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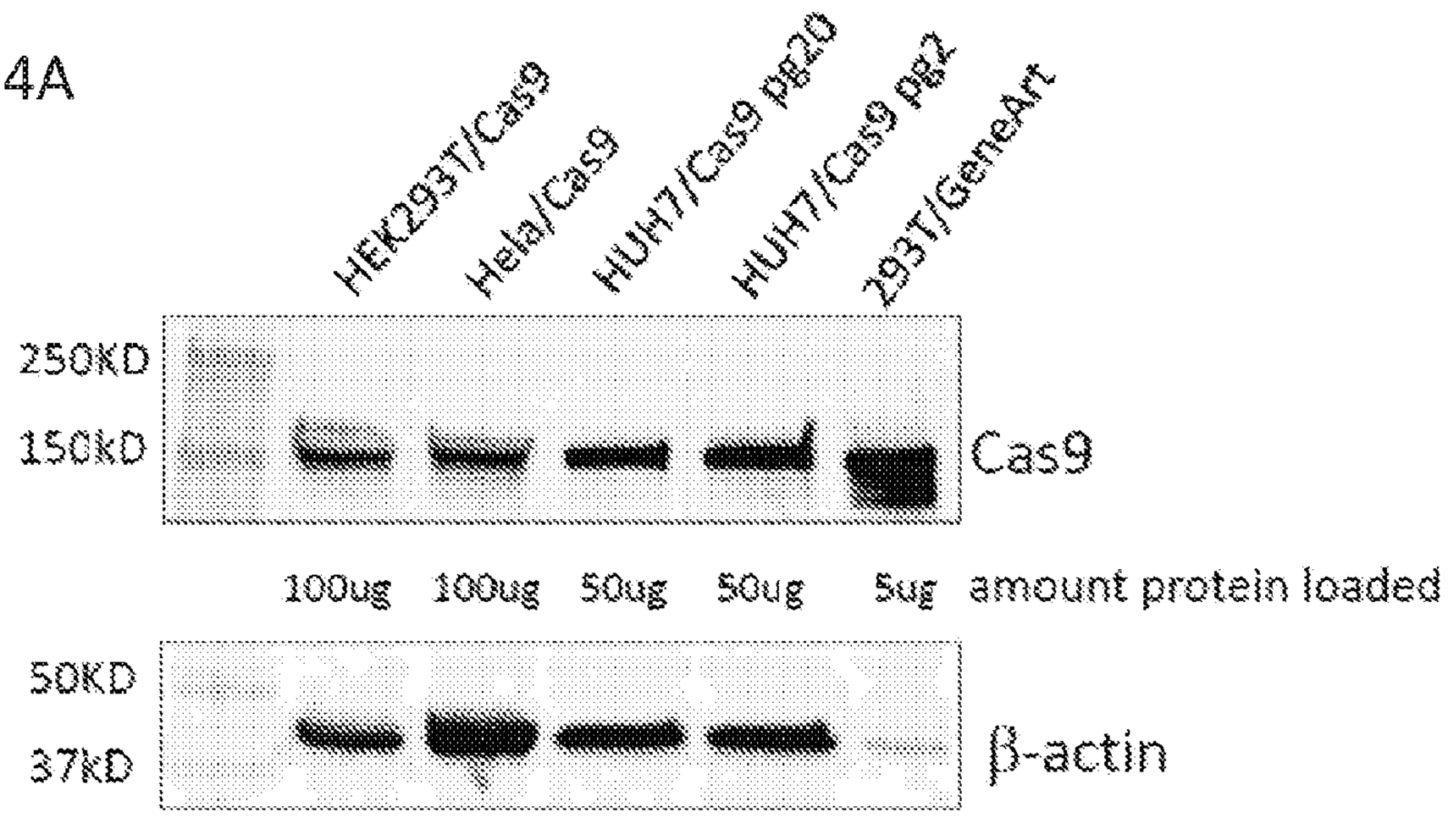
(54) Titre : SUBSTANCES ET PROCEDES DE TRAITEMENT DE GLYCOGENOSE DE DE TYPE 1A
(54) Title: MATERIALS AND METHODS FOR TREATMENT OF GLYCOGEN STORAGE DISEASE TYPE 1A

Fig. 94A



(57) Abrégé/Abstract:
The present application provides materials and methods for treating a patient with Glycogen Storage Disease type 1a (GSD1a) both ex vivo and in vivo. In addition, the present application provides materials and methods for modulating the expression, function, and/or activity of the glucose-6-phosphatase, catalytic (G6PC) and/or the glucose-6-phosphatase (G6Pase) protein in a cell by genome editing.

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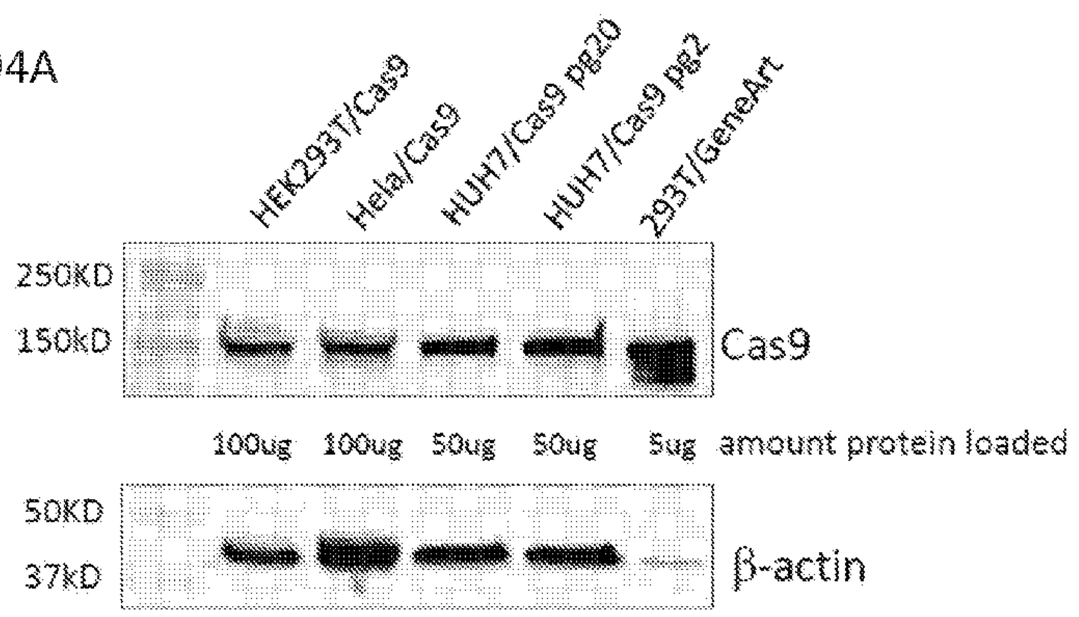
(54) **Title**: MATERIALS AND METHODS FOR TREATMENT OF GLYCOGEN STORAGE DISEASE TYPE 1A

Fig. 94A



(57) **Abstract**: The present application provides materials and methods for treating a patient with Glycogen Storage Disease type 1a (GSD1a) both *ex vivo* and *in vivo*. In addition, the present application provides materials and methods for modulating the expression, function, and/or activity of the glucose-6-phosphatase, catalytic (G6PC) and/or the glucose-6-phosphatase (G6Pase) protein in a cell by genome editing.

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MATERIALS AND METHODS FOR TREATMENT OF GLYCOGEN STORAGE DISEASE TYPE 1A

Related Applications

[0001] This application claims the benefit of U.S. Provisional Application No. 62/252,208, filed November 6, 2015; U.S. Provisional Application No. 62/265,678, filed December 10, 2015; and U.S. Provisional Application No. 62/324,113, filed April 18, 2016; the contents of each of which are incorporated herein by reference in their entirety

Field of the Invention

[0002] The present application provides materials and methods for treating a patient with Glycogen Storage Disease type 1a (GSD1a) both *ex vivo* and *in vivo*. In addition, the present application provides materials and methods for modulating the expression, function, and/or activity of the glucose-6-phosphatase, catalytic (G6PC) gene and/or the glucose-6-phosphatase (G6Pase) protein in a cell by genome editing.

Incorporation by Reference of Sequence Listing

[0003] This application contains a Sequence Listing in computer readable form (filename: CRIS009001WO_ST25.txt; 13,024,421 bytes – ASCII text file; created November 3, 2016), which is incorporated herein by reference in its entirety and forms part of the disclosure.

Background of the Invention

[0004] Glycogen storage disease type 1 (GSD1) is a group of diseases resulting from defects of proteins involved in the removal of phosphates from glucose-6-phosphate, which, as the final step in both gluconeogenesis and glycogenolysis, is crucial for the maintenance of blood glucose levels (Arion, W. J., & Canfield, W. K. (1993). Glucose-6-phosphatase and type 1 glycogen storage disease: some critical considerations. Eur J Pediatr, 152(S1), S7-S13; Froissart, R., et al. (2011). Glucose-6-phosphatase deficiency. Orphanet Journal Of Rare Diseases, 6(27); van Schaftingen, E., & Gerin, I. (2002). The glucose-6-phosphatase system. Biochem J,

362(Pt 3), 513-532). GSD1 is clinically recognized by hepatomegaly (enlargement of the liver due to accumulation of glycogen) and hypoglycemia, and is usually diagnosed between 6 and 8 months of age (Koeberl, et al. (2007). Glycogen storage disease types I and II: treatment updates. J Inherit Metab Dis, 30(2), 159-164. doi:10.1007/s10545-007-0519-9; Rake, J. P. (2002). Glycogen storage disease type I: diagnosis, management, clinical course and outcome. Results of the European Study on Glycogen Storage Disease Type I (ESGSDI). Eur J Pediatr, 161, S20-S34).

[0005] The most common form of GSD1 (about 80% of all cases) is GSD1a, which is caused by inactivating mutations to the glucose-6-phosphatase catalytic unit. In addition to the genetic association in patients, the mechanism of the disease was confirmed by association in both mouse and dog disease models (Froissart, R., et al. Orphanet Journal Of Rare Diseases, 2011; Kishnani, P. S., et al. (2001). Canine model and genomic structural organization of glycogen storage disease type Ia (GSD Ia). Vet Pathol, 38(1), 83-91; Mutel, E., et al. (2011). Targeted deletion of liver glucose-6 phosphatase mimics glycogen storage disease type 1a including development of multiple adenomas. J Hepatol, 54(3), 529-537. doi:10.1016/j.jhep.2010.08.014). Without the ability to dephosphorylate glucose for release into the blood, the breakdown of glycogen in liver cells is affected, along with the maintenance of normal blood glucose. This inability to release glucose underlies the symptoms of GSD1, as the body must then rely on alternative fuel sources, which can lead to lactic acidemia and hyperlipidemia (van Schaftingen, E., & Gerin, I. Biochem J, 2002).

[0006] GSD1a is a recessively inherited genetic disorder associated with various mutations to the G6PC gene that render it unable to dephosphorylate glucose (Chou, J. Y., & Mansfield, B. C. (2008). Mutations in the Glucose-6-Phosphatase-alpha (G6PC) Gene that Cause Type 1a Glycogen Storage Disease. Hum Mutat, 29(7), 921-930). Preclinical mouse models demonstrate that restoration of 20% of normal glucose-6-phosphatase activity using adeno-associated virus (AAV) gene delivery can normalize blood glucose, triglycerides and uric acid, as well as reduce hepatomegaly and renomegaly (Zingone, A., et al. (2000). Correction of glycogen storage disease type 1a in a mouse model by gene therapy. J Biol Chem, 275(2),

828-832). Another estimate based on human studies places the therapeutic threshold at 10% of normal glucose-6-phosphatase activity (Koeberl, et al. J Inherit Metab Dis, 2007). Both estimates indicate a reasonable and likely achievable goal for gene editing efficacy, suggesting that the G6PC gene may be a good target.

[0007] The other aspect of GSD1a that makes it a good candidate for gene therapy is the lack of satisfactory treatments. Current treatments are primarily limited to nutritional supplementation in an effort to maintain normal blood glucose and prevent seizures caused by hypoglycemia (Koeberl, D. D., et al. (2009). Emerging therapies for glycogen storage disease type I. Trends Endocrinol Metab, 20(5), 252-258. doi:10.1016/j.tem.2009.02.003). The primary nutritional therapies are continuous naso-gastric infusion of glucose and frequent administration of uncooked cornstarch (Lee, P. J., et al. (1996). Uncooked cornstarch--efficacy in type I glycogenosis. Arch Dis Child, 74(6), 546-547). While these therapies can help to maintain normoglycemia and aid with amelioration of growth retardation, they do not address renomegaly or hepatomegaly. Though liver transplantation can cure the hepatic manifestations (hepatomegaly, hepatic adenomas) of GSD1, as well as aiding in maintaining normoglycemia, it cannot address all the issues caused by GSD1 (Selby, R., et al. (1993). Liver transplantation for type I and type IV glycogen storage disease. Eur J Pediatr, 152 Suppl 1, S71-76). Hepatocyte transplantation has also been investigated as a possible treatment option, however, long-term engraftment was not achieved and the therapy ultimately failed (Koeberl, et al. Trends Endocrinol Metab, 2009).

[0008] To address incomplete and unsatisfactory treatment options, several groups have been working on gene therapy in animal models of the disease, including mice and dogs. Most of these studies have used an AAV vector to convey a corrected version of the gene into hepatocytes, although one used a lentiviral vector (Clar, J., et al. (2015). Hepatic lentiviral gene transfer prevents the long-term onset of hepatic tumours of glycogen storage disease type 1a in mice. Hum Mol Genet, 24(8), 2287-2296. doi:10.1093/hmg/ddu746; Koeberl, et al. Trends Endocrinol Metab, 2009). There have been some successes with this approach, with some studies achieving a temporary or longer term reversal of some disease symptoms with less than 20% restoration of glucose-6-phosphatase activity (Clar,

J., et al. Hum Mol Genet, 2015; Lee, Y. M., et al. (2012). Prevention of hepatocellular adenoma and correction of metabolic abnormalities in murine glycogen storage disease type Ia by gene therapy. Hepatology, 56(5), 1719-1729. doi:10.1002/hep.25717; Zingone, A., et al. J Biol Chem, 2000). There is also some evidence in dogs that AAV vector gene therapy can temporarily reduce symptoms of the disease (reviewed in Koeberl, et al. J Inherit Metab Dis, 2007). One mouse study also demonstrated that AAV mediated expression of glucose-6-phosphatase in the liver of as little as 3% normal glucose-6-phosphatase expression could ameliorate GSD1 symptoms and prevent formation of hepatic adenomas. They also demonstrated that even distribution of glucose-6-phosphatase activity is not necessary to observe a phenotypic change, instead noting foci of higher glucose-6-phosphatase activity 9 Clar, J., et al. Hum Mol Genet, 2015; Lee, Y. M., et al. Hepatology, 2012). Overall, the limited-term success of the AAV therapies combined with the lack of adequate available therapies and the reasonable estimates for therapeutic threshold make this disease a good candidate for gene editing therapy based on endonucleases

[0009] Genome engineering refers to the strategies and techniques for the targeted, specific modification of the genetic information (genome) of living organisms. Genome engineering is a very active field of research because of the wide range of possible applications, particularly in the areas of human health; the correction of a gene carrying a harmful mutation, for example, or to explore the function of a gene. Early technologies developed to insert a gene into a living cell, such as transgenesis, were often limited by the random nature of the insertion of the new sequence into the genome. The new gene was usually positioned blindly, and may have inactivated or disturbed the functioning of other genes, or even caused severe unwanted effects. Furthermore, these technologies generally offered no degree of reproducibility, as there was no guarantee that the new sequence would be inserted at the same place in two different cells. More recent genome engineering strategies, such as ZFNs, TALENs, HEs and MegaTALs, enable a specific area of the DNA to be modified, thereby increasing the precision of the correction or insertion compared to early technologies, and offering some degree of reproducibility. Despite this, such recent genome engineering strategies have limitations.

[0010] Despite efforts from researchers and medical professionals worldwide who have been trying to address GSD1a, and despite the promise of genome engineering approaches, there still remains a critical need for developing safe and effective treatments for GSD1a.

[0011] Prior approaches addressing GSD1a have severe limitations, such as limited success and lack of adequate available therapies. The present invention solves these problems by using genome engineering tools to create permanent changes to the genome that can restore the glucose-6-phosphatase (G6Pase) protein activity with a single treatment. Thus, the present invention corrects the underlying genetic defect causing the disease.

Summary of the Invention

[0012] Provided herein are cellular, *ex vivo* and *in vivo* methods for creating permanent changes to the genome by inserting, correcting, or modulating the expression or function of one or more exons within or near the glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the G6PC gene by genome editing and restoring glucose-6-phosphatase (G6Pase) protein activity, which can be used to treat Glycogen Storage Disease type 1a (GSD1a). Also provided herein are components, kits and compositions for performing such methods. Also provided are cells produced by such methods.

[0013] Provided herein is a method for editing a G6PC gene in a human cell by genome editing, the method comprising the step of introducing into the human cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or one or more double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene that results in at least one of a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus that results in a permanent insertion of the G6PC gene and results in restoration of G6Pase protein activity. The human cell can be a liver cell.

[0014] Also provided herein is a method for inserting a G6PC gene in a human cell by genome editing, the method comprising the step of: introducing into the

human cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near a safe harbor locus that results in a permanent insertion of the G6PC gene, and results in restoration of G6Pase protein activity.

[0015] In one aspect, provided herein is a method for inserting the glucose-6-phosphatase, catalytic (G6PC) gene in a human cell by genome editing comprising introducing into the human cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene that results in a permanent insertion or correction of one or more mutations within the G6PC gene and restoration of G6Pase protein activity.

[0016] In another aspect, provided herein is an *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a) comprising the steps of: creating a patient specific induced pluripotent stem cell (iPSC); editing within or near the glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the G6PC gene of the iPSC or editing within or near a safe harbor locus of the iPSC; or editing within or near a locus in the first exon of the HGD gene of the iPSC; differentiating the genome edited iPSC into a hepatocyte; and implanting the hepatocyte into the patient.

[0017] In some embodiments, the step of creating a patient specific iPSC comprises: isolating a somatic cell from the patient; and introducing a set of pluripotency-associated genes into the somatic cell to induce the cell to become a pluripotent stem cell. In some embodiments, the somatic cell is a fibroblast. In some embodiments, the set of pluripotency-associated genes is one or more of the genes selected from the group consisting of OCT4, SOX2, KLF4, Lin28, NANOG and cMYC.

[0018] The step of editing within or near a G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene of the iPSC or editing within or near a safe harbor locus of the G6PC gene of the iPSC or editing within or near a locus of the first exon of the HGD gene of the iPSC can comprise introducing into the iPSC one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near

the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus that results in a permanent insertion of the G6PC gene or within or near a locus in the first exon of HGD that results in a permanent insertion of the G6PC gene and results in restoration of G6Pase protein activity. The safe harbor locus can be selected from the group consisting of: AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR. The safe harbor locus can be selected from the group consisting of: exon 1-2 of AAVS1 (PPP1R12C), exon 1-2 of ALB, exon 1-2 of Angptl3, exon 1-2 of ApoC3, exon 1-2 of ASGR2, exon 1-2 of CCR5, exon 1-2 of FIX (F9), exon 1-2 of Gys2, exon 1-2 of HGD, exon 1-2 of Lp(a), exon 1-2 of Pcsk9, exon 1-2 of Serpina1, exon 1-2 of TF, and exon
1-2 of TTR.

[0019] In some embodiments, the step of editing the G6PC gene of the iPSC comprises introducing into the iPSC one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more double-strand breaks (DSBs) within the G6PC gene that results in permanent correction of one or more mutations within the G6PC gene and restoration of G6Pase protein activity.

[0020] In some embodiments, the step of differentiating the genome edited iPSC into a liver progenitor cell or a hepatocyte comprises one or more of the following: contacting the genome edited iPSC with one or more of activin, B27 supplement, FGF4, HGF, BMP2, BMP4, Oncostatin M, or Dexametason.

[0021] In some embodiments, the step of implanting the hepatocyte into the patient comprises implanting the hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

[0022] In yet another aspect, provided herein is an *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a) comprising the steps of: performing a biopsy of the patient's liver; isolating a liver specific progenitor cell or primary hepatocyte; editing within or near the glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the

G6PC gene of the progenitor cell or primary hepatocyte or editing within or near a safe harbor locus of the progenitor cell or primary hepatocyte; and implanting the genome-edited progenitor cell or primary hepatocyte into the patient.

[0023] In some embodiments, the step of isolating a liver specific progenitor cell or primary hepatocyte from the patient comprises: perfusion of fresh liver tissues with digestion enzymes, cell differential centrifugation, cell culturing, or combinations thereof.

[0024] In some embodiments, the step of editing within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene of the progenitor cell or primary hepatocyte or editing within or near a safe harbor locus of the white blood cell of the progenitor cell or primary hepatocyte comprises introducing into the progenitor cell or primary hepatocyte one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of theG6PC gene that results in permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus that results in a permanent insertion or correction of one or more mutations within the G6PC gene and restoration of G6Pase protein activity. The safe harbor locus can be selected from the group consisting of: AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR. The safe harbor locus can be selected from the group consisting of: exon 1-2 of AAVS1 (PPP1R12C), exon 1-2 of ALB, exon 1-2 of Angptl3, exon 1-2 of ApoC3, exon 1-2 of ASGR2, exon 1-2 of CCR5, exon 1-2 of FIX (F9), exon 1-2 of Gys2, exon 1-2 of HGD, exon 1-2 of Lp(a), exon 1-2 of Pcsk9, exon 1-2 of Serpina1, exon 1-2 of TF, and exon 1-2 of TTR.

[0025] In some embodiments, the step of implanting the genome-edited liver-specific progenitor cell or primary hepatocyte into the patient comprises implanting the genome-edited liver-specific progenitor cell or primary hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

[0026] Also provided herein is an ex vivo method for treating a patient (e.g., a human) with Glycogen Storage Disease type 1a (GSD1a), the method comprising the steps of: i) isolating a mesenchymal stem cell from the patient; ii) editing within or near a G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene of the mesenchymal stem cell or editing within or near a safe harbor locus of the G6PC gene of the mesenchymal cell; iii) differentiating the genome-edited mesenchymal stem cell into a hepatocyte; and iv) implanting the hepatocyte into the patient.

[0027] In another aspect, provided herein is an *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a) comprising the steps of: performing a biopsy of the patient's bone marrow; isolating a mesenchymal stem cell; editing the glucose-6-phosphatase, catalytic (G6PC) gene of the stem cell; differentiating the stem cell into a hepatocyte; and implanting the hepatocyte into the patient.

[0028] The mesenchymal stem cell can be isolated from the patient's bone marrow by performing a biopsy of the patient's bone marrow or the mesenchymal stem cell can be isolated from peripheral blood.

[0029] In some embodiments, the step of isolating a mesenchymal stem cell comprises: aspiration of bone marrow and isolation of mesenchymal cells by density centrifugation using Percoll™.

[0030] In some embodiments, the step of editing within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene of the mesenchymal stem cell comprises introducing into the mesenchymal stem cell one or more deoxyribonucleic acid (DNA) endonucleases to effect single-strand breaks (SSBs) or one or more double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or editing within or near a safe harbor locus of the G6PC gene that results in permanent correction or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus that results of one or more mutations within the G6PC gene and restoration of G6Pase protein activity. The safe harbor locus can be selected from the group consisting of: AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3,

ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR. The safe harbor locus can be selected from the group consisting of: exon 1-2 of AAVS1 (PPP1R12C), exon 1-2 of ALB, exon 1-2 of Angptl3, exon 1-2 of ApoC3, exon 1-2 of ASGR2, exon 1-2 of CCR5, exon 1-2 of FIX (F9), exon 1-2 of Gys2, exon 1-2 of HGD, exon 1-2 of Lp(a), exon 1-2 of Pcsk9, exon 1-2 of Serpina1, exon 1-2 of TF, and exon 1-2 of TTR.

[0031] In some embodiments, the step of differentiating the genome-edited mesenchymal stem cell into a hepatocyte comprises one or more of the following: contacting the genome edited mesenchymal stem cell with one or more of insulin, transferrin, FGF4, HGF, or bile acids.

[0032] In some embodiments, the step of implanting the hepatocyte into the patient comprises implanting the hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

[0033] In a further aspect, provided herein is an *in vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a) comprising the step of editing the glucose-6-phosphatase, catalytic (G6PC) gene in a cell of the patient, or other DNA sequences that encode regulatory elements of the G6PC gene, or editing within or near a safe harbor locus in a cell of the patient. The cell can be a liver cell.

[0034] In some embodiments, the step of editing the G6PC gene in a cell of the patient comprises introducing into the cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more double-strand breaks (DSBs) within the G6PC gene that results in permanent correction of one or more mutations within the G6PC gene and restoration of G6Pase protein activity.

[0035] In some embodiments, the step of editing a G6PC gene in a cell of the patient comprises introducing into the cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or editing within or near a safe harbor locus of the G6PC gene that results in a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the

expression or function of the G6PC gene and restoration of G6Pase protein activity. The cell can be a hepatocyte, a liver progenitor cell, or combinations thereof.

[0036] In some embodiments, the one or more DNA endonucleases is a Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas100, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, or Cpf1 endonuclease; a homolog thereof, recombination of the naturally occurring molecule, codon-optimized, or modified version thereof, and combinations of any of the foregoing.

[0037] In some embodiments, the method comprises introducing into the cell one or more polynucleotides encoding the DNA endonuclease. In some embodiments, the method comprises introducing into the cell one or more ribonucleic acids (RNAs) encoding the DNA endonuclease. In some embodiments, the one or more polynucleotides or one or more RNAs is one or more modified polynucleotides or one or more modified RNAs. In some embodiments, the method comprises introducing into the cell one or more DNA endonucleases wherein the endonuclease is a protein or polypeptide.

[0038] In some embodiments, the method further comprises introducing into the cell one or more guide ribonucleic acids (gRNAs). In some embodiments, the one or more gRNAs are single-molecule guide RNA (sgRNAs). In some embodiments, the one or more gRNAs or one or more sgRNAs is one or more modified gRNAs, one or more modified sgRNAs, or combinations thereof.

[0039] In some embodiments, the one or more DNA endonucleases is pre-complexed with one or more gRNAs, one or more sgRNAs, or combinations thereof.

[0040] In some embodiments, the method further comprises introducing into the cell a polynucleotide donor template comprising at least a portion of the wild-type G6PC gene, DNA sequences that encode wild-type regulatory elements of the G6PC gene, and/or cDNA. The at least a portion of the wild-type G6PC gene or cDNA can be exon 1, exon 2, exon 3, exon 4, exon 5, intronic regions, fragments or combinations thereof, or the entire G6PC gene or cDNA. The donor template can

be either a single or double stranded polynucleotide. The donor template can have homologous arms to the 17q21 region.

[0041] In some embodiments, the method further comprises introducing into the cell one guide ribonucleic acid (gRNA) and a polynucleotide donor template comprising at least a portion of the wild-type G6PC gene. In some embodiments, the method further comprises introducing into the cell one guide ribonucleic acid (gRNA) and a polynucleotide donor template comprising at least a portion of a codon optimized or modified G6PC gene. The one or more DNA endonucleases is one or more Cas9 or Cpf1 endonucleases that effect single-strand break (SSB) or one double-strand break (DSB) at a DSB locus within or near the G6PC gene (or codon optimized or modified G6PC gene) or other DNA sequences that encode regulatory elements of the G6PC gene, or within or near a safe harbor locus, that facilitates insertion of a new sequence from the polynucleotide donor template into the chromosomal DNA at the locus or safe harbor locus that results in a permanent correction of a part of the chromosomal DNA of the G6PC gene or other DNA sequences that encode regulator elements of the G6PC gene proximal to the locus or safe harbor locus and restoration of G6Pase protein activity. In some embodiments, the gRNA comprises a spacer sequence that is complementary to a segment of the locus or safe harbor locus. In some embodiments, proximal means nucleotides both upstream and downstream of the locus or safe harbor locus.

[0042] In some embodiments, the method further comprises introducing into the cell two guide ribonucleic acid (gRNAs) and a polynucleotide donor template comprising at least a portion of the wild-type G6PC gene, and wherein the one or more DNA endonucleases is two or more Cas9 or Cpf1 endonucleases that effect or create at least two (e.g., a pair) single-strand breaks (SSBs) and/or a pair of double-strand breaks (DSBs), the first at a 5' DSB locus and the second at a 3' DSB locus, within the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor locus, that facilitates insertion of a new sequence from the polynucleotide donor template into the chromosomal DNA between the 5' DSB locus and the 3' DSB locus that results in permanent correction of the chromosomal DNA between the 5' DSB locus and the 3' DSB locus within the G6PC gene or other DNA sequences that encode

regulatory elements of the G6PC gene or within or near a safe harbor locus and restoration of G6Pase protein activity, and wherein the first guide RNA comprises a spacer sequence that is complementary to a segment of the 5' DSB locus and the second guide RNA comprises a spacer sequence that is complementary to a segment of the 3' DSB locus.

[0043] In some embodiments, the one or more gRNAs are single-molecule guide RNA (sgRNAs). In some embodiments, the one or more gRNAs or one or more sgRNAs is a modified gRNAs or one or more modified sgRNAs.

[0044] In some embodiments, the one or more DNA endonucleases is pre-complexed with one or more gRNAs or one or more sgRNAs.

[0045] In some embodiments, the part of the wild-type G6PC gene or cDNA is the entire G6PC gene or cDNA.

[0046] In some embodiments, the DSB, or 5' DSB and 3' DSB are in the first exon, first intron, or both the first exon and first intron of the G6PC gene.

[0047] In some embodiments, the gRNA or sgRNA is directed to one or more of the following pathological variants: rs80356479, rs80356486, rs606231368, rs80356488, rs587776757, rs104894565, rs104894566, rs1801175, rs1801176, rs104894567, rs104894571, rs80356482, rs80356483, rs104894563, rs367727229, rs387906505, rs104894568, rs104894569, rs80356487, rs764920787, rs80356485, rs780226142, rs80356484.

[0048] The at least a portion of the wild-type G6PC gene or cDNA can be exon 1, exon 2, exon 3, exon 4, exon 5, intronic regions, fragments or combinations thereof, or the entire G6PC gene or cDNA.

[0049] The donor template can be either a single or double stranded polynucleotide. The donor template can have homologous arms to the 17q21 region.

[0050] The SSB, DSB, 5' DSB, and/or 3' DSB can be in the first, second, third, fourth, or fifth exon or introns of the G6PC gene.

[0051] In some embodiments, the correction is by homology directed repair (HDR).

[0052] In some embodiments, the Cas9 or Cpf1 mRNA, gRNA, and donor template are either each formulated separately into lipid nanoparticles or all co-formulated into a lipid nanoparticle.

[0053] In some embodiments, the Cas9 or Cpf1 mRNA, gRNA, and donor template are formulated into separate exosomes or are co-formulated into an exosome.

[0054] In some embodiments, the Cas9 or Cpf1 mRNA is formulated into a lipid nanoparticle, and both the gRNA and donor template are delivered to the cell by a viral vector. In some embodiments, the viral vector is an adeno-associated virus (AAV). In some embodiments, the AAV vector is an AAV6 vector.

[0055] The Cas9 or Cpf1 mRNA can be formulated into a lipid nanoparticle, and the gRNA can be delivered to the cell by electroporation and donor template can be delivered to the cell by a viral vector. In some embodiments, the viral vector is an adeno-associated virus (AAV) vector. In some embodiments, the AAV vector is an AAV6 vector.

[0056] In some embodiments, the G6PC gene is located on Chromosome 17: 42,900,796 - 42,914,432 (Genome Reference Consortium – GRCh38/hg38).

[0057] The restoration of G6Pase protein activity can be compared to wild-type or normal G6Pase protein activity.

[0058] In another aspect, provided herein is one or more guide ribonucleic acids (gRNAs) comprising a spacer sequence selected from the group consisting of the sequences in Figures 1-90 for editing the glucose-6-phosphatase, catalytic gene in a cell from a patient with Glycogen Storage Disease type 1a. In some embodiments, the one or more gRNAs are single-molecule guide RNAs (sgRNAs). In some embodiments, the one or more gRNAs or one or more sgRNAs is one or more modified gRNAs or one or more modified sgRNAs.

[0059] In another aspect, provided herein are cells that have been modified by the preceding methods to permanently correct one or more mutations within the glucose-6-phosphatase, catalytic (G6PC) gene and restore G6Pase protein activity. Further provided herein are methods for ameliorating Glycogen Storage Disease

type 1a (GSD1a) by the administration of cells that have been modified by the preceding methods to a GSD1a patient.

[0060] In some embodiments, the methods and compositions of the disclosure comprise one or more modified guide ribonucleic acids (gRNAs). Non-limiting examples of modifications can comprise one or more nucleotides modified at the 2' position of the sugar, in some embodiments a 2'-O-alkyl, 2'-O-alkyl-O-alkyl, or 2'-fluoro-modified nucleotide. In some embodiments, RNA modifications include 2'-fluoro, 2'-amino or 2' O-methyl modifications on the ribose of pyrimidines, abasic residues, desoxy nucleotides, or an inverted base at the 3' end of the RNA.

[0061] In some embodiments, the one or more modified guide ribonucleic acids (gRNAs) comprise a modification that makes the modified gRNA more resistant to nuclease digestion than the native oligonucleotide. Non-limiting examples of such modifications include those comprising modified backbones, for example, phosphorothioates, phosphorothyos, phosphotriesters, methyl phosphonates, short chain alkyl or cycloalkyl intersugar linkages or short chain heteroatomic or heterocyclic intersugar linkages.

[0062] Various other aspects are described and exemplified herein.

Brief Description of the Drawings

[0063] Various aspects of materials and methods for treatment of Glycogen Storage Disease type 1a (GSD1a) disclosed and described in this specification can be better understood by reference to the accompanying figures, in which:

[0064] Figure 1 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *S. pyogenes* Cas9 endonuclease.

[0065] Figure 2 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *S. aureus* Cas9 endonuclease.

[0066] Figure 3 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting

exons 1-2 of an AAVS1 (PPP1R12C) gene with a *S. thermophilus* Cas9 endonuclease.

[0067] Figure 4 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *T. denticola* Cas9 endonuclease.

[0068] Figure 5 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *N. meningitides* Cas9 endonuclease.

[0069] Figure 6 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[0070] Figure 7 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an Alb gene with a *S. pyogenes* Cas9 endonuclease.

[0071] Figure 8 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an Alb gene with a *S. aureus* Cas9 endonuclease.

[0072] Figure 9 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Alb gene with a *S. thermophilus* Cas9 endonuclease.

[0073] Figure 10 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Alb gene with a *T. denticola* Cas9 endonuclease.

[0074] Figure 11 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Alb gene with a *N. meningitides* Cas9 endonuclease.

[0075] Figure 12 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting

exons 1-2 of an Alb gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[0076] Figure 13 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an Angpt13 gene with a *S. pyogenes* Cas9 endonuclease.

[0077] Figure 14 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an Angpt13 gene with a *S. aureus* Cas9 endonuclease.

[0078] Figure 15 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Angpt13 gene with a *S. thermophilus* Cas9 endonuclease.

[0079] Figure 16 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Angpt13 gene with a *T. denticola* Cas9 endonuclease.

[0080] Figure 17 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Angpt13 gene with a *N. meningitides* Cas9 endonuclease.

[0081] Figure 18 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of an Angpt13 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[0082] Figure 19 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an ApoC3 gene with a *S. pyogenes* Cas9 endonuclease.

[0083] Figure 20 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an ApoC3 gene with a *S. aureus* Cas9 endonuclease.

[0084] Figure 21 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an ApoC3 gene with a *S. thermophilus* Cas9 endonuclease.

[0085] Figure 22 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an ApoC3 gene with a *T. denticola* Cas9 endonuclease.

[0086] Figure 23 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an ApoC3 gene with a *N. meningitides* Cas9 endonuclease.

[0087] Figure 24 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of an ApoC3 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[0088] Figure 25 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an ASGR2 gene with a *S. pyogenes* Cas9 endonuclease.

[0089] Figure 26 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an ASGR2 gene with a *S. aureus* Cas9 endonuclease.

[0090] Figure 27 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an ASGR2 gene with a *S. thermophilus* Cas9 endonuclease.

[0091] Figure 28 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an ASGR2 gene with a *T. denticola* Cas9 endonuclease.

[0092] Figure 29 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an ASGR2 gene with a *N. meningitides* Cas9 endonuclease.

[0093] Figure 30 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of an ASGR2 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[0094] Figure 31 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a CCR5 gene with a *S. pyogenes* Cas9 endonuclease.

[0095] Figure 32 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a CCR5 gene with a *S. aureus* Cas9 endonuclease.

[0096] Figure 33 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a CCR5 gene with a *S. thermophilus* Cas9 endonuclease.

[0097] Figure 34 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a CCR5 gene with a *T. denticola* Cas9 endonuclease.

[0098] Figure 35 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a CCR5 gene with a *N. meningitides* Cas9 endonuclease.

[0099] Figure 36 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of a CCR5 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00100] Figure 37 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an F9 gene with a *S. pyogenes* Cas9 endonuclease.

[00101] Figure 38 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an F9 gene with a *S. aureus* Cas9 endonuclease.

[00102] Figure 39 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an F9 gene with a *S. thermophilus* Cas9 endonuclease.

[00103] Figure 40 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an F9 gene with a *T. denticola* Cas9 endonuclease.

[00104] Figure 41 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an F9 gene with a *N. meningitides* Cas9 endonuclease.

[00105] Figure 42 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of an F9 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00106] Figure 43 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a Gys2 gene with a *S. pyogenes* Cas9 endonuclease.

[00107] Figure 44 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a Gys2 gene with a *S. aureus* Cas9 endonuclease.

[00108] Figure 45 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a Gys2 gene with a *S. thermophilus* Cas9 endonuclease.

[00109] Figure 46 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a Gys2 gene with a *T. denticola* Cas9 endonuclease.

[00110] Figure 47 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a Gys2 gene with a *N. meningitides* Cas9 endonuclease.

[00111] Figure 48 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of a Gys2 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00112] Figure 49 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an HGD gene with a *S. pyogenes* Cas9 endonuclease.

[00113] Figure 50 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an HGD gene with a *S. aureus* Cas9 endonuclease.

[00114] Figure 51 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an HGD gene with a *S. thermophilus* Cas9 endonuclease.

[00115] Figure 52 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an HGD gene with a *T. denticola* Cas9 endonuclease.

[00116] Figure 53 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an HGD gene with a *N. meningitides* Cas9 endonuclease.

[00117] Figure 54 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of an HGD gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00118] Figure 55 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an Lp(a) gene with a *S. pyogenes* Cas9 endonuclease.

[00119] Figure 56 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of an Lp(a) gene with a *S. aureus* Cas9 endonuclease.

[00120] Figure 57 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Lp(a) gene with a *S. thermophilus* Cas9 endonuclease.

[00121] Figure 58 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Lp(a) gene with a *T. denticola* Cas9 endonuclease.

[00122] Figure 59 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of an Lp(a) gene with a *N. meningitides* Cas9 endonuclease.

[00123] Figure 60 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of an Lp(a) gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00124] Figure 61 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a PCSK9 gene with a *S. pyogenes* Cas9 endonuclease.

[00125] Figure 62 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a PCSK9 gene with a *S. aureus* Cas9 endonuclease.

[00126] Figure 63 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a PCSK9 gene with a *S. thermophilus* Cas9 endonuclease.

[00127] Figure 64 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a PCSK9 gene with a *T. denticola* Cas9 endonuclease.

[00128] Figure 65 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a PCSK9 gene with a *N. meningitides* Cas9 endonuclease.

[00129] Figure 66 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of a PCSK9 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00130] Figure 67 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a Serpina1 gene with a *S. pyogenes* Cas9 endonuclease.

[00131] Figure 68 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a Serpina1 gene with a *S. aureus* Cas9 endonuclease.

[00132] Figure 69 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a Serpina1 gene with a *S. thermophilus* Cas9 endonuclease.

[00133] Figure 70 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a Serpina1 gene with a *T. denticola* Cas9 endonuclease.

[00134] Figure 71 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a Serpina1 gene with a *N. meningitides* Cas9 endonuclease.

[00135] Figure 72 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of a Serpina1 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00136] Figure 73 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a TF gene with a *S. pyogenes* Cas9 endonuclease.

[00137] Figure 74 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a TF gene with a *S. aureus* Cas9 endonuclease.

[00138] Figure 75 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a TF gene with a *S. thermophilus* Cas9 endonuclease.

[00139] Figure 76 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a TF gene with a *T. denticola* Cas9 endonuclease.

[00140] Figure 77 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a TF gene with a *N. meningitides* Cas9 endonuclease.

[00141] Figure 78 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of a TF gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00142] Figure 79 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a TTR gene with a *S. pyogenes* Cas9 endonuclease.

[00143] Figure 80 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting exons 1-2 of a TTR gene with a *S. aureus* Cas9 endonuclease.

[00144] Figure 81 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a TTR gene with a *S. thermophilus* Cas9 endonuclease.

[00145] Figure 82 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a TTR gene with a *T. denticola* Cas9 endonuclease.

[00146] Figure 83 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting exons 1-2 of a TTR gene with a *N. meningitides* Cas9 endonuclease.

[00147] Figure 84 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting exons 1-2 of a TTR gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00148] Figure 85 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting the G6PC gene with a *S. pyogenes* Cas9 endonuclease.

[00149] Figure 86 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target sequence, cut site, and strand for targeting the G6PC gene with a *S. aureus* Cas9 endonuclease.

[00150] Figure 87 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting the G6PC gene with a *S. thermophilus* Cas9 endonuclease.

[00151] Figure 88 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting the G6PC gene with a *T. denticola* Cas9 endonuclease.

[00152] Figure 89 is a list of gRNA 20 bp spacer sequences, associated PAM, chromosomal and gene location of the target, cut site, and strand for targeting the G6PC gene with a *N. meningitides* Cas9 endonuclease.

[00153] Figure 90 is a list of gRNA 22 bp spacer sequences, associated PAM, chromosomal and gene location of the target, two cut sites, and strand for targeting the G6PC gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00154] Figure 91A is a list of pathological variants of the G6PC gene, the start and stop locations of the variants on the chromosome, the type of variant, and the HGVS_g.

[00155] Figure 91B is a list of pathological variants of the G6PC gene, the molecular consequences of the variant, the variant allele, the transcript change, and the protein change.

[00156] Figure 92A is an illustration of a plasmid (referred to herein as “CTx-1”) comprising a codon optimized gene for S. pyogenes Cas9 endonuclease. The CTx-1 plasmid also comprises a gRNA scaffold sequence, which includes a 20 bp spacer sequence from the sequences listed in Figures 1, 7, 13, 19, 25, 31, 37, 43, 49, 55, 61, 67, 73, 79, 85, and 91.

[00157] Figure 92B is an illustration of a plasmid (referred to herein as "CTx-2") comprising a different codon optimized gene for S. pyogenes Cas9 endonuclease. The CTx-2 plasmid also comprises a gRNA scaffold sequence, which includes a 20 bp spacer sequence from the sequences listed in Figures 1, 7, 13, 19, 25, 31, 37, 43, 49, 55, 61, 67, 73, 79, 85, and 91.

[00158] Figure 92C is an illustration of a plasmid (referred to herein as "CTx-3") comprising yet another different codon optimized gene for S. pyogenes Cas9 endonuclease. The CTx-3 plasmid also comprises a gRNA scaffold sequence, which includes a 20 bp spacer sequence from the sequences listed in Figures 1, 7, 13, 19, 25, 31, 37, 43, 49, 55, 61, 67, 73, 79, 85, and 91.

[00159] Figure 93A is an illustration depicting the type II CRISPR/Cas system.

[00160] Figure 93B is another illustration depicting the type II CRISPR/Cas system.

[00161] Figure 94A is an illustration depicting detection of Cas9 mRNA in different cells with constitutive expression (HEK293T, Hela, Huh7) or transient expression (HEK293T) of Cas9. pg2, pg20 – 2nd and 20th passages are presented for Huh7 cells.

[00162] Figure 94B is an illustration depicting Cas9 expression in HepG2 transfected with mRNA.

[00163] Figure 94C is an illustration depicting Cas9 expression in human primary hepatocytes transfected with Cas9 mRNA.

[00164] Figures 95A and 95B are a series of graphs depicting activity of gRNA CH31, comparison of split gRNA (crRNA+tracerRNA) and single stranded gRNA with various chemical modifications.

[00165] Figure 96 is an illustration depicting a comparison of the single stranded donor oligonucleotide and wt allele, where mismatches are highlighted.

[00166] Figure 97A is a graph depicting efficiency of Cas9/gRNA promoted HDR (- minus strand donor, + plus strand donor, no donor) using NextGen sequencing analysis of different gRNAs.

[00167] Figure 97B is a graph depicting efficiency of Cas9/gRNA promoted HDR (- minus strand donor, + plus strand donor, no donor) using Sanger sequencing analysis (200 individual sequences) of the HDR gRNA3 (+ donor).

[00168] Figure 97C is a graph depicting efficiency of Cas9/gRNA promoted HDR (- minus strand donor, + plus strand donor, no donor) using representative sequence with correct recombination vs wt allele.

[00169] Figure 98 is a graph depicting specific G6PC activity measured in HEK293 cells transfected with plasmids encoding G6PC protein: wildtype and mutant forms.

[00170] Figures 99A-99C are a series of illustrations depicting a schematic representation of the donors for knock-in strategies described herein.

Brief Description of the Sequence Listing

[00171] SEQ ID NOs: 1-2,032 are 20 bp spacer sequences for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *S. pyogenes* Cas9 endonuclease.

[00172] SEQ ID NOs: 2,033-2,203 are 20 bp spacer sequences for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *S. aureus* Cas9 endonuclease.

[00173] SEQ ID NOs: 2,204-2,221 are 20 bp spacer sequences for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *S. thermophilus* Cas9 endonuclease.

[00174] SEQ ID NOs: 2,222-2,230 are 20 bp spacer sequences for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *T. denticola* Cas9 endonuclease.

[00175] SEQ ID NOs: 2,231-2,305 are 20 bp spacer sequences for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with a *N. meningitides* Cas9 endonuclease.

[00176] SEQ ID NOs: 2,306-3,481 are 22 bp spacer sequences for targeting exons 1-2 of an AAVS1 (PPP1R12C) gene with an *Acidominococcus*, *Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00177] SEQ ID NOs: 3,482-3,649 are 20 bp spacer sequences for targeting exons 1-2 of an Alb gene with a *S. pyogenes* Cas9 endonuclease.

[00178] SEQ ID NOs: 3,650-3,677 are 20 bp spacer sequences for targeting exons 1-2 of an Alb gene with a *S. aureus* Cas9 endonuclease.

[00179] SEQ ID NOs: 3,678-3,695 are 20 bp spacer sequences for targeting exons 1-2 of an Alb gene with a *S. thermophilus* Cas9 endonuclease.

[00180] SEQ ID NOs: 3,696-3,700 are 20 bp spacer sequences for targeting exons 1-2 of an Alb gene with a *T. denticola* Cas9 endonuclease.

[00181] SEQ ID NOs: 3,701-3,724 are 20 bp spacer sequences for targeting exons 1-2 of an Alb gene with a *N. meningitides* Cas9 endonuclease.

[00182] SEQ ID NOs: 3,725-4,103 are 22 bp spacer sequences for targeting exons 1-2 of an Alb gene with an *Acidominococcus*, *Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00183] SEQ ID NOs: 4,104-4,448 are 20 bp spacer sequences for targeting exons 1-2 of an Angpt13 gene with a *S. pyogenes* Cas9 endonuclease.

[00184] SEQ ID NOs: 4,449-4,484 are 20 bp spacer sequences for targeting exons 1-2 of an Angpt13 gene with a *S. aureus* Cas9 endonuclease.

[00185] SEQ ID NOs: 4,485-4,507 are 20 bp spacer sequences for targeting exons 1-2 of an Angpt13 gene with a *S. thermophilus* Cas9 endonuclease.

[00186] SEQ ID NOs: 4,508-4,520 are 20 bp spacer sequences for targeting exons 1-2 of an Angpt13 gene with a *T. denticola* Cas9 endonuclease.

[00187] SEQ ID NOs: 4,521-4,583 are 20 bp spacer sequences for targeting exons 1-2 of an Angpt13 gene with a *N. meningitides* Cas9 endonuclease.

[00188] SEQ ID NOs: 4,584-5,431 are 22 bp spacer sequences for targeting exons 1-2 of an Angpt13 gene with an *Acidominococcus*, *Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00189] SEQ ID NOs: 5,432-5,834 are 20 bp spacer sequences for targeting exons 1-2 of an ApoC3 gene with a *S. pyogenes* Cas9 endonuclease.

[00190] SEQ ID NOs: 5,835-5,859 are 20 bp spacer sequences for targeting exons 1-2 of an ApoC3 gene with a *S. aureus* Cas9 endonuclease.

[00191] SEQ ID NOs: 5,860-5,862 are 20 bp spacer sequences for targeting exons 1-2 of an ApoC3 gene with a *S. thermophilus* Cas9 endonuclease.

[00192] SEQ ID NOs: 5,863-5,864 are 20 bp spacer sequences for targeting exons 1-2 of an ApoC3 gene with a *T. denticola* Cas9 endonuclease.

[00193] SEQ ID NOs: 5,865-5,876 are 20 bp spacer sequences for targeting exons 1-2 of an ApoC3 gene with a *N. meningitides* Cas9 endonuclease.

[00194] SEQ ID NOs: 5,877-6,108 are 22 bp spacer sequences for targeting exons 1-2 of an ApoC3 gene with an *Acidominococcus*, *Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00195] SEQ ID NOs: 6,109-7,876 are 20 bp spacer sequences for targeting exons 1-2 of an ASGR2 gene with a *S. pyogenes* Cas9 endonuclease.

[00196] SEQ ID NOs: 7,877-8,082 are 20 bp spacer sequences for targeting exons 1-2 of an ASGR2 gene with a *S. aureus* Cas9 endonuclease.

[00197] SEQ ID NOs: 8,083-8,106 are 20 bp spacer sequences for targeting exons 1-2 of an ASGR2 gene with a *S. thermophilus* Cas9 endonuclease.

[00198] SEQ ID NOs: 8,107-8,118 are 20 bp spacer sequences for targeting exons 1-2 of an ASGR2 gene with a *T. denticola* Cas9 endonuclease.

[00199] SEQ ID NOs: 8,119-8,201 are 20 bp spacer sequences for targeting exons 1-2 of an ASGR2 gene with a *N. meningitides* Cas9 endonuclease.

[00200] SEQ ID NOs: 8,202-9,641 are 22 bp spacer sequences for targeting exons 1-2 of an ASGR2 gene with an *Acidominococcus*, *Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00201] SEQ ID NOs: 9,642-9,844 are 20 bp spacer sequences for targeting exons 1-2 of a CCR5 gene with a *S. pyogenes* Cas9 endonuclease.

[00202] SEQ ID NOs: 9,845-9,876 are 20 bp spacer sequences for targeting exons 1-2 of a CCR5 gene with a *S. aureus* Cas9 endonuclease.

[00203] SEQ ID NOs: 9,877-9,890 are 20 bp spacer sequences for targeting exons 1-2 of a CCR5 gene with a *S. thermophilus* Cas9 endonuclease.

[00204] SEQ ID NOs: 9,891-9,892 are 20 bp spacer sequences for targeting exons 1-2 of a CCR5 gene with a *T. denticola* Cas9 endonuclease.

[00205] SEQ ID NOs: 9,893-9,920 are 20 bp spacer sequences for targeting exons 1-2 of a CCR5 gene with a *N. meningitides* Cas9 endonuclease.

[00206] SEQ ID NOs: 9,921-10,220 are 22 bp spacer sequences for targeting exons 1-2 of a CCR5 gene with an *Acidominococcus*, *Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00207] SEQ ID NOs: 10,221-11,686 are 20 bp spacer sequences for targeting exons 1-2 of an F9 gene with a *S. pyogenes* Cas9 endonuclease.

[00208] SEQ ID NOs: 11,687-11,849 are 20 bp spacer sequences for targeting exons 1-2 of an F9 gene with a *S. aureus* Cas9 endonuclease.

[00209] SEQ ID NOs: 11,850-11,910 are 20 bp spacer sequences for targeting exons 1-2 of an F9 gene with a *S. thermophilus* Cas9 endonuclease.

[00210] SEQ ID NOs: 11,911-11,935 are 20 bp spacer sequences for targeting exons 1-2 of an F9 gene with a *T. denticola* Cas9 endonuclease.

[00211] SEQ ID NOs: 11,936-12,088 are 20 bp spacer sequences for targeting exons 1-2 of an F9 gene with a *N. meningitides* Cas9 endonuclease.

[00212] SEQ ID NOs: 12,089-14,229 are 22 bp spacer sequences for targeting exons 1-2 of an F9 gene with an *Acidominococcus*, *Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00213] SEQ ID NOs: 14,230-19,722 are 20 bp spacer sequences for targeting exons 1-2 of an Gys2 gene with a *S. pyogenes* Cas9 endonuclease.

[00214] SEQ ID NOs: 19,723-20,398 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Gys2 gene with a *S. aureus* Cas9 endonuclease.

[00215] SEQ ID NOs: 20,399-20,676 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Gys2 gene with a *S. thermophilus* Cas9 endonuclease.

[00216] SEQ ID NOs: 20,677-20,790 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Gys2 gene with a *T. denticola* Cas9 endonuclease.

[00217] SEQ ID NOs: 20,791-21,470 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Gys2 gene with a *N. meningitides* Cas9 endonuclease.

[00218] SEQ ID NOs: 21,471-29,902 are gRNA 22 bp spacer sequences for targeting exons 1-2 of an Gys2 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00219] SEQ ID NOs: 29,903-31,595 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an HGD gene with a *S. pyogenes* Cas9 endonuclease.

[00220] SEQ ID NOs: 31,596-31,809 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an HGD gene with a *S. aureus* Cas9 endonuclease.

[00221] SEQ ID NOs: 31,810-31,892 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an HGD gene with a *S. thermophilus* Cas9 endonuclease.

[00222] SEQ ID NOs: 31,893-31,911 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an HGD gene with a *T. denticola* Cas9 endonuclease.

[00223] SEQ ID NOs: 31,912-32,112 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an HGD gene with a *N. meningitides* Cas9 endonuclease.

[00224] SEQ ID NOs: 32,113-34,437 are gRNA 22 bp spacer sequences for targeting exons 1-2 of an HGD gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00225] SEQ ID NOs: 34,438-38,232 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Lp(a) gene with a *S. pyogenes* Cas9 endonuclease.

[00226] SEQ ID NOs: 38,233-38,642 are gRNA 20 bp spacer sequences for exons 1-2 of targeting the Lp(a) gene with a *S. aureus* Cas9 endonuclease.

[00227] SEQ ID NOs: 38,643-38,778 are gRNA 20 bp spacer sequences for targeting the exons 1-2 of Lp(a) gene with a *S. thermophilus* Cas9 endonuclease.

[00228] SEQ ID NOs: 38,779-38,813 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Lp(a) gene with a *T. denticola* Cas9 endonuclease.

[00229] SEQ ID NOs: 38,814-39,181 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Lp(a) gene with a *N. meningitides* Cas9 endonuclease.

[00230] SEQ ID NOs: 39,182-43,802 are gRNA 22 bp spacer sequences for targeting exons 1-2 of an Lp(a) gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00231] SEQ ID NOs: 43,803-45,822 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an PCSK9 gene with a *S. pyogenes* Cas9 endonuclease.

[00232] SEQ ID NOs: 45,823-46,009 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an PCSK9 gene with a *S. aureus* Cas9 endonuclease.

[00233] SEQ ID NOs: 46,010-46,045 are gRNA 20 bp spacer sequences, for targeting exons 1-2 of an PCSK9 gene with a *S. thermophilus* Cas9 endonuclease.

[00234] SEQ ID NOs: 46,046-46,059 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an PCSK9 gene with a *T. denticola* Cas9 endonuclease.

[00235] SEQ ID NOs: 46,060-46,199 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an PCSK9 gene with a *N. meningitides* Cas9 endonuclease.

[00236] SEQ ID NOs: 46,200-47,993 are gRNA 22 bp spacer sequences for targeting exons 1-2 of an PCSK9 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00237] SEQ ID NOs: 47,994-49,131 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Serpina1 gene with a *S. pyogenes* Cas9 endonuclease.

[00238] SEQ ID NOs: 49,132-49,224 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Serpina1 gene with a *S. aureus* Cas9 endonuclease.

[00239] SEQ ID NOs: 49,225-49,236 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Serpina1 gene with a *S. thermophilus* Cas9 endonuclease.

[00240] SEQ ID NOs: 49,237-49,239 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Serpina1 gene with a *T. denticola* Cas9 endonuclease.

[00241] SEQ ID NOs: 49,240-49,290 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an Serpina1 gene with a *N. meningitides* Cas9 endonuclease.

[00242] SEQ ID NOs: 49,291-50,094 are gRNA 22 bp spacer sequences for targeting exons 1-2 of an Serpina1 gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00243] SEQ ID NOs: 50,095-50,926 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TF gene with a *S. pyogenes* Cas9 endonuclease.

[00244] SEQ ID NOs: 50,927-51,012 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TF gene with a *S. aureus* Cas9 endonuclease.

[00245] SEQ ID NOs: 51,013-51,024 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TF gene with a *S. thermophilus* Cas9 endonuclease.

[00246] SEQ ID NOs: 51,025-51,031 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TF gene with a *T. denticola* Cas9 endonuclease.

[00247] SEQ ID NOs: 51,032-51,075 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TF gene with a *N. meningitides* Cas9 endonuclease.

[00248] SEQ ID NOs: 51,076-51,711 are gRNA 22 bp spacer sequences targeting exons 1-2 of an TF gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00249] SEQ ID NOs: 51,712-52,011 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TTR gene with a *S. pyogenes* Cas9 endonuclease.

[00250] SEQ ID NOs: 52,012-52,052 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TTR gene with a *S. aureus* Cas9 endonuclease.

[00251] SEQ ID NOs: 52,053-52,069 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TTR gene with a *S. thermophilus* Cas9 endonuclease.

[00252] SEQ ID NOs: 52,070-52,071 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TTR gene with a *T. denticola* Cas9 endonuclease.

[00253] SEQ ID NOs: 52,072-52,106 are gRNA 20 bp spacer sequences for targeting exons 1-2 of an TTR gene with a *N. meningitides* Cas9 endonuclease.

[00254] SEQ ID NOs: 52,107-52,508 are gRNA 22 bp spacer sequences for targeting exons 1-2 of an TTR gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

[00255] SEQ ID NOs: 52,509-57,754 are gRNA 20 bp spacer sequences for targeting the G6PC gene with a *S. pyogenes* Cas9 endonuclease.

[00256] SEQ ID NOs: 57,755-58,367 are gRNA 20 bp spacer sequences for targeting the G6PC gene with a *S. aureus* Cas9 endonuclease.

[00257] SEQ ID NOs: 58,368-58,512 are gRNA 20 bp spacer sequences for targeting the G6PC gene with a *S. thermophilus* Cas9 endonuclease.

[00258] SEQ ID NOs: 58,513-58,583 are gRNA 20 bp spacer sequences for targeting the G6PC gene with a *T. denticola* Cas9 endonuclease.

[00259] SEQ ID NOs: 58,584-59,035 are gRNA 20 bp spacer sequences for targeting the G6PC gene with a *N. meningitides* Cas9 endonuclease.

[00260] SEQ ID NOs: 59,036-64,789 are gRNA 22 bp spacer sequences for targeting the G6PC gene with an *Acidominococcus, Lachnospiraceae*, and *Francisella novicida* Cpf1 endonuclease.

Detailed Description

[00261] Glycogen Storage Disease type 1a (GSD1a)

[00262] GSD1a is caused by a homozygous or compound heterozygous mutation that inactivates both copies of the glucose-6-phosphatase, catalytic (G6PC) gene. This gene is located at 17q21 and consists of five exons (OMIM #23220). Glucose-6-Phosphatase (G6Pase) is an endoplasmic reticulum membrane-bound enzyme that catalyzes the removal of phosphate from Glucose-6-Phosphate (van Schaftingen, E., & Gerin, I. Biochem J, 2002). The glucose-6-phosphatase system. Biochem J, 362(Pt 3), 513-532). This is the final step in both gluconeogenesis and glycogenolysis, making G6Pase very important for glucose homeostasis (van Schaftingen, E., & Gerin, I. Biochem J, 2002).

[00263] A G6PC knockout mouse model has been generated that demonstrates many of the same disease symptoms, including hyperlipidemia, lactic acidosis, hypoglycemia and hepatomegaly (Mutel, E., et al. J Hepatol, 2011). Not only do G6Pase deficient mice exhibit symptoms similar to those of human GSD1a patients, when these mice are given adenoviral based gene therapy with G6PC, many of the phenotypes associated with GSD1a are reversed (Lee, Y. M., et al.

Hepatology, 2012 ; Zingone, A., et al. J Biol Chem, 2000). These combined studies, as well as results obtained from dogs with a mutation to this gene, indicate that G6PC is the underlying cause of GSD1a (Kishnani, P. S., et al. Vet Pathol, 2001).

[00264] There are various mutations associated with GSD1a, which are a combination of missense, nonsense, frameshift and other mutations, with the common effect of inactivating G6Pase (van Schaftingen, E., & Gerin, I. Biochem J, 2002). The various mutations are distributed across the five exons of the gene and appear to be roughly distributed in incidence based on heritage (*e.g.*: 50% of Caucasians have 130X, while 91% of Japanese patients and carriers have a G>T at base 727) (Kajihara, S., et al. (1995). Exon Redefinition by a Point Mutation within Exon 5 of the Glucose-6-Phosphatase Gene Is the Major Cause of Glycogen Storage Disease type Ia in Japan. Am. J. Hum. Genet., 57, 549-555; Lei, K. J., et al. (1995). Genetic Basis of Glycogen Storage Disease type 1a: Prevalent Mutations at the Glucose-6-Phosphatase Locus. Am. J. Hum. Genet., 57, 766-771). Overall, the most prevalent mutations were at codon 83, with a change from arginine to cysteine or histidine; and at codon 347, with a premature stop (Lei, K. J., et al. Am. J. Hum. Genet., 1995). Codon site 83 resides in the active site of the enzyme, and its charge is critical to its functionality, thus the amino acid change abolishes the action of the enzyme (Chou, J. Y., & Mansfield, B. C. Hum Mutat, 2008). Though the incidence of the various mutations that cause GSD1a seem to vary based upon population, the overall incidence of the disease is 1/100,000, with a carrier frequency of 1/150 (Koeberl, et al. Trends Endocrinol Metab, 2009). There is also an increased prevalence in Ashkenazi Jews, with an incidence of 1/20,000 (Ekstein, J., et al. (2004). Mutation frequencies for glycogen storage disease Ia in the Ashkenazi Jewish population. Am J Med Genet A, 129A(2), 162-164. doi:10.1002/ajmg.a.30232).

[00265] Therapeutic approach

[00266] As the known forms of GSD1a are monogenic disorders with recessive inheritance, it is likely that correcting one of the mutant alleles per cell will be sufficient for correction and restoration or partial restoration of GSD1a function. The correction of one allele can coincide with one copy that remains with the original mutation, or a copy that was cleaved and repaired by non-homologous end joining

(NHEJ) and therefore was not properly corrected. Bi-allelic correction can also occur. Various editing strategies that can be employed for specific mutations are discussed below.

[00267] Correction of one or possibly both of the mutant alleles provides an important improvement over existing or potential therapies, such as introduction of G6PC expression cassettes through lentivirus delivery and integration. Gene editing has the advantage of precise genome modification and lower adverse effects, for example, the mutation can be corrected by the insertions or deletions that arise due to the NHEJ repair pathway. If the patient's G6PC gene has an inserted or deleted base, a targeted cleavage can result in a NHEJ-mediated insertion or deletion that restores the frame. Missense mutations can also be corrected through NHEJ-mediated correction using one or more guide RNA. The ability or likelihood of the cut(s) to correct the mutation can be designed or evaluated based on the local sequence and micro-homologies. NHEJ can also be used to delete segments of the gene, either directly or by altering splice donor or acceptor sites through cleavage by one gRNA targeting several locations, or several gRNAs. This may be useful if an amino acid, domain or exon contains the mutations and can be removed or inverted, or if the deletion otherwise restored function to the protein. Pairs of guide strands have been used for deletions and corrections of inversions.

[00268] Alternatively, the donor for correction by HDR contains the corrected sequence with small or large flanking homology arms to allow for annealing. HDR is essentially an error-free mechanism that uses a supplied homologous DNA sequence as a template during DSB repair. The rate of HDR is a function of the distance between the mutation and the cut site so choosing overlapping or nearby target sites is important. Templates can include extra sequences flanked by the homologous regions or can contain a sequence that differs from the genomic sequence, thus allowing sequence editing.

[00269] In addition to correcting mutations by NHEJ or HDR, a range of other options are possible. If there are small or large deletions or multiple mutations, a cDNA can be knocked in that contains the exons affected. A full length cDNA can be knocked into any "safe harbor"— i.e., non-deleterious insertion point that is not

the G6PC gene itself--, with or without suitable regulatory sequences. If this construct is knocked-in near the G6PC regulatory elements, it should have physiological control, similar to the normal gene. Two or more (e.g., a pair) nucleases can be used to delete mutated gene regions, though a donor would usually have to be provided to restore function. In this case two gRNA and one donor sequence would be supplied.

[00270] Provided herein are methods to correct the specific mutation in the gene by inducing a double stranded break with Cas9 and a sgRNA or a pair of double stranded breaks around the mutation using two appropriate sgRNAs, and to provide a donor DNA template to induce Homology-Directed Repair (HDR). In some embodiments, the donor DNA template can be a short single stranded oligonucleotide, a short double stranded oligonucleotide, a long single or double stranded DNA molecule. These methods use gRNAs and donor DNA molecules for each of the variants of G6PC.

[00271] Provided herein are methods to knock-in G6PC cDNA or a minigene (comprised of one or more exons and introns or natural or synthetic introns) into the locus of the corresponding gene. These methods use a pair of sgRNA targeting the first exon and/or the first intron of the G6PC gene. In some embodiments, the donor DNA is single or double stranded DNA having homologous arms to the 17q21 region.

[00272] Provided herein are methods to knock-in G6PC cDNA or a minigene (comprised of one or more exons and introns or natural or synthetic introns) into the locus of the hot-spot, e.g. ALB gene. These methods use a pair of sgRNA targeting the first exon and/or the first intron of the gene located in the liver hotspot. In some embodiments, the donor DNA is single or double stranded DNA having homologous arms to the corresponding region.

[00273] Provided herein are cellular, ex vivo and in vivo methods for using genome engineering tools to create permanent changes to the genome by: 1) correcting, by insertions or deletions that arise due to the imprecise NHEJ pathway, one or more mutations within or near the G6PC gene, 2) correcting, by HDR, one or more mutations within or near the G6PC gene, or 3) deletion of the mutant region and knocking-in G6PC cDNA or a minigene (comprised of one or more exons and

introns or natural or synthetic introns) into the gene locus or a safe harbor locus in the glucose-6-phosphatase, catalytic (G6PC) gene and restoring G6Pase protein activity. Such methods use endonucleases, such as CRISPR-associated (CRISPR/Cas9, Cpf1 and the like) nucleases, to permanently delete, insert, edit, correct, or replace one or more exons (i.e., mutations within or near the coding and/or splicing sequences) in the genomic locus of the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene. In this way, examples set forth in the present disclosure can help to restore the reading frame or the wild-type sequence of, or otherwise correct, the gene with a single treatment (rather than deliver potential therapies for the lifetime of the patient).G6PC gene.

[00274] Provided herein are methods for treating a patient with GSD1a. An embodiment of such method is an *ex vivo* cell based therapy. For example, a patient specific induced pluripotent stem cell (iPSC) is created. Then, the chromosomal DNA of these iPS cells is edited using the materials and methods described herein. Next, the genome-edited iPSCs are differentiated into hepatocytes. Finally, the hepatocytes are implanted into the patient.

[00275] Another embodiment of such method is an *ex vivo* cell based therapy. For example, a biopsy of the patient's liver is performed. Then, a liver specific progenitor cell or primary hepatocyte is isolated from the patient, e.g., by a biopsy. Next, the chromosomal DNA of these progenitor cells or primary hepatocytes is edited using the materials and methods described herein. Finally, the genome-edited progenitor cells or primary hepatocytes are implanted into the patient.

[00276] Yet another embodiment of such method is an *ex vivo* cell based therapy. For example, a biopsy of the patient's bone marrow is performed. Then, a mesenchymal stem cell is isolated from the patient, which can be isolated from the patient's bone marrow, e.g., by biopsy, or peripheral blood. Next, the chromosomal DNA of these mesenchymal stem cells is edited using the materials and methods described herein. Next, the genome-edited mesenchymal stem cells are differentiated into hepatocytes. Finally, these hepatocytes are implanted into the patient.

[00277] One advantage of an *ex vivo* cell therapy approach is the ability to conduct a comprehensive analysis of the therapeutic prior to administration. All

nuclease based therapeutics have some level of off-target effects. Performing gene correction *ex vivo* allows one to fully characterize the corrected cell population prior to implantation. Aspects of the invention include sequencing the entire genome of the corrected cells to ensure that the off-target cuts, if any, are in genomic locations associated with minimal risk to the patient. Furthermore, populations of specific cells, including clonal populations, can be isolated prior to implantation.

[00278] Another advantage of *ex vivo* cell therapy relates to genetic correction in iPSCs compared to other primary cell sources. iPSCs are prolific, making it easy to obtain the large number of cells that will be required for a cell based therapy. Furthermore, iPSCs are an ideal cell type for performing clonal isolations. This allows screening for the correct genomic correction, without risking a decrease in viability. In contrast, other potential cell types, such as primary hepatocytes, are viable for only a few passages and difficult to clonally expand. Thus, manipulation of GSD1a iPSCs will be much easier, and will shorten the amount of time needed to make the desired genetic correction.

[00279] Another embodiment of such method is an *in vivo* based therapy. In this method, the chromosomal DNA of the cells in the patient is corrected using the materials and methods described herein.

[00280] An advantage of *in vivo* gene therapy is the ease of therapeutic production and administration. The same therapeutic approach and therapy will have the potential to be used to treat more than one patient, for example a number of patients who share the same or similar genotype or allele. In contrast, *ex vivo* cell therapy typically requires using a patient's own cells, which are isolated, manipulated and returned to the same patient.

[00281] Also provided herein is a cellular method for editing the glucose-6-phosphatase, catalytic (G6PC) gene in a cell by genome editing. For example, a cell is isolated from a patient or animal. Then, the chromosomal DNA of the cell is edited using the materials and methods described herein.

[00282] The methods of the invention, regardless of whether a cellular or *ex vivo* or *in vivo* method, can involve one or a combination of the following: 1) correcting, by insertions or deletions that arise due to the imprecise NHEJ pathway, one or more mutations within or near the G6PC gene or other DNA sequences that

encode regulatory elements of the G6PC gene, 2) correcting, by HDR, one or more mutations within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene, 3) deletion of the mutant region and knocking-in G6PC cDNA or a minigene (comprised of one or more exons and introns or natural or synthetic introns) into the gene locus or at a heterologous location in the genome (such as a safe harbor locus, such as, *e.g.*, targeting exon 1-2 of, an albumin gene, an AAVS1 (PPP1R12C) gene, an ALB gene, an Angptl3 gene, an ApoC3 gene, an ASGR2 gene, a CCR5 gene, a FIX (F9) gene, a Gys2 gene, an HGD gene, an Lp(a) gene, a Pcsk9 gene, a Serpina1 gene, a TF gene, and/or a TTR gene, or 4) deletion of the mutant region and knocking-in G6PC cDNA or a minigene (comprised of one or more exons and introns or natural or synthetic introns) into the first exon of HGD, leading to disruption of HGD expression. HGD-/- hepatocytes have proliferation advantage when FAH activity is absent or reduced. Inhibition of FAH can be achieved by treatment with shRNA (AAV) targeting FAH, or siRNA (LNP formulated, or conjugate with GalNAc, or with cholesterol) or treatment with CEHPOBA (see e.g., Paulk et al. “In vivo selection of transplanted hepatocytes by pharmacological inhibition of fumarylacetoacetate hydrolase in wild-type mice.” Mol Ther 2012, 20(10):1981-1987). Assessment of efficiency of HDR mediated knock-in of cDNA into the first exon can utilize cDNA knock-in into “safe harbor” sites such as: single-stranded or double-stranded DNA having homologous arms to one of the following regions, for example: ApoC3 (chr11:116829908-116833071), Angptl3 (chr1:62,597,487-62,606,305), Serpina1 (chr14:94376747-94390692), Lp(a) (chr6:160531483-160664259), Pcsk9 (chr1:55,039,475-55,064,852), FIX (chrX:139,530,736-139,563,458), ALB (chr4:73,404,254-73,421,411), TTR (chr18:31,591,766-31,599,023), TF (chr3:133,661,997-133,779,005), Gys2 (chr12:21,536,188-21,604,857), AAVS1(PPP1R12C) (chr19:55,090,912-55,117,599), HGD (chr3:120,628,167-120,682,570), CCR5 (chr3:46,370,854-46,376,206), ASGR2 (chr17:7,101,322-7,114,310), 5’UTR correspondent to ASS1 or alternative 5’ UTR, complete CDS of G6PC and 3’ UTR of G6PC or modified 3’ UTR and at least 80 nt of the first intron, alternatively same DNA template sequence will be delivered by AAV. Both the HDR and knock-in strategies utilize a donor DNA template in Homology-Directed Repair (HDR). HDR in either strategy may be accomplished by making one or more single-

stranded breaks (SSBs) or one or more double-stranded breaks (DSBs) at specific sites in the genome by using one or more endonucleases.

[00283] For example, the NHEJ correction strategy can involve restoring the reading frame in the G6PC gene by inducing one single stranded break or double stranded break in the gene of interest with one or more CRISPR endonucleases and a gRNA (e.g., crRNA + tracrRNA, or sgRNA), or two or more single stranded breaks or double stranded breaks in the gene of interest with two or more CRISPR endonucleases and two or more sgRNAs. This approach can require development and optimization of sgRNAs for the G6PC gene.

[00284] For example, the HDR correction strategy involves restoring the reading frame in the G6PC gene by inducing one single stranded break or double stranded break in the gene of interest one or more CRISPR endonucleases and gRNA (e.g., crRNA + tracrRNA, or sgRNA), or two or more single stranded breaks or double stranded breaks in the gene of interest with one or more CRISPR endonucleases and two or more appropriate gRNAs, in the presence of a donor DNA template introduced exogenously to direct the cellular DSB response to Homology-Directed Repair (the donor DNA template can be a short single stranded oligonucleotide, a short double stranded oligonucleotide, a long single or double stranded DNA molecule). This approach requires development and optimization of gRNAS and donor DNA molecules for all major variants of the G6PC gene.

[00285] For example, the knock-in strategy involves knocking-in G6PC cDNA or a minigene (comprised of one or more exons and introns or natural or synthetic introns) into the locus of the gene using a gRNA (e.g., crRNA + tracrRNA, or sgRNA) or a pair of gRNAs targeting upstream of or in the first or other exon and/or intron of the G6PC gene, or in a safe harbor site (such as, *e.g.*, exon 1-2 of, AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and/or TTR). The donor DNA will be single or double stranded DNA having homologous arms to the 17q21 region.

[00286] The advantages for both strategies (correction and knock-in) are similar, including in principle both short and long term beneficial clinical and laboratory effects. In addition, it may be that only a low percentage of G6Pase activity is required to provide therapeutic benefit. Another advantage for both strategies is

that most patients have low-level gene and protein activity, therefore suggesting that additional protein expression, for example following gene correction, should not necessarily lead to an immune response against the target gene product. The knock-in approach does provide one advantage over the correction approach – the ability to treat all patients versus only a subset of patients. While there is a common mutation in this gene (at codon 83), there are also many other possible mutations, and using the knock-in method could treat all of them. The other issue with gene editing in this manner is the need for a DNA donor for HDR.

[00287] In addition to the above genome editing strategies, another strategy involves modulating expression, function, or activity of G6PC by editing in the regulatory sequence.

[00288] In addition to the editing options listed above, Cas9 or similar proteins can be used to target effector domains to the same target sites that can be identified for editing, or additional target sites within range of the effector domain. A range of chromatin modifying enzymes, methylases or demethlyases can be used to alter expression of the target gene. One possibility is increasing the expression of the G6Pase protein if the mutation leads to lower activity. These types of epigenetic regulation have some advantages, particularly as they are limited in possible off-target effects.

[00289] A number of types of genomic target sites are present in addition to mutations in the coding and splicing sequences.

[00290] The regulation of transcription and translation implicates a number of different classes of sites that interact with cellular proteins or nucleotides. Often the DNA binding sites of transcription factors or other proteins can be targeted for mutation or deletion to study the role of the site, though they can also be targeted to change gene expression. Sites can be added through non-homologous end joining (NHEJ) or direct genome editing by homology directed repair (HDR). Increased use of genome sequencing, RNA expression and genome-wide studies of transcription factor binding have increased the ability to identify how the sites lead to developmental or temporal gene regulation. These control systems may be direct or may involve extensive cooperative regulation that can require the integration of activities from multiple enhancers. Transcription factors typically bind

6–12 bp-long degenerate DNA sequences. The low level of specificity provided by individual sites suggests that complex interactions and rules are involved in binding and the functional outcome. Binding sites with less degeneracy may provide simpler means of regulation. Artificial transcription factors can be designed to specify longer sequences that have less similar sequences in the genome and have lower potential for off-target cleavage. Any of these types of binding sites can be mutated, deleted or even created to enable changes in gene regulation or expression (Canver, M.C. *et al.*, *Nature* (2015)).

[00291] Another class of gene regulatory regions having these features is microRNA (miRNA) binding sites. miRNAs are non-coding RNAs that play key roles in post-transcriptional gene regulation. miRNA may regulate the expression of 30% of all mammalian protein-encoding genes. Specific and potent gene silencing by double stranded RNA (RNAi) was discovered, plus additional small noncoding RNA (Canver, M.C. *et al.*, *Nature* (2015)). The largest class of noncoding RNAs important for gene silencing are miRNAs. In mammals, miRNAs are first transcribed as a long RNA transcripts, which can be separate transcriptional units, part of protein introns, or other transcripts. The long transcripts are called primary miRNA (pri-miRNA) that include imperfectly base-paired hairpin structures. These pri-miRNA are cleaved into one or more shorter precursor miRNAs (pre-miRNAs) by Microprocessor, a protein complex in the nucleus, involving Drosha.

[00292] Pre-miRNAs are short stem loops ~70 nucleotides in length with a 2-nucleotide 3'-overhang that are exported, into the mature 19-25 nucleotide miRNA:miRNA* duplexes. The miRNA strand with lower base pairing stability (the guide strand) is loaded onto the RNA-induced silencing complex (RISC). The passenger guide strand (marked with *), may be functional, but is usually degraded. The mature miRNA tethers RISC to partly complementary sequence motifs in target mRNAs predominantly found within the 3′ untranslated regions (UTRs) and induces posttranscriptional gene silencing (Bartel, D.P. *Cell* 136, 215-233 (2009); Saj, A. & Lai, E.C. *Curr Opin Genet Dev* 21, 504-510 (2011)).

[00293] miRNAs are important in development, differentiation, cell cycle and growth control, and in virtually all biological pathways in mammals and other multicellular organisms. miRNAs are also involved in cell cycle control, apoptosis

and stem cell differentiation, hematopoiesis, hypoxia, muscle development, neurogenesis, insulin secretion, cholesterol metabolism, aging, viral replication and immune responses.

[00294] A single miRNA can target hundreds of different mRNA transcripts, while an individual transcript can be targeted by many different miRNAs. More than 28645 microRNAs have been annotated in the latest release of miRBase (v.21). Some miRNAs are encoded by multiple loci, some of which are expressed from tandemly co-transcribed clusters. The features allow for complex regulatory networks with multiple pathways and feedback controls. miRNAs are integral parts of these feedback and regulatory circuits and can help regulate gene expression by keeping protein production within limits (Herranz, H. & Cohen, S.M. *Genes Dev* 24, 1339-1344 (2010); Posadas, D.M. & Carthew, R.W. *Curr Opin Genet Dev* 27, 1-6 (2014)).

[00295] miRNA are also important in a large number of human diseases that are associated with abnormal miRNA expression. This association underscores the importance of the miRNA regulatory pathway. Recent miRNA deletion studies have linked miRNA with regulation of the immune responses (Stern-Ginossar, N. *et al*., *Science* 317, 376-381 (2007)).

[00296] miRNA also have a strong link to cancer and may play a role in different types of cancer. miRNAs have been found to be downregulated in a number of tumors. miRNA are important in the regulation of key cancer-related pathways, such as cell cycle control and the DNA damage response, and are therefore used in diagnosis and are being targeted clinically. MicroRNAs delicately regulate the balance of angiogenesis, such that experiments depleting all microRNAs suppresses tumor angiogenesis (Chen, S. *et al*., *Genes Dev* 28, 1054-1067 (2014)).

[00297] As has been shown for protein coding genes, miRNA genes are also subject to epigenetic changes occurring with cancer. Many miRNA loci are associated with CpG islands increasing their opportunity for regulation by DNA methylation (Weber, B., Stresemann, C., Brueckner, B. & Lyko, F. *Cell Cycle* 6, 1001-1005 (2007)). The majority of studies have used treatment with chromatin remodeling drugs to reveal epigenetically silenced miRNAs.

[00298] In addition to their role in DNA silencing, miRNA can also activate translation (Posadas, D.M. & Carthew, R.W. *Curr Opin Genet Dev* 27, 1-6 (2014)). Knocking out these sites may lead to decreased expression of the targeted gene, while introducing these sites may increase expression.

[00299] Individual miRNA can be knocked out most effectively by mutating the seed sequence (bases 2-8 of the microRNA), which is important for binding specificity. Cleavage in this region, followed by mis-repair by NHEJ can effectively abolish miRNA function by blocking binding to target sites. miRNA could also be inhibited by specific targeting of the special loop region adjacent to the palindromic sequence. Catalytically inactive Cas9 can also be used to inhibit shRNA expression (Zhao, Y. *et al.*, *Sci Rep* 4, 3943 (2014)). In addition to targeting the miRNA, the binding sites can also be targeted and mutated to prevent the silencing by miRNA.

[00300] Human Cells

[00301] For ameliorating GSD1a, as described and illustrated herein, the principal targets for gene editing are human cells. For example, in the *ex vivo* methods, the human cells are somatic cells, which after being modified using the techniques as described, can give rise to hepatocytes or progenitor cells. For example, in the *in vivo* methods, the human cells are hepatocytes, renal cells or cells from other affected organs.

[00302] By performing gene editing in autologous cells that are derived from and therefore already completely matched with the patient in need, it is possible to generate cells that can be safely re-introduced into the patient, and effectively give rise to a population of cells that will be effective in ameliorating one or more clinical conditions associated with the patient's disease.

[00303] Progenitor cells (also referred to as stem cells herein) are capable of both proliferation and giving rise to more progenitor cells, these in turn having the ability to generate a large number of mother cells that can in turn give rise to differentiated or differentiable daughter cells. The daughter cells themselves can be induced to proliferate and produce progeny that subsequently differentiate into one or more mature cell types, while also retaining one or more cells with parental developmental potential. The term "stem cell" refers then, to a cell with the capacity or potential, under particular circumstances, to differentiate to a more specialized or

differentiated phenotype, and which retains the capacity, under certain circumstances, to proliferate without substantially differentiating. In one embodiment, the term progenitor or stem cell refers to a generalized mother cell whose descendants (progeny) specialize, often in different directions, by differentiation, *e.g.*, by acquiring completely individual characters, as occurs in progressive diversification of embryonic cells and tissues. Cellular differentiation is a complex process typically occurring through many cell divisions. A differentiated cell may derive from a multipotent cell that itself is derived from a multipotent cell, and so on. While each of these multipotent cells may be considered stem cells, the range of cell types that each can give rise to may vary considerably. Some differentiated cells also have the capacity to give rise to cells of greater developmental potential. Such capacity may be natural or may be induced artificially upon treatment with various factors. In many biological instances, stem cells are also "multipotent" because they can produce progeny of more than one distinct cell type, but this is not required for "stem-ness."

[00304] Self-renewal is another important aspect of the stem cell. In theory, self-renewal can occur by either of two major mechanisms. Stem cells may divide asymmetrically, with one daughter retaining the stem state and the other daughter expressing some distinct other specific function and phenotype. Alternatively, some of the stem cells in a population can divide symmetrically into two stems, thus maintaining some stem cells in the population as a whole, while other cells in the population give rise to differentiated progeny only. Generally, "progenitor cells" have a cellular phenotype that is more primitive (*i.e.*, is at an earlier step along a developmental pathway or progression than is a fully differentiated cell). Often, progenitor cells also have significant or very high proliferative potential. Progenitor cells can give rise to multiple distinct differentiated cell types or to a single differentiated cell type, depending on the developmental pathway and on the environment in which the cells develop and differentiate.

[00305] In the context of cell ontogeny, the adjective "differentiated," or "differentiating" is a relative term. A "differentiated cell" is a cell that has progressed further down the developmental pathway than the cell to which it is being compared. Thus, stem cells can differentiate into lineage-restricted precursor cells

(such as a myocyte progenitor cell), which in turn can differentiate into other types of precursor cells further down the pathway (such as a myocyte precursor), and then to an end-stage differentiated cell, such as a myocyte, which plays a characteristic role in a certain tissue type, and may or may not retain the capacity to proliferate further.

[00306] Induced Pluripotent Stem Cells

[00307] In some embodiments, the genetically engineered human cells described herein are induced pluripotent stem cells (iPSCs). An advantage of using iPSCs is that the cells can be derived from the same subject to which the progenitor cells are to be administered. That is, a somatic cell can be obtained from a subject, reprogrammed to an induced pluripotent stem cell, and then re-differentiated into a progenitor cell to be administered to the subject (*e.g.*, autologous cells). Because the progenitors are essentially derived from an autologous source, the risk of engraftment rejection or allergic response is reduced compared to the use of cells from another subject or group of subjects. In addition, the use of iPSCs negates the need for cells obtained from an embryonic source. Thus, in one embodiment, the stem cells used in the disclosed methods are not embryonic stem cells.

[00308] Although differentiation is generally irreversible under physiological contexts, several methods have been recently developed to reprogram somatic cells to iPSCs. Exemplary methods are known to those of skill in the art and are described briefly herein below.

[00309] The term "reprogramming" refers to a process that alters or reverses the differentiation state of a differentiated cell (*e.g.*, a somatic cell). Stated another way, reprogramming refers to a process of driving the differentiation of a cell backwards to a more undifferentiated or more primitive type of cell. It should be noted that placing many primary cells in culture can lead to some loss of fully differentiated characteristics. Thus, simply culturing such cells included in the term differentiated cells does not render these cells non-differentiated cells (*e.g.*, undifferentiated cells) or pluripotent cells. The transition of a differentiated cell to pluripotency requires a reprogramming stimulus beyond the stimuli that lead to partial loss of differentiated character in culture. Reprogrammed cells also have the characteristic of the capacity of extended passaging without loss of growth potential, relative to primary

cell parents, which generally have capacity for only a limited number of divisions in culture.

[00310] The cell to be reprogrammed can be either partially or terminally differentiated prior to reprogramming. In some embodiments, reprogramming encompasses complete reversion of the differentiation state of a differentiated cell (*e.g.*, a somatic cell) to a pluripotent state or a multipotent state. In some embodiments, reprogramming encompasses complete or partial reversion of the differentiation state of a differentiated cell (*e.g.*, a somatic cell) to an undifferentiated cell (*e.g.*, an embryonic-like cell). Reprogramming can result in expression of particular genes by the cells, the expression of which further contributes to reprogramming. In certain embodiments described herein, reprogramming of a differentiated cell (*e.g.*, a somatic cell) causes the differentiated cell to assume an undifferentiated state (*e.g.*, is an undifferentiated cell). The resulting cells are referred to as "reprogrammed cells," or "induced pluripotent stem cells (iPSCs or iPS cells)."

[00311] Reprogramming can involve alteration, *e.g.*, reversal, of at least some of the heritable patterns of nucleic acid modification (*e.g.*, methylation), chromatin condensation, epigenetic changes, genomic imprinting, etc., that occur during cellular differentiation. Reprogramming is distinct from simply maintaining the existing undifferentiated state of a cell that is already pluripotent or maintaining the existing less than fully differentiated state of a cell that is already a multipotent cell (*e.g.*, a myogenic stem cell). Reprogramming is also distinct from promoting the self-renewal or proliferation of cells that are already pluripotent or multipotent, although the compositions and methods described herein can also be of use for such purposes, in some embodiments.

[00312] Many methods are known in the art that can be used to generate pluripotent stem cells from somatic cells. Any such method that reprograms a somatic cell to the pluripotent phenotype would be appropriate for use in the methods described herein.

[00313] Reprogramming methodologies for generating pluripotent cells using defined combinations of transcription factors have been described. Mouse somatic cells can be converted to ES cell-like cells with expanded developmental potential

by the direct transduction of Oct4, Sox2, Klf4, and c-Myc; see, *e.g.*, Takahashi and Yamanaka, Cell 126(4): 663–76 (2006). iPSCs resemble ES cells, as they restore the pluripotency-associated transcriptional circuitry and much of the epigenetic landscape. In addition, mouse iPSCs satisfy all the standard assays for pluripotency: specifically, *in vitro* differentiation into cell types of the three germ layers, teratoma formation, contribution to chimeras, germline transmission [see, *e.g.*, Maherali and Hochedlinger, Cell Stem Cell. 3(6):595-605 (2008)], and tetraploid complementation.

[00314] Human iPSCs can be obtained using similar transduction methods, and the transcription factor trio, OCT4, SOX2, and NANOG, has been established as the core set of transcription factors that govern pluripotency; see, *e.g.*, Budniatzky and Gepstein, Stem Cells Transl Med. 3(4):448-57 (2014); Barrett *et al.*, Stem Cells Trans Med 3:1-6 sctm.2014-0121 (2014); Focosi *et al.*, Blood Cancer Journal 4: e211 (2014); and references cited therein. The production of iPSCs can be achieved by the introduction of nucleic acid sequences encoding stem cell-associated genes into an adult, somatic cell, historically using viral vectors.

[00315] iPSCs can be generated or derived from terminally differentiated somatic cells, as well as from adult stem cells, or somatic stem cells. That is, a non-pluripotent progenitor cell can be rendered pluripotent or multipotent by reprogramming. In such instances, it may not be necessary to include as many reprogramming factors as required to reprogram a terminally differentiated cell. Further, reprogramming can be induced by the non-viral introduction of reprogramming factors, *e.g.*, by introducing the proteins themselves, or by introducing nucleic acids that encode the reprogramming factors, or by introducing messenger RNAs that upon translation produce the reprogramming factors (see *e.g.*, Warren *et al.*, Cell Stem Cell, 7(5):618-30 (2010). Reprogramming can be achieved by introducing a combination of nucleic acids encoding stem cell-associated genes, including, for example, Oct-4 (also known as Oct-3/4 or Pouf51), Soxl, Sox2, Sox3, Sox 15, Sox 18, NANOG, Klfl, Klf2, Klf4, Klf5, NR5A2, c-Myc, 1-Myc, n-Myc, Rem2, Tert, and LIN28. In one embodiment, reprogramming using the methods and compositions described herein can further comprise introducing one or more of Oct-3/4, a member of the Sox family, a member of the Klf family, and a

member of the Myc family to a somatic cell. In one embodiment, the methods and compositions described herein further comprise introducing one or more of each of Oct-4, Sox2, Nanog, c-MYC and Klf4 for reprogramming. As noted above, the exact method used for reprogramming is not necessarily critical to the methods and compositions described herein. However, where cells differentiated from the reprogrammed cells are to be used in, *e.g.*, human therapy, in one embodiment the reprogramming is not effected by a method that alters the genome. Thus, in such embodiments, reprogramming is achieved, *e.g.*, without the use of viral or plasmid vectors.

[00316] The efficiency of reprogramming (*i.e.*, the number of reprogrammed cells) derived from a population of starting cells can be enhanced by the addition of various agents, *e.g.*, small molecules, as shown by Shi *et al.*, Cell-Stem Cell 2:525-528 (2008); Huangfu *et al.*, Nature Biotechnology 26(7):795-797 (2008) and Marson *et al.*, Cell-Stem Cell 3: 132-135 (2008). Thus, an agent or combination of agents that enhance the efficiency or rate of induced pluripotent stem cell production can be used in the production of patient-specific or disease-specific iPSCs. Some non-limiting examples of agents that enhance reprogramming efficiency include soluble Wnt, Wnt conditioned media, BIX-01294 (a G9a histone methyltransferase), PD0325901 (a MEK inhibitor), DNA methyltransferase inhibitors, histone deacetylase (HDAC) inhibitors, valproic acid, 5'-azacytidine, dexamethasone, suberoylanilide, hydroxamic acid (SAHA), vitamin C, and trichostatin (TSA), among others.

[00317] Other non-limiting examples of reprogramming enhancing agents include: Suberoylanilide Hydroxamic Acid (SAHA (*e.g.*, MK0683, vorinostat) and other hydroxamic acids), BML-210, Depudecin (*e.g.*, (-)-Depudecin), HC Toxin, Nullscript (4-(l,3-Dioxo-lH,3H-benzo[de]isoquinolin-2-yl)-N-hydroxybutanamide), Phenylbutyrate (*e.g.*, sodium phenylbutyrate) and Valproic Acid ((VP A) and other short chain fatty acids), Scriptaid, Suramin Sodium, Trichostatin A (TSA), APHA Compound 8, Apicidin, Sodium Butyrate, pivaloyloxymethyl butyrate (Pivanex, AN-9), Trapoxin B, Chlamydocin, Depsipeptide (also known as FR901228 or FK228), benzamides (*e.g.*, CI-994 (*e.g.*, N-acetyl dinaline) and MS-27-275), MGCD0103, NVP-LAQ-824, CBHA (m-carboxycinnaminic acid bishydroxamic acid),

JNJ16241199, Tubacin, A-161906, proxamide, oxamflatin, 3-Cl-UCHA (*e.g.*, 6-(3-chlorophenylureido)caproic hydroxamic acid), AOE (2-amino-8-oxo-9, 10-epoxydecanoic acid), CHAP31 and CHAP 50. Other reprogramming enhancing agents include, for example, dominant negative forms of the HDACs (*e.g.*, catalytically inactive forms), siRNA inhibitors of the HDACs, and antibodies that specifically bind to the HDACs. Such inhibitors are available, *e.g.*, from BIOMOL International, Fukasawa, Merck Biosciences, Novartis, Gloucester Pharmaceuticals, Titan Pharmaceuticals, MethylGene, and Sigma Aldrich.

[00318] To confirm the induction of pluripotent stem cells for use with the methods described herein, isolated clones can be tested for the expression of a stem cell marker. Such expression in a cell derived from a somatic cell identifies the cells as induced pluripotent stem cells. Stem cell markers are selected from the non-limiting group including SSEA3, SSEA4, CD9, Nanog, Fbxl5, Ecatl, Esgl, Eras, Gdf3, Fgf4, Cripto, Daxl, Zpf296, Slc2a3, Rexl, Utfl, and Natl. In one embodiment, a cell that expresses Oct4 or Nanog is identified as pluripotent. Methods for detecting the expression of such markers can include, for example, RT-PCR and immunological methods that detect the presence of the encoded polypeptides, such as Western blots or flow cytometric analyses. In some embodiments, detection involves not only RT-PCR, but also includes detection of protein markers. Intracellular markers may be best identified via RT-PCR, or protein detection methods such as immunocytochemistry, while cell surface markers are readily identified, *e.g.*, by immunocytochemistry.

[00319] The pluripotent stem cell character of isolated cells can be confirmed by tests evaluating the ability of the iPSCs to differentiate into cells of each of the three germ layers. As one example, teratoma formation in nude mice can be used to evaluate the pluripotent character of the isolated clones. The cells are introduced into nude mice and histology and/or immunohistochemistry is performed on a tumor arising from the cells. The growth of a tumor comprising cells from all three germ layers, for example, further indicates that the cells are pluripotent stem cells.

[00320] Hepatocytes

[00321] In some embodiments, the genetically engineered human cells described herein are hepatocytes. A hepatocyte is a cell of the main parenchymal

tissue of the liver. Hepatocytes make up 70-85% of the liver's mass. These cells are involved in: protein synthesis; protein storage; transformation of carbohydrates; synthesis of cholesterol, bile salts and phospholipids; detoxification, modification, and excretion of exogenous and endogenous substances; and initiation of formation and secretion of bile.

[00322] G6PC is primarily expressed in hepatocytes (parenchymal liver cells) with secondary expression in the cells of the kidney, intestine and salivary glands. Therefore, the correction of G6PC is primarily targeted at hepatocytes and the liver, as well as the secondary sites of expression that are associated with clinical manifestation, for example the kidney.

[00323] Creating patient specific iPSCs

[00324] One step of the *ex vivo* methods of the invention involves creating a patient specific iPS cell, patient specific iPS cells, or a patient specific iPS cell line. There are many established methods in the art for creating patient specific iPS cells, as described in Takahashi and Yamanaka 2006; Takahashi, Tanabe *et al*. 2007. For example, the creating step comprises: a) isolating a somatic cell, such as a skin cell or fibroblast from the patient; and b) introducing a set of pluripotency-associated genes into the somatic cell in order to induce the cell to become a pluripotent stem cell. In some embodiments, the set of pluripotency-associated genes is one or more of the genes selected from the group consisting of OCT4, SOX2, KLF4, Lin28, NANOG, and cMYC.

[00325] Performing a biopsy or aspirate of the patient's liver or bone marrow

[00326] A biopsy or aspirate is a sample of tissue or fluid taken from the body. There are many different kinds of biopsies or aspirates. Nearly all of them involve using a sharp tool to remove a small amount of tissue. If the biopsy will be on the skin or other sensitive area, numbing medicine is applied first. A biopsy or aspirate may be performed according to any of the known methods in the art. For example, in a liver biopsy, a needle is injected into the liver through the skin of the belly, capturing the liver tissue. For example, in a bone marrow aspirate, a large needle is used to enter the pelvis bone to collect bone marrow.

[00327] Isolating a liver specific progenitor cell or primary hepatocyte

[00328] Liver specific progenitor cells and primary hepatocytes may be isolated according to any method known in the art. For example, human hepatocytes are isolated from fresh surgical specimens (e.g., an autologous sample). Healthy liver tissue is used to isolate hepatocytes by collagenase digestion. The obtained cell suspension is filtered through a 100-mm nylon mesh and sedimented by centrifugation at 50g for 5 minutes, resuspended, and washed two to three times in cold wash medium. Human liver stem cells are obtained by culturing under stringent conditions of hepatocytes obtained from fresh liver preparations. Hepatocytes seeded on collagen-coated plates are cultured for 2 weeks. After 2 weeks, surviving cells are removed, and characterized for expression of stem cells markers (Herrera *et al*, STEM CELLS 2006;24: 2840 –2850).

[00329] Isolating a mesenchymal stem cell

[00330] Mesenchymal stem cells may be isolated according to any method known in the art, such as from a patient's bone marrow or peripheral blood. For example, marrow aspirate is collected into a syringe with heparin. Cells are washed and centrifuged on a Percoll™. Cells, such as blood cells, liver cells, interstitial cells, macrophages, mast cells, and thymocytes, are separated using Percoll™. The cells are cultured in Dulbecco's modified Eagle's medium (DMEM) (low glucose) containing 10% fetal bovine serum (FBS) (Pittinger MF, Mackay AM, Beck SC *et al*., Science 1999; 284:143–147).

[00331] Genome Editing

[00332] Genome editing generally refers to the process of modifying the nucleotide sequence of a genome, preferably in a precise or pre-determined manner. Examples of methods of genome editing described herein include methods of using site-directed nucleases to cut deoxyribonucleic acid (DNA) at precise target locations in the genome, thereby creating double-strand or single-strand DNA breaks at particular locations within the genome. Such breaks can be and regularly are repaired by natural, endogenous cellular processes, such as homology-directed repair (HDR) and non-homologous end-joining (NHEJ), as recently reviewed in Cox *et al*., Nature Medicine 21(2), 121-31 (2015). These two main DNA repair processes consist of a family of alternative pathways. NHEJ

directly joins the DNA ends resulting from a double-strand break, sometimes with the loss or addition of nucleotide sequence, which may disrupt or enhance gene expression. HDR utilizes a homologous sequence, or donor sequence, as a template for inserting a defined DNA sequence at the break point. The homologous sequence may be in the endogenous genome, such as a sister chromatid. Alternatively, the donor may be an exogenous nucleic acid, such as a plasmid, a single-strand oligonucleotide, a double-stranded oligonucleotide, a duplex oligonucleotide or a virus, that has regions of high homology with the nuclease-cleaved locus, but which may also contain additional sequence or sequence changes including deletions that can be incorporated into the cleaved target locus. A third repair mechanism is microhomology-mediated end joining (MMEJ), also referred to as "Alternative NHEJ", in which the genetic outcome is similar to NHEJ in that small deletions and insertions can occur at the cleavage site. MMEJ makes use of homologous sequences of a few basepairs flanking the DNA break site to drive a more favored DNA end joining repair outcome, and recent reports have further elucidated the molecular mechanism of this process; see, *e.g.*, Cho and Greenberg, Nature 518, 174-76 (2015); Kent *et a*l., Nature Structural and Molecular Biology, Adv. Online doi:10.1038/nsmb.2961(2015); Mateos-Gomez *et al.*, Nature 518, 254-57 (2015); Ceccaldi *et al.*, Nature 528, 258-62 (2015). In some instances it may be possible to predict likely repair outcomes based on analysis of potential microhomologies at the site of the DNA break.

[00333] Each of these genome editing mechanisms can be used to create desired genomic alterations. A step in the genome editing process is to create one or two DNA breaks, the latter as double-strand breaks or as two single-stranded breaks, in the target locus as close as possible to the site of intended mutation. This can be achieved via the use of site-directed polypeptides, as described and illustrated herein.

[00334] Site-directed polypeptides, such as a DNA endonuclease, can introduce double-strand breaks or single-strand breaks in nucleic acids, *e.g.*, genomic DNA. The double-strand break can stimulate a cell's endogenous DNA-repair pathways (*e.g.*, homology-dependent repair or non-homologous end joining or alternative non-homologous end joining (A-NHEJ) or microhomology-mediated end joining).

NHEJ can repair cleaved target nucleic acid without the need for a homologous template. This can sometimes result in small deletions or insertions (indels) in the target nucleic acid at the site of cleavage, and can lead to disruption or alteration of gene expression. HDR can occur when a homologous repair template, or donor, is available. The homologous donor template comprises sequences that are homologous to sequences flanking the target nucleic acid cleavage site. The sister chromatid is generally used by the cell as the repair template. However, for the purposes of genome editing, the repair template is often supplied as an exogenous nucleic acid, such as a plasmid, duplex oligonucleotide, single-strand oligonucleotide, double-stranded oligonucleotide, or viral nucleic acid. With exogenous donor templates, it is common to introduce an additional nucleic acid sequence (such as a transgene) or modification (such as a single or multiple base change or a deletion) between the flanking regions of homology so that the additional or altered nucleic acid sequence also becomes incorporated into the target locus. MMEJ results in a genetic outcome that is similar to NHEJ in that small deletions and insertions can occur at the cleavage site. MMEJ makes use of homologous sequences of a few basepairs flanking the cleavage site to drive a favored end-joining DNA repair outcome. In some instances it may be possible to predict likely repair outcomes based on analysis of potential microhomologies in the nuclease target regions.

[00335] Thus, in some cases, homologous recombination is used to insert an exogenous polynucleotide sequence into the target nucleic acid cleavage site. An exogenous polynucleotide sequence is termed a donor polynucleotide (or donor or donor sequence or polynucleotide donor template) herein. In some embodiments, the donor polynucleotide, a portion of the donor polynucleotide, a copy of the donor polynucleotide, or a portion of a copy of the donor polynucleotide is inserted into the target nucleic acid cleavage site. In some embodiments, the donor polynucleotide is an exogenous polynucleotide sequence, *i.e.*, a sequence that does not naturally occur at the target nucleic acid cleavage site.

[00336] The modifications of the target DNA due to NHEJ and/or HDR can lead to, for example, mutations, deletions, alterations, integrations, gene correction, gene replacement, gene tagging, transgene insertion, nucleotide deletion, gene

disruption, translocations and/or gene mutation. The processes of deleting genomic DNA and integrating non-native nucleic acid into genomic DNA are examples of genome editing.

[00337] CRISPR Endonuclease System

[00338] A CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) genomic locus can be found in the genomes of many prokaryotes (*e.g.*, bacteria and archaea). In prokaryotes, the CRISPR locus encodes products that function as a type of immune system to help defend the prokaryotes against foreign invaders, such as virus and phage. There are three stages of CRISPR locus function: integration of new sequences into the CRISPR locus, expression of CRISPR RNA (crRNA), and silencing of foreign invader nucleic acid. Five types of CRISPR systems (*e.g.*, Type I, Type II, Type III, Type U, and Type V) have been identified.

[00339] A CRISPR locus includes a number of short repeating sequences referred to as "repeats." When expressed, the repeats can form secondary hairpin structures (e.g., hairpins) and/or comprise unstructured single-stranded sequences. The repeats usually occur in clusters and frequently diverge between species. The repeats are regularly interspaced with unique intervening sequences referred to as "spacers," resulting in a repeat-spacer-repeat locus architecture. The spacers are identical to or have high homology with known foreign invader sequences. A spacer-repeat unit encodes a crisprRNA (crRNA), which is processed into a mature form of the spacer-repeat unit. A crRNA comprises a "seed" or spacer sequence that is involved in targeting a target nucleic acid (in the naturally occurring form in prokaryotes, the spacer sequence targets the foreign invader nucleic acid). A spacer sequence is located at the 5' or 3' end of the crRNA.

[00340] A CRISPR locus also comprises polynucleotide sequences encoding CRISPR Associated (Cas) genes. Cas genes encode endonucleases involved in the biogenesis and the interference stages of crRNA function in prokaryotes. Some Cas genes comprise homologous secondary and/or tertiary structures.

[00341] Type II CRISPR Systems

[00342] crRNA biogenesis in a Type II CRISPR system in nature requires a trans-activating CRISPR RNA (tracrRNA). The tracrRNA is modified by

endogenous RNaseIII, and then hybridizes to a crRNA repeat in the pre-crRNA array. Endogenous RNaseIII is recruited to cleave the pre-crRNA. Cleaved crRNAs are subjected to exoribonuclease trimming to produce the mature crRNA form (*e.g.*, 5' trimming). The tracrRNA remains hybridized to the crRNA, and the tracrRNA and the crRNA associate with a site-directed polypeptide (*e.g.*, Cas9). The crRNA of the crRNA-tracrRNA-Cas9 complex guides the complex to a target nucleic acid to which the crRNA can hybridize. Hybridization of the crRNA to the target nucleic acid activates Cas9 for targeted nucleic acid cleavage. The target nucleic acid in a Type II CRISPR system is referred to as a protospacer adjacent motif (PAM). In nature, the PAM is essential to facilitate binding of a site-directed polypeptide (*e.g.*, Cas9) to the target nucleic acid. Type II systems (also referred to as Nmeni or CASS4) are further subdivided into Type II-A (CASS4) and II-B (CASS4a). Jinek *et al.*, *Science, 337*(6096):816-821 (2012) showed that the CRISPR/Cas9 system is useful for RNA-programmable genome editing, and international patent application publication number WO2013/176772 provides numerous examples and applications of the CRISPR/Cas endonuclease system for site-specific gene editing.

[00343] Type V CRISPR Systems

[00344] Type V CRISPR systems have several important differences from Type II systems. For example, Cpf1 is a single RNA-guided endonuclease that, in contrast to Type II systems, lacks tracrRNA. In fact, Cpf1-associated CRISPR arrays are processed into mature crRNAS without the requirement of an additional trans-activating tracrRNA. The Type V CRISPR array is processed into short mature crRNAs of 42-44 nucleotides in length, with each mature crRNA beginning with 19 nucleotides of direct repeat followed by 23-25 nucleotides of spacer sequence. In contrast, mature crRNAs in Type II systems start with 20-24 nucleotides of spacer sequence followed by about 22 nucleotides of direct repeat. Also, Cpf1 utilizes a T-rich protospacer-adjacent motif such that Cpf1-crRNA complexes efficiently cleave target DNA preceded by a short T-rich PAM, which is in contrast to the G-rich PAM following the target DNA for Type II systems. Thus, Type V systems cleave at a point that is distant from the PAM, while Type II systems cleave at a point that is adjacent to the PAM. In addition, in contrast to

Type II systems, Cpf1 cleaves DNA via a staggered DNA double-stranded break with a 4 or 5 nucleotide 5' overhang. Type II systems cleave via a blunt double-stranded break. Similar to Type II systems, Cpf1 contains a predicted RuvC-like endonuclease domain, but lacks a second HNH endonuclease domain, which is in contrast to Type II systems.

[00345] Cas Genes/Polypeptides and Protospacer Adjacent Motifs

[00346] Exemplary CRISPR/Cas polypeptides include the Cas9 polypeptides in Fig. 1 of Fonfara *et al.*, *Nucleic Acids Research, 42*: 2577-2590 (2014). The CRISPR/Cas gene naming system has undergone extensive rewriting since the Cas genes were discovered. Fig. 5 of Fonfara, *supra*, provides PAM sequences for the Cas9 polypeptides from various species.

[00347] Site-Directed Polypeptides

[00348] A site-directed polypeptide is a nuclease used in genome editing to cleave DNA. The site-directed may be administered to a cell or a patient as either: one or more polypeptides, or one or more mRNAs encoding the polypeptide.

[00349] In the context of a CRISPR/Cas or CRISPR/Cpf1 system, the site-directed polypeptide can bind to a guide RNA that, in turn, specifies the site in the target DNA to which the polypeptide is directed. In embodiments of CRISPR/Cas or CRISPR/Cpf1 systems herein, the site-directed polypeptide is an endonuclease, such as a DNA endonuclease.

[00350] In some embodiments, a site-directed polypeptide comprises a plurality of nucleic acid-cleaving (*i.e.*, nuclease) domains. Two or more nucleic acid-cleaving domains can be linked together via a linker. In some embodiments, the linker comprises a flexible linker. Linkers may comprise 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, 30, 35, 40 or more amino acids in length.

[00351] Naturally-occurring wild-type Cas9 enzymes comprise two nuclease domains, a HNH nuclease domain and a RuvC domain. Herein, the "Cas9" refers to both naturally-occurring and recombinant Cas9s. Cas9 enzymes contemplated herein comprise a HNH or HNH-like nuclease domain, and/or a RuvC or RuvC-like nuclease domain.

[00352] HNH or HNH-like domains comprise a McrA-like fold. HNH or HNH-like domains comprises two antiparallel β-strands and an α-helix. HNH or HNH-like domains comprises a metal binding site (*e.g.*, a divalent cation binding site). HNH or HNH-like domains can cleave one strand of a target nucleic acid (*e.g.*, the complementary strand of the crRNA targeted strand).

[00353] RuvC or RuvC-like domains comprise an RNaseH or RNaseH-like fold. RuvC/RNaseH domains are involved in a diverse set of nucleic acid-based functions including acting on both RNA and DNA. The RNaseH domain comprises 5 β-strands surrounded by a plurality of α-helices. RuvC/RNaseH or RuvC/RNaseH-like domains comprise a metal binding site (*e.g.*, a divalent cation binding site). RuvC/RNaseH or RuvC/RNaseH-like domains can cleave one strand of a target nucleic acid (*e.g.*, the non-complementary strand of a double-stranded target DNA).

[00354] Site-directed polypeptides can introduce double-strand breaks or single-strand breaks in nucleic acids, *e.g.*, genomic DNA. The double-strand break can stimulate a cell's endogenous DNA-repair pathways (*e.g.*, homology-dependent repair (HDR) or non-homologous end joining (NHEJ) or alternative non-homologous end joining (A-NHEJ) or microhomology-mediated end joining (MMEJ)). NHEJ can repair cleaved target nucleic acid without the need for a homologous template. This can sometimes result in small deletions or insertions (indels) in the target nucleic acid at the site of cleavage, and can lead to disruption or alteration of gene expression. HDR can occur when a homologous repair template, or donor, is available. The homologous donor template comprises sequences that are homologous to sequences flanking the target nucleic acid cleavage site. The sister chromatid is generally used by the cell as the repair template. However, for the purposes of genome editing, the repair template is often supplied as an exogenous nucleic acid, such as a plasmid, duplex oligonucleotide, single-strand oligonucleotide or viral nucleic acid. With exogenous donor templates, it is common to introduce an additional nucleic acid sequence (such as a transgene) or modification (such as a single or multiple base change or a deletion) between the flanking regions of homology so that the additional or altered nucleic acid sequence also becomes incorporated into the target locus. MMEJ results in a genetic

outcome that is similar to NHEJ in that small deletions and insertions can occur at the cleavage site. MMEJ makes use of homologous sequences of a few basepairs flanking the cleavage site to drive a favored end-joining DNA repair outcome. In some instances it may be possible to predict likely repair outcomes based on analysis of potential microhomologies in the nuclease target regions.

[00355] Thus, in some cases, homologous recombination is used to insert an exogenous polynucleotide sequence into the target nucleic acid cleavage site. An exogenous polynucleotide sequence is termed a donor polynucleotide (or donor or donor sequence) herein. In some embodiments, the donor polynucleotide, a portion of the donor polynucleotide, a copy of the donor polynucleotide, or a portion of a copy of the donor polynucleotide is inserted into the target nucleic acid cleavage site. In some embodiments, the donor polynucleotide is an exogenous polynucleotide sequence, *i.e.*, a sequence that does not naturally occur at the target nucleic acid cleavage site.

[00356] The modifications of the target DNA due to NHEJ and/or HDR can lead to, for example, mutations, deletions, alterations, integrations, gene correction, gene replacement, gene tagging, transgene insertion, nucleotide deletion, gene disruption, translocations and/or gene mutation. The processes of deleting genomic DNA and integrating non-native nucleic acid into genomic DNA are examples of genome editing.

[00357] In some embodiments, the site-directed polypeptide comprises an amino acid sequence having at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or 100% amino acid sequence identity to a wild-type exemplary site-directed polypeptide [*e.g.*, Cas9 from *S. pyogenes*, US2014/0068797 Sequence ID No. 8 or Sapranauskas *et al., Nucleic Acids Res, 39*(21): 9275-9282 (2011)], and various other site-directed polypeptides).

[00358] In some embodiments, the site-directed polypeptide comprises an amino acid sequence having at least 10%, at least 15%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 99%, or 100% amino acid sequence

identity to the nuclease domain of a wild-type exemplary site-directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*).

[00359] In some embodiments, a site-directed polypeptide comprises at least 70, 75, 80, 85, 90, 95, 97, 99, or 100% identity to a wild-type site-directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*) over 10 contiguous amino acids. In some embodiments, a site-directed polypeptide comprises at most: 70, 75, 80, 85, 90, 95, 97, 99, or 100% identity to a wild-type site-directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*) over 10 contiguous amino acids. In some embodiments, a site-directed polypeptide comprises at least: 70, 75, 80, 85, 90, 95, 97, 99, or 100% identity to a wild-type site-directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*) over 10 contiguous amino acids in a HNH nuclease domain of the site-directed polypeptide. In some embodiments, a site-directed polypeptide comprises at most: 70, 75, 80, 85, 90, 95, 97, 99, or 100% identity to a wild-type site-directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*) over 10 contiguous amino acids in a HNH nuclease domain of the site-directed polypeptide. In some embodiments, a site-directed polypeptide comprises at least: 70, 75, 80, 85, 90, 95, 97, 99, or 100% identity to a wild-type site-directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*) over 10 contiguous amino acids in a RuvC nuclease domain of the site-directed polypeptide. In some embodiments, a site-directed polypeptide comprises at most: 70, 75, 80, 85, 90, 95, 97, 99, or 100% identity to a wild-type site-directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*) over 10 contiguous amino acids in a RuvC nuclease domain of the site-directed polypeptide.

[00360] In some embodiments, the site-directed polypeptide comprises a modified form of a wild-type exemplary site-directed polypeptide. The modified form of the wild- type exemplary site-directed polypeptide comprises a mutation that reduces the nucleic acid-cleaving activity of the site-directed polypeptide. In some embodiments, the modified form of the wild-type exemplary site-directed polypeptide has less than 90%, less than 80%, less than 70%, less than 60%, less than 50%, less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, or less than 1% of the nucleic acid-cleaving activity of the wild-type exemplary site-directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*). The modified form of the site-directed polypeptide can have no substantial nucleic acid-cleaving

activity. When a site-directed polypeptide is a modified form that has no substantial nucleic acid-cleaving activity, it is referred to herein as "enzymatically inactive."

[00361] In some embodiments, the modified form of the site-directed polypeptide comprises a mutation such that it can induce a single-strand break (SSB) on a target nucleic acid (*e.g.*, by cutting only one of the sugar-phosphate backbones of a double-strand target nucleic acid). In some embodiments, the mutation results in less than 90%, less than 80%, less than 70%, less than 60%, less than 50%, less than 40%, less than 30%, less than 20%, less than 10%, less than 5%, or less than 1% of the nucleic acid-cleaving activity in one or more of the plurality of nucleic acid-cleaving domains of the wild-type site directed polypeptide (*e.g.*, Cas9 from *S. pyogenes*, *supra*). In some embodiments, the mutation results in one or more of the plurality of nucleic acid-cleaving domains retaining the ability to cleave the complementary strand of the target nucleic acid, but reducing its ability to cleave the non-complementary strand of the target nucleic acid. In some embodiments, the mutation results in one or more of the plurality of nucleic acid-cleaving domains retaining the ability to cleave the non-complementary strand of the target nucleic acid, but reducing its ability to cleave the complementary strand of the target nucleic acid. For example, residues in the wild-type exemplary *S. pyogenes* Cas9 polypeptide, such as Asp10, His840, Asn854 and Asn856, are mutated to inactivate one or more of the plurality of nucleic acid-cleaving domains (*e.g.*, nuclease domains). In some embodiments, the residues to be mutated correspond to residues Asp10, His840, Asn854 and Asn856 in the wild-type exemplary *S. pyogenes* Cas9 polypeptide (*e.g.*, as determined by sequence and/or structural alignment). Non-limiting examples of mutations include D10A, H840A, N854A or N856A. One skilled in the art will recognize that mutations other than alanine substitutions are suitable.

[00362] In some embodiments, a D10A mutation is combined with one or more of H840A, N854A, or N856A mutations to produce a site-directed polypeptide substantially lacking DNA cleavage activity. In some embodiments, a H840A mutation is combined with one or more of D10A, N854A, or N856A mutations to produce a site-directed polypeptide substantially lacking DNA cleavage activity. In some embodiments, a N854A mutation is combined with one or more of H840A,

D10A, or N856A mutations to produce a site-directed polypeptide substantially lacking DNA cleavage activity. In some embodiments, a N856A mutation is combined with one or more of H840A, N854A, or D10A mutations to produce a site-directed polypeptide substantially lacking DNA cleavage activity. Site-directed polypeptides that comprise one substantially inactive nuclease domain are referred to as “nickases”.

[00363] Nickase variants of RNA-guided endonucleases, for example Cas9, can be used to increase the specificity of CRISPR-mediated genome editing. Wild type Cas9 is typically guided by a single guide RNA designed to hybridize with a specified ~20 nucleotide sequence in the target sequence (such as an endogenous genomic locus). However, several mismatches can be tolerated between the guide RNA and the target locus, effectively reducing the length of required homology in the target site to, for example, as little as 13 nt of homology, and thereby resulting in elevated potential for binding and double-strand nucleic acid cleavage by the CRISPR/Cas9 complex elsewhere in the target genome – also known as off-target cleavage. Because nickase variants of Cas9 each only cut one strand, in order to create a double-strand break it is necessary for a pair of nickases to bind in close proximity and on opposite strands of the target nucleic acid, thereby creating a pair of nicks, which is the equivalent of a double-strand break. This requires that two separate guide RNAs - one for each nickase - must bind in close proximity and on opposite strands of the target nucleic acid. This requirement essentially doubles the minimum length of homology needed for the double-strand break to occur, thereby reducing the likelihood that a double-strand cleavage event will occur elsewhere in the genome, where the two guide RNA sites - if they exist - are unlikely to be sufficiently close to each other to enable the double-strand break to form. As described in the art, nickases can also be used to promote HDR versus NHEJ. HDR can be used to introduce selected changes into target sites in the genome through the use of specific donor sequences that effectively mediate the desired changes. Descriptions of various CRISPR/Cas systems for use in gene editing can be found, *e.g.*, in international patent application publication number WO2013/176772, and in *Nature Biotechnology 32*, 347–355 (2014), and references cited therein.

[00364] Mutations contemplated include substitutions, additions, and deletions, or any combination thereof. In some embodiments, the mutation converts the mutated amino acid to alanine. In some embodiments, the mutation converts the mutated amino acid to another amino acid (*e.g.*, glycine, serine, threonine, cysteine, valine, leucine, isoleucine, methionine, proline, phenylalanine, tyrosine, tryptophan, aspartic acid, glutamic acid, asparagines, glutamine, histidine, lysine, or arginine). In some embodiments, the mutation converts the mutated amino acid to a non-natural amino acid (*e.g.*, selenomethionine). In some embodiments, the mutation converts the mutated amino acid to amino acid mimics (*e.g.*, phosphomimics). In some embodiments, the mutation is a conservative mutation. For example, the mutation can convert the mutated amino acid to amino acids that resemble the size, shape, charge, polarity, conformation, and/or rotamers of the mutated amino acids (*e.g.*, cysteine/serine mutation, lysine/asparagine mutation, histidine/phenylalanine mutation). In some embodiments, the mutation causes a shift in reading frame and/or the creation of a premature stop codon. In some embodiments, mutations cause changes to regulatory regions of genes or loci that affect expression of one or more genes.

[00365] In some embodiments, the site-directed polypeptide (*e.g.*, variant, mutated, enzymatically inactive and/or conditionally enzymatically inactive site-directed polypeptide) targets nucleic acid. In some embodiments, the site-directed polypeptide (*e.g.*, variant, mutated, enzymatically inactive and/or conditionally enzymatically inactive endoribonuclease) targets DNA. In some embodiments, the site-directed polypeptide (*e.g.*, variant, mutated, enzymatically inactive and/or conditionally enzymatically inactive endoribonuclease) targets RNA.

[00366] In some embodiments, the site-directed polypeptide comprises one or more non-native sequences (*e.g.*, the site-directed polypeptide is a fusion protein).

[00367] In some embodiments, the site-directed polypeptide comprises an amino acid sequence comprising at least 15% amino acid identity to a Cas9 from a bacterium (*e.g.*, *S. pyogenes*), a nucleic acid binding domain, and two nucleic acid cleaving domains (*i.e.*, a HNH domain and a RuvC domain).

[00368] In some embodiments, the site-directed polypeptide comprises an amino acid sequence comprising at least 15% amino acid identity to a Cas9 from a

bacterium (*e.g.*, *S. pyogenes*), and two nucleic acid cleaving domains (*i.e.*, a HNH domain and a RuvC domain).

[00369] In some embodiments, the site-directed polypeptide comprises an amino acid sequence comprising at least 15% amino acid identity to a Cas9 from a bacterium (*e.g.*, *S. pyogenes*), and two nucleic acid cleaving domains, wherein one or both of the nucleic acid cleaving domains comprise at least 50% amino acid identity to a nuclease domain from Cas9 from a bacterium (*e.g.*, *S. pyogenes*).

[00370] In some embodiments, the site-directed polypeptide comprises an amino acid sequence comprising at least 15% amino acid identity to a Cas9 from a bacterium (*e.g.*, *S. pyogenes*), two nucleic acid cleaving domains (*i.e.*, a HNH domain and a RuvC domain), and non-native sequence (for example, a nuclear localization signal) or a linker linking the site-directed polypeptide to a non-native sequence.

[00371] In some embodiments, the site-directed polypeptide comprises an amino acid sequence comprising at least 15% amino acid identity to a Cas9 from a bacterium (*e.g.*, *S. pyogenes*), two nucleic acid cleaving domains (*i.e.*, a HNH domain and a RuvC domain), wherein the site-directed polypeptide comprises a mutation in one or both of the nucleic acid cleaving domains that reduces the cleaving activity of the nuclease domains by at least 50%.

[00372] In some embodiments, the site-directed polypeptide comprises an amino acid sequence comprising at least 15% amino acid identity to a Cas9 from a bacterium (*e.g.*, *S. pyogenes*), and two nucleic acid cleaving domains (*i.e.*, a HNH domain and a RuvC domain), wherein one of the nuclease domains comprises mutation of aspartic acid 10, and/or wherein one of the nuclease domains comprises mutation of histidine 840, and wherein the mutation reduces the cleaving activity of the nuclease domain(s) by at least 50%.

[00373] In some embodiments of the invention, the one or more site-directed polypeptides, e.g. DNA endonucleases, include two nickases that together effect one double-strand break at a specific locus in the genome, or four nickases that together effect two double-strand breaks at specific loci in the genome. Alternatively, one site-directed polypeptide, e.g. DNA endonuclease, effects one double-strand break at a specific locus in the genome.

[00374] Genome-targeting Nucleic Acid

[00375] The present disclosure provides a genome-targeting nucleic acid that can direct the activities of an associated polypeptide (*e.g.*, a site-directed polypeptide) to a specific target sequence within a target nucleic acid. In some embodiments, the genome-targeting nucleic acid is an RNA. A genome-targeting RNA is referred to as a "guide RNA" or "gRNA" herein. A guide RNA comprises at least a spacer sequence that hybridizes to a target nucleic acid sequence of interest, and a CRISPR repeat sequence. In Type II systems, the gRNA also comprises a second RNA called the tracrRNA sequence. In the Type II guide RNA (gRNA), the CRISPR repeat sequence and tracrRNA sequence hybridize to each other to form a duplex. In the Type V guide RNA (gRNA), the crRNA forms a duplex. In both systems, the duplex binds a site-directed polypeptide, such that the guide RNA and site-direct polypeptide form a complex. The genome-targeting nucleic acid provides target specificity to the complex by virtue of its association with the site-directed polypeptide. The genome-targeting nucleic acid thus directs the activity of the site-directed polypeptide.

[00376] Exemplary guide RNAs include the spacer sequences in Figures 1-90, shown with the genome location of their target sequence and the associated Cas9 or Cpf1 cut site, wherein the genome location is based on the GRCh38/hg38 human genome assembly. As is understood by the person of ordinary skill in the art, each guide RNA is designed to include a spacer sequence complementary to its genomic target sequence. For example, each of the spacer sequences in Figures 1-90 may be put into a single RNA chimera or a crRNA (along with a corresponding tracrRNA). See Jinek *et al.*, Science, 337, 816-821 (2012) and Deltcheva *et al.*, Nature, 471, 602-607 (2011).

[00377] In some embodiments, the genome-targeting nucleic acid is a double-molecule guide RNA. In some embodiments, the genome-targeting nucleic acid is a single-molecule guide RNA.

[00378] A double-molecule guide RNA comprises two strands of RNA. The first strand comprises in the 5' to 3' direction, an optional spacer extension sequence, a spacer sequence and a minimum CRISPR repeat sequence. The second strand comprises a minimum tracrRNA sequence (complementary to the minimum

CRISPR repeat sequence), a 3' tracrRNA sequence and an optional tracrRNA extension sequence.

[00379] A single-molecule guide RNA (sgRNA) in a Type II system comprises, in the 5' to 3' direction, an optional spacer extension sequence, a spacer sequence, a minimum CRISPR repeat sequence, a single-molecule guide linker, a minimum tracrRNA sequence, a 3' tracrRNA sequence and an optional tracrRNA extension sequence. The optional tracrRNA extension may comprise elements that contribute additional functionality (*e.g.*, stability) to the guide RNA. The single-molecule guide linker links the minimum CRISPR repeat and the minimum tracrRNA sequence to form a hairpin structure. The optional tracrRNA extension comprises one or more hairpins.

[00380] A single-molecule guide RNA (sgRNA) in a Type V system comprises, in the 5' to 3' direction, a minimum CRISPR repeat sequence and a spacer sequence.

[00381] By way of illustration, guide RNAs used in the CRISPR/Cas system, or other smaller RNAs can be readily synthesized by chemical means, as illustrated below and described in the art. While chemical synthetic procedures are continually expanding, purifications of such RNAs by procedures such as high performance liquid chromatography (HPLC, which avoids the use of gels such as PAGE) tends to become more challenging as polynucleotide lengths increase significantly beyond a hundred or so nucleotides. One approach used for generating RNAs of greater length is to produce two or more molecules that are ligated together. Much longer RNAs, such as those encoding a Cas9 or Cpf1 endonuclease, are more readily generated enzymatically. Various types of RNA modifications can be introduced during or after chemical synthesis and/or enzymatic generation of RNAs, *e.g.*, modifications that enhance stability, reduce the likelihood or degree of innate immune response, and/or enhance other attributes, as described in the art.

[00382] Spacer Extension Sequence

[00383] In some embodiments of genome-targeting nucleic acids, a spacer extension sequence can provide stability and/or provide a location for modifications of a genome-targeting nucleic acid. A spacer extension sequence can modify on- or off-target activity or specificity. In some embodiments, a spacer extension sequence is provided. A spacer extension sequence may have a length of more

than 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400, 1000, 2000, 3000, 4000, 5000, 6000, or 7000 or more nucleotides. A spacer extension sequence may have a length of less than 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400, 1000, 2000, 3000, 4000, 5000, 6000, 7000 or more nucleotides. In some embodiments, a spacer extension sequence is less than 10 nucleotides in length. In some embodiments, a spacer extension sequence is between 10-30 nucleotides in length. In some embodiments, a spacer extension sequence is between 30-70 nucleotides in length.

[00384] In some embodiments, the spacer extension sequence comprises another moiety (*e.g.*, a stability control sequence, an endoribonuclease binding sequence, a ribozyme). In some embodiments, the moiety decreases or increases the stability of a nucleic acid targeting nucleic acid. In some embodiments, the moiety is a transcriptional terminator segment (*i.e.*, a transcription termination sequence). In some embodiments, the moiety functions in a eukaryotic cell. In some embodiments, the moiety functions in a prokaryotic cell. In some embodiments, the moiety functions in both eukaryotic and prokaryotic cells. Non-limiting examples of suitable moieties include: a 5' cap (*e.g.*, a 7-methylguanylate cap (m7 G)), a riboswitch sequence (*e.g.*, to allow for regulated stability and/or regulated accessibility by proteins and protein complexes), a sequence that forms a dsRNA duplex (*i.e.*, a hairpin), a sequence that targets the RNA to a subcellular location (*e.g.*, nucleus, mitochondria, chloroplasts, and the like), a modification or sequence that provides for tracking (*e.g.*, direct conjugation to a fluorescent molecule, conjugation to a moiety that facilitates fluorescent detection, a sequence that allows for fluorescent detection, etc.), and/or a modification or sequence that provides a binding site for proteins (*e.g.*, proteins that act on DNA, including transcriptional activators, transcriptional repressors, DNA methyltransferases, DNA demethylases, histone acetyltransferases, histone deacetylases, and the like).

[00385] Spacer Sequence

[00386] The spacer sequence hybridizes to a sequence in a target nucleic acid of interest. The spacer of a genome-targeting nucleic acid interacts with a target

nucleic acid in a sequence-specific manner via hybridization (*i.e.*, base pairing). The nucleotide sequence of the spacer thus varies depending on the sequence of the target nucleic acid of interest.

[00387] In a CRISPR/Cas system herein, the spacer sequence is designed to hybridize to a target nucleic acid that is located 5' of a PAM of the Cas9 enzyme used in the system. The spacer may perfectly match the target sequence or may have mismatches. Each Cas9 enzyme has a particular PAM sequence that it recognizes in a target DNA. For example, *S. pyogenes* recognizes in a target nucleic acid a PAM that comprises the sequence 5'-NRG-3', where R comprises either A or G, where N is any nucleotide and N is immediately 3' of the target nucleic acid sequence targeted by the spacer sequence.

[00388] In some embodiments, the target nucleic acid sequence comprises 20 nucleotides. In some embodiments, the target nucleic acid comprises less than 20 nucleotides. In some embodiments, the target nucleic acid comprises more than 20 nucleotides. In some embodiments, the target nucleic acid comprises at least: 5, 10, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30 or more nucleotides. In some embodiments, the target nucleic acid comprises at most: 5, 10, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 30 or more nucleotides. In some embodiments, the target nucleic acid sequence comprises 20 bases immediately 5' of the first nucleotide of the PAM. For example, in a sequence comprising 5'-NNNNNNNNNNNNNNNNNNNNNRG-3' (SEQ ID NO: 64,790), the target nucleic acid comprises the sequence that corresponds to the Ns, wherein N is any nucleotide, and the underlined NRG sequence is the *S. pyogenes* PAM.

[00389] In some embodiments, the spacer sequence that hybridizes to the target nucleic acid has a length of at least about 6 nucleotides (nt). The spacer sequence can be at least about 6 nt, at least about 10 nt, at least about 15 nt, at least about 18 nt, at least about 19 nt, at least about 20 nt, at least about 25 nt, at least about 30 nt, at least about 35 nt or at least about 40 nt, from about 6 nt to about 80 nt, from about 6 nt to about 50 nt, from about 6 nt to about 45 nt, from about 6 nt to about 40 nt, from about 6 nt to about 35 nt, from about 6 nt to about 30 nt, from about 6 nt to about 25 nt, from about 6 nt to about 20 nt, from about 6 nt to about 19 nt, from about 10 nt to about 50 nt, from about 10 nt to about 45 nt, from about

10 nt to about 40 nt, from about 10 nt to about 35 nt, from about 10 nt to about 30 nt, from about 10 nt to about 25 nt, from about 10 nt to about 20 nt, from about 10 nt to about 19 nt, from about 19 nt to about 25 nt, from about 19 nt to about 30 nt, from about 19 nt to about 35 nt, from about 19 nt to about 40 nt, from about 19 nt to about 45 nt, from about 19 nt to about 50 nt, from about 19 nt to about 60 nt, from about 20 nt to about 25 nt, from about 20 nt to about 30 nt, from about 20 nt to about 35 nt, from about 20 nt to about 40 nt, from about 20 nt to about 45 nt, from about 20 nt to about 50 nt, or from about 20 nt to about 60 nt. In some embodiments, the spacer sequence comprises 20 nucleotides. In some embodiments, the spacer comprises 19 nucleotides.

[00390] In some embodiments, the percent complementarity between the spacer sequence and the target nucleic acid is at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 97%, at least about 98%, at least about 99%, or 100%. In some embodiments, the percent complementarity between the spacer sequence and the target nucleic acid is at most about 30%, at most about 40%, at most about 50%, at most about 60%, at most about 65%, at most about 70%, at most about 75%, at most about 80%, at most about 85%, at most about 90%, at most about 95%, at most about 97%, at most about 98%, at most about 99%, or 100%. In some embodiments, the percent complementarity between the spacer sequence and the target nucleic acid is 100% over the six contiguous 5'-most nucleotides of the target sequence of the complementary strand of the target nucleic acid. In some embodiments, the percent complementarity between the spacer sequence and the target nucleic acid is at least 60% over about 20 contiguous nucleotides. The length of the spacer sequence and the target nucleic acid can differ by 1 to 6 nucleotides, which may be thought of as a bulge or bulges.

[00391] In some embodiments, a spacer sequence is designed or chosen using a computer program. The computer program can use variables, such as predicted melting temperature, secondary structure formation, predicted annealing temperature, sequence identity, genomic context, chromatin accessibility, % GC, frequency of genomic occurrence (*e.g.*, of sequences that are identical or are

similar but vary in one or more spots as a result of mismatch, insertion or deletion), methylation status, presence of SNPs, and the like.

[00392] Minimum CRISPR Repeat Sequence

[00393] In some embodiments, a minimum CRISPR repeat sequence is a sequence with at least about 30%, about 40%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or 100% sequence identity to a reference CRISPR repeat sequence (*e.g.*, crRNA from *S. pyogenes*).

[00394] A minimum CRISPR repeat sequence comprises nucleotides that can hybridize to a minimum tracrRNA sequence in a cell. The minimum CRISPR repeat sequence and a minimum tracrRNA sequence form a duplex, *i.e.* a base-paired double-stranded structure. Together, the minimum CRISPR repeat sequence and the minimum tracrRNA sequence bind to the site-directed polypeptide. At least a part of the minimum CRISPR repeat sequence hybridizes to the minimum tracrRNA sequence. In some embodiments, at least a part of the minimum CRISPR repeat sequence comprises at least about 30%, about 40%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or 100% complementary to the minimum tracrRNA sequence. In some embodiments, at least a part of the minimum CRISPR repeat sequence comprises at most about 30%, about 40%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or 100% complementary to the minimum tracrRNA sequence.

[00395] The minimum CRISPR repeat sequence can have a length from about 7 nucleotides to about 100 nucleotides. For example, the length of the minimum CRISPR repeat sequence is from about 7 nucleotides (nt) to about 50 nt, from about 7 nt to about 40 nt, from about 7 nt to about 30 nt, from about 7 nt to about 25 nt, from about 7 nt to about 20 nt, from about 7 nt to about 15 nt, from about 8 nt to about 40 nt, from about 8 nt to about 30 nt, from about 8 nt to about 25 nt, from about 8 nt to about 20 nt, from about 8 nt to about 15 nt, from about 15 nt to about 100 nt, from about 15 nt to about 80 nt, from about 15 nt to about 50 nt, from about 15 nt to about 40 nt, from about 15 nt to about 30 nt, or from about 15 nt to about 25 nt. In some embodiments, the minimum CRISPR repeat sequence is

approximately 9 nucleotides in length. In some embodiments, the minimum CRISPR repeat sequence is approximately 12 nucleotides in length.

[00396] In some embodiments, the minimum CRISPR repeat sequence is at least about 60% identical to a reference minimum CRISPR repeat sequence (*e.g.*, wild-type crRNA from *S. pyogenes*) over a stretch of at least 6, 7, or 8 contiguous nucleotides. For example, the minimum CRISPR repeat sequence is at least about 65% identical, at least about 70% identical, at least about 75% identical, at least about 80% identical, at least about 85% identical, at least about 90% identical, at least about 95% identical, at least about 98% identical, at least about 99% identical or 100% identical to a reference minimum CRISPR repeat sequence over a stretch of at least 6, 7, or 8 contiguous nucleotides.

[00397] Minimum tracrRNA Sequence

[00398] In some embodiments, a minimum tracrRNA sequence is a sequence with at least about 30%, about 40%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or 100% sequence identity to a reference tracrRNA sequence (*e.g.*, wild type tracrRNA from *S. pyogenes*).

[00399] A minimum tracrRNA sequence comprises nucleotides that hybridize to a minimum CRISPR repeat sequence in a cell. A minimum tracrRNA sequence and a minimum CRISPR repeat sequence form a duplex, *i.e.* a base-paired double-stranded structure. Together, the minimum tracrRNA sequence and the minimum CRISPR repeat bind to a site-directed polypeptide. At least a part of the minimum tracrRNA sequence can hybridize to the minimum CRISPR repeat sequence. In some embodiments, the minimum tracrRNA sequence is at least about 30%, about 40%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or 100% complementary to the minimum CRISPR repeat sequence.

[00400] The minimum tracrRNA sequence can have a length from about 7 nucleotides to about 100 nucleotides. For example, the minimum tracrRNA sequence can be from about 7 nucleotides (nt) to about 50 nt, from about 7 nt to about 40 nt, from about 7 nt to about 30 nt, from about 7 nt to about 25 nt, from about 7 nt to about 20 nt, from about 7 nt to about 15 nt, from about 8 nt to about

40 nt, from about 8 nt to about 30 nt, from about 8 nt to about 25 nt, from about 8 nt to about 20 nt, from about 8 nt to about 15 nt, from about 15 nt to about 100 nt, from about 15 nt to about 80 nt, from about 15 nt to about 50 nt, from about 15 nt to about 40 nt, from about 15 nt to about 30 nt or from about 15 nt to about 25 nt long. In some embodiments, the minimum tracrRNA sequence is approximately 9 nucleotides in length. In some embodiments, the minimum tracrRNA sequence is approximately 12 nucleotides. In some embodiments, the minimum tracrRNA consists of tracrRNA nt 23-48 described in Jinek *et al., supra*.

[00401] In some embodiments, the minimum tracrRNA sequence is at least about 60% identical to a reference minimum tracrRNA (*e.g.*, wild type, tracrRNA from *S. pyogenes*) sequence over a stretch of at least 6, 7, or 8 contiguous nucleotides. For example, the minimum tracrRNA sequence is at least about 65% identical, about 70% identical, about 75% identical, about 80% identical, about 85% identical, about 90% identical, about 95% identical, about 98% identical, about 99% identical or 100% identical to a reference minimum tracrRNA sequence over a stretch of at least 6, 7, or 8 contiguous nucleotides.

[00402] In some embodiments, the duplex between the minimum CRISPR RNA and the minimum tracrRNA comprises a double helix. In some embodiments, the duplex between the minimum CRISPR RNA and the minimum tracrRNA comprises at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more nucleotides. In some embodiments, the duplex between the minimum CRISPR RNA and the minimum tracrRNA comprises at most about 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more nucleotides.

[00403] In some embodiments, the duplex comprises a mismatch (*i.e.*, the two strands of the duplex are not 100% complementary). In some embodiments, the duplex comprises at least about 1, 2, 3, 4, or 5 or mismatches. In some embodiments, the duplex comprises at most about 1, 2, 3, 4, or 5 or mismatches. In some embodiments, the duplex comprises no more than 2 mismatches.

[00404] Bulges

[00405] In some embodiments, there is a “bulge” in the duplex between the minimum CRISPR RNA and the minimum tracrRNA. The bulge is an unpaired region of nucleotides within the duplex. In some embodiments, the bulge

contributes to the binding of the duplex to the site-directed polypeptide. A bulge comprises, on one side of the duplex, an unpaired 5'-XXXY-3' where X is any purine and Y comprises a nucleotide that can form a wobble pair with a nucleotide on the opposite strand, and an unpaired nucleotide region on the other side of the duplex. The number of unpaired nucleotides on the two sides of the duplex can be different.

[00406] In one example, the bulge comprises an unpaired purine (*e.g.*, adenine) on the minimum CRISPR repeat strand of the bulge. In some embodiments, a bulge comprises an unpaired 5'-AAGY-3' of the minimum tracrRNA sequence strand of the bulge, where Y comprises a nucleotide that can form a wobble pairing with a nucleotide on the minimum CRISPR repeat strand.

[00407] In some embodiments, a bulge on the minimum CRISPR repeat side of the duplex comprises at least 1, 2, 3, 4, or 5 or more unpaired nucleotides. In some embodiments, a bulge on the minimum CRISPR repeat side of the duplex comprises at most 1, 2, 3, 4, or 5 or more unpaired nucleotides. In some embodiments, a bulge on the minimum CRISPR repeat side of the duplex comprises 1 unpaired nucleotide.

[00408] In some embodiments, a bulge on the minimum tracrRNA sequence side of the duplex comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more unpaired nucleotides. In some embodiments, a bulge on the minimum tracrRNA sequence side of the duplex comprises at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 or more unpaired nucleotides. In some embodiments, a bulge on a second side of the duplex (*e.g.*, the minimum tracrRNA sequence side of the duplex) comprises 4 unpaired nucleotides.

[00409] In some embodiments, a bulge comprises at least one wobble pairing. In some embodiments, a bulge comprises at most one wobble pairing. In some embodiments, a bulge comprises at least one purine nucleotide. In some embodiments, a bulge comprises at least 3 purine nucleotides. In some embodiments, a bulge sequence comprises at least 5 purine nucleotides. In some embodiments, a bulge sequence comprises at least one guanine nucleotide. In some embodiments, a bulge sequence comprises at least one adenine nucleotide.

[00410] Hairpins

[00411] In various embodiments, one or more hairpins are located 3' to the minimum tracrRNA in the 3' tracrRNA sequence.

[00412] In some embodiments, the hairpin starts at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20 or more nucleotides 3' from the last paired nucleotide in the minimum CRISPR repeat and minimum tracrRNA sequence duplex. In some embodiments, the hairpin can start at most about 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more nucleotides 3' of the last paired nucleotide in the minimum CRISPR repeat and minimum tracrRNA sequence duplex.

[00413] In some embodiments, a hairpin comprises at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or 20 or more consecutive nucleotides. In some embodiments, a hairpin comprises at most about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, or more consecutive nucleotides.

[00414] In some embodiments, a hairpin comprises a CC dinucleotide (*i.e.*, two consecutive cytosine nucleotides).

[00415] In some embodiments, a hairpin comprises duplexed nucleotides (*e.g.*, nucleotides in a hairpin, hybridized together). For example, a hairpin comprises a CC dinucleotide that is hybridized to a GG dinucleotide in a hairpin duplex of the 3' tracrRNA sequence.

[00416] One or more of the hairpins can interact with guide RNA-interacting regions of a site-directed polypeptide.

[00417] In some embodiments, there are two or more hairpins, and in some embodiments there are three or more hairpins.

[00418] 3' tracrRNA sequence

[00419] In some embodiments, a 3' tracrRNA sequence comprises a sequence with at least about 30%, about 40%, about 50%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 95%, or 100% sequence identity to a reference tracrRNA sequence (*e.g.*, a tracrRNA from *S. pyogenes*).

[00420] In some embodiments, the 3' tracrRNA sequence has a length from about 6 nucleotides to about 100 nucleotides. For example, the 3' tracrRNA

sequence can have a length from about 6 nucleotides (nt) to about 50 nt, from about 6 nt to about 40 nt, from about 6 nt to about 30 nt, from about 6 nt to about 25 nt, from about 6 nt to about 20 nt, from about 6 nt to about 15 nt, from about 8 nt to about 40 nt, from about 8 nt to about 30 nt, from about 8 nt to about 25 nt, from about 8 nt to about 20 nt, from about 8 nt to about 15 nt, from about 15 nt to about 100 nt, from about 15 nt to about 80 nt, from about 15 nt to about 50 nt, from about 15 nt to about 40 nt, from about 15 nt to about 30 nt, or from about 15 nt to about 25 nt. In some embodiments, the 3' tracrRNA sequence has a length of approximately 14 nucleotides.

[00421] In some embodiments, the 3' tracrRNA sequence is at least about 60% identical to a reference 3' tracrRNA sequence (*e.g.*, wild type 3' tracrRNA sequence from *S. pyogenes*) over a stretch of at least 6, 7, or 8 contiguous nucleotides. For example, the 3' tracrRNA sequence is at least about 60% identical, about 65% identical, about 70% identical, about 75% identical, about 80% identical, about 85% identical, about 90% identical, about 95% identical, about 98% identical, about 99% identical, or 100% identical, to a reference 3' tracrRNA sequence (*e.g.*, wild type 3' tracrRNA sequence from *S. pyogenes*) over a stretch of at least 6, 7, or 8 contiguous nucleotides.

[00422] In some embodiments, a 3' tracrRNA sequence comprises more than one duplexed region (*e.g.*, hairpin, hybridized region). In some embodiments, a 3' tracrRNA sequence comprises two duplexed regions.

[00423] In some embodiments, the 3' tracrRNA sequence comprises a stem loop structure. In some embodiments, a stem loop structure in the 3' tracrRNA comprises at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15 or 20 or more nucleotides. In some embodiments, the stem loop structure in the 3' tracrRNA comprises at most 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 or more nucleotides. In some embodiments, the stem loop structure comprises a functional moiety. For example, the stem loop structure may comprise an aptamer, a ribozyme, a protein-interacting hairpin, a CRISPR array, an intron, or an exon. In some embodiments, the stem loop structure comprises at least about 1, 2, 3, 4, or 5 or more functional moieties. In some embodiments, the stem loop structure comprises at most about 1, 2, 3, 4, or 5 or more functional moieties.

[00424] In some embodiments, the hairpin in the 3' tracrRNA sequence comprises a P-domain. In some embodiments, the P-domain comprises a double-stranded region in the hairpin.

[00425] tracrRNA Extension Sequence

[00426] A tracrRNA extension sequence may be provided whether the tracrRNA is in the context of single-molecule guides or double-molecule guides. In some embodiments, a tracrRNA extension sequence has a length from about 1 nucleotide to about 400 nucleotides. In some embodiments, a tracrRNA extension sequence has a length of more than 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, or 400 nucleotides. In some embodiments, a tracrRNA extension sequence has a length from about 20 to about 5000 or more nucleotides. In some embodiments, a tracrRNA extension sequence has a length of more than 1000 nucleotides. In some embodiments, a tracrRNA extension sequence has a length of less than 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 320, 340, 360, 380, 400 or more nucleotides. In some embodiments, a tracrRNA extension sequence can have a length of less than 1000 nucleotides. In some embodiments, a tracrRNA extension sequence comprises less than 10 nucleotides in length. In some embodiments, a tracrRNA extension sequence is 10-30 nucleotides in length. In some embodiments, tracrRNA extension sequence is 30-70 nucleotides in length.

[00427] In some embodiments, the tracrRNA extension sequence comprises a functional moiety (*e.g.*, a stability control sequence, ribozyme, endoribonuclease binding sequence). In some embodiments, the functional moiety comprises a transcriptional terminator segment (*i.e.*, a transcription termination sequence). In some embodiments, the functional moiety has a total length from about 10 nucleotides (nt) to about 100 nucleotides, from about 10 nt to about 20 nt, from about 20 nt to about 30 nt, from about 30 nt to about 40 nt, from about 40 nt to about 50 nt, from about 50 nt to about 60 nt, from about 60 nt to about 70 nt, from about 70 nt to about 80 nt, from about 80 nt to about 90 nt, or from about 90 nt to about 100 nt, from about 15 nt to about 80 nt, from about 15 nt to about 50 nt, from about 15 nt to about 40 nt, from about 15 nt to about 30 nt, or from about 15 nt to

about 25 nt. In some embodiments, the functional moiety functions in a eukaryotic cell. In some embodiments, the functional moiety functions in a prokaryotic cell. In some embodiments, the functional moiety functions in both eukaryotic and prokaryotic cells.

[00428] Non-limiting examples of suitable tracrRNA extension functional moieties include a 3' poly-adenylated tail, a riboswitch sequence (*e.g.*, to allow for regulated stability and/or regulated accessibility by proteins and protein complexes), a sequence that forms a dsRNA duplex (*i.e.*, a hairpin), a sequence that targets the RNA to a subcellular location (*e.g.*, nucleus, mitochondria, chloroplasts, and the like), a modification or sequence that provides for tracking (*e.g.*, direct conjugation to a fluorescent molecule, conjugation to a moiety that facilitates fluorescent detection, a sequence that allows for fluorescent detection, etc.), and/or a modification or sequence that provides a binding site for proteins (*e.g.*, proteins that act on DNA, including transcriptional activators, transcriptional repressors, DNA methyltransferases, DNA demethylases, histone acetyltransferases, histone deacetylases, and the like). In some embodiments, a tracrRNA extension sequence comprises a primer binding site or a molecular index (*e.g.*, barcode sequence). In some embodiments, the tracrRNA extension sequence comprises one or more affinity tags.

[00429] Single-Molecule Guide Linker Sequence

[00430] In some embodiments, the linker sequence of a single-molecule guide nucleic acid has a length from about 3 nucleotides to about 100 nucleotides. In Jinek *et al.*, *supra,* for example, a simple 4 nucleotide "tetraloop" (-GAAA-) was used, Science, 337(6096):816-821 (2012). An illustrative linker has a length from about 3 nucleotides (nt) to about 90 nt, from about 3 nt to about 80 nt, from about 3 nt to about 70 nt, from about 3 nt to about 60 nt, from about 3 nt to about 50 nt, from about 3 nt to about 40 nt, from about 3 nt to about 30 nt, from about 3 nt to about 20 nt, from about 3 nt to about 10 nt. For example, the linker can have a length from about 3 nt to about 5 nt, from about 5 nt to about 10 nt, from about 10 nt to about 15 nt, from about 15 nt to about 20 nt, from about 20 nt to about 25 nt, from about 25 nt to about 30 nt, from about 30 nt to about 35 nt, from about 35 nt to about 40 nt, from about 40 nt to about 50 nt, from about 50 nt to about 60 nt, from

about 60 nt to about 70 nt, from about 70 nt to about 80 nt, from about 80 nt to about 90 nt, or from about 90 nt to about 100 nt. In some embodiments, the linker of a single-molecule guide nucleic acid is between 4 and 40 nucleotides. In some embodiments, a linker is at least about 100, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, or 7000 or more nucleotides. In some embodiments, a linker is at most about 100, 500, 1000, 1500, 2000, 2500, 3000, 3500, 4000, 4500, 5000, 5500, 6000, 6500, or 7000 or more nucleotides.

[00431] Linkers can comprise any of a variety of sequences, although preferably the linker will not comprise sequences that have extensive regions of homology with other portions of the guide RNA, which might cause intramolecular binding that could interfere with other functional regions of the guide. In Jinek *et al.*, *supra,* a simple 4 nucleotide sequence -GAAA- was used, Science, 337(6096):816-821 (2012), but numerous other sequences, including longer sequences can likewise be used.

[00432] In some embodiments, the linker sequence comprises a functional moiety. For example, the linker sequence may comprise one or more features, including an aptamer, a ribozyme, a protein-interacting hairpin, a protein binding site, a CRISPR array, an intron, or an exon. In some embodiments, the linker sequence comprises at least about 1, 2, 3, 4, or 5 or more functional moieties. In some embodiments, the linker sequence comprises at most about 1, 2, 3, 4, or 5 or more functional moieties.

[00433] Genome engineering strategies to correct cells by insertion, correction or replacement of one or more mutations within or near the gene or by knocking-in G6PC cDNA or a minigene into the locus of the corresponding gene or safe harbor site

[00434] The methods of the present disclosure can involve correction of one or both of the mutant alleles. Gene editing to correct the mutation has the advantage of restoration of correct expression levels and temporal control. Sequencing the patient's G6PC alleles allows for design of the gene editing strategy to best correct the identified mutation(s).

[00435] A step of the *ex vivo* methods of the invention involves editing/correcting the patient specific iPS cells using genome engineering. Alternatively, a step of the

ex vivo methods of the invention involves editing/correcting the progenitor cell, primary hepatocyte, or mesenchymal stem cell, or a liver progenitor cell. Likewise, a step of the *in vivo* methods of the invention involves editing/correcting the cells in a GSD1a patient using genome engineering. Similarly, a step in the cellular methods of the invention involves editing/correcting the G6PC gene in a human cell by genome engineering.

[00436] GSD1a patients exhibit one or more mutations in the G6PC gene. Therefore, different patients will generally require different correction strategies. Any CRISPR endonuclease may be used in the methods of the invention, each CRISPR endonuclease having its own associated PAM, which may or may not be disease specific. For example, gRNA spacer sequences for targeting the G6PC gene with a CRISPR/Cas9 endonuclease from *S. pyogenes* have been identified in Figure 85. gRNA spacer sequences for targeting the G6PC gene with a CRISPR/Cas9 endonuclease from *S. aureus* have been identified in Figure 86. gRNA spacer sequences for targeting the G6PC gene with a CRISPR/Cas9 endonuclease from *S. thermophilus* have been identified in Figure 87. gRNA spacer sequences for targeting the G6PC gene with a CRISPR/Cas9 endonuclease from *T. denticola* have been identified in Figure 88. gRNA spacer sequences for targeting the G6PC gene with a CRISPR/Cas9 endonuclease from *N. meningitides* have been identified in Figure 89. gRNA spacer sequences for targeting the G6PC gene with a CRISPR/Cpf1 endonuclease from *Acidominococcus*, *Lachnospiracea*, and *Francisella novicida* have been identified in Figure 90. gRNA spacer sequences for targeting, *e.g.*, targeting exon 1-2 of, AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR with a CRISPR/Cas9 endonuclease from *S. pyogenes* have been identified in Figures 1, 7, 13, 19, 25, 31, 37, 43, 49, 55, 61, 67, 73, and 79 respectively. gRNA spacer sequences for targeting, *e.g.*, targeting exon 1-2 of, AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR with a CRISPR/Cas9 endonuclease from *S. aureus* have been identified in Figures 8, 14, 20, 26, 32, 38, 44, 50, 56, 62, 68, 74, and 80, respectively. gRNA spacer sequences for targeting, *e.g.*, targeting exon 1-2 of, AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR with a CRISPR/Cas9 endonuclease

from *S. thermophilus* have been identified in Figures 9, 15, 21, 27, 33, 39, 45, 51, 57,63, 69, 75, and 81, respectively. gRNA spacer sequences for targeting, *e.g.*, targeting exon 1-2 of, AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR with a CRISPR/Cas9 endonuclease from *T. denticola* have been identified in Figures 10, 16, 22, 28, 34, 40, 46, 52, 58, 64, 70, 76, and 82, respectively. gRNA spacer sequences for targeting, *e.g.*, targeting exon 1-2 of, AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR with a CRISPR/Cas9 endonuclease from *N. meningitides* have been identified in Figures 11, 17, 23, 29, 35, 41, 47, 53, 59, 65, 71, 77, and 83, respectively. gRNA spacer sequences for targeting, *e.g.*, targeting exon 1-2 of, AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR with a CRISPR/Cas9 endonuclease from *Acidominococcus, Lachnospiraceae, and Francisella novicida* have been identified in Figures 12, 18, 24, 30, 36, 42, 48, 54, 60, 66, 72, 78, and 84, respectively.

[00437] For example, the mutation can be corrected by the insertions or deletions that arise due to the imprecise NHEJ repair pathway. If the patient's G6PC gene has an inserted or deleted base, a targeted cleavage can result in a NHEJ-mediated insertion or deletion that restores the frame. Missense mutations can also be corrected through NHEJ-mediated correction using one or more guide RNA. The ability or likelihood of the cut(s) to correct the mutation can be designed or evaluated based on the local sequence and micro-homologies. NHEJ can also be used to delete segments of the gene, either directly or by altering splice donor or acceptor sites through cleavage by one gRNA targeting several locations, or several gRNAs. This may be useful if an amino acid, domain or exon contains the mutations and can be removed or inverted, or if the deletion otherwise restored function to the protein. Pairs of guide strands have been used for deletions and corrections of inversions.

[00438] Alternatively, the donor for correction by HDR contains the corrected sequence with small or large flanking homology arms to allow for annealing. HDR is essentially an error-free mechanism that uses a supplied homologous DNA sequence as a template during DSB repair. The rate of homology directed repair

(HDR) is a function of the distance between the mutation and the cut site so choosing overlapping or nearest target sites is important. Templates can include extra sequences flanked by the homologous regions or can contain a sequence that differs from the genomic sequence, thus allowing sequence editing.

[00439] In addition to correcting mutations by NHEJ or HDR, a range of other options are possible. If there are small or large deletions or multiple mutations, a cDNA can be knocked in that contains the exons affected. A full length cDNA can be knocked into any “safe harbor”, but must use a supplied or other promoter. If this construct is knocked into the correct location, it will have physiological control, similar to the normal gene. Pairs of nucleases can be used to delete mutated gene regions, though a donor would usually have to be provided to restore function. In this case two gRNA would be supplied and one donor sequence.

[00440] Some genome engineering strategies involve correction of one or more mutations in or near the gene, or deleting the mutant G6PC DNA and knocking-in G6PC cDNA or a minigene (comprised of one or more exons and introns or natural or synthetic introns) into the locus of the corresponding gene or a safe harbor locus by homology directed repair (HDR), which is also known as homologous recombination (HR). Homology directed repair is one strategy for treating patients that have inactivating mutations in or near the glucose-6-phosphatase catalytic unit. These strategies will restore the glucose-6-phosphatase catalytic unit and completely reverse, treat, and/or mitigate the diseased state. This strategy will require a more custom approach based on the location of the patient’s inactivating mutation(s). Donor nucleotides for correcting mutations are small (< 300 bp). This is advantageous, as HDR efficiencies may be inversely related to the size of the donor molecule. Also, it is expected that the donor templates can fit into size constrained viral vector molecules, e.g., adeno-associated virus (AAV) molecules, which have been shown to be an effective means of donor template delivery. Also, it is expected that the donor templates can fit into other size constrained molecules, including, by way of non-limiting example, platelets and/or exosomes or other microvesicles.

[00441] Homology direct repair is a cellular mechanism for repairing double-stranded breaks (DSBs). The most common form is homologous recombination.

There are additional pathways for HDR, including single-strand annealing and alternative-HDR. Genome engineering tools allow researchers to manipulate the cellular homologous recombination pathways to create site-specific modifications to the genome. It has been found that cells can repair a double-stranded break using a synthetic donor molecule provided in trans. Therefore, by introducing a double-stranded break near a specific mutation and providing a suitable donor, targeted changes can be made in the genome. Specific cleavage increases the rate of HDR more than 1,000 fold above the rate of 1 in 10^6 cells receiving a homologous donor alone. The rate of homology directed repair (HDR) at a particular nucleotide is a function of the distance to the cut site, so choosing overlapping or nearest target sites is important. Gene editing offers the advantage over gene addition, as correcting in situ leaves the rest of the genome unperturbed.

[00442] Supplied donors for editing by HDR vary markedly but generally contain the intended sequence with small or large flanking homology arms to allow annealing to the genomic DNA. The homology regions flanking the introduced genetic changes can be 30 bp or smaller, or as large as a multi-kilobase cassette that can contain promoters, cDNAs, etc. Both single-stranded and double-stranded oligonucleotide donors have been used. These oligonucleotides range in size from less than 100 nt to over many kb, though longer ssDNA can also be generated and used. Double-stranded donors are often used, including PCR amplicons, plasmids, and mini-circles. In general, it has been found that an AAV vector is a very effective means of delivery of a donor template, though the packaging limits for individual donors is <5kb. Active transcription of the donor increased HDR three-fold, indicating the inclusion of promoter may increase conversion. Conversely, CpG methylation of the donor decreased gene expression and HDR.

[00443] In addition to wildtype endonucleases, such as Cas9, nickase variants exist that have one or the other nuclease domain inactivated resulting in cutting of only one DNA strand. HDR can be directed from individual Cas nickases or using pairs of nickases that flank the target area. Donors can be single-stranded, nicked, or dsDNA.

[00444] The donor DNA can be supplied with the nuclease or independently by a variety of different methods, for example by transfection, nano-particle, micro-

injection, or viral transduction. A range of tethering options has been proposed to increase the availability of the donors for HDR. Examples include attaching the donor to the nuclease, attaching to DNA binding proteins that bind nearby, or attaching to proteins that are involved in DNA end binding or repair.

[00445] The repair pathway choice can be guided by a number of culture conditions, such as those that influence cell cycling, or by targeting of DNA repair and associated proteins. For example, to increase HDR, key NHEJ molecules can be suppressed, such as KU70, KU80 or DNA ligase IV.

[00446] Without a donor present, the ends from a DNA break or ends from different breaks can be joined using the several nonhomologous repair pathways in which the DNA ends are joined with little or no base-pairing at the junction. In addition to canonical NHEJ, there are similar repair mechanisms, such as alt-NHEJ. If there are two breaks, the intervening segment can be deleted or inverted. NHEJ repair pathways can lead to insertions, deletions or mutations at the joints.

[00447] NHEJ was used to insert a 15-kb inducible gene expression cassette into a defined locus in human cell lines after nuclease cleavage. Maresca, M., Lin, V.G., Guo, N. & Yang, Y., *Genome Res* 23, 539-546 (2013).

[00448] In addition to genome editing by NHEJ or HDR, site-specific gene insertions have been conducted that use both the NHEJ pathway and HR. A combination approach may be applicable in certain settings, possibly including intron/exon borders. NHEJ may prove effective for ligation in the intron, while the error-free HDR may be better suited in the coding region.

[00449] As stated previously, the G6PC gene contains 5 exons. Any one or more of the 5 exons or nearby introns may be repaired in order to correct a mutation and restore the inactive G6Pase catalytic unit. Alternatively, there are various mutations associated with GSD1a, which are a combination of insertions, deletions, missense, nonsense, frameshift and other mutations, with the common effect of inactivating G6Pase. Any one or more of the mutations may be repaired in order to restore the inactive G6Pase catalytic unit. For example, one or more of the following pathological variants may be corrected: rs80356479, rs80356486, rs606231368, rs80356488, rs587776757, rs104894565, rs104894566, rs1801175, rs1801176, rs104894567, rs104894571, rs80356482, rs80356483, rs104894563, rs367727229,

rs387906505, rs104894568, rs104894569, rs80356487, rs764920787, rs80356485, rs780226142, rs80356484 (see Figures 91A and 91B). These variants include deletions, insertions and single nucleotide polymorphisms. As a further alternative, G6PC cDNA or a minigene (comprised of one or more exons and introns or natural or synthetic introns) may be knocked-in to the locus of the corresponding gene or knocked-in to a safe harbor site, such as AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and/or TTR. The safe harbor locus can be selected from the group consisting of: exon 1-2 of AAVS1 (PPP1R12C), exon 1-2 of ALB, exon 1-2 of Angptl3, exon 1-2 of ApoC3, exon 1-2 of ASGR2, exon 1-2 of CCR5, exon 1-2 of FIX (F9), exon 1-2 of Gys2, exon 1-2 of HGD, exon 1-2 of Lp(a), exon 1-2 of Pcsk9, exon 1-2 of Serpina1, exon 1-2 of TF, and exon 1-2 of TTR. In some embodiments, the methods provide one gRNA or a pair of gRNAs that can be used to facilitate incorporation of a new sequence from a polynucleotide donor template to correct one or more mutations or to knock-in a part of or the entire G6PC gene or cDNA.

[00450] Some embodiments of the methods provide gRNA pairs that make a deletion by cutting the gene twice, one gRNA cutting at the 5' end of one or more mutations and the other gRNA cutting at the 3' end of one or more mutations that facilitates insertion of a new sequence from a polynucleotide donor template to replace the one or more mutations, or deletion may exclude mutant amino acids or amino acids adjacent to it (e.g., premature stop codon) and lead to expression of a functional protein, or restore an open reading frame. The cutting may be accomplished by a pair of DNA endonucleases that each makes a DSB in the genome, or by multiple nickases that together make a DSB in the genome.

[00451] Alternatively, some embodiments of the methods provide one gRNA to make one double-strand cut around one or more mutations that facilitates insertion of a new sequence from a polynucleotide donor template to replace the one or more mutations. The double-strand cut may be made by a single DNA endonuclease or multiple nickases that together make a DSB in the genome, or single gRNA may lead to deletion (MMEJ), which may exclude mutant amino acid (e.g., premature stop codon) and lead to expression of a functional protein, or restore an open reading frame.

[00452] Illustrative modifications within the G6PC gene include replacements within or near (proximal) to the mutations referred to above, such as within the region of less than 3 kb, less than 2kb, less than 1 kb, less than 0.5 kb upstream or downstream of the specific mutation. Given the relatively wide variations of mutations in the G6PC gene, it will be appreciated that numerous variations of the replacements referenced above (including without limitation larger as well as smaller deletions), would be expected to result in restoration of G6Pase protein activity.

[00453] Such variants include replacements that are larger in the 5' and/or 3' direction than the specific mutation in question, or smaller in either direction. Accordingly, by “near” or "proximal" with respect to specific replacements, it is intended that the SSB or DSB locus associated with a desired replacement boundary (also referred to herein as an endpoint) may be within a region that is less than about 3 kb from the reference locus noted. In some embodiments, the DSB locus is more proximal and within 2 kb, within 1 kb, within 0.5 kb, or within 0.1 kb. In the case of small replacement, the desired endpoint is at or "adjacent to" the reference locus, by which it is intended that the endpoint is within 100 bp, within 50 bp, within 25 bp, or less than about 10 bp to 5 bp from the reference locus.

[00454] Embodiments comprising larger or smaller replacements are expected to provide the same benefit, as long as the G6Pase catalytic unit is restored. It is thus expected that many variations of the replacements described and illustrated herein will be effective for ameliorating GSD1a.

[00455] Another genome engineering strategy involves exon deletion. Targeted deletion of specific exons can be an attractive strategy for treating a large subset of patients with a single therapeutic cocktail. Deletions can either be single exon deletions or multi-exon deletions. While multi-exon deletions can reach a larger number of patients, for larger deletions the efficiency of deletion greatly decreases with increased size. Therefore, deletions range can be from 40 to 10,000 base pairs (bp) in size. For example, deletions can range from 40-100; 100-300; 300-500; 500-1,000; 1,000-2,000; 2,000-3,000; 3,000-5,000; or 5,000-10,000 base pairs in size.

[00456] Deletions can occur in enhancer, promoter, 1st intron, and/or 3'UTR leading to upregulation of the gene expression, and/or through deletion of the regulatory elements.

[00457] In order to ensure that the pre-mRNA is properly processed following deletion, the surrounding splicing signals can be deleted. Splicing donor and acceptors are generally within 100 base pairs of the neighboring intron. Therefore, in some examples, methods can provide all gRNAs that cut approximately +/- 100-3100 bp with respect to each exon/intron junction of interest.

[00458] For any of the genome editing strategies, gene editing can be confirmed by sequencing or PCR analysis.

[00459] Target Sequence Selection

[00460] Shifts in the location of the 5' boundary and/or the 3' boundary relative to particular reference loci are used to facilitate or enhance particular applications of gene editing, which depend in part on the endonuclease system selected for the editing, as further described and illustrated herein.

[00461] In a first, non-limiting example of such target sequence selection, many endonuclease systems have rules or criteria that guide the initial selection of potential target sites for cleavage, such as the requirement of a PAM sequence motif in a particular position adjacent to the DNA cleavage sites in the case of CRISPR Type II or Type V endonucleases.

[00462] In another non-limiting example of target sequence selection or optimization, the frequency of "off-target" activity for a particular combination of target sequence and gene editing endonuclease (*i.e.* the frequency of DSBs occurring at sites other than the selected target sequence) is assessed relative to the frequency of on-target activity. In some cases, cells that have been correctly edited at the desired locus may have a selective advantage relative to other cells. Illustrative, but nonlimiting, examples of a selective advantage include the acquisition of attributes such as enhanced rates of replication, persistence, resistance to certain conditions, enhanced rates of successful engraftment or persistence *in vivo* following introduction into a patient, and other attributes associated with the maintenance or increased numbers or viability of such cells. In

other cases, cells that have been correctly edited at the desired locus may be positively selected for by one or more screening methods used to identify, sort or otherwise select for cells that have been correctly edited. Both selective advantage and directed selection methods may take advantage of the phenotype associated with the correction. In some embodiments, cells may be edited two or more times in order to create a second modification that creates a new phenotype that is used to select or purify the intended population of cells. Such a second modification could be created by adding a second gRNA for a selectable or screenable marker. In some cases, cells can be correctly edited at the desired locus using a DNA fragment that contains the cDNA and also a selectable marker.

[00463] Whether any selective advantage is applicable or any directed selection is to be applied in a particular case, target sequence selection is also guided by consideration of off-target frequencies in order to enhance the effectiveness of the application and/or reduce the potential for undesired alterations at sites other than the desired target. As described further and illustrated herein and in the art, the occurrence of off-target activity is influenced by a number of factors including similarities and dissimilarities between the target site and various off target sites, as well as the particular endonuclease used. Bioinformatics tools are available that assist in the prediction of off-target activity, and frequently such tools can also be used to identify the most likely sites of off-target activity, which can then be assessed in experimental settings to evaluate relative frequencies of off-target to on-target activity, thereby allowing the selection of sequences that have higher relative on-target activities. Illustrative examples of such techniques are provided herein, and others are known in the art.

[00464] Another aspect of target sequence selection relates to homologous recombination events. Sequences sharing regions of homology can serve as focal points for homologous recombination events that result in deletion of intervening sequences. Such recombination events occur during the normal course of replication of chromosomes and other DNA sequences, and also at other times when DNA sequences are being synthesized, such as in the case of repairs of double-strand breaks (DSBs), which occur on a regular basis during the normal cell replication cycle but may also be enhanced by the occurrence of various events

(such as UV light and other inducers of DNA breakage) or the presence of certain agents (such as various chemical inducers). Many such inducers cause DSBs to occur indiscriminately in the genome, and DSBs are regularly being induced and repaired in normal cells. During repair, the original sequence may be reconstructed with complete fidelity, however, in some cases, small insertions or deletions (referred to as "indels") are introduced at the DSB site.

[00465] DSBs may also be specifically induced at particular locations, as in the case of the endonucleases systems described herein, which can be used to cause directed or preferential gene modification events at selected chromosomal locations. The tendency for homologous sequences to be subject to recombination in the context of DNA repair (as well as replication) can be taken advantage of in a number of circumstances, and is the basis for one application of gene editing systems, such as CRISPR, in which homology directed repair is used to insert a sequence of interest, provided through use of a "donor" polynucleotide, into a desired chromosomal location.

[00466] Regions of homology between particular sequences, which can be small regions of "microhomology" that may comprise as few as ten basepairs or less, can also be used to bring about desired deletions. For example, a single DSB is introduced at a site that exhibits microhomology with a nearby sequence. During the normal course of repair of such DSB, a result that occurs with high frequency is the deletion of the intervening sequence as a result of recombination being facilitated by the DSB and concomitant cellular repair process.

[00467] In some circumstances, however, selecting target sequences within regions of homology can also give rise to much larger deletions, including gene fusions (when the deletions are in coding regions), which may or may not be desired given the particular circumstances.

[00468] The examples provided herein further illustrate the selection of various target regions for the creation of DSBs designed to induce replacements that result in restoration of G6Pase activity, as well as the selection of specific target sequences within such regions that are designed to minimize off-target events relative to on-target events.

[00469] Nucleic acid modifications

[00470] In some embodiments, polynucleotides introduced into cells comprise one or more modifications that can be used individually or in combination, for example, to enhance activity, stability or specificity, alter delivery, reduce innate immune responses in host cells, or for other enhancements, as further described herein and known in the art.

[00471] In certain embodiments, modified polynucleotides are used in the CRISPR/Cas9/CPf1 system, in which case the guide RNAs (either single-molecule guides or double-molecule guides) and/or a DNA or an RNA encoding a Cas or Cpf1 endonuclease introduced into a cell can be modified, as described and illustrated below. Such modified polynucleotides can be used in the CRISPR/Cas9/CPf1 system to edit any one or more genomic loci.

[00472] Using the CRISPR/Cas9/CPf1 system for purposes of nonlimiting illustrations of such uses, modifications of guide RNAs can be used to enhance the formation or stability of the CRISPR/Cas9/CPf1 genome editing complex comprising guide RNAs, which may be single-molecule guides or double-molecule, and a Cas or Cpf1 endonuclease. Modifications of guide RNAs can also or alternatively be used to enhance the initiation, stability or kinetics of interactions between the genome editing complex with the target sequence in the genome, which can be used, for example, to enhance on-target activity. Modifications of guide RNAs can also or alternatively be used to enhance specificity, *e.g.*, the relative rates of genome editing at the on-target site as compared to effects at other (off-target) sites.

[00473] Modifications can also or alternatively be used to increase the stability of a guide RNA, *e.g.*, by increasing its resistance to degradation by ribonucleases (RNases) present in a cell, thereby causing its half-life in the cell to be increased. Modifications enhancing guide RNA half-life can be particularly useful in embodiments in which a Cas or Cpf1 endonuclease is introduced into the cell to be edited via an RNA that needs to be translated in order to generate endonuclease, because increasing the half-life of guide RNAs introduced at the same time as the RNA encoding the endonuclease can be used to increase the time that the guide RNAs and the encoded Cas or Cpf1 endonuclease co-exist in the cell.

[00474] Modifications can also or alternatively be used to decrease the likelihood or degree to which RNAs introduced into cells elicit innate immune responses. Such responses, which have been well characterized in the context of RNA interference (RNAi), including small-interfering RNAs (siRNAs), as described below and in the art, tend to be associated with reduced half-life of the RNA and/or the elicitation of cytokines or other factors associated with immune responses.

[00475] One or more types of modifications can also be made to RNAs encoding an endonuclease that are introduced into a cell, including, without limitation, modifications that enhance the stability of the RNA (such as by increasing its degradation by RNAses present in the cell), modifications that enhance translation of the resulting product (*i.e.* the endonuclease), and/or modifications that decrease the likelihood or degree to which the RNAs introduced into cells elicit innate immune responses.

[00476] Combinations of modifications, such as the foregoing and others, can likewise be used. In the case of CRISPR/Cas9/CPf1, for example, one or more types of modifications can be made to guide RNAs (including those exemplified above), and/or one or more types of modifications can be made to RNAs encoding Cas endonuclease (including those exemplified above).

[00477] By way of illustration, guide RNAs used in the CRISPR/Cas9/CPf1 system, or other smaller RNAs can be readily synthesized by chemical means, enabling a number of modifications to be readily incorporated, as illustrated below and described in the art. While chemical synthetic procedures are continually expanding, purifications of such RNAs by procedures such as high performance liquid chromatography (HPLC, which avoids the use of gels such as PAGE) tends to become more challenging as polynucleotide lengths increase significantly beyond a hundred or so nucleotides. One approach used for generating chemically-modified RNAs of greater length is to produce two or more molecules that are ligated together. Much longer RNAs, such as those encoding a Cas9 endonuclease, are more readily generated enzymatically. While fewer types of modifications are generally available for use in enzymatically produced RNAs, there are still modifications that can be used to, *e.g.*, enhance stability, reduce the likelihood or degree of innate immune response, and/or enhance other attributes,

as described further below and in the art; and new types of modifications are regularly being developed.

[00478] By way of illustration of various types of modifications, especially those used frequently with smaller chemically synthesized RNAs, modifications can comprise one or more nucleotides modified at the 2' position of the sugar, in some embodiments a 2'-O-alkyl, 2'-O-alkyl-O-alkyl, or 2'-fluoro-modified nucleotide. In some embodiments, RNA modifications include 2'-fluoro, 2'-amino or 2' O-methyl modifications on the ribose of pyrimidines, abasic residues, or an inverted base at the 3' end of the RNA. Such modifications are routinely incorporated into oligonucleotides and these oligonucleotides have been shown to have a higher Tm (*i.e.*, higher target binding affinity) than 2'-deoxyoligonucleotides against a given target.

[00479] A number of nucleotide and nucleoside modifications have been shown to make the oligonucleotide into which they are incorporated more resistant to nuclease digestion than the native oligonucleotide; these modified oligos survive intact for a longer time than unmodified oligonucleotides. Specific examples of modified oligonucleotides include those comprising modified backbones, for example, phosphorothioates, phosphotriesters, methyl phosphonates, short chain alkyl or cycloalkyl intersugar linkages or short chain heteroatomic or heterocyclic intersugar linkages. Some oligonucleotides are oligonucleotides with phosphorothioate backbones and those with heteroatom backbones, particularly CH2 -NH-O-CH2, CH,~N(CH3)~O~CH2 (known as a methylene(methylimino) or MMI backbone), CH2 --O--N (CH3)-CH2, CH2 -N (CH3)-N (CH3)-CH2 and O-N (CH3)- CH2 -CH2 backbones, wherein the native phosphodiester backbone is represented as O- P-- O- CH,); amide backbones [see De Mesmaeker *et al.*, Ace. Chem. Res., 28:366-374 (1995)]; morpholino backbone structures (see Summerton and Weller, U.S. Pat. No. 5,034,506); peptide nucleic acid (PNA) backbone (wherein the phosphodiester backbone of the oligonucleotide is replaced with a polyamide backbone, the nucleotides being bound directly or indirectly to the aza nitrogen atoms of the polyamide backbone, see Nielsen *et al.*, Science 1991, 254, 1497). Phosphorus-containing linkages include, but are not limited to, phosphorothioates, chiral phosphorothioates, phosphorodithioates,

phosphotriesters, aminoalkylphosphotriesters, methyl and other alkyl phosphonates comprising 3'alkylene phosphonates and chiral phosphonates, phosphinates, phosphoramidates comprising 3'-amino phosphoramidate and aminoalkylphosphoramidates, thionophosphoramidates, thionoalkylphosphonates, thionoalkylphosphotriesters, and boranophosphates having normal 3'-5' linkages, 2'-5' linked analogs of these, and those having inverted polarity wherein the adjacent pairs of nucleoside units are linked 3'-5' to 5'-3' or 2'-5' to 5'-2'; see US Patent Nos. 3,687,808; 4,469,863; 4,476,301; 5,023,243; 5,177,196; 5,188,897; 5,264,423; 5,276,019; 5,278,302; 5,286,717; 5,321,131; 5,399,676; 5,405,939; 5,453,496; 5,455,233; 5,466,677; 5,476,925; 5,519,126; 5,536,821; 5,541,306; 5,550,111; 5,563,253; 5,571,799; 5,587,361; and 5,625,050.

[00480] Morpholino-based oligomeric compounds are described in Braasch and David Corey, Biochemistry, 41(14): 4503-4510 (2002); Genesis, Volume 30, Issue 3, (2001); Heasman, Dev. Biol., 243: 209-214 (2002); Nasevicius *et al.*, Nat. Genet., 26:216-220 (2000); Lacerra *et al.*, Proc. Natl. Acad. Sci., 97: 9591-9596 (2000); and U.S. Pat. No. 5,034,506, issued Jul. 23, 1991.

[00481] Cyclohexenyl nucleic acid oligonucleotide mimetics are described in Wang *et al.*, J. Am. Chem. Soc., 122: 8595-8602 (2000).

[00482] Modified oligonucleotide backbones that do not include a phosphorus atom therein have backbones that are formed by short chain alkyl or cycloalkyl internucleoside linkages, mixed heteroatom and alkyl or cycloalkyl internucleoside linkages, or one or more short chain heteroatomic or heterocyclic internucleoside linkages. These comprise those having morpholino linkages (formed in part from the sugar portion of a nucleoside); siloxane backbones; sulfide, sulfoxide and sulfone backbones; formacetyl and thioformacetyl backbones; methylene formacetyl and thioformacetyl backbones; alkene containing backbones; sulfamate backbones; methyleneimino and methylenehydrazino backbones; sulfonate and sulfonamide backbones; amide backbones; and others having mixed N, O, S, and CH2 component parts; see US patent nos. 5,034,506; 5,166,315; 5,185,444; 5,214,134; 5,216,141; 5,235,033; 5,264,562; 5,264,564; 5,405,938; 5,434,257; 5,466,677; 5,470,967; 5,489,677; 5,541,307; 5,561,225; 5,596,086; 5,602,240; 5,610,289; 5,602,240; 5,608,046; 5,610,289; 5,618,704; 5,623,070; 5,663,312;

5,633,360; 5,677,437; and 5,677,439, each of which is herein incorporated by reference.

[00483] One or more substituted sugar moieties can also be included, *e.g.*, one of the following at the 2' position: OH, SH, SCH3, F, OCN, OCH3 OCH3, OCH3 O(CH2)n CH3, O(CH2)n NH2, or O(CH2)n CH3, where n is from 1 to about 10; C1 to C10 lower alkyl, alkoxyalkoxy, substituted lower alkyl, alkaryl or aralkyl; Cl; Br; CN; CF3; OCF3; O-, S-, or N-alkyl; O-, S-, or N-alkenyl; SOCH3; SO2 CH3; ONO2; NO2; N3; NH2; heterocycloalkyl; heterocycloalkaryl; aminoalkylamino; polyalkylamino; substituted silyl; an RNA cleaving group; a reporter group; an intercalator; a group for improving the pharmacokinetic properties of an oligonucleotide; or a group for improving the pharmacodynamic properties of an oligonucleotide and other substituents having similar properties. In some embodiments, a modification includes 2'-methoxyethoxy (2'-0-CH2CH2OCH3, also known as 2'-O-(2-methoxyethyl)) (Martin *et al*, Helv. Chim. Acta, 1995, 78, 486). Other modifications include 2'-methoxy (2'-0-CH3), 2'-propoxy (2'-OCH2 CH2CH3) and 2'-fluoro (2'-F). Similar modifications may also be made at other positions on the oligonucleotide, particularly the 3' position of the sugar on the 3' terminal nucleotide and the 5' position of 5' terminal nucleotide. Oligonucleotides may also have sugar mimetics, such as cyclobutyls in place of the pentofuranosyl group.

[00484] In some embodiments, both a sugar and an internucleoside linkage, *i.e.*, the backbone, of the nucleotide units are replaced with novel groups. The base units are maintained for hybridization with an appropriate nucleic acid target compound. One such oligomeric compound, an oligonucleotide mimetic that has been shown to have excellent hybridization properties, is referred to as a peptide nucleic acid (PNA). In PNA compounds, the sugar-backbone of an oligonucleotide is replaced with an amide containing backbone, for example, an aminoethylglycine backbone. The nucleobases are retained and are bound directly or indirectly to aza nitrogen atoms of the amide portion of the backbone. Representative United States patents that teach the preparation of PNA compounds comprise, but are not limited to, US patent nos. 5,539,082; 5,714,331; and 5,719,262. Further teaching of PNA compounds can be found in Nielsen *et al*, Science, 254: 1497-1500 (1991).

[00485] Guide RNAs can also include, additionally or alternatively, nucleobase (often referred to in the art simply as "base") modifications or substitutions. As used herein, "unmodified" or "natural" nucleobases include adenine (A), guanine (G), thymine (T), cytosine (C), and uracil (U). Modified nucleobases include nucleobases found only infrequently or transiently in natural nucleic acids, *e.g.*, hypoxanthine, 6-methyladenine, 5-Me pyrimidines, particularly 5-methylcytosine (also referred to as 5-methyl-2' deoxycytosine and often referred to in the art as 5-Me-C), 5-hydroxymethylcytosine (HMC), glycosyl HMC and gentobiosyl HMC, as well as synthetic nucleobases, *e.g.*, 2-aminoadenine, 2-(methylamino)adenine, 2-(imidazolylalkyl)adenine, 2-(aminoalklyamino)adenine or other heterosubstituted alkyladenines, 2-thiouracil, 2-thiothymine, 5-bromouracil, 5-hydroxymethyluracil, 8-azaguanine, 7-deazaguanine, N6 (6-aminohexyl)adenine, and 2,6-diaminopurine. Kornberg, A., DNA Replication, W. H. Freeman & Co., San Francisco, pp75-77 (1980); Gebeyehu *et al*., Nucl. Acids Res. 15:4513 (1997). A "universal" base known in the art, *e.g.*, inosine, can also be included. 5-Me-C substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2 ºC. (Sanghvi, Y. S., in Crooke, S. T. and Lebleu, B., eds., Antisense Research and Applications, CRC Press, Boca Raton, 1993, pp. 276-278) and are embodiments of base substitutions.

[00486] Modified nucleobases comprise other synthetic and natural nucleobases, such as 5-methylcytosine (5-me-C), 5-hydroxymethyl cytosine, xanthine, hypoxanthine, 2-aminoadenine, 6-methyl and other alkyl derivatives of adenine and guanine, 2-propyl and other alkyl derivatives of adenine and guanine, 2-thiouracil, 2-thiothymine and 2-thiocytosine, 5-halouracil and cytosine, 5-propynyl uracil and cytosine, 6-azo uracil, cytosine and thymine, 5-uracil (pseudo-uracil), 4-thiouracil, 8-halo, 8-amino, 8-thiol, 8- thioalkyl, 8-hydroxyl and other 8-substituted adenines and guanines, 5-halo particularly 5- bromo, 5-trifluoromethyl and other 5-substituted uracils and cytosines, 7-methylquanine and 7-methyladenine, 8-azaguanine and 8-azaadenine, 7-deazaguanine and 7-deazaadenine, and 3-deazaguanine and 3-deazaadenine.

[00487] Further, nucleobases comprise those disclosed in United States Patent No. 3,687,808, those disclosed in 'The Concise Encyclopedia of Polymer Science And Engineering', pages 858-859, Kroschwitz, J.I., ed. John Wiley & Sons, 1990,

those disclosed by Englisch *et al.*, Angewandle Chemie, International Edition', 1991, 30, page 613, and those disclosed by Sanghvi, Y. S., Chapter 15, Antisense Research and Applications', pages 289- 302, Crooke, S.T. and Lebleu, B. ea., CRC Press, 1993. Certain of these nucleobases are particularly useful for increasing the binding affinity of the oligomeric compounds of the invention. These include 5-substituted pyrimidines, 6-azapyrimidines and N-2, N-6 and 0-6 substituted purines, comprising 2-aminopropyladenine, 5-propynyluracil and 5-propynylcytosine. 5-methylcytosine substitutions have been shown to increase nucleic acid duplex stability by 0.6-1.2ºC (Sanghvi, Y.S., Crooke, S.T. and Lebleu, B., eds, 'Antisense Research and Applications', CRC Press, Boca Raton, 1993, pp. 276-278) and are embodiments of base substitutions, even more particularly when combined with 2'-O-methoxyethyl sugar modifications. Modified nucleobases are described in US patent nos. 3,687,808, as well as 4,845,205; 5,130,302; 5,134,066; 5,175,273; 5,367,066; 5,432,272; 5,457,187; 5,459,255; 5,484,908; 5,502,177; 5,525,711; 5,552,540; 5,587,469; 5,596,091; 5,614,617; 5,681,941; 5,750,692; 5,763,588; 5,830,653; 6,005,096; and U.S. Patent Application Publication 2003/0158403.

[00488] Thus, the term “modified” refers to a non-natural sugar, phosphate, or base that is incorporated into a guide RNA, an endonuclease, or both a guide RNA and an endonuclease. It is not necessary for all positions in a given oligonucleotide to be uniformly modified, and in fact more than one of the aforementioned modifications may be incorporated in a single oligonucleotide, or even in a single nucleoside within an oligonucleotide.

[00489] In some embodiments, the guide RNAs and/or mRNA (or DNA) encoding an endonuclease are chemically linked to one or more moieties or conjugates that enhance the activity, cellular distribution, or cellular uptake of the oligonucleotide. Such moieties comprise, but are not limited to, lipid moieties such as a cholesterol moiety [Letsinger *et al.*, Proc. Natl. Acad. Sci. USA, 86: 6553-6556 (1989)]; cholic acid [Manoharan *et al.*, Bioorg. Med. Chem. Let., 4: 1053-1060 (1994)]; a thioether, *e.g.*, hexyl-S- tritylthiol [Manoharan *et al*, Ann. N. Y. Acad. Sci., 660: 306-309 (1992) and Manoharan *et al.*, Bioorg. Med. Chem. Let., 3: 2765-2770 (1993)]; a thiocholesterol [Oberhauser *et al.*, Nucl. Acids Res., 20: 533-538 (1992)]; an aliphatic chain, *e.g.*, dodecandiol or undecyl residues [Kabanov *et al.*, FEBS

Lett., 259: 327-330 (1990) and Svinarchuk *et al*., Biochimie, 75: 49- 54 (1993)]; a phospholipid, *e.g*., di-hexadecyl-rac-glycerol or triethylammonium 1 ,2-di-O-hexadecyl- rac-glycero-3-H-phosphonate [Manoharan et al., Tetrahedron Lett., 36: 3651-3654 (1995) and Shea *et al*., Nucl. Acids Res., 18: 3777-3783 (1990)]; a polyamine or a polyethylene glycol chain [Mancharan *et al*., Nucleosides & Nucleotides, 14: 969-973 (1995)]; adamantane acetic acid [Manoharan *et al*., Tetrahedron Lett., 36: 3651-3654 (1995)]; a palmityl moiety [(Mishra *et a*l., Biochim. Biophys. Acta, 1264: 229-237 (1995)]; or an octadecylamine or hexylamino-carbonyl-t oxycholesterol moiety [Crooke *et al*., J. Pharmacol. Exp. Ther., 277: 923-937 (1996)]. See also US Patent Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599, 928 and 5,688,941.

[00490] Sugars and other moieties can be used to target proteins and complexes comprising nucleotides, such as cationic polysomes and liposomes, to particular sites. For example, hepatic cell directed transfer can be mediated via asialoglycoprotein receptors (ASGPRs); see, *e.g*., Hu, *et al*., Protein Pept Lett. 21(10):1025-30 (2014). Other systems known in the art and regularly developed can be used to target biomolecules of use in the present case and/or complexes thereof to particular target cells of interest.

[00491] These targeting moieties or conjugates can include conjugate groups covalently bound to functional groups, such as primary or secondary hydroxyl groups. Conjugate groups of the invention include intercalators, reporter molecules, polyamines, polyamides, polyethylene glycols, polyethers, groups that enhance the pharmacodynamic properties of oligomers, and groups that enhance the pharmacokinetic properties of oligomers. Typical conjugate groups include cholesterols, lipids, phospholipids, biotin, phenazine, folate, phenanthridine,

anthraquinone, acridine, fluoresceins, rhodamines, coumarins, and dyes. Groups that enhance the pharmacodynamic properties, in the context of this invention, include groups that improve uptake, enhance resistance to degradation, and/or strengthen sequence-specific hybridization with the target nucleic acid. Groups that enhance the pharmacokinetic properties, in the context of this invention, include groups that improve uptake, distribution, metabolism or excretion of the compounds of the present invention. Representative conjugate groups are disclosed in International Patent Application No. PCT/US92/09196, filed Oct. 23, 1992, and U.S. Pat. No. 6,287,860, which are incorporated herein by reference. Conjugate moieties include, but are not limited to, lipid moieties such as a cholesterol moiety, cholic acid, a thioether, *e.g.*, hexyl-5-tritylthiol, a thiocholesterol, an aliphatic chain, *e.g.*, dodecandiol or undecyl residues, a phospholipid, *e.g.*, di-hexadecyl-rac-glycerol or triethylammonium l,2-di-O-hexadecyl-rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, or adamantane acetic acid, a palmityl moiety, or an octadecylamine or hexylamino-carbonyl-oxy cholesterol moiety. See, *e.g.*, U.S. Pat. Nos. 4,828,979; 4,948,882; 5,218,105; 5,525,465; 5,541,313; 5,545,730; 5,552,538; 5,578,717, 5,580,731; 5,580,731; 5,591,584; 5,109,124; 5,118,802; 5,138,045; 5,414,077; 5,486,603; 5,512,439; 5,578,718; 5,608,046; 4,587,044; 4,605,735; 4,667,025; 4,762,779; 4,789,737; 4,824,941; 4,835,263; 4,876,335; 4,904,582; 4,958,013; 5,082,830; 5,112,963; 5,214,136; 5,082,830; 5,112,963; 5,214,136; 5,245,022; 5,254,469; 5,258,506; 5,262,536; 5,272,250; 5,292,873; 5,317,098; 5,371,241, 5,391,723; 5,416,203, 5,451,463; 5,510,475; 5,512,667; 5,514,785; 5,565,552; 5,567,810; 5,574,142; 5,585,481; 5,587,371; 5,595,726; 5,597,696; 5,599,923; 5,599,928 and 5,688,941.

[00492] Longer polynucleotides that are less amenable to chemical synthesis and are typically produced by enzymatic synthesis can also be modified by various means. Such modifications can include, for example, the introduction of certain nucleotide analogs, the incorporation of particular sequences or other moieties at the 5' or 3' ends of molecules, and other modifications. By way of illustration, the mRNA encoding Cas9 is approximately 4 kb in length and can be synthesized by *in vitro* transcription. Modifications to the mRNA can be applied to, *e.g.*, increase its translation or stability (such as by increasing its resistance to degradation with a cell), or to reduce the tendency of the RNA to elicit an innate immune response that

is often observed in cells following introduction of exogenous RNAs, particularly longer RNAs such as that encoding Cas9.

[00493] Numerous such modifications have been described in the art, such as polyA tails, 5' cap analogs (*e.g.*, Anti Reverse Cap Analog (ARCA) or m7G(5')ppp(5')G (mCAP)), modified 5' or 3' untranslated regions (UTRs), use of modified bases (such as Pseudo-UTP, 2-Thio-UTP, 5-Methylcytidine-5'-Triphosphate (5-Methyl-CTP) or N6-Methyl-ATP), or treatment with phosphatase to remove 5' terminal phosphates. These and other modifications are known in the art, and new modifications of RNAs are regularly being developed.

[00494] There are numerous commercial suppliers of modified RNAs, including for example, TriLink Biotech, AxoLabs, Bio-Synthesis Inc., Dharmacon and many others. As described by TriLink, for example, 5-Methyl-CTP can be used to impart desirable characteristics, such as increased nuclease stability, increased translation or reduced interaction of innate immune receptors with *in vitro* transcribed RNA. 5-Methylcytidine-5'-Triphosphate (5-Methyl-CTP), N6-Methyl-ATP, as well as Pseudo-UTP and 2-Thio-UTP, have also been shown to reduce innate immune stimulation in culture and *in vivo* while enhancing translation, as illustrated in publications by Kormann *et al*. and Warren *et al*. referred to below.

[00495] It has been shown that chemically modified mRNA delivered *in vivo* can be used to achieve improved therapeutic effects; see, *e.g.*, Kormann *et al.*, Nature Biotechnology 29, 154–157 (2011). Such modifications can be used, for example, to increase the stability of the RNA molecule and/or reduce its immunogenicity. Using chemical modifications such as Pseudo-U, N6-Methyl-A, 2-Thio-U and 5-Methyl-C, it was found that substituting just one quarter of the uridine and cytidine residues with 2-Thio-U and 5-Methyl-C respectively resulted in a significant decrease in toll-like receptor (TLR) mediated recognition of the mRNA in mice. By reducing the activation of the innate immune system, these modifications can be used to effectively increase the stability and longevity of the mRNA *in vivo*; see, *e.g.*, Kormann *et al*., *supra*.

[00496] It has also been shown that repeated administration of synthetic messenger RNAs incorporating modifications designed to bypass innate anti-viral responses can reprogram differentiated human cells to pluripotency. See, *e.g.*,

Warren, *et al.*, Cell Stem Cell, 7(5):618-30 (2010). Such modified mRNAs that act as primary reprogramming proteins can be an efficient means of reprogramming multiple human cell types. Such cells are referred to as induced pluripotency stem cells (iPSCs), and it was found that enzymatically synthesized RNA incorporating 5-Methyl-CTP, Pseudo-UTP and an Anti Reverse Cap Analog (ARCA) could be used to effectively evade the cell's antiviral response; see, *e.g.*, Warren *et al.*, *supra*.

[00497] Other modifications of polynucleotides described in the art include, for example, the use of polyA tails, the addition of 5' cap analogs (such as m7G(5')ppp(5')G (mCAP)), modifications of 5' or 3' untranslated regions (UTRs), or treatment with phosphatase to remove 5' terminal phosphates – and new approaches are regularly being developed.

[00498] A number of compositions and techniques applicable to the generation of modified RNAs for use herein have been developed in connection with the modification of RNA interference (RNAi), including small-interfering RNAs (siRNAs). siRNAs present particular challenges *in vivo* because their effects on gene silencing via mRNA interference are generally transient, which can require repeat administration. In addition, siRNAs are double-stranded RNAs (dsRNA) and mammalian cells have immune responses that have evolved to detect and neutralize dsRNA, which is often a by-product of viral infection. Thus, there are mammalian enzymes such as PKR (dsRNA-responsive kinase), and potentially retinoic acid-inducible gene I (RIG-I), that can mediate cellular responses to dsRNA, as well as Toll-like receptors (such as TLR3, TLR7 and TLR8) that can trigger the induction of cytokines in response to such molecules; see, *e.g.*, the reviews by Angart *et al.*, Pharmaceuticals (Basel) 6(4): 440–468 (2013); Kanasty *et al.*, Molecular Therapy 20(3): 513–524 (2012); Burnett *et al.*, Biotechnol J. 6(9):1130-46 (2011); Judge and MacLachlan, Hum Gene Ther 19(2):111-24 (2008); and references cited therein.

[00499] A large variety of modifications have been developed and applied to enhance RNA stability, reduce innate immune responses, and/or achieve other benefits that can be useful in connection with the introduction of polynucleotides into human cells, as described herein; see, *e.g.*, the reviews by Whitehead KA *et al.*, Annual Review of Chemical and Biomolecular Engineering, 2: 77-96 (2011);

Gaglione and Messere, Mini Rev Med Chem, 10(7):578-95 (2010); Chernolovskaya *et al*, Curr Opin Mol Ther., 12(2):158-67 (2010); Deleavey *et al*., Curr Protoc Nucleic Acid Chem Chapter 16:Unit 16.3 (2009); Behlke, Oligonucleotides 18(4):305-19 (2008); Fucini *et al*., Nucleic Acid Ther 22(3): 205–210 (2012); Bremsen *et al*., Front Genet 3:154 (2012).

[00500] As noted above, there are a number of commercial suppliers of modified RNAs, many of which have specialized in modifications designed to improve the effectiveness of siRNAs. A variety of approaches are offered based on various findings reported in the literature. For example, Dharmacon notes that replacement of a non-bridging oxygen with sulfur (phosphorothioate, PS) has been extensively used to improve nuclease resistance of siRNAs, as reported by Kole, Nature Reviews Drug Discovery 11:125-140 (2012). Modifications of the 2'-position of the ribose have been reported to improve nuclease resistance of the internucleotide phosphate bond while increasing duplex stability (Tm), which has also been shown to provide protection from immune activation. A combination of moderate PS backbone modifications with small, well-tolerated 2'-substitutions (2'-O-Methyl, 2'-Fluoro, 2'-Hydro) have been associated with highly stable siRNAs for applications *in vivo*, as reported by Soutschek *et al*. Nature 432:173-178 (2004); and 2'-O-Methyl modifications have been reported to be effective in improving stability as reported by Volkov, Oligonucleotides 19:191-202 (2009). With respect to decreasing the induction of innate immune responses, modifying specific sequences with 2'-O-Methyl, 2'-Fluoro, 2'-Hydro have been reported to reduce TLR7/TLR8 interaction while generally preserving silencing activity; see, *e.g*., Judge *et al*., Mol. Ther. 13:494-505 (2006); and Cekaite *et al*., J. Mol. Biol. 365:90-108 (2007). Additional modifications, such as 2-thiouracil, pseudouracil, 5-methylcytosine, 5-methyluracil, and N6-methyladenosine have also been shown to minimize the immune effects mediated by TLR3, TLR7, and TLR8; see, *e.g*., Kariko, K. *et al*., Immunity 23:165-175 (2005).

[00501] As is also known in the art, and commercially available, a number of conjugates can be applied to polynucleotides, such as RNAs, for use herein that can enhance their delivery and/or uptake by cells, including for example, cholesterol, tocopherol and folic acid, lipids, peptides, polymers, linkers and

aptamers; see, *e.g.*, the review by Winkler, Ther. Deliv. 4:791-809 (2013), and references cited therein.

[00502] Codon-Optimization

[00503] In some embodiments, a polynucleotide encoding a site-directed polypeptide is codon-optimized according to methods standard in the art for expression in the cell containing the target DNA of interest. For example, if the intended target nucleic acid is in a human cell, a human codon-optimized polynucleotide encoding Cas9 is contemplated for use for producing the Cas9 polypeptide.

[00504] Complexes of a Genome-targeting Nucleic Acid and a Site-Directed Polypeptide

[00505] A genome-targeting nucleic acid interacts with a site-directed polypeptide (*e.g.*, a nucleic acid-guided nuclease such as Cas9), thereby forming a complex. The genome-targeting nucleic acid guides the site-directed polypeptide to a target nucleic acid.

[00506] RNPs

[00507] As stated previously, the site-directed polypeptide and genome-targeting nucleic acid may each be administered separately to a cell or a patient. On the other hand, the site-directed polypeptide may be pre-complexed with one or more guide RNAs, or one or more crRNA together with a tracrRNA. The pre-complexed material may then be administered to a cell or a patient. Such pre-complexed material is known as a ribonucleoprotein particle (RNP).

[00508] Nucleic Acids Encoding System Components

[00509] In another aspect, the present disclosure provides a nucleic acid comprising a nucleotide sequence encoding a genome-targeting nucleic acid of the disclosure, a site-directed polypeptide of the disclosure, and/or any nucleic acid or proteinaceous molecule necessary to carry out the embodiments of the methods of the disclosure.

[00510] In some embodiments, the nucleic acid encoding a genome-targeting nucleic acid of the disclosure, a site-directed polypeptide of the disclosure, and/or

any nucleic acid or proteinaceous molecule necessary to carry out the embodiments of the methods of the disclosure comprises a vector (*e.g.*, a recombinant expression vector).

[00511] The term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double-stranded DNA loop into which additional nucleic acid segments can be ligated. Another type of vector is a viral vector, wherein additional nucleic acid segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome.

[00512] In some embodiments, vectors are capable of directing the expression of nucleic acids to which they are operatively linked. Such vectors are referred to herein as "recombinant expression vectors", or more simply "expression vectors", which serve equivalent functions.

[00513] The term "operably linked" means that the nucleotide sequence of interest is linked to regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence. The term "regulatory sequence" is intended to include, for example, promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are well known in the art and are described, for example, in Goeddel; Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cells, and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the target cell, the level of expression desired, and the like.

[00514] Expression vectors contemplated include, but are not limited to, viral vectors based on vaccinia virus, poliovirus, adenovirus, adeno-associated virus,

SV40, herpes simplex virus, human immunodeficiency virus, retrovirus (*e.g.*, Murine Leukemia Virus, spleen necrosis virus, and vectors derived from retroviruses such as Rous Sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, a lentivirus, human immunodeficiency virus, myeloproliferative sarcoma virus, and mammary tumor virus) and other recombinant vectors. Other vectors contemplated for eukaryotic target cells include, but are not limited to, the vectors pXT1, pSG5, pSVK3, pBPV, pMSG, and pSVLSV40 (Pharmacia). Additional vectors contemplated for eukaryotic target cells include, but are not limited to, the vectors pCTx-1, pCTx-2, and pCTx-3, which are described in Figures 92A to 92C. Other vectors may be used so long as they are compatible with the host cell.

[00515] In some embodiments, a vector comprises one or more transcription and/or translation control elements. Depending on the host/vector system utilized, any of a number of suitable transcription and translation control elements, including constitutive and inducible promoters, transcription enhancer elements, transcription terminators, etc. may be used in the expression vector. In some embodiments, the vector is a self-inactivating vector that either inactivates the viral sequences or the components of the CRISPR machinery or other elements.

[00516] Non-limiting examples of suitable eukaryotic promoters (*i.e.,* promoters functional in a eukaryotic cell) include those from cytomegalovirus (CMV) immediate early, herpes simplex virus (HSV) thymidine kinase, early and late SV40, long terminal repeats (LTRs) from retrovirus, human elongation factor-1 promoter (EF1), a hybrid construct comprising the cytomegalovirus (CMV) enhancer fused to the chicken beta-actin promoter (CAG), murine stem cell virus promoter (MSCV), phosphoglycerate kinase-1 locus promoter (PGK), and mouse metallothionein-I.

[00517] For expressing small RNAs, including guide RNAs used in connection with Cas endonuclease, various promoters such as RNA polymerase III promoters, including for example U6 and H1, can be advantageous. Descriptions of and parameters for enhancing the use of such promoters are known in art, and additional information and approaches are regularly being described; see, *e.g.*, Ma, H. *et al.*, *Molecular Therapy - Nucleic Acids 3*, e161 (2014) doi:10.1038/mtna.2014.12.

[00518] The expression vector may also contain a ribosome binding site for translation initiation and a transcription terminator. The expression vector may also include appropriate sequences for amplifying expression. The expression vector may also include nucleotide sequences encoding non-native tags (*e.g.*, histidine tag, hemagglutinin tag, green fluorescent protein, etc.) that are fused to the site-directed polypeptide, thus resulting in a fusion protein.

[00519] In some embodiments, a promoter is an inducible promoter (*e.g.*, a heat shock promoter, tetracycline-regulated promoter, steroid-regulated promoter, metal-regulated promoter, estrogen receptor-regulated promoter, etc.). In some embodiments, a promoter is a constitutive promoter (*e.g.*, CMV promoter, UBC promoter). In some embodiments, the promoter is a spatially restricted and/or temporally restricted promoter (*e.g.*, a tissue specific promoter, a cell type specific promoter, etc.).

[00520] In some embodiments, the nucleic acid encoding a genome-targeting nucleic acid of the disclosure and/or a site-directed polypeptide are packaged into or on the surface of delivery vehicles for delivery to cells. Delivery vehicles contemplated include, but are not limited to, nanospheres, liposomes, quantum dots, nanoparticles, polyethylene glycol particles, hydrogels, and micelles. As described in the art, a variety of targeting moieties can be used to enhance the preferential interaction of such vehicles with desired cell types or locations.

[00521] Introduction of the complexes, polypeptides, and nucleic acids of the disclosure into cells can occur by viral or bacteriophage infection, transfection, conjugation, protoplast fusion, lipofection, electroporation, nucleofection, calcium phosphate precipitation, polyethyleneimine (PEI)-mediated transfection, DEAE-dextran mediated transfection, liposome-mediated transfection, particle gun technology, calcium phosphate precipitation, direct micro-injection, nanoparticle-mediated nucleic acid delivery, and the like.

[00522] Delivery

[00523] Guide RNA polynucleotides (RNA or DNA) and/or endonuclease polynucleotide(s) (RNA or DNA) can be delivered by viral or non-viral delivery vehicles known in the art. Alternatively, endonuclease polypeptide(s) may be delivered by non-viral delivery vehicles known in the art, such as electroporation or

lipid nanoparticles. In some embodiments, the DNA endonuclease may be delivered as one or more polypeptides, either alone or pre-complexed with one or more guide RNAs, or one or more crRNA together with a tracrRNA.

[00524] Polynucleotides may be delivered by non-viral delivery vehicles including, but not limited to, nanoparticles, liposomes, ribonucleoproteins, positively charged peptides, small molecule RNA-conjugates, aptamer-RNA chimeras, and RNA-fusion protein complexes. Some exemplary non-viral delivery vehicles are described in Peer and Lieberman, Gene Therapy, 18: 1127–1133 (2011) (which focuses on non-viral delivery vehicles for siRNA that are also useful for delivery of other polynucleotides).

[00525] Polynucleotides, such as guide RNA, sgRNA, and mRNA encoding an endonuclease, may be delivered to a cell or a patient by a lipid nanoparticle (LNP).

[00526] A LNP refers to any particle having a diameter of less than 1000 nm, 500 nm, 250 nm, 200 nm, 150 nm, 100 nm, 75 nm, 50 nm, or 25 nm. Alternatively, a nanoparticle may range in size from 1-1000 nm, 1-500 nm, 1-250 nm, 25-200 nm, 25-100 nm, 35-75 nm, or 25-60 nm.

[00527] LNPs may be made from cationic, anionic, or neutral lipids. Neutral lipids, such as the fusogenic phospholipid DOPE or the membrane component cholesterol, may be included in LNPs as 'helper lipids' to enhance transfection activity and nanoparticle stability. Limitations of cationic lipids include low efficacy owing to poor stability and rapid clearance, as well as the generation of inflammatory or anti-inflammatory responses.

[00528] LNPs may also be comprised of hydrophobic lipids, hydrophilic lipids, or both hydrophobic and hydrophilic lipids.

[00529] Any lipid or combination of lipids that are known in the art may be used to produce a LNP. Examples of lipids used to produce LNPs are: DOTMA, DOSPA, DOTAP, DMRIE, DC-cholesterol, DOTAP–cholesterol, GAP-DMORIE–DPyPE, and GL67A–DOPE–DMPE–polyethylene glycol (PEG). Examples of cationic lipids are: 98N12-5, C12-200, DLin-KC2-DMA (KC2), DLin-MC3-DMA (MC3), XTC, MD1, and 7C1. Examples of neutral lipids are: DPSC, DPPC, POPC, DOPE, and SM. Examples of PEG-modified lipids are: PEG-DMG, PEG-CerC14, and PEG-CerC20.

[00530] The lipids may be combined in any number of molar ratios to produce a LNP. In addition, the polynucleotide(s) may be combined with lipid(s) in a wide range of molar ratios to produce a LNP.

[00531] As stated previously, the site-directed polypeptide and genome-targeting nucleic acid may each be administered separately to a cell or a patient. On the other hand, the site-directed polypeptide may be pre-complexed with one or more guide RNAs, or one or more crRNA together with a tracrRNA. The pre-complexed material may then be administered to a cell or a patient. Such pre-complexed material is known as a ribonucleoprotein particle (RNP).

[00532] RNA is capable of forming specific interactions with RNA or DNA. While this property is exploited in many biological processes, it also comes with the risk of promiscuous interactions in a nucleic acid-rich cellular environment. One solution to this problem is the formation of ribonucleoprotein particles (RNPs), in which the RNA is pre-complexed with an endonuclease. Another benefit of the RNP is protection of the RNA from degradation.

[00533] The endonuclease in the RNP may be modified or unmodified. Likewise, the gRNA, crRNA, tracrRNA, or sgRNA may be modified or unmodified. Numerous modifications are known in the art and may be used.

[00534] The endonuclease and sgRNA are generally combined in a 1:1 molar ratio. Alternatively, the endonuclease, crRNA and tracrRNA are generally combined in a 1:1:1 molar ratio. However, a wide range of molar ratios may be used to produce a RNP.

[00535] A recombinant adeno-associated virus (AAV) vector may be used for delivery. Techniques to produce rAAV particles, in which an AAV genome to be packaged that includes the polynucleotide to be delivered, rep and cap genes, and helper virus functions are provided to a cell are standard in the art. Production of rAAV requires that the following components are present within a single cell (denoted herein as a packaging cell): a rAAV genome, AAV rep and cap genes separate from (*i.e.*, not in) the rAAV genome, and helper virus functions. The AAV rep and cap genes may be from any AAV serotype for which recombinant virus can be derived, and may be from a different AAV serotype than the rAAV genome ITRs, including, but not limited to, AAV serotypes AAV-1, AAV-2, AAV-3, AAV-4, AAV-5,

AAV-6, AAV-7, AAV-8, AAV-9, AAV-10, AAV-11, AAV-12, AAV-13 and AAV rh.74. Production of pseudotyped rAAV is disclosed in, for example, international patent application publication number WO 01/83692. See Table 1.

Table 1

AAV Serotype	**Genbank Accession No.**
AAV-1	NC_002077.1
AAV-2	NC_001401.2
AAV-3	NC_001729.1
AAV-3B	AF028705.1
AAV-4	NC_001829.1
AAV-5	NC_006152.1
AAV-6	AF028704.1
AAV-7	NC_006260.1
AAV-8	NC_006261.1
AAV-9	AX753250.1
AAV-10	AY631965.1
AAV-11	AY631966.1
AAV-12	DQ813647.1
AAV-13	EU285562.1

[00536] A method of generating a packaging cell involves creating a cell line that stably expresses all of the necessary components for AAV particle production. For example, a plasmid (or multiple plasmids) comprising a rAAV genome lacking AAV rep and cap genes, AAV rep and cap genes separate from the rAAV genome, and a selectable marker, such as a neomycin resistance gene, are integrated into the genome of a cell. AAV genomes have been introduced into bacterial plasmids by procedures such as GC tailing (Samulski *et al.*, 1982, Proc. Natl. Acad. S6. USA,

79:2077-2081), addition of synthetic linkers containing restriction endonuclease cleavage sites (Laughlin *et al.*, 1983, Gene, 23:65-73) or by direct, blunt-end ligation (Senapathy & Carter, 1984, J. Biol. Chem., 259:4661-4666). The packaging cell line is then infected with a helper virus, such as adenovirus. The advantages of this method are that the cells are selectable and are suitable for large-scale production of rAAV. Other examples of suitable methods employ adenovirus or baculovirus, rather than plasmids, to introduce rAAV genomes and/or rep and cap genes into packaging cells.

[00537] General principles of rAAV production are reviewed in, for example, Carter, 1992, Current Opinions in Biotechnology, 1533-539; and Muzyczka, 1992, Curr. Topics in Microbial. and Immunol., 158:97-129). Various approaches are described in Ratschin *et al.*, Mol. Cell. Biol. 4:2072 (1984); Hermonat *et al.*, Proc. Natl. Acad. Sci. USA, 81:6466 (1984); Tratschin *et al.*, Mo1. Cell. Biol. 5:3251 (1985); McLaughlin *et al.*, J. Virol., 62:1963 (1988); and Lebkowski *et al.*, 1988 Mol. Cell. Biol., 7:349 (1988). Samulski *et al.* (1989, J. Virol., 63:3822-3828); U.S. Patent No. 5,173,414; WO 95/13365 and corresponding U.S. Patent No. 5,658.776 ; WO 95/13392; WO 96/17947; PCT/US98/18600; WO 97/09441 (PCT/US96/14423); WO 97/08298 (PCT/US96/13872); WO 97/21825 (PCT/US96/20777); WO 97/06243 (PCT/FR96/01064); WO 99/11764; Perrin *et al.* (1995) Vaccine 13:1244-1250; Paul *et al.* (1993) Human Gene Therapy 4:609-615; Clark *et al.* (1996) Gene Therapy 3:1124-1132; U.S. Patent. No. 5,786,211; U.S. Patent No. 5,871,982; and U.S. Patent. No. 6,258,595.

[00538] AAV vector serotypes can be matched to target cell types. For example, the following exemplary cell types may be transduced by the indicated AAV serotypes among others. See Table 2.

Table 2

Tissue/Cell Type	**Serotype**
Liver	AAV3, AAV5, AAV8, AAV9
Skeletal muscle	AAV1, AAV7, AAV6, AAV8, AAV9
Central nervous system	AAV5, AAV1, AAV4

RPE	AAV5, AAV4
Photoreceptor cells	AAV5
Lung	AAV9
Heart	AAV8
Pancreas	AAV8
Kidney	AAV2, AAV8

[00539] In addition to adeno-associated viral vectors, other viral vectors can be used. Such viral vectors include, but are not limited to, lentivirus, alphavirus, enterovirus, pestivirus, baculovirus, herpesvirus, Epstein Barr virus, papovavirusr, poxvirus, vaccinia virus, and herpes simplex virus.

[00540] In some embodiments, Cas9 mRNA, sgRNA targeting one or two loci in G6PC genes, and donor DNA are each separately formulated into lipid nanoparticles, or are all co-formulated into one lipid nanoparticle, or co-formulated into two or more lipid nanoparticles.

[00541] In some embodiments, Cas9 mRNA is formulated in a lipid nanoparticle, while sgRNA and donor DNA are delivered in an AAV vector. In some embodiments, Cas9 mRNA and sgRNA are co-formulated in a lipid nanoparticle, while donor DNA is delivered in an AAV vector.

[00542] Options are available to deliver the Cas9 nuclease as a DNA plasmid, as mRNA or as a protein. The guide RNA can be expressed from the same DNA, or can also be delivered as an RNA. The RNA can be chemically modified to alter or improve its half-life, or decrease the likelihood or degree of immune response. The endonuclease protein can be complexed with the gRNA prior to delivery. Viral vectors allow efficient delivery; split versions of Cas9 and smaller orthologs of Cas9 can be packaged in AAV, as can donors for HDR. A range of non-viral delivery methods also exist that can deliver each of these components, or non-viral and viral methods can be employed in tandem. For example, nano-particles can be used to deliver the protein and guide RNA, while AAV can be used to deliver a donor DNA.

[00543] Exosomes

[00544] Exosomes, a type of microvesicle bound by phospholipid bilayer, can be used to deliver nucleic acids to specific tissue. Many different types of cells within the body naturally secrete exosomes. Exosomes form within the cytoplasm when endosomes invaginate and form multivesicular-endosomes (MVE). When the MVE fuses with the cellular membrane, the exosomes are secreted in the extracellular space. Ranging between 30-120nm in diameter, exosomes can shuttle various molecules from one cell to another in a form of cell-to-cell communication. Cells that naturally produce exosomes, such as mast cells, can be genetically altered to produce exosomes with surface proteins that target specific tissues, alternatively exosomes can be isolated from the bloodstream. Specific nucleic acids can be placed within the engineered exosomes with electroporation. When introduced systemically, the exosomes can deliver the nucleic acids to the specific target tissue.

[00545] Genetically Modified Cells

[00546] The term "genetically modified cell" refers to a cell that comprises at least one genetic modification introduced by genome editing (*e.g.*, using the CRISPR/Cas system). In some *ex vivo* embodiments herein, the genetically modified cell is a genetically modified progenitor cell. In some *in vivo* embodiments herein, the genetically modified cell is a genetically modified liver cell. A genetically modified cell comprising an exogenous genome-targeting nucleic acid and/or an exogenous nucleic acid encoding a genome-targeting nucleic acid is contemplated herein.

[00547] The term "control treated population" describes a population of cells that has been treated with identical media, viral induction, nucleic acid sequences, temperature, confluency, flask size, pH, etc., with the exception of the addition of the genome editing components. Any method known in the art can be used to measure restoration of G6Pase gene or protein expression or activity, for example, Western Blot analysis of the G6Pase protein or quantifying G6PC mRNA.

[00548] The term "isolated cell" refers to a cell that has been removed from an organism in which it was originally found, or a descendant of such a cell. Optionally, the cell has been cultured *in vitro*, *e.g.*, under defined conditions or in the presence of other cells. Optionally, the cell is later introduced into a second organism or re-

introduced into the organism from which it (or the cell from which it is descended) was isolated.

[00549] The term "isolated population" with respect to an isolated population of cells refers to a population of cells that has been removed and separated from a mixed or heterogeneous population of cells. In some embodiments, an isolated population is a substantially pure population of cells, as compared to the heterogeneous population from which the cells were isolated or enriched. In some embodiments, the isolated population is an isolated population of human progenitor cells, *e.g.*, a substantially pure population of human progenitor cells, as compared to a heterogeneous population of cells comprising human progenitor cells and cells from which the human progenitor cells were derived.

[00550] The term "substantially enhanced," with respect to a particular cell population, refers to a population of cells in which the occurrence of a particular type of cell is increased relative to pre-existing or reference levels, by at least 2-fold, at least 3-, at least 4-, at least 5-, at least 6-, at least 7-, at least 8-, at least 9, at least 10-, at least 20-, at least 50-, at least 100-, at least 400-, at least 1000-, at least 5000-, at least 20000-, at least 100000- or more fold depending, *e.g.*, on the desired levels of such cells for ameliorating GSD1a.

[00551] The term "substantially enriched" with respect to a particular cell population, refers to a population of cells that is at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70% or more with respect to the cells making up a total cell population.

[00552] The terms "substantially enriched" or "substantially pure" with respect to a particular cell population, refers to a population of cells that is at least about 75%, at least about 85%, at least about 90%, or at least about 95% pure, with respect to the cells making up a total cell population. That is, the terms "substantially pure" or "essentially purified," with regard to a population of progenitor cells, refers to a population of cells that contain fewer than about 20%, about 15%, about 10%, about 9%, about 8%, about 7%, about 6%, about 5%, about 4%, about 3%, about 2%, about 1%, or less than 1%, of cells that are not progenitor cells as defined by the terms herein.

[00553] Differentiation of genome edited iPSCs into hepatocytes

[00554] Another step of the *ex vivo* methods of the invention involves differentiating the genome edited iPSCs into hepatocytes. The differentiating step may be performed according to any method known in the art. For example, hiPSC are differentiated into definitive endoderm using various treatments, including activin and B27 supplement (Life Technology). The definitive endoderm is further differentiated into hepatocyte, the treatment includes: FGF4, HGF, BMP2, BMP4, Oncostatin M, Dexametason, etc. (Duan et al, STEM CELLS; 2010;28:674–686, Ma et al, STEM CELLS TRANSLATIONAL MEDICINE *2013;2:409–419*).

[00555] Differentiation of genome edited mesenchymal stem cells into hepatocytes

[00556] Another step of the *ex vivo* methods of the invention involves differentiating the genome edited mesenchymal stem cells into hepatocytes. The differentiating step may be performed according to any method known in the art. For example, hMSC are treated with various factors and hormones, including insulin, transferrin, FGF4, HGF, bile acids (Sawitza I *et al*, Sci Rep. 2015; 5: 13320).

[00557] Implanting cells into patients

[00558] Another step of the *ex vivo* methods of the invention involves implanting the hepatocytes into patients. This implanting step may be accomplished using any method of implantation known in the art. For example, the genetically modified cells may be injected directly in the patient's liver or otherwise administered to the patient.

[00559] Another step of the *ex vivo* methods of the invention involves implanting the progenitor cells or primary hepatocytes into patients. This implanting step may be accomplished using any method of implantation known in the art. For example, the genetically modified cells may be injected directly in the patient's liver or otherwise administered to the patient. The genetically modified cells may be purified *ex vivo* using a selected marker.

[00560] Pharmaceutically Acceptable Carriers

[00561] The *ex vivo* methods of administering progenitor cells to a subject contemplated herein involve the use of therapeutic compositions comprising progenitor cells.

[00562] Therapeutic compositions contain a physiologically tolerable carrier together with the cell composition, and optionally at least one additional bioactive agent as described herein, dissolved or dispersed therein as an active ingredient. In some embodiments, the therapeutic composition is not substantially immunogenic when administered to a mammal or human patient for therapeutic purposes, unless so desired.

[00563] In general, the progenitor cells described herein are administered as a suspension with a pharmaceutically acceptable carrier. One of skill in the art will recognize that a pharmaceutically acceptable carrier to be used in a cell composition will not include buffers, compounds, cryopreservation agents, preservatives, or other agents in amounts that substantially interfere with the viability of the cells to be delivered to the subject. A formulation comprising cells can include *e.g.*, osmotic buffers that permit cell membrane integrity to be maintained, and optionally, nutrients to maintain cell viability or enhance engraftment upon administration. Such formulations and suspensions are known to those of skill in the art and/or can be adapted for use with the progenitor cells, as described herein, using routine experimentation.

[00564] A cell composition can also be emulsified or presented as a liposome composition, provided that the emulsification procedure does not adversely affect cell viability. The cells and any other active ingredient can be mixed with excipients that are pharmaceutically acceptable and compatible with the active ingredient, and in amounts suitable for use in the therapeutic methods described herein.

[00565] Additional agents included in a cell composition can include pharmaceutically acceptable salts of the components therein. Pharmaceutically acceptable salts include the acid addition salts (formed with the free amino groups of the polypeptide) that are formed with inorganic acids, such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, tartaric, mandelic and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases, such as, for example, sodium, potassium, ammonium, calcium or

ferric hydroxides, and such organic bases as isopropylamine, trimethylamine, 2-ethylamino ethanol, histidine, procaine and the like.

[00566] Physiologically tolerable carriers are well known in the art. Exemplary liquid carriers are sterile aqueous solutions that contain no materials in addition to the active ingredients and water, or contain a buffer such as sodium phosphate at physiological pH value, physiological saline or both, such as phosphate-buffered saline. Still further, aqueous carriers can contain more than one buffer salt, as well as salts such as sodium and potassium chlorides, dextrose, polyethylene glycol and other solutes. Liquid compositions can also contain liquid phases in addition to and to the exclusion of water. Exemplary of such additional liquid phases are glycerin, vegetable oils such as cottonseed oil, and water-oil emulsions. The amount of an active compound used in the cell compositions that is effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques.

[00567] Administration & Efficacy

[00568] The terms "administering," "introducing" and "transplanting" are used interchangeably in the context of the placement of cells, *e.g.*, progenitor cells, into a subject, by a method or route that results in at least partial localization of the introduced cells at a desired site, such as a site of injury or repair, such that a desired effect(s) is produced. The cells *e.g.*, progenitor cells, or their differentiated progeny can be administered by any appropriate route that results in delivery to a desired location in the subject where at least a portion of the implanted cells or components of the cells remain viable. The period of viability of the cells after administration to a subject can be as short as a few hours, *e.g.*, twenty-four hours, to a few days, to as long as several years, or even the life time of the patient, *i.e.*, long-term engraftment. For example, in some embodiments described herein, an effective amount of myogenic progenitor cells is administered via a systemic route of administration, such as an intraperitoneal or intravenous route.

[00569] The terms “individual”, “subject,” “host” and “patient” are used interchangeably herein and refer to any subject for whom diagnosis, treatment or therapy is desired. In some embodiments, the subject is a mammal. In some embodiments, the subject is a human being.

[00570] When provided prophylactically, progenitor cells described herein can be administered to a subject in advance of any symptom of GSD1a, *e.g.*, prior to the development of seizures caused by hypoglycemia. Accordingly, the prophylactic administration of a liver progenitor cell population serves to prevent GSD1a.

[00571] When provided therapeutically, liver progenitor cells are provided at (or after) the onset of a symptom or indication of GSD1a, *e.g.*, upon the onset of abnormal glucose metabolism.

[00572] In some embodiments described herein, the liver progenitor cell population being administered according to the methods described herein comprises allogeneic liver progenitor cells obtained from one or more donors. "Allogeneic" refers to a liver progenitor cell or biological samples comprising liver progenitor cells or biological samples obtained from one or more different donors of the same species, where the genes at one or more loci are not identical. For example, a liver progenitor cell population being administered to a subject can be derived from one more unrelated donor subjects, or from one or more non-identical siblings. In some embodiments, syngeneic liver progenitor cell populations can be used, such as those obtained from genetically identical animals, or from identical twins. In other embodiments, the liver progenitor cells are autologous cells; that is, the liver progenitor cells are obtained or isolated from a subject and administered to the same subject, *i.e.*, the donor and recipient are the same.

[00573] In one embodiment, the term "effective amount" refers to the amount of a population of progenitor cells or their progeny needed to prevent or alleviate at least one or more signs or symptoms of GSD1a, and relates to a sufficient amount of a composition to provide the desired effect, *e.g.*, to treat a subject having GSD1a. The term "therapeutically effective amount" therefore refers to an amount of progenitor cells or a composition comprising progenitor cells that is sufficient to promote a particular effect when administered to a typical subject, such as one who has or is at risk for GSD1a. An effective amount would also include an amount sufficient to prevent or delay the development of a symptom of the disease, alter the course of a symptom of the disease (for example but not limited to, slow the progression of a symptom of the disease), or reverse a symptom of the disease. It

is understood that for any given case, an appropriate "effective amount" can be determined by one of ordinary skill in the art using routine experimentation.

[00574] For use in the various embodiments described herein, an effective amount of progenitor cells comprises at least 10^2 progenitor cells, at least 5 X 10^2 progenitor cells, at least 10^3 progenitor cells, at least 5 X 10^3 progenitor cells, at least 10^4 progenitor cells, at least 5 X 10^4 progenitor cells, at least 10^5 progenitor cells, at least 2 X 10^5 progenitor cells, at least 3 X 10^5 progenitor cells, at least 4 X 10^5 progenitor cells, at least 5 X 10^5 progenitor cells, at least 6 X 10^5 progenitor cells, at least 7 X 10^5 progenitor cells, at least 8 X 10^5 progenitor cells, at least 9 X 10^5 progenitor cells, at least 1 X 10^6 progenitor cells, at least 2 X 10^6 progenitor cells, at least 3 X 10^6 progenitor cells, at least 4 X 10^6 progenitor cells, at least 5 X 10^6 progenitor cells, at least 6 X 10^6 progenitor cells, at least 7 X 10^6 progenitor cells, at least 8 X 10^6 progenitor cells, at least 9 X 10^6 progenitor cells, or multiples thereof. The progenitor cells are derived from one or more donors, or are obtained from an autologous source. In some embodiments described herein, the progenitor cells are expanded in culture prior to administration to a subject in need thereof.

[00575] Modest and incremental increases in the levels of functional G6Pase expressed in cells of patients having GSD1a can be beneficial for ameliorating one or more symptoms of the disease, for increasing long-term survival, and/or for reducing side effects associated with other treatments. Upon administration of such cells to human patients, the presence of liver progenitors that are producing increased levels of functional G6Pase is beneficial. In some embodiments, effective treatment of a subject gives rise to at least about 3%, 5% or 7% functional G6Pase relative to total G6Pase in the treated subject. In some embodiments, functional G6Pase will be at least about 10% of total G6Pase. In some embodiments, functional G6Pase will be at least about 20% to 30% of total G6Pase. Similarly, the introduction of even relatively limited subpopulations of cells having significantly elevated levels of functional G6Pase can be beneficial in various patients because in some situations normalized cells will have a selective advantage relative to diseased cells. However, even modest levels of liver progenitors with elevated levels of functional G6Pase can be beneficial for ameliorating one or more aspects of GSD1a in patients. In some embodiments, about 10%, about 20%, about 30%,

about 40%, about 50%, about 60%, about 70%, about 80%, about 90% or more of the liver progenitors in patients to whom such cells are administered are producing increased levels of functional G6Pase.

[00576] "Administered" refers to the delivery of a progenitor cell composition into a subject by a method or route that results in at least partial localization of the cell composition at a desired site. A cell composition can be administered by any appropriate route that results in effective treatment in the subject, *i.e.* administration results in delivery to a desired location in the subject where at least a portion of the composition delivered, *i.e.* at least 1 x 10^4 cells are delivered to the desired site for a period of time. Modes of administration include injection, infusion, instillation, or ingestion. "Injection" includes, without limitation, intravenous, intramuscular, intra-arterial, intrathecal, intraventricular, intracapsular, intraorbital, intracardiac, intradermal, intraperitoneal, transtracheal, subcutaneous, subcuticular, intraarticular, sub capsular, subarachnoid, intraspinal, intracerebro spinal, and intrasternal injection and infusion. In some embodiments, the route is intravenous. For the delivery of cells, administration by injection or infusion can be made.

[00577] In one embodiment, the cells are administered systemically. The phrases "systemic administration," "administered systemically", "peripheral administration" and "administered peripherally" refer to the administration of a population of progenitor cells other than directly into a target site, tissue, or organ, such that it enters, instead, the subject's circulatory system and, thus, is subject to metabolism and other like processes.

[00578] The efficacy of a treatment comprising a composition for the treatment of GSD1a can be determined by the skilled clinician. However, a treatment is considered "effective treatment," if any one or all of the signs or symptoms of, as but one example, levels of functional G6Pase are altered in a beneficial manner (*e.g.*, increased by at least 10%), or other clinically accepted symptoms or markers of disease are improved or ameliorated. Efficacy can also be measured by failure of an individual to worsen as assessed by hospitalization or need for medical interventions (*e.g.*, normal glucose metabolism, or progression of the disease is halted or at least slowed). Methods of measuring these indicators are known to those of skill in the art and/or described herein. Treatment includes any treatment of

a disease in an individual or an animal (some non-limiting examples include a human, or a mammal) and includes: (1) inhibiting the disease, *e.g.*, arresting, or slowing the progression of symptoms; or (2) relieving the disease, *e.g.*, causing regression of symptoms; and (3) preventing or reducing the likelihood of the development of symptoms.

[00579] The treatment according to the present invention ameliorates one or more symptoms associated with GSD1a by increasing the amount of functional G6Pase in the individual. Early signs typically associated with GSD1a, include for example, seizures due to hypoglycemia.

[00580] Kits

[00581] The present disclosure provides kits for carrying out the methods of the invention. A kit can include one or more of a genome-targeting nucleic acid, a polynucleotide encoding a genome-targeting nucleic acid, a site-directed polypeptide, a polynucleotide encoding a site-directed polypeptide, and/or any nucleic acid or proteinaceous molecule necessary to carry out the embodiments of the methods of the invention, or any combination thereof.

[00582] In some embodiments, a kit comprises: (1) a vector comprising a nucleotide sequence encoding a genome-targeting nucleic acid, and (2) the site-directed polypeptide or a vector comprising a nucleotide sequence encoding the site-directed polypeptide and (3) a reagent for reconstitution and/or dilution of the vector(s) and or polypeptide.

[00583] In some embodiments, a kit comprises: (1) a vector comprising (i) a nucleotide sequence encoding a genome-targeting nucleic acid, and (ii) a nucleotide sequence encoding the site-directed polypeptide and (2) a reagent for reconstitution and/or dilution of the vector.

[00584] In some embodiments of any of the above kits, the kit comprises a single-molecule guide genome-targeting nucleic acid. In some embodiments of any of the above kits, the kit comprises a double-molecule genome-targeting nucleic acid. In some embodiments of any of the above kits, the kit comprises two or more double-molecule guides or single-molecule guides. In some embodiments, the kits comprise a vector that encodes the nucleic acid targeting nucleic acid.

[00585] In some embodiments of any of the above kits, the kit can further comprise a polynucleotide to be inserted to effect the desired genetic modification.

[00586] Components of a kit may be in separate containers, or combined in a single container.

[00587] In some embodiments, a kit described above further comprises one or more additional reagents, where such additional reagents are selected from a buffer, a buffer for introducing a polypeptide or polynucleotide into a cell, a wash buffer, a control reagent, a control vector, a control RNA polynucleotide, a reagent for *in vitro* production of the polypeptide from DNA, adaptors for sequencing and the like. A buffer can be a stabilization buffer, a reconstituting buffer, a diluting buffer, or the like. In some embodiments, a kit can also include one or more components that may be used to facilitate or enhance the on-target binding or the cleavage of DNA by the endonuclease, or improve the specificity of targeting.

[00588] In addition to the above-mentioned components, a kit can further include instructions for using the components of the kit to practice the methods. The instructions for practicing the methods are generally recorded on a suitable recording medium. For example, the instructions may be printed on a substrate, such as paper or plastic, etc. The instructions may be present in the kits as a package insert, in the labeling of the container of the kit or components thereof (*i.e.*, associated with the packaging or subpackaging), etc. The instructions can be present as an electronic storage data file present on a suitable computer readable storage medium, *e.g.* CD-ROM, diskette, flash drive, etc. In some instances, the actual instructions are not present in the kit, but means for obtaining the instructions from a remote source (*e.g.* via the Internet), can be provided. An example of this embodiment is a kit that includes a web address where the instructions can be viewed and/or from which the instructions can be downloaded. As with the instructions, this means for obtaining the instructions can be recorded on a suitable substrate.

[00589] Guide RNA Formulation

[00590] Guide RNAs of the invention are formulated with pharmaceutically acceptable excipients such as carriers, solvents, stabilizers, adjuvants, diluents, etc., depending upon the particular mode of administration and dosage form. Guide

RNA compositions are generally formulated to achieve a physiologically compatible pH, and range from a pH of about 3 to a pH of about 11, about pH 3 to about pH 7, depending on the formulation and route of administration. In some embodiments, the pH is adjusted to a range from about pH 5.0 to about pH 8. In some embodiments, the compositions comprise a therapeutically effective amount of at least one compound as described herein, together with one or more pharmaceutically acceptable excipients. Optionally, the compositions comprise a combination of the compounds described herein, or may include a second active ingredient useful in the treatment or prevention of bacterial growth (for example and without limitation, anti-bacterial or anti-microbial agents), or may include a combination of reagents of the invention.

[00591] Suitable excipients include, for example, carrier molecules that include large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Other exemplary excipients include antioxidants (for example and without limitation, ascorbic acid), chelating agents (for example and without limitation, EDTA), carbohydrates (for example and without limitation, dextrin, hydroxyalkylcellulose, and hydroxyalkylmethylcellulose), stearic acid, liquids (for example and without limitation, oils, water, saline, glycerol and ethanol), wetting or emulsifying agents, pH buffering substances, and the like.

[00592] Other Possible Therapeutic Approaches

[00593] Gene editing can be conducted using nucleases engineered to target specific sequences. To date there are four major types of nucleases: meganucleases and their derivatives, zinc finger nucleases (ZFNs), transcription activator like effector nucleases (TALENs), and CRISPR-Cas9 nuclease systems. The nuclease platforms vary in difficulty of design, targeting density and mode of action, particularly as the specificity of ZFNs and TALENs is through protein-DNA interactions, while RNA-DNA interactions primarily guide Cas9. Cas9 cleavage also requires an adjacent motif, the PAM, which differs between different CRISPR systems. Cas9 from *Streptococcus pyogenes* cleaves using a NRG PAM, CRISPR from Neisseria meningitidis can cleave at sites with PAMs including NNNNGATT,

NNNNNGTTT and NNNNGCTT. A number of other Cas9 orthologs target protospacer adjacent to alternative PAMs.

[00594] CRISPR endonucleases, such as Cas9 can be used in the methods of the invention. However, the teachings described herein, such as therapeutic target sites, could be applied to other forms of endonucleases, such as ZFNs, TALENs, HEs, or MegaTALs, or using combinations of nucleases. However, in order to apply the teachings of the present invention to such endonucleases, one would need to, among other things, engineer proteins directed to the specific target sites.

[00595] Additional binding domains can be fused to the Cas9 protein to increase specificity. The target sites of these constructs would map to the identified gRNA specified site, but would require additional binding motifs, such as for a zinc finger domain. In the case of Mega-TAL, a meganuclease can be fused to a TALE DNA-binding domain. The meganuclease domain can increase specificity and provide the cleavage. Similarly, inactivated or dead Cas9 (dCas9) can be fused to a cleavage domain and require the sgRNA/Cas9 target site and adjacent binding site for the fused DNA-binding domain. This likely would require some protein engineering of the dCas9, in addition to the catalytic inactivation, to decrease binding without the additional binding site.

[00596] Zinc Finger Nucleases

[00597] Zinc finger nucleases (ZFNs) are modular proteins comprised of an engineered zinc finger DNA binding domain linked to the catalytic domain of the type II endonuclease FokI. Because FokI functions only as a dimer, a pair of ZFNs must be engineered to bind to cognate target “half-site” sequences on opposite DNA strands and with precise spacing between them to enable the catalytically active FokI dimer to form. Upon dimerization of the FokI domain, which itself has no sequence specificity per se, a DNA double-strand break is generated between the ZFN half-sites as the initiating step in genome editing.

[00598] The DNA binding domain of each ZFN is typically comprised of 3-6 zinc fingers of the abundant Cys2-His2 architecture, with each finger primarily recognizing a triplet of nucleotides on one strand of the target DNA sequence, although cross-strand interaction with a fourth nucleotide also can be important. Alteration of the amino acids of a finger in positions that make key contacts with the

DNA alters the sequence specificity of a given finger. Thus, a four-finger zinc finger protein will selectively recognize a 12 bp target sequence, where the target sequence is a composite of the triplet preferences contributed by each finger, although triplet preference can be influenced to varying degrees by neighboring fingers. An important aspect of ZFNs is that they can be readily re-targeted to almost any genomic address simply by modifying individual fingers, although considerable expertise is required to do this well. In most applications of ZFNs, proteins of 4-6 fingers are used, recognizing 12-18 bp respectively. Hence, a pair of ZFNs will typically recognize a combined target sequence of 24-36 bp, not including the 5-7 bp spacer between half-sites. The binding sites can be separated further with larger spacers, including 15-17 bp. A target sequence of this length is likely to be unique in the human genome, assuming repetitive sequences or gene homologs are excluded during the design process. Nevertheless, the ZFN protein-DNA interactions are not absolute in their specificity so off-target binding and cleavage events do occur, either as a heterodimer between the two ZFNs, or as a homodimer of one or the other of the ZFNs. The latter possibility has been effectively eliminated by engineering the dimerization interface of the FokI domain to create “plus” and “minus” variants, also known as obligate heterodimer variants, which can only dimerize with each other, and not with themselves. Forcing the obligate heterodimer prevents formation of the homodimer. This has greatly enhanced specificity of ZFNs, as well as any other nuclease that adopts these FokI variants.

[00599] A variety of ZFN-based systems have been described in the art, modifications thereof are regularly reported, and numerous references describe rules and parameters that are used to guide the design of ZFNs; see, *e.g.*, Segal *et al.*, *Proc Natl Acad Sci USA 96*(6):2758-63 (1999); Dreier B *et al.*, *J Mol Biol. 303*(4):489-502 (2000); Liu Q *et al.*, *J Biol Chem. 277*(6):3850-6 (2002); Dreier *et al.*, *J Biol Chem 280*(42):35588-97 (2005); and Dreier *et al.*, *J Biol Chem. 276*(31):29466-78 (2001).

[00600] Transcription Activator-Like Effector Nucleases (TALENs)

[00601] TALENs represent another format of modular nucleases whereby, as with ZFNs, an engineered DNA binding domain is linked to the FokI nuclease

domain, and a pair of TALENs operate in tandem to achieve targeted DNA cleavage. The major difference from ZFNs is the nature of the DNA binding domain and the associated target DNA sequence recognition properties. The TALEN DNA binding domain derives from TALE proteins, which were originally described in the plant bacterial pathogen *Xanthomonas sp*. TALEs are comprised of tandem arrays of 33-35 amino acid repeats, with each repeat recognizing a single basepair in the target DNA sequence that is typically up to 20 bp in length, giving a total target sequence length of up to 40 bp. Nucleotide specificity of each repeat is determined by the repeat variable diresidue (RVD), which includes just two amino acids at positions 12 and 13. The bases guanine, adenine, cytosine and thymine are predominantly recognized by the four RVDs: Asn-Asn, Asn-Ile, His-Asp and Asn-Gly, respectively. This constitutes a much simpler recognition code than for zinc fingers, and thus represents an advantage over the latter for nuclease design. Nevertheless, as with ZFNs, the protein-DNA interactions of TALENs are not absolute in their specificity, and TALENs have also benefitted from the use of obligate heterodimer variants of the FokI domain to reduce off-target activity.

[00602] Additional variants of the FokI domain have been created that are deactivated in their catalytic function. If one half of either a TALEN or a ZFN pair contains an inactive FokI domain, then only single-strand DNA cleavage (nicking) will occur at the target site, rather than a DSB. The outcome is comparable to the use of CRISPR/Cas9 “nickase” mutants in which one of the Cas9 cleavage domains has been deactivated. DNA nicks can be used to drive genome editing by HDR, but at lower efficiency than with a DSB. The main benefit is that off-target nicks are quickly and accurately repaired, unlike the DSB, which is prone to NHEJ-mediated mis-repair.

[00603] A variety of TALEN-based systems have been described in the art, and modifications thereof are regularly reported; see, *e.g.*, Boch, *Science* *326*(5959):1509-12 (2009); Mak *et al.*, *Science 335*(6069):716-9 (2012); and Moscou *et al.*, *Science 326*(5959):1501 (2009). The use of TALENs based on the "Golden Gate" platform, or cloning scheme, has been described by multiple groups; see, *e.g.*, Cermak *et al.*, *Nucleic Acids Res. 39*(12):e82 (2011); Li *et al.*, *Nucleic Acids Res. 39*(14):6315-25(2011); Weber *et al.*, *PLoS One. 6*(2):e16765 (2011);

Wang *et al.*, *J Genet Genomics 41*(6):339-47, Epub 2014 May 17 (2014); and Cermak T *et al.*, *Methods Mol Biol. 1239*:133-59 (2015).

[00604] Homing Endonucleases

[00605] Homing endonucleases (HEs) are sequence-specific endonucleases that have long recognition sequences (14-44 base pairs) and cleave DNA with high specificity – often at sites unique in the genome. There are at least six known families of HEs as classified by their structure, including LAGLIDADG (SEQ ID NO: 64,791), GIY-YIG, His-Cis box, H-N-H, PD-(D/E)xK, and Vsr-like that are derived from a broad range of hosts, including eukarya, protists, bacteria, archaea, cyanobacteria and phage. As with ZFNs and TALENs, HEs can be used to create a DSB at a target locus as the initial step in genome editing. In addition, some natural and engineered HEs cut only a single strand of DNA, thereby functioning as site-specific nickases. The large target sequence of HEs and the specificity that they offer have made them attractive candidates to create site-specific DSBs.

[00606] A variety of HE-based systems have been described in the art, and modifications thereof are regularly reported; see, *e.g.*, the reviews by Steentoft *et al.*, *Glycobiology 24*(8):663-80 (2014); Belfort and Bonocora, *Methods Mol Biol. 1123*:1-26 (2014); Hafez and Hausner, *Genome 55*(8):553-69 (2012); and references cited therein.

[00607] MegaTAL / Tev-mTALEN / MegaTev

[00608] As further examples of hybrid nucleases, the MegaTAL platform and Tev-mTALEN platform use a fusion of TALE DNA binding domains and catalytically active HEs, taking advantage of both the tunable DNA binding and specificity of the TALE, as well as the cleavage sequence specificity of the HE; see, *e.g.*, Boissel *et al., NAR 42*: 2591-2601 (2014); Kleinstiver *et al.*, *G3 4*:1155-65 (2014); and Boissel and Scharenberg, *Methods Mol. Biol. 1239*: 171-96 (2015).

[00609] In a further variation, the MegaTev architecture is the fusion of a meganuclease (Mega) with the nuclease domain derived from the GIY-YIG homing endonuclease I-TevI (Tev). The two active sites are positioned ~30 bp apart on a DNA substrate and generate two DSBs with non-compatible cohesive ends; see, *e.g.*, Wolfs *et al.*, *NAR 42*, 8816-29 (2014). It is anticipated that other combinations

of existing nuclease-based approaches will evolve and be useful in achieving the targeted genome modifications described herein.

[00610] dCas9-FokI and Other Nucleases

[00611] Combining the structural and functional properties of the nuclease platforms described above offers a further approach to genome editing that can potentially overcome some of the inherent deficiencies. As an example, the CRISPR genome editing system typically uses a single Cas9 endonuclease to create a DSB. The specificity of targeting is driven by a 20 or 24 nucleotide sequence in the guide RNA that undergoes Watson-Crick base-pairing with the target DNA (plus an additional 2 bases in the adjacent NAG or NGG PAM sequence in the case of Cas9 or Cpf1 from *S. pyogenes*). Such a sequence is long enough to be unique in the human genome, however, the specificity of the RNA/DNA interaction is not absolute, with significant promiscuity sometimes tolerated, particularly in the 5' half of the target sequence, effectively reducing the number of bases that drive specificity. One solution to this has been to completely deactivate the Cas9 catalytic function – retaining only the RNA-guided DNA binding function – and instead fusing a FokI domain to the deactivated Cas9; see, *e.g.*, Tsai *et al., Nature Biotech 32:* 569-76 (2014); and Guilinger *et al.*, *Nature Biotech. 32:* 577-82 (2014). Because FokI must dimerize to become catalytically active, two guide RNAs are required to tether two FokI fusions in close proximity to form the dimer and cleave DNA. This essentially doubles the number of bases in the combined target sites, thereby increasing the stringency of targeting by CRISPR-based systems.

[00612] As further example, fusion of the TALE DNA binding domain to a catalytically active HE, such as I-TevI, takes advantage of both the tunable DNA binding and specificity of the TALE, as well as the cleavage sequence specificity of I-TevI, with the expectation that off-target cleavage may be further reduced.

[00613] Methods and Compositions of the Invention

[00614] Accordingly, the present disclosure relates in particular to the following non-limiting inventions: In a first method, Method 1, the present disclosure provides a I method for editing the glucose-6-phosphatase, catalytic (G6PC) gene in a human cell by genome editing, the method comprising the step of: introducing into

the human cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction, or modulation of expression of function of one or more exons within or near or affecting the expression or function of the G6PC gene and results in restoration of glucose-6-phosphatase (G6Pase) protein activity.

[00615] In another method, Method 2, the present disclosure provides a method for inserting a G6PC gene in a human cell by genome editing, the method comprising introducing into the human cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near a safe harbor locus that results in a permanent insertion of the G6PC gene, and results in restoration of G6Pase protein activity.

[00616] In another method, Method 3, the present disclosure provides an *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a), the method comprising the steps of: i) creating a patient specific induced pluripotent stem cell (iPSC) , or editing within or near a safe harbor locus of the iPSC; ii) editing within or near a glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the G6PC gene of the iPSC; iii) differentiating the genome edited iPSC into a hepatocyte; and iv) implanting the hepatocyte into the patient.

[00617] In another method, Method 4, the present disclosure provides the method of Method 3, wherein the creating step comprises: a) isolating a somatic cell from the patient; and b) introducing a set of pluripotency-associated genes into the somatic cell to induce the somatic cell to become a pluripotent stem cell.

[00618] In another method, Method 5, the present disclosure provides the method of Method 4, wherein the somatic cell is a fibroblast.

[00619] In another method, Method 6, the present disclosure provides the method of Method 4, wherein the set of pluripotency-associated genes is one or more of the genes selected from the group consisting of OCT4, SOX2, KLF4, Lin28, NANOG and cMYC.

[00620] In another method, Method 7, the present disclosure provides the method of any one of Methods 3-6, wherein the editing step comprises introducing into the iPSC one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus and results in restoration of glucose-6-phosphatase (G6Pase) protein activity.

[00621] In another method, Method 8, the present disclosure provides the method of Method 7, wherein the safe harbor locus is selected from the group consisting of AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR. The safe harbor locus can be selected from the group consisting of: exon 1-2 of AAVS1 (PPP1R12C), exon 1-2 of ALB, exon 1-2 of Angptl3, exon 1-2 of ApoC3, exon 1-2 of ASGR2, exon 1-2 of CCR5, exon 1-2 of FIX (F9), exon 1-2 of Gys2, exon 1-2 of HGD, exon 1-2 of Lp(a), exon 1-2 of Pcsk9, exon 1-2 of Serpina1, exon 1-2 of TF, and exon 1-2 of TTR.

[00622] In another method, Method 9, the present disclosure provides the method of any one of Methods 3-8, wherein the differentiating step comprises one or more of the following to differentiate the genome edited iPSC into a hepatocyte: contacting the genome edited iPSC with one or more of activin, B27 supplement, FGF4, HGF, BMP2, BMP4, Oncostatin M, Dexametason.

[00623] In another method, Method 10, the present disclosure provides the method of any one of Methods 3-9, wherein the implanting step comprises implanting the hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

[00624] In another method, Method 11, the present disclosure provides an *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a), the method comprising the steps of: i) performing a biopsy of the patient's liver; ii) isolating a liver specific progenitor cell or primary hepatocyte; iii) editing within or near the glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the G6PC gene of the progenitor cell or primary

hepatocyte or editing within or near a safe harbor locus of the progenitor cell or primary hepatocyte; and iv) implanting the genome-edited progenitor cell or primary hepatocyte into the patient.

[00625] In another method, Method 12, the present disclosure provides the method of Method 11, wherein the isolating step comprises: perfusion of fresh liver tissues with digestion enzymes, cell differential centrifugation, cell culturing, or combinations thereof.

[00626] In another method, Method 13, the present disclosure provides the method of any one of Methods 11-12, wherein the editing step comprises introducing into the progenitor cell or primary hepatocyte one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor that results in a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus and restoration of glucose-6-phosphatase (G6Pase) protein activity.

[00627] In another method, Method 14, the present disclosure provides the method of Method 13, wherein the safe harbor locus is selected from the group consisting of AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR. The safe harbor locus can be selected from the group consisting of: exon 1-2 of AAVS1 (PPP1R12C), exon 1-2 of ALB, exon 1-2 of Angptl3, exon 1-2 of ApoC3, exon 1-2 of ASGR2, exon 1-2 of CCR5, exon 1-2 of FIX (F9), exon 1-2 of Gys2, exon 1-2 of HGD, exon 1-2 of Lp(a), exon 1-2 of Pcsk9, exon 1-2 of Serpina1, exon 1-2 of TF, and exon 1-2 of TTR.

[00628] In another method, Method 15, the present disclosure provides the method of any one of Methods 11-14, wherein the implanting step comprises implanting the genome-edited progenitor cell or primary hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

[00629] In another method, Method 16, the present disclosure provides an *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a), the method comprising the steps of: i) performing a biopsy of the patient's bone

marrow; ii) isolating a mesenchymal stem cell from the patient; iii) editing within or near the glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the G6PC gene of the mesenchymal stem cell or editing within or near a safe harbor locus of the mesenchymal stem cell; iv) differentiating the genome-edited mesenchymal stem cell into a hepatocyte; and v) implanting the hepatocyte into the patient.

[00630] In another method, Method 17, the present disclosure provides the method of Method 16, wherein the mesenchymal stem cell is isolated from the patient's bone marrow or peripheral blood.

[00631] In another method, Method 18, the present disclosure provides the method of Method 16, wherein the isolating step comprises: aspiration of bone marrow and isolation of mesenchymal cells by density centrifugation using Percoll™.

[00632] In another method, Method 19, the present disclosure provides the method of any one of Methods 16-18, wherein the editing step comprises introducing into the mesenchymal stem cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus and restoration of glucose-6-phosphatase (G6Pase) protein activity.

[00633] In another method, Method 20, the present disclosure provides the method of Method 19, wherein the safe harbor locus is selected from the group consisting of AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR. The safe harbor locus can be selected from the group consisting of: exon 1-2 of AAVS1 (PPP1R12C), exon 1-2 of ALB, exon 1-2 of Angptl3, exon 1-2 of ApoC3, exon 1-2 of ASGR2, exon 1-2 of CCR5, exon 1-2 of FIX (F9), exon 1-2 of Gys2, exon 1-2 of HGD, exon 1-2 of Lp(a), exon 1-2 of Pcsk9, exon 1-2 of Serpina1, exon 1-2 of TF, and exon 1-2 of TTR.

[00634] In another method, Method 21, the present disclosure provides the method of any one of Methods 16-19, wherein the differentiating step comprises one or more of the following to differentiate the genome edited mesenchymal stem cell into a hepatocyte: contacting the genome edited stem cell with one or more of insulin, transferrin, FGF4, HGF, or bile acids.

[00635] In another method, Method 22, the present disclosure provides the method of any one of Methods 16-21, wherein the implanting step comprises implanting the hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

[00636] In another method, Method 23, the present disclosure provides an *in vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a), the method comprising the step of editing the glucose-6-phosphatase, catalytic (G6PC) gene in a cell of the patient, or other DNA sequences that encode regulatory elements of the G6PC gene, or editing within or near a safe harbor locus in a cell of the patient.

[00637] In another method, Method 24, the present disclosure provides the method of Method 23, wherein the editing step comprises introducing into the cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus that results in a permanent insertion of the G6PC gene and restoration of glucose-6-phosphatase (G6Pase) protein activity.

[00638] In another method, Method 25, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19, or 24, wherein the one or more DNA endonucleases is a Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas100, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, or Cpf1 endonuclease; or a homolog thereof,

recombination of the naturally occurring molecule, codon-optimized, or modified version thereof, and combinations thereof.

[00639] In another method, Method 26, the present disclosure provides the method of Method 25, wherein the method comprises introducing into the cell one or more polynucleotides encoding the one or more DNA endonucleases.

[00640] In another method, Method 27, the present disclosure provides the method of Method 25, wherein the method comprises introducing into the cell one or more ribonucleic acids (RNAs) encoding the one or more DNA endonucleases.

[00641] In another method, Method 28, the present disclosure provides the method of any one of Methods 26 or 27, wherein the one or more polynucleotides or one or more RNAs is one or more modified polynucleotides or one or more modified RNAs.

[00642] In another method, Method 29, the present disclosure provides the method of Method 26, wherein the DNA endonuclease is a protein or polypeptide.

[00643] In another method, Method 30, the present disclosure provides the method of any one of the preceding Methods, wherein the method further comprises introducing into the cell one or more guide ribonucleic acids (gRNAs).

[00644] In another method, Method 31, the present disclosure provides the method of Method 30, wherein the one or more gRNAs are single-molecule guide RNA (sgRNAs).

[00645] In another method, Method 32, the present disclosure provides the method of any one of Methods 30-31, wherein the one or more gRNAs or one or more sgRNAs is one or more modified gRNAs or one or more modified sgRNAs.

[00646] In another method, Method 33, the present disclosure provides the method of any one of Methods 30-32, wherein the one or more DNA endonucleases is pre-complexed with one or more gRNAs or one or more sgRNAs.

[00647] In another method, Method 34, the present disclosure provides the method of any one of the preceding Methods, wherein the method further comprises introducing into the cell a polynucleotide donor template comprising at least a portion of the wild-type G6PC gene or cDNA.

[00648] In another method, Method 35, the present disclosure provides the method of Method 34, wherein the at least a portion of the wild-type G6PC gene or cDNA is exon 1, exon 2, exon 3, exon 4, exon 5, intronic regions, fragments or combinations thereof, the entire G6PC gene, DNA sequences that encode wild-type regulatory elements of the G6PC gene, or cDNA.

[00649] In another method, Method 36, the present disclosure provides the method of any one of Methods 34-35, wherein the donor template is either a single or double stranded polynucleotide.

[00650] In another method, Method 37, the present disclosure provides the method of any one of Methods 34-36, wherein the donor template has homologous arms to the 17q21 region.

[00651] In another method, Method 38, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19, or 24, wherein the method further comprises introducing into the cell one guide ribonucleic acid (gRNA) and a polynucleotide donor template comprising at least a portion of the wild-type G6PC gene, and wherein the one or more DNA endonucleases is one or more Cas9 endonucleases that effect one single-strand break (SSB) or double-strand break (DSB) at a DSB locus within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor locus that facilitates insertion of a new sequence from the polynucleotide donor template into the chromosomal DNA at the locus or safe harbor locus that results in a permanent insertion or correction of a part of the chromosomal DNA of the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene proximal to the locus or safe harbor locus and restoration of G6Pase protein activity, and wherein the gRNA comprises a spacer sequence that is complementary to a segment of the locus or safe harbor locus.

[00652] In another method, Method 39, the present disclosure provides the method of Method 38, wherein proximal means nucleotides both upstream and downstream of the locus or safe harbor locus.

[00653] In another method, Method 40, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19, or 24, wherein the method further comprises introducing into the cell two guide ribonucleic acid (gRNAs) and a

polynucleotide donor template comprising at least a portion of the wild-type G6PC gene, and wherein the one or more DNA endonucleases is two or more Cas9 or Cpf1 endonucleases that effect a pair of single-strand breaks (SSBs) or double-strand breaks (DSBs), the first at a 5' locus and the second at a 3' locus, within the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor locus that facilitates insertion of a new sequence from the polynucleotide donor template into the chromosomal DNA between the 5' locus and the 3' locus that results in permanent correction of the chromosomal DNA between the 5' locus and the 3' locus within the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor locus and restoration of G6Pase protein activity, and wherein the first guide RNA comprises a spacer sequence that is complementary to a segment of the 5' locus and the second guide RNA comprises a spacer sequence that is complementary to a segment of the 3' locus.

[00654] In another method, Method 41, the present disclosure provides the method of any one of Methods 38-40, wherein the one or two gRNAs are one or two single-molecule guide RNA (sgRNAs).

[00655] In another method, Method 42, the present disclosure provides the method of any one of Methods 38-41, wherein the one or two gRNAs or one or two sgRNAs is one or two modified gRNA or one or two modified sgRNA.

[00656] In another method, Method 43, the present disclosure provides the method of any one of Methods 38-42, wherein the one or more DNA endonucleases is pre-complexed with one or two gRNAs or one or two sgRNAs.

[00657] In another method, Method 44, the present disclosure provides the method of any one of Methods 38-43, wherein the at least a portion of the wild-type G6PC gene or cDNA is exon 1, exon 2, exon 3, exon 4, exon 5, intronic regions, fragments or combinations thereof, the entire G6PC gene, DNA sequences that encode wild-type regulatory elements of the G6PC gene, or cDNA.

[00658] In another method, Method 45, the present disclosure provides the method of any one of Methods 38-44, wherein the donor template is either a single or double stranded polynucleotide.

[00659] In another method, Method 46, the present disclosure provides the method of any one of Methods 38-45, wherein the donor template has homologous arms to the 17q21 region.

[00660] In another method, Method 47, the present disclosure provides the method of Method 3644, wherein the SSB, DSB, or 5' DSB and 3' DSB are in the first, second, third, fourth, fifth exon or intron of the G6PC gene.

[00661] In another method, Method 48, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19, 24, 30-33, or 38-41, wherein the gRNA or sgRNA is directed to one or more of the following pathological variants: rs80356479, rs80356486, rs606231368, rs80356488, rs587776757, rs104894565, rs104894566, rs1801175, rs1801176, rs104894567, rs104894571, rs80356482, rs80356483, rs104894563, rs367727229, rs387906505, rs104894568, rs104894569, rs80356487, rs764920787, rs80356485, rs780226142, rs80356484.

[00662] In another method, Method 49, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19 or 24-48, wherein the insertion or correction is by homology directed repair (HDR).

[00663] In another method, Method 50, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19 or 24-49, wherein the Cas9 mRNA, gRNA, and donor template are either each formulated into separate lipid nanoparticles or all co-formulated into a lipid nanoparticle.

[00664] In another method, Method 51, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19 or 24-49, wherein the Cas9 or Cpf1 mRNA is formulated into a lipid nanoparticle, and both the gRNA and donor template are delivered to the cell by a viral vector.

[00665] In another method, Method 52, the present disclosure provides the method of Method 51, wherein the viral vector is an adeno-associated virus (AAV).

[00666] In another method, Method 53, the present disclosure provides the method of Method 52, wherein the AAV vector is an AAV6 vector.

[00667] In another method, Method 54, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19 or 24-49, wherein the Cas9 or Cpf1

mRNA, gRNA and a donor template are either each formulated into separate exosomes or all co-formulated into an exosome.

[00668] 5In another method, Method 55, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19 or 24-49, wherein the Cas9 or Cpf1 mRNA is formulated into a lipid nanoparticle, and the gRNA is delivered to the cell by electroporation and donor template is delivered to the cell by a viral vector.

[00669] In another method, Method 56, the present disclosure provides the method of Method 55, wherein the viral vector is an adeno-associated virus (AAV) vector.

[00670] In another method, Method 57, the present disclosure provides the method of Method 56, wherein the AAV vector is an AAV6 vector.

[00671] In another method, Method 58, the present disclosure provides the method of any one of the preceding Methods, wherein the G6PC gene is located on Chromosome 17: 42,900,796 - 42,914,432 (Genome Reference Consortium – GRCh38/hg38).

[00672] In another method, Method 59, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19 or 24-49, wherein the restoration of G6Pase protein activity is compared to wild-type or normal G6Pase protein activity.

[00673] In another method, Method 60, the present disclosure provides the method of Method 1, wherein the human cell is a liver cell.

[00674] In another method, Method 61, the present disclosure provides the method of Method 23, wherein the cell is a liver cell.

[00675] In another method, Method 62, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19 or 24-49, wherein the G6PC gene is operably linked to an exogenous promoter that drives expression of the G6PC gene.

[00676] In another method, Method 63, the present disclosure provides the method of any one of Methods 1, 2, 7, 13, 19 or 24-49, wherein the one or more SSBs or DSBs occurs at a location immediately 3’ to an endogenous promoter locus.

[00677] The present disclosure also provides a composition, Composition 1, comprising one or more guide ribonucleic acids (gRNAs) or editing a G6PC gene in a cell from a patient with Glycogen Storage Disease type 1a (GSD1a), the one or more gRNAs comprising a spacer sequence selected from the group consisting of the nucleic acid sequences in Figures 1-90 for editing the glucose-6-phosphatase, catalytic gene in a cell from a patient with Glycogen Storage Disease type 1a.

[00678] In another composition, Composition 2, the present disclosure provides the one or more gRNAs of Composition 1, wherein the one or more gRNAs are one or more single-molecule guide RNAs (sgRNAs).

[00679] In another composition, Composition 3, the present disclosure provides the one or more gRNAs or sgRNAs of Composition 1 or 2, wherein the one or more gRNAs or one or more sgRNAs is one or more modified gRNA or one or more modified sgRNA.

[00680] In another composition, Composition 4, the present disclosure provides the one or more gRNAs or sgRNAs of Compositions 63-65, wherein the cell is a liver cell.

[00681] Definitions

[00682] The term "comprising" or "comprises" is used in reference to compositions, methods, and respective component(s) thereof, that are essential to the invention, yet open to the inclusion of unspecified elements, whether essential or not.

[00683] The term "consisting essentially of" refers to those elements required for a given embodiment. The term permits the presence of additional elements that do not materially affect the basic and novel or functional characteristic(s) of that embodiment of the invention.

[00684] The term "consisting of" refers to compositions, methods, and respective components thereof as described herein, which are exclusive of any element not recited in that description of the embodiment.

[00685] The singular forms "a," "an," and "the" include plural references, unless the context clearly dictates otherwise.

[00686] Certain numerical values presented herein are preceded by the term "about." The term "about" is used to provide literal support for the numerical value the term "about" precedes, as well as a numerical value that is approximately the numerical value, that is the approximating unrecited numerical value may be a number which, in the context it is presented, is the substantial equivalent of the specifically recited numerical value. The term "about" means numerical values within ± 10% of the recited numerical value.

[00687] When a range of numerical values is presented herein, it is contemplated that each intervening value between the lower and upper limit of the range, the values that are the upper and lower limits of the range, and all stated values with the range are encompassed within the disclosure. All the possible sub-ranges within the lower and upper limits of the range are also contemplated by the disclosure.

Examples

[00688] The invention will be more fully understood by reference to the following examples, which provide illustrative non-limiting embodiments of the invention.

[00689] The examples describe the use of the CRISPR system as an illustrative genome editing technique to create defined therapeutic genomic replacements, termed "genomic modifications" herein, in the G6PC gene that lead to permanent correction of mutations in the genomic locus, or expression at a heterologous locus, that restore G6Pase activity. Introduction of the defined therapeutic modifications represents a novel therapeutic strategy for the potential amelioration of GSD1a, as described and illustrated herein.

Example 1 - CRISPR/SpCas9 target sites for the AAVS1 (PPP1R12C) gene

[00690] Exons 1-2 of the AAVS1 (PPP1R12C) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 1.

Example 2 - CRISPR/SaCas9 target sites for the AAVS1 (PPP1R12C) gene

[00691] Exons 1-2 of the AAVS1 (PPP1R12C) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 2.

Example 3 - CRISPR/StCas9 target sites for the AAVS1 (PPP1R12C) gene

[00692] Exons 1-2 of the AAVS1 (PPP1R12C) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 3.

Example 4 - CRISPR/TdCas9 target sites for the AAVS1 (PPP1R12C) gene

[00693] Exons 1-2 of the AAVS1 (PPP1R12C) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 4.

Example 5 - CRISPR/NmCas9 target sites for the AAVS1 (PPP1R12C) gene

[00694] Exons 1-2 of the AAVS1 (PPP1R12C) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 5.

Example 6 - CRISPR/Cpf1 target sites for the AAVS1 (PPP1R12C) gene

[00695] Exons 1-2 of the AAVS1 (PPP1R12C) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 6.

Example 7 - CRISPR/SpCas9 target sites for the ALB gene

[00696] Exons 1-2 of the ALB gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG.

gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 7.

Example 8 - CRISPR/SaCas9 target sites for the ALB gene

[00697] Exons 1-2 of the ALB gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 8.

Example 9 - CRISPR/StCas9 target sites for the ALB gene

[00698] Exons 1-2 of the ALB gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 9.

Example 10 - CRISPR/TdCas9 target sites for the ALB gene

[00699] Exons 1-2 of the ALB gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 10.

Example 11 - CRISPR/NmCas9 target sites for the ALB gene

[00700] Exons 1-2 of the ALB gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 11.

Example 12 - CRISPR/Cpf1 target sites for the ALB gene

[00701] Exons 1-2 of the ALB gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 12.

Example 13 - CRISPR/SpCas9 target sites for the Angptl3 gene

[00703] Exons 1-2 of the Angptl3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 13.

Example 14 - CRISPR/SaCas9 target sites for the Angptl3 gene

[00704] Exons 1-2 of the Angptl3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 14.

Example 15 - CRISPR/StCas9 target sites for the Angptl3 gene

[00705] Exons 1-2 of the Angptl3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 15.

Example 16 - CRISPR/TdCas9 target sites for the Angptl3 gene

[00706] Exons 1-2 of the Angptl3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 16.

Example 17 - CRISPR/NmCas9 target sites for the Angptl3 gene

[00707] Exons 1-2 of the Angptl3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 17.

Example 18 - CRISPR/Cpf1 target sites for the Angptl3 gene

[00708] Exons 1-2 of the Angptl3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN.

gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 18.

Example 19 - CRISPR/SpCas9 target sites for the ApoC3 gene

[00709] Exons 1-2 of the ApoC3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 19.

Example 20 - CRISPR/SaCas9 target sites for the ApoC3 gene

[00710] Exons 1-2 of the ApoC3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 20.

Example 21 - CRISPR/StCas9 target sites for the ApoC3 gene

[00711] Exons 1-2 of the ApoC3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 21.

Example 22 - CRISPR/TdCas9 target sites for the ApoC3 gene

[00712] Exons 1-2 of the ApoC3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 22.

Example 23 - CRISPR/NmCas9 target sites for the ApoC3 gene

[00713] Exons 1-2 of the ApoC3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 23.

Example 24 - CRISPR/Cpf1 target sites for the ApoC3 gene

[00714] Exons 1-2 of the ApoC3 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 24.

Example 25 - CRISPR/SpCas9 target sites for the ASGR2 gene

[00715] Exons 1-2 of the ASGR2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 25.

Example 26 - CRISPR/SaCas9 target sites for the ASGR2 gene

[00716] Exons 1-2 of the ASGR2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 26.

Example 27 - CRISPR/StCas9 target sites for the ASGR2 gene

[00717] Exons 1-2 of the ASGR2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 27.

Example 28 - CRISPR/TdCas9 target sites for the ASGR2 gene

[00718] Exons 1-2 of the ASGR2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 28.

Example 29 - CRISPR/NmCas9 target sites for the ASGR2 gene

[00719] Exons 1-2 of the ASGR2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence

NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 29.

Example 30 - CRISPR/Cpf1 target sites for the ASGR2 gene

[00720] Exons 1-2 of the ASGR2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 30.

Example 31 - CRISPR/SpCas9 target sites for the CCR5 gene

[00721] Exons 1-2 of the CCR5 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 31.

Example 32 - CRISPR/SaCas9 target sites for the CCR5 gene

[00722] Exons 1-2 of the CCR5 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 32.

Example 33 - CRISPR/StCas9 target sites for the CCR5 gene

[00723] Exons 1-2 of the CCR5 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 33.

Example 34 - CRISPR/TdCas9 target sites for the CCR5 gene

[00724] Exons 1-2 of the CCR5 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 34.

Example 35 - CRISPR/NmCas9 target sites for the CCR5 gene

[00725] Exons 1-2 of the CCR5 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 35.

Example 36 - CRISPR/Cpf1 target sites for the CCR5 gene

[00726] Exons 1-2 of the CCR5 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 36.

Example 37 - CRISPR/SpCas9 target sites for the FIX (F9) gene

[00727] Exons 1-2 of the FIX (F9) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 37.

Example 38 - CRISPR/SaCas9 target sites for the FIX (F9) gene

[00728] Exons 1-2 of the FIX (F9) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 38.

Example 39 - CRISPR/StCas9 target sites for the FIX (F9) gene

[00729] Exons 1-2 of the FIX (F9) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 39.

Example 40 - CRISPR/TdCas9 target sites for the FIX (F9) gene

[00730] Exons 1-2 of the FIX (F9) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence

NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 40.

Example 41 - CRISPR/NmCas9 target sites for the FIX (F9) gene

[00731] Exons 1-2 of the FIX (F9) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 41.

Example 42 - CRISPR/Cpf1 target sites for the FIX (F9) gene

[00732] Exons 1-2 of the FIX (F9) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 42.

Example 43 - CRISPR/SpCas9 target sites for the Gys2 gene

[00733] Exons 1-2 of the Gys2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 43

Example 44 - CRISPR/SaCas9 target sites for the Gys2 gene

[00734] Exons 1-2 of the Gys2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 44.

Example 45 - CRISPR/StCas9 target sites for the Gys2 gene

[00735] Exons 1-2 of the Gys2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 45.

Example 46 - CRISPR/TdCas9 target sites for the Gys2 gene

[00736] Exons 1-2 of the Gys2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 46.

Example 47 - CRISPR/NmCas9 target sites for the Gys2 gene

[00737] Exons 1-2 of the Gys2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 47.

Example 48 - CRISPR/Cpf1 target sites for the Gys2 gene

[00738] Exons 1-2 of the Gys2 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 48.

Example 49 - CRISPR/SpCas9 target sites for the HGD gene

[00739] Exons 1-2 of the HGD gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 49.

Example 50 - CRISPR/SaCas9 target sites for the HGD gene

[00740] Exons 1-2 of the HGD gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 50.

Example 51 - CRISPR/StCas9 target sites for the HGD gene

[00741] Exons 1-2 of the HGD gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence

NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 51.

Example 52 - CRISPR/TdCas9 target sites for the HGD gene

[00742] Exons 1-2 of the HGD gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 52.

Example 53 - CRISPR/NmCas9 target sites for the HGD gene

[00743] Exons 1-2 of the HGD gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 53.

Example 54 - CRISPR/Cpf1 target sites for the HGD gene

[00744] Exons 1-2 of the HGD gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 54.

Example 55 - CRISPR/SpCas9 target sites for the Lp(a) gene

[00745] Exons 1-2 of the Lp(a) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 55.

Example 56 - CRISPR/SaCas9 target sites for the Lp(a) gene

[00746] Exons 1-2 of the Lp(a) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 56.

Example 57 - CRISPR/StCas9 target sites for the Lp(a) gene

[00747] Exons 1-2 of the Lp(a) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 57.

Example 58 - CRISPR/TdCas9 target sites for the Lp(a) gene

[00748] Exons 1-2 of the Lp(a) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 58.

Example 59 - CRISPR/NmCas9 target sites for the Lp(a) gene

[00749] Exons 1-2 of the Lp(a) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 59.

Example 60 - CRISPR/Cpf1 target sites for the Lp(a) gene

[00750] Exons 1-2 of the Lp(a) gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 60.

Example 61 - CRISPR/SpCas9 target sites for the PCSK9 gene

[00751] Exons 1-2 of the PCSK9 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 61.

Example 62 - CRISPR/SaCas9 target sites for the PCSK9 gene

[00752] Exons 1-2 of the PCSK9 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence

NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 62.

Example 63 - CRISPR/StCas9 target sites for the PCSK9 gene

[00753] Exons 1-2 of the PCSK9 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 63.

Example 64 - CRISPR/TdCas9 target sites for the PCSK9 gene

[00754] Exons 1-2 of the PCSK9 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 64.

Example 65 - CRISPR/NmCas9 target sites for the PCSK9 gene

[00755] Exons 1-2 of the PCSK9 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 65.

Example 66 - CRISPR/Cpf1 target sites for the PCSK9 gene

[00756] Exons 1-2 of the PCSK9 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 66.

Example 67 - CRISPR/SpCas9 target sites for the Serpina1 gene

[00757] Exons 1-2 of the Serpina1 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 67.

Example 68 - CRISPR/SaCas9 target sites for the Serpina1 gene

[00759] Exons 1-2 of the Serpina1 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 68.

Example 69 - CRISPR/StCas9 target sites for the Serpina1 gene

[00760] Exons 1-2 of the Serpina1 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 69.

Example 70 - CRISPR/TdCas9 target sites for the Serpina1 gene

[00761] Exons 1-2 of the Serpina1 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 70.

Example 71 - CRISPR/NmCas9 target sites for the Serpina1 gene

[00762] Exons 1-2 of the Serpina1 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 71.

Example 72 - CRISPR/Cpf1 target sites for the Serpina1 gene

[00763] Exons 1-2 of the Serpina1 gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 72.

Example 73 - CRISPR/SpCas9 target sites for the TF gene

[00764] Exons 1-2 of the TF gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA

20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 73.

Example 74 - CRISPR/SaCas9 target sites for the TF gene

[00765] Exons 1-2 of the TF gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 74.

Example 75 - CRISPR/StCas9 target sites for the TF gene

[00766] Exons 1-2 of the TF gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 75.

Example 76 - CRISPR/TdCas9 target sites for the TF gene

[00767] Exons 1-2 of the TF gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 76.

Example 77 - CRISPR/NmCas9 target sites for the TF gene

[00768] Exons 1-2 of the TF gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 77.

Example 78 - CRISPR/Cpf1 target sites for the TF gene

[00769] Exons 1-2 of the TF gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 78.

Example 79 - CRISPR/SpCas9 target sites for the TTR gene

[00771] Exons 1-2 of the TTR gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 79.

Example 80 - CRISPR/SaCas9 target sites for the TTR gene

[00772] Exons 1-2 of the TTR gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 80.

Example 81 - CRISPR/StCas9 target sites for the TTR gene

[00773] Exons 1-2 of the TTR gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 81.

Example 82 - CRISPR/TdCas9 target sites for the TTR gene

[00774] Exons 1-2 of the TTR gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 82.

Example 83 - CRISPR/NmCas9 target sites for the TTR gene

[00775] Exons 1-2 of the TTR gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 83.

Example 84 - CRISPR/Cpf1 target sites for the TTR gene

[00776] Exons 1-2 of the TTR gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN.

gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 84.

Example 85 - CRISPR/SpCas9 target sites for the G6PC gene

[00777] Regions of the G6PC gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NRG. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 85.

Example 86 - CRISPR/SaCas9 target sites for the G6PC gene

[00778] Regions of the G6PC gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNGRRT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 86.

Example 87 - CRISPR/StCas9 target sites for the G6PC gene

[00779] Regions of the G6PC gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNAGAAW. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 87.

Example 88 - CRISPR/TdCas9 target sites for the G6PC gene

[00780] Regions of the G6PC gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NAAAAC. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 88.

Example 89 - CRISPR/NmCas9 target sites for the G6PC gene

[00781] Regions of the G6PC gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence NNNNGHTT. gRNA 20 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 89.

Example 90 - CRISPR/Cpf1 target sites for the G6PC gene

[00783] Regions of the G6PC gene were scanned for target sites. Each area was scanned for a protospacer adjacent motif (PAM) having the sequence YTN. gRNA 22 bp spacer sequences corresponding to the PAM were identified, as shown in Figure 90.

Example 91 – Bioinformatics analysis of the guide strands

[00784] Candidate guides will be screened and selected in a multi-step process that involves both theoretical binding and experimentally assessed activity. By way of illustration, candidate guides having sequences that match a particular on-target site, such as a site within the G6PC gene, with adjacent PAM can be assessed for their potential to cleave at off-target sites having similar sequences, using one or more of a variety of bioinformatics tools available for assessing off-target binding, as described and illustrated in more detail below, in order to assess the likelihood of effects at chromosomal positions other than those intended. Candidates predicted to have relatively lower potential for off-target activity can then be assessed experimentally to measure their on-target activity, and then off-target activities at various sites. Preferred guides have sufficiently high on-target activity to achieve desired levels of gene editing at the selected locus, and relatively lower off-target activity to reduce the likelihood of alterations at other chromosomal loci. The ratio of on-target to off-target activity is often referred to as the "specificity" of a guide.

[00785] For initial screening of predicted off-target activities, there are a number of bioinformatics tools known and publicly available that can be used to predict the most likely off-target sites; and since binding to target sites in the CRISPR/Cas9/Cpf1 nuclease system is driven by Watson-Crick base pairing between complementary sequences, the degree of dissimilarity (and therefore reduced potential for off-target binding) is essentially related to primary sequence differences: mismatches and bulges, *i.e*. bases that are changed to a non-complementary base, and insertions or deletions of bases in the potential off-target site relative to the target site. An exemplary bioinformatics tool called COSMID (CRISPR Off-target Sites with Mismatches, Insertions and Deletions) (available on the web at crispr.bme.gatech.edu) compiles such similarities. Other bioinformatics tools include, but are not limited to, GUIDO, autoCOSMID, and CCtop.

[00786] Bioinformatics were used to minimize off-target cleavage in order to reduce the detrimental effects of mutations and chromosomal rearrangements. Studies on CRISPR /Cas9 systems suggested the possibility of high off-target activity due to nonspecific hybridization of the guide strand to DNA sequences with base pair mismatches and/or bulges, particularly at positions distal from the PAM region. Therefore, it is important to have a bioinformatics tool that can identify potential off-target sites that have insertions and/or deletions between the RNA guide strand and genomic sequences, in addition to base-pair mismatches. The bioinformatics-based tool, COSMID (CRISPR Off-target Sites with Mismatches, Insertions and Deletions) was therefore used to search genomes for potential CRISPR off-target sites (available on the web at crispr.bme.gatech.edu). COSMID output ranked lists of the potential off-target sites based on the number and location of mismatches, allowing more informed choice of target sites, and avoiding the use of sites with more likely off-target cleavage.

[00787] Additional bioinformatics pipelines were employed that weigh the estimated on- and/or off-target activity of gRNA targeting sites in a region. Other features that may be used to predict activity include information about the cell type in question, DNA accessibility, chromatin state, transcription factor binding sites, transcription factor binding data, and other CHIP-seq data. Additional factors are weighed that predict editing efficiency, such as relative positions and directions of pairs of gRNAs, local sequence features and micro-homologies.

Example 92 – Testing of preferred guides in cells for on-target activity

[00788] The gRNAs predicted to have the lowest off target activity will then be tested for on-target activity in a model cell line, such as Huh-7 cells and evaluated for indel frequency using TIDE or next generation sequencing. TIDE is a web tool to rapidly assess genome editing by CRISPR-Cas9 of a target locus determined by a guide RNA (gRNA or sgRNA). Based on the quantitative sequence trace data from two standard capillary sequencing reactions, the TIDE software quantifies the editing efficacy and identifies the predominant types of insertions and deletions (indels) in the DNA of a targeted cell pool. See Brinkman *et al*, Nucl. Acids Res. (2014) for a detailed explanation and examples. Next-generation sequencing (NGS), also known as high-throughput sequencing, is the catch-all term used to

describe a number of different modern sequencing technologies including: Illumina (Solexa) sequencing, Roche 454 sequencing, Ion torrent: Proton/PGM sequencing, and SOLiD sequencing. These recent technologies allow one to sequence DNA and RNA much more quickly and cheaply than the previously used Sanger sequencing, and as such have revolutionized the study of genomics and molecular biology.

[00789] Transfection of tissue culture cells, allows screening of different constructs and a robust means of testing activity and specificity. Tissue culture cell lines, such as Huh-7 cells, are easily transfected and result in high activity. These or other cell lines will be evaluated to determine the cell lines that provide the best surrogate. These cells will then be used for many early stage tests. For example, individual gRNAs for *S. pyogenes* Cas9 will be transfected into the cells using plasmids, such as, for example, CTx-1, CTx-2, or CTx-3 described in Figure 92A-92C, which are suitable for expression in human cells. Several days later, the genomic DNA is harvested and the target site amplified by PCR. The cutting activity can be measured by the rate of insertions, deletions and mutations introduced by NHEJ repair of the free DNA ends. Although this method cannot differentiate correctly repaired sequences from uncleaved DNA, the level of cutting can be gauged by the amount of mis-repair. Off-target activity can be observed by amplifying identified putative off-target sites and using similar methods to detect cleavage. Translocation can also be assayed using primers flanking cut sites, to determine if specific cutting and translocations happen. Un-guided assays have been developed allowing complementary testing of off-target cleavage including guide-seq. The gRNA or pairs of gRNA with significant activity can then be followed up in cultured cells to measure correction of G6PC mutation. Off-target events can be followed again. These experiments allow optimization of nuclease and donor design and delivery.

Example 93 – Testing of preferred guides in cells for off-target activity

[00791] The gRNAs having the best on-target activity from the TIDE and next generation sequencing studies in the above example will then be tested for off-target activity using whole genome sequencing.

Example 94 – Testing different approaches for HDR gene editing

[00792] After testing the gRNAs for both on-target activity and off-target activity, the mutation correction and knock-in strategies will be tested for HDR gene editing.

[00793] For the mutation correction approach, the donor DNA template will be provided as a short single-stranded oligonucleotide, a short double-stranded oligonucleotide (PAM sequence intact/PAM sequence mutated), a long single-stranded DNA molecule (PAM sequence intact/PAM sequence mutated) or a long double-stranded DNA molecule (PAM sequence intact/PAM sequence mutated). In addition, the donor DNA template will be delivered by AAV.

[00794] For the cDNA knock-in approach, a single-stranded or double-stranded DNA having homologous arms to the 17q21 region may include more than 40 nt of the first exon (the first coding exon) of the G6PC gene, the complete CDS of the G6PC gene and 3'UTR of the G6PC gene, and at least 40 nt of the following intron. The single-stranded or double-stranded DNA having homologous arms to the 17q21 region, which includes more than 80 nt of the first exon of the G6PC gene, the complete CDS of the G6PC gene and 3'UTR of the G6PC gene, and at least 80 nt of the following intron. The single-stranded or double-stranded DNA having homologous arms to the 17q21 region may include more than 100 nt of the first exon of the G6PC gene, the complete CDS of the G6PC gene and 3'UTR of the G6PC gene, and at least 100 nt of the following intron. The single-stranded or double-stranded DNA having homologous arms to the 17q21 region may include more than 150 nt of the first exon of the G6PC gene, the complete CDS of the G6PC gene and 3'UTR of the G6PC gene, and at least 150 nt of the following intron. The single-stranded or double-stranded DNA having homologous arms to the 17q21 region may include more than 300 nt of the first exon of the G6PC gene, the complete CDS of the G6PC gene and 3'UTR of the G6PC gene, and at least 300 nt of the following intron. The single-stranded or double-stranded DNA having

homologous arms to the 17q21 region may include more than 400 nt of the first exon of the G6PC gene, the complete CDS of the G6PC gene and 3'UTR of the G6PC gene, and at least 400 nt of the following the first intron. Alternatively, the DNA template will be delivered by AAV.

[00795] Next, the efficiency of HDR mediated correction of the common mutation of G6PC R83 and knock-in of cDNA into the 1st exon will be assessed.

Example 95 – Re-assessment of lead CRISPR-Cas9/DNA donor combinations

[00796] After testing the different strategies for HDR gene editing, the lead CRISPR-Cas9/DNA donor combinations will be re-assessed in primary human hepatocytes for efficiency of deletion, recombination, and off-target specificity. Cas9 mRNA or RNP will be formulated into lipid nanoparticles for delivery, sgRNAs will be formulated into nanoparticles or delivered as AAV, and donor DNA will be formulated into nanoparticles or delivered as AAV.

Example 96 – *In vivo* testing in relevant mouse model

[00797] After the CRISPR-Cas9/DNA donor combinations have been re-assessed, the lead formulations will be tested *in vivo* in an animal model. Suitable animal models include, by way of non-limiting example a FGR mouse model with the livers repopulated with human hepatocytes or iPSC derived hepatocytes (normal or G6PC deficient).

[00798] Culture in human cells allows direct testing on the human target and the background human genome, as described above.

[00799] Preclinical efficacy and safety evaluations can be observed through engraftment of modified mouse or human hepatocytes in FGR mice. The modified cells can be observed in the months after engraftment.

Example 97 – Screening of gRNAs

[00800] The G6PC region (chr17:42,897,797-42,917,433) was used to design 20-nt recognition sites using the CCTOP protocol (Stemmer, M., Thumberger, T., del Sol Keyer, M., Wittbrodt, J. and Mateo, J.L. *CCTop: an intuitive, flexible and reliable CRISPR/Cas9 target prediction tool.* PLOS ONE (2015). doi:10.1371/journal.pone.0124633) to design gRNA targeting various regions of the

gene. The gRNAs with lowest off-target scores targeting Exon 1, Exon 2 and 5'end of Exon 5 were purchased from Integrated DNA Technologies in the format of Alt-R™ CRISPR crRNA. crRNAs were annealed with tracerRNA in the equimolar ratio (incubation at 70°C, 2 min, and 20°C for 20 min, and keep at 4°C). The activity of the gRNAs was tested in HuH7 cells constitutively expressing the Cas9 (transduced by lentivirus), Figures 94A-94C. 10K cells per well (96-well plate) were plated, and transfected in 16-18h after plating, briefly, gRNAs were incubated with lipofectamine RNAiMAX according to the manufacturer's protocol, final concentration 25nM. Cells were incubated with gRNA-lipofectamine complexes for 16-96h in the complete media comprising DMEM, supplemented by 10%FBS. Cells were lysed in prepGEM (ZyGem) according to the manufacture protocol.

[00801] Efficiency of the gRNA was analyzed by Tracking of Indels by Decomposition(TIDE) analysis (Brinkman EK, Chen T, Amendola M, van Steensel B. Easy quantitative assessment of genome editing by sequence trace decomposition. Nucleic Acids Res. 2014 Dec 16;42(22):e168. doi: 10.1093/nar/gku936), briefly, genomic DNA was used as a template for PCR using KAPA HiFi PCR Kit using the following primers (Table 3).

Table 3. gRNA sequences and activity in Huh7-Cas9

Exon #	guide ID	gRNA sequence (SEQ ID NO)	Forward TIDE primer	Reverse TIDE primer	Sequencing Primer	Eff.	SD
1	CH01	TGTCCGTGATCGCAGACCTC (52,943)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	6.1	2.5
1	CH02	AGAGCCCTTGCAGTTATTCC (57,319)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	32.9	2.7
1	CH03	CCTGGAGGTAATGTGTTGAC (57,306)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	44.8	0.0
1	CH04	CCAGTCAACACATTACCTCC (52,935)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	68.2	2.2
1	CH05	AGTCTTGGTAATTCACCTGG (57,305)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	52.2	4.4
1	CH06	GGGAGTCTTGGTAATTCACC (57,303)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	6.2	0.6
1	CH07	GGTGAATTACCAAGACTCCC (52,938)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	45.0	7.2
1	CH08	CTCCCAGGACTGGTTCATCT (52,940)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	55.5	1.1
1	CH09	CACCAAGATGAACCAGTCCT (57,300)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	10.7	1.6
1	CH10	ATTCCTGAGGTCTGCGATCA (57,296)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	34.9	2.3
1	CH11	TGTGGGCATTAAACTCCTTT (52,951)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	66.3	0.0
1	CH12	GGGCATATAAAACAGGGGCA (52,910)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	20.9	1.5
1	CH13	TGCAGTTATTCCAGGCTTGG (57,321)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	29.7	11.8
1	CH14	CCAAGCCTGGAATAACTGCA (52,918)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	68.7	0.0
1	CH15	CCTTGCAGTTATTCCAGGCT (57,320)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	34.0	0.0
1	CH16	CAAGCCTGGAATAACTGCAA (52,919)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	60.2	1.5
1	CH17	GACATCTTCCTGAGGTGCCA (52,923)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	35.5	2.7
1	CH18	CCTCATTTCCTTGGCACCTC (57,312)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	24.8	1.0

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Exon #	guide ID	gRNA sequence (SEQ ID NO)	Forward TIDE primer	Reverse TIDE primer	Sequencing Primer	Eff.	SD
1	CH19	TTGACTGGATCCCAAAGTCA (57,308)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	43.7	0.0
1	CH20	ATTACCAAGACTCCCAGGAC (52,939)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	28.7	4.0
1	CH21	TGAACCAGTCCTGGGAGTCT (57,302)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	9.2	2.7
1	CH22	ACACCAAGATGAACCAGTCC (57,299)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	20.0	5.5
1	CH23	GGACGTAGAAGGCATTCCTG (57,295)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	55.9	0.4
1	CH24	TCTACGTCCTCTTCCCCATC (52,944)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	16.6	5.6
1	CH25	GGCTCAACCTCGTCTTTAAG (52,957)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	13.9	6.5
1	CH26	GTTCTTACCACTTAAAGACG (57,274)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	19.3	2.1
1	CH27	GTGGTAAGAACCATATAGAG (52,962)	ATTGGCCCTGCTGAGTACAT (64,792)	ATAGCCTGGGGAAAGCAACT (64,795)	ATAGCCTGGGGAAAGCAACT (64,795)	57.4	3.6
2	CH28	TCAGGCTACACTCTTCTTGA (53,360)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	34.3	9.2
2	CH29	TACACTCTTCTTGAAGGTGT (53,362)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	35.7	20.9
2	CH30	TTCTTGAAGGTGTAGGCTTT (53,364)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	11.3	1.5
2	CH31	GCTGTCCAAAGAGAATCCTA (56,893)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	56.2	14.4
2	CH32	TCTTTGGACAGCGTCCATAC (53,372)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	46.0	36.6
2	CH33	TTGGACAGCGTCCATACTGG (53,373)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	29.7	26.5
2	CH34	TGGACAGCGTCCATACTGGT (53,374)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	63.6	14.0
2	CH35	GCGTCCATACTGGTGGGTTT (53,375)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	16.5	14.5
2	CH36	GTATCCAAAACCCACCAGTA (56,890)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	63.6	11.3
2	CH37	GAACTGCTTTATCAGGGGCA (56,884)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	9.7	5.6
2	CH38	ACAGGGAACTGCTTTATCAG (56,883)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	75.5	7.3

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Exon #	guide ID	gRNA sequence (SEQ ID NO)	Forward TIDE primer	Reverse TIDE primer	Sequencing Primer	Eff.	SD
2	CH39	TACAGGGAACTGCTTTATCA (56,882)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	23.0	11.2
2	CH40	TTACAGGGAACTGCTTTATC (56,881)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	36.3	16.8
2	CH41	TTCCCTGTAACCTGTGAGAC (53,380)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	42.9	26.4
2	CH42	GTCCAGTCTCACAGGTTACA (56,879)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	73.9	16.1
2	CH43	GGTCCAGTCTCACAGGTTAC (56,878)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	54.3	19.1
2	CH44	GTAACCTGTGAGACTGGACC (53,382)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	49.3	5.7
2	CH45	CTTACCTGGTCCAGTCTCAC (56,876)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	60.9	14.3
2	CH46	CAGGGGCTGGGACGCTTACC (56,873)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	29.2	23.5
2	CH47	TGGACCTCGTTTACCTGTTA (59,984)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	38.9	26.3
2	CH48	TCATCCATAACAGGTAAACG (56,865)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	44.1	12.3
2	CH49	AGGTCAGTTTCATCCATAAC (56,863)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	39.5	18.2
2	CH50	TATGGATGAAACTGACCTTG (53,392)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	24.9	16.7
2	CH51	CCTGAATAGCACAGTAGTAT (53,403)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	21.8	12.9
2	CH79	TTTCACATGTTGCCTCTAGA (56,909)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	60.1	4.1
2	CH80	CAACATGTGAAATCCTTCTC (53,358)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	65.1	4.1
2	CH81	AAGAAGAGTGTAGCCTGAGA (56,906)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	5.7	0.7
2	CH82	CTTCTTGAAGGTGTAGGCTT (53,363)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	16.5	3.1
2	CH83	AAAAACAGAACAAGTTTCTG (56,898)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	57.4	3.6
2	CH84	GAAAAACAGAACAAGTTTCT (56,897)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	7.2	1.0
2	CH85	AACTTGTTCTGTTTTTCCAT (53,369)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	42.3	3.8

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Exon #	guide ID	gRNA sequence (SEQ ID NO)	Forward TIDE primer	Reverse TIDE primer	Sequencing Primer	Eff.	SD
2	CH86	TTTTTCCATAGGATTCTCTT (53,370)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	51.7	1.6
2	CH87	GCTCTCCTCATGTCCCCTCA (56,860)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	36.0	3.2
5	CH52	ACTTCTTGTGCGGCTGGCCC (55,848)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	5.1	3.0
5	CH53	ACAACGACTTCTTGTGCGGC (55,846)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	2.4	0.9
5	CH54	TCTTACAACGACTTCTTGTG (55,845)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	44.3	15.8
5	KB55	ACCCCCATCCCAAGTCGAGC (54,506)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	13.1	0.7
5	KB56	ACCAGCTCGACTTGGGATGG (55,875)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	17.2	2.8
5	KB57	GACCAGCTCGACTTGGGATG (55,874)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	13.4	4.8
5	KB58	AGACCAGCTCGACTTGGGAT (55,873)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	11.4	3.7
5	KB59	AAGACCAGCTCGACTTGGGA (55,872)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	11.1	3.0
5	KB60	GTAGAAGACCAGCTCGACTT (55,871)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	3.5	1.7
5	KB61	CGTAGAAGACCAGCTCGACT (55,870)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	2.2	0.8
5	KB62	CACTACCGCACTCTTGCAGA (55,865)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	3.7	1.4
5	KB63	CAAGAGTGCGGTAGTGCCCC (54,511)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	14.8	0.2
5	KB64	GATGACACTGACGGATGCCA (55,861)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	20.5	4.3
5	KB65	GGATGACACTGACGGATGCC (55,860)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	2.2	1.1
5	KB66	TAGTAGTCCTCCTCAATCCC (55,842)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	50.1	2.1
5	KB67	TGCCATCCATTCTGCCGTCG (54,540)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	4.0	1.0
5	KB68	TTCCACGACGGCAGAATGGA (55,838)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	41.6	0.2
5	KB69	TTAATTCCACGACGGCAGAA (55,837)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	24.4	4.1

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Exon #	guide ID	gRNA sequence (SEQ ID NO)	Forward TIDE primer	Reverse TIDE primer	Sequencing Primer	Eff.	SD
5	KB70	GCCGTCGTGGAATTAAATCA (54,541)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	50.5	2.8
5	KB71	TCCGTGATTTAATTCCACGA (55,835)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	2.8	1.0
5	KB72	TCGTGGAATTAAATCACGGA (54,542)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	12.3	5.2
5	KB73	TTAAATCACGGATGGCAGAT (54,544)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	17.5	1.6
5	KB74	TGGCAGATTGGAGGGTCGCC (54,548)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	4.4	0.5
5	KB75	TGCATATGGTGTACGTGATA (55,820)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	35.6	4.1
5	KB76	CCATATGCAAGTTTCCCGCC (54,558)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	19.0	0.9
5	KB77	CCTGGCGGGAAACTTGCATA (55,819)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	1.6	0.8
5	KB78	TATGCAAGTTTCCCGCCAGG (54,560)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)	41.4	2.5

exon 1 15 27

exon 2 22 33

exon 3 6 27

*Eff. = efficiency (% indels)

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[00802] PCR amplicons were purified using the AxyPrep Mag PCR clean-up kit (Axygen). Amplicons were sequenced using the primers listed below and analyzed using decomposition algorithm. gRNA activity was measured as a ratio of alleles with various indels (insertions of 1 to 50 nt, or deletions of 1 to 50 nt) adjacent to predicted cut site of the S.py. Cas9 (i.e., between nucleotides -4 and -3 upstream of PAM (NRG) on a non-target strand and between 3 and 4 nucleotides downstream of PAM complementary sequence (CCN) on a target strand. The activity of the gRNA is listed in Table 3.

[00803] These studies demonstrate that 15 out of 27 gRNAs targeting exon 1, 22 out of 33 targeting exon 2 and 6 out of exon 27 targeting exon 5 had *in vitro* indel efficiency higher than 30%.

Example 98 – Activity of the gRNA targeting mutant allele in HuH7 cells (wildtype alleles)

[00804] To assess the activity of the gRNAs preferentially targeting mutant alleles, gRNA overlapping with two the most prevalent mutations of G6PC R83C (rs1801175) and Q347X (rs80356487) were designed, with perfect match with mutant sequence (Table 4). As a surrogate of the activity of the mutant gRNAs, their activity in Huh7-Cas9 cells has been assessed as shown below in Table 4.

Table 4. gRNA sequences and activity in Huh7-Cas9

Exon #	guide ID	gRNA sequence	Forward TIDE primer	Reverse TIDE primer	Sequencing Primer	Eff.	SD
2	CH31	GCTGTCCAAAGAGAATCCTA (56,893)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	59.65	7
2	CH31 mutant	**A**CTGTCCAAAGAGAATCCTA (64,798)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	43.65	7.4
2	CH32	TCTTTGGACAG**C**GTCCATAC (53,372)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	44.25	6.2
2	CH32 mutant	TCTTTGGACAG**T**GTCCATAC (64,799)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	22.65	0.7
2	CH33	TTGGACAG**C**GTCCATACTGG (53,373)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	13.95	0.8
2	CH33 mutant	TTGGACAG**T**GTCCATACTGG (64,800)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	6.75	2
2	CH34	TGGACAGCGTCCATACTGGT (53,374)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	51.6	6
2	CH34 mutant	TGGACAG**T**GTCCATACTGGT (64,801)	cccaggaggtagaggtcacaatga (64,793)	agagagggcaagggattggacg (64,835)	agagagggcaagggattggacg (64,835)	38	4.2
5	ex5-d1	CTACTGCCTCGCC**T**AGGTCC (64,802)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)		
5	ex5-d2	CATCCCCTACTGCCTCGCC**T** (64,803)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)		
5	ex5-d3	TACTGCCTCGCC**T**AGGTCCT (64,804)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)		
5	ex5-d4	AGGACCT**A**GGCGAGGCAGTA (64,805)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)		
5	ex5-d5	GCTGGCCCAGGACCTAGGCG (64,806)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)		
5	ex5-d6	CAGGACCT**A**GGCGAGGCAGT (64,807)	AACCTGGGCACGCTCTTT (64,794)	AGAGGACCACCTGAGCTGAC (64,796)	TGTAAAAGAGGACCACCTGAGC (64,797)		

*Eff. = efficiency (% indels)

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[00805] These studies demonstrate that gRNAs targeting mutant allele and having one mismatch comparing to wildtype sequence retained 50-74% of the wild type analogues.

Example 99 – Activity of 19-mer, 18-mer, 17-mer gRNA

[00806] To analyze whether gRNA with recognition part shorter than 20-mer have some activity, Alt-R gRNA activity in Huh7-Cas9 cells was analyzed, and whether the substitution of Gs to one or two 5' nucleotides would affect the gRNA activity was also analyzed, as shown below in Table 5. These modified lengths and or sequences of gRNA may modify kinetics of double stranded cutting and/or its specificity.

Table 5. gRNA sequences and activity in Huh7-Cas9

gRNA ID	Sequence (SEQ ID NO)	Efficiency	SD
CH31_N20	GCTGTCCAAAGAGAATCCTA (56,893)	29.83	3.21
CH31_GGN18	GGTGTCCAAAGAGAATCCTA (64,808)	23.97	2.72
CH31_N19	CTGTCCAAAGAGAATCCTA (64,809)	22.67	2.41
CH31_GN18	GTGTCCAAAGAGAATCCTA (64,810)	19.77	3.32
CH31_N18	TGTCCAAAGAGAATCCTA (64,811)	21.10	4.45
CH31_GN17	GGTCCAAAGAGAATCCTA (64,812)	20.37	5.68
CH31_N17	GTCCAAAGAGAATCCTA (64,813)	21.20	4.60
CH32_N20	TCTTTGGACAGCGTCCATAC (53,372)	14.87	1.18
CH32_GN19	GCTTTGGACAGCGTCCATAC (64,814)	9.17	0.62
CH32_GGN18	GGTTTGGACAGCGTCCATAC (64,815)	3.07	0.61
CH32_N19	CTTTGGACAGCGTCCATAC (64,816)	13.13	0.65
CH32_GN18	GTTTGGACAGCGTCCATAC (64,817)	1.27	0.05
CH32_N18	TTTGGACAGCGTCCATAC (64,818)	4.37	0.45
CH32_GN17	GTTGGACAGCGTCCATAC (64,819)	3.30	1.36
CH32_N17	TTGGACAGCGTCCATAC (64,820)	6.87	1.69

[00807] These studies demonstrate that all shorter analogues of the gRNA CH31 retained more than 66% of indel activity. Only 19-mer analogues of the gRNA CH32 retained activity >60% of the full gRNA.

Example 100 – Format of gRNAs

[00808] Selected gRNAs were tested in a form of single-stranded gRNA with various chemical modifications, and double-stranded gRNA conjugated by click chemistry with various chemical modifications as shown below in Table 6. Transfection of the gRNAs was performed as described above and their activities at various concentrations (3nM – 25 nM) are presented in Figures 95A-95B.

Table 6. Examples of the chemical modifications of gRNA

gRNA name	Chemical modification scheme	Sequence 5' to 3'
CH31	CTX0	gscsusGUCCAAAGAGAAUCCUAGUUUUAGAGCUAGAAAUAGCAAGUU AAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCusususU (SEQ ID NO: 64,821)
CH31	CTX0split	gscsusGUCCAAAGAGAAUCCUAGUUUUAGAgcuaGAAA (SEQ ID NO: 64,822)-(ABA)(COM)-uagcAAGUUAAAAUAAGGCUAGUCCGUUAUCaacuuGAAAaaguggcaccgagucggugcusususU (SEQ ID NO: 64,836)
CH31	CTX1	gscsusGUCCAAAGAGAAUCCUAGUUUUAGAGCUAGAAAUAGCAAGUU AAAAUAAGGCUAGUCCGUUAUCAACUUGAAAAAGUGGCACCGAGUC GGUGCusususU (SEQ ID NO: 64,821)
CH31	CTX1split	gscsusGUCCAAAGAGAAUCCUAguuuuagagcuagaaa (SEQ ID NO: 64,823)-(NHC6)(ABA)(COM)-uagcAAGUUAAAAUAAGGCUAGUCCGUUAUCaacuuGAAAaaguggcaccgagucggugcusususU (SEQ ID NO: 64,836)

CH31	CTX2split	gscsusGUCCAAAGAGAAUCCUAGUUUUAGAGCUAUGCU (SEQ ID NO: 64,824)-(NHC6)(ABA)(COM)-AGCAUAGCAAGUUAAAAUAAGGCUAGUCCGUUAUCaacuuGAAAaaguggcaccgagucggugcusususU (SEQ ID NO: 64,837)

a, c, g, u: 2'-O-methyl residues

s: phosphorothioate

A, C, G, U: RNA residues

[00809] These studies demonstrate that single stranded gRNA or click-conjugated split gRNAs had superior activity than split gRNAs, especially at lower concentrations.

Example 101 – gRNA activity in primary human hepatocytes and HepG2

[00810] Selected gRNAs were tested in a form of single-stranded gRNA with various chemical modifications (see Table 6 above). Transfection of the gRNAs was performed using Lipofectamine MessengerMax according to the manufacture protocol. The gRNAs activities at 12.5nM are presented below in Table 7.

Table 7. gRNA activity in HepG2 and PHH transfected with Cas9 mRNA and gRNA

gRNA	Activity, In-del%	SD	Cell type
CH31-CTX0	43.96805556	17.657448	HepG2
CH31-CTX1	41.12261905	20.441894	HepG2
CH32-AltR	13.89166667	13.517525	HepG2
CH31-CTX2	20.36944444	8.9200085	PHH

[00811] These studies demonstrate that single stranded gRNAs transfected with Cas9 mRNA were active in both HepG2 cells and primary human hepatocytes.

Example 102 – Analysis of the off-target activity of selected gRNAs

[00812] Off-targets (loci in the genome targeted by the CRISPR endonuclease beyond the locus of interest) were predicted by two algorithms, CCTOP (see Example 97) and COSMID (COSMID: A Web-based Tool for Identifying and

Validating CRISPR/Cas Off-target Sites. TJ Cradick, P Qiu, CM Lee, EJ Fine, G Bao. Molecular Therapy -Nucleic Acids 3 (12), e214).

[00813] Selected gRNAs were transfected into Huh-7 cells as described above in 24 well format. gDNA was isolated using DNAeasy isolation kit (Qiagen). Off-target activities for the selected gRNAs were measured by two methods:

- TIDE analysis for the top 5-6 off-targets (similar to on target activity), see Table 8B for the example (3-5% of indel is considered as background).
- HiSeq of 200-500 off-target sites. DNA correspondent to off-target sites was enriched by TargetGxOne™ enrichment library preparation and analyzed by 2x125bp paired end (PE) sequencing on Illumina HiSeq2500 in High Output mode (V4 Chemistry). Off-target activity is defined as the ratio of reads with indels adjacent to the predicted off-target locus to the total number of reads correspondent to the locus, see Table 8A for the example.

Table 8A. Examples of analysis of off-target activity by Capture-Seq, in del frequency

	CH31	Control	Comment
chr12:98076278-98076300 (-)	0.1%	0.0%	
chr13:84282989-84283011 (+)	0.3%	0.0%	
chr17:10714406-10714427 (-)	0.4%	0.0%	
chr17:42903925-42903947 (-)	58.6%	2.0%	On-Target
chr2:158676009-158676031 (+)	0.5%	0.0%	
chr2:208579757-208579779 (-)	1.7%	0.0%	
chr3:56776643-56776665 (+)	0.4%	0.0%	
chr3:142796927-142796949 (+)	0.3%	0.0%	
chr4:32556942-32556964 (-)	3.0%	0.0%	
chr6:45288091-45288113 (+)	0.2%	0.0%	
chr6:167947988-167948010 (-)	0.1%	0.0%	
chr7:20703389-20703411 (-)	0.3%	0.0%	

Table 8B. Examples of analysis of off-target activity by TIDE analysis

	CH32	
ch17:42903936-42903958 (+)	~90%	On-Target
Ch19: 53480959-53480938 (-)	~5%	
Chr2: 64486187-64486165 (-)	~5%	

[00814] These studies demonstrate that although constitutive expression of Cas9 increases off-targeting potential, the indels in predicted off-target sites for the identified gRNAs were either non-detected or lower than 5% of on-target activity of the correspondent gRNA.

Example 103 – Correction of mutations (missense, nonsense) by HDR

[00815] gRNA targeting DNA in the proximity of the mutation of interest (e.g. R83C (rs1801175) and donor DNA was provided as single stranded (+ or – strands) or double stranded DNA oligo nucleotides (+ strand is presented in Figure 96). The donor DNA had several sense mismatches (therapeutic donor will have wildtype sequence or sequence with homology to wt >90%).

[00816] gRNA and oligonucleotide were co-transfected into Huh-7 cells expressing Cas9 and genomic DNAs were harvested 48-96 hours post transfection. The locus of interest was amplified using primers 5'-cccaggaggtagaggtcacaatga-3' (SEQ ID NO: 64,793) and 5'-agagagggcaagggattggacg-3' (SEQ ID NO: 64,795), and the amplicons were cloned into TOPO-blunt vector and sequenced by Sanger Sequencing. Efficiency of the gene editing as well as an example of the mutated sequence are presented in Figures 99A-99C.

[00817] NextGen Sequencing, briefly, primers (5'-cccaggaggtagaggtcacaatga-3' (SEQ ID NO: 64,793) and 5'-agagagggcaagggattggacg-3' (SEQ ID NO: 64,795)) were used to generate amplicons, amplicons were used for nested PCR using following primers (NextGen_G6PC_R83_rev GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGGGCACGGAAGTGTTGCTG TAGT (SEQ ID NO: 64,825) and NextGen_G6PC_R83_for TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGCCCTTCTAGAGGCAACATGT GAA (SEQ ID NO: 64,826) and finally the library was generated using the

barcoding primers. The efficiencies of HDR with the above mentioned donor and several gRNAs are presented in the Figures 97A-97C.

[00818] These studies demonstrate that the *in vitro* assay provided comparison of the efficiency of different gRNAs to promote HDR around position of interest. This *in vitro* assay also highlighted the importance of the proximity of the cut site to the mutation.

Example 104 – Restoration of the G6PC activity by small deletion around mutation

[00819] One or two gRNAs targeting DNA in the proximity of the mutation of interest (e.g. Q347X (rs80356487). The DNA cutting will lead to small deletion or insertion around the premature stop codon and may lead to modified amino acid sequence. Examples are shown below:

G6PC Q347X

MEEGMNVLHDFGIQSTHYLQVNYQDSQDWFILVSVIADLRNAFYVLFPIWFHLQE
AVGIKLLWVAVIGDWLNLVFKWILFGQRPYWWVLDTDYYSNTSVPLIKQFPVTCET
GPGSPSGHAMGTAGVYYVMVTSTLSIFQGKIKPTYRFRCLNVILWLGFWAVQLNV
CLSRIYLAAHFPHQVVAGVLSGIAVAETFSHIHSIYNASLKKYFLITFFLFSFAIGFYL
LLKGLGVDLLWTLEKAQRWCEQPEWVHIDTTPFASLLKNLGTLFGLGLALNSSMY
RESCKGKLSKWLPFRLSSIVASLVLLHVFDSLKPPSQVELVFYVLSFCKSAVVPLA
SVSVIPYC**LAXVL**GQPHKKSL (SEQ ID NO: 64,827)

G6PC Δ346-347

MEEGMNVLHDFGIQSTHYLQVNYQDSQDWFILVSVIADLRNAFYVLFPIWFHLQE
AVGIKLLWVAVIGDWLNLVFKWILFGQRPYWWVLDTDYYSNTSVPLIKQFPVTCET
GPGSPSGHAMGTAGVYYVMVTSTLSIFQGKIKPTYRFRCLNVILWLGFWAVQLNV
CLSRIYLAAHFPHQVVAGVLSGIAVAETFSHIHSIYNASLKKYFLITFFLFSFAIGFYL
LLKGLGVDLLWTLEKAQRWCEQPEWVHIDTTPFASLLKNLGTLFGLGLALNSSMY
RESCKGKLSKWLPFRLSSIVASLVLLHVFDSLKPPSQVELVFYVLSFCKSAVVPLA
SVSVIPYC**LVL**GQPHKKSL (SEQ ID NO: 64,828)

G6PC Δ 347-348

MEEGMNVLHDFGIQSTHYLQVNYQDSQDWFILVSVIADLRNAFYVLFPIWFHLQE
AVGIKLLWVAVIGDWLNLVFKWILFGQRPYWWVLDTDYYSNTSVPLIKQFPVTCET
GPGSPSGHAMGTAGVYYVMVTSTLSIFQGKIKPTYRFRCLNVILWLGFWAVQLNV
CLSRIYLAAHFPHQVVAGVLSGIAVAETFSHIHSIYNASLKKYFLITFFLFSFAIGFYL
LLKGLGVDLLWTLEKAQRWCEQPEWVHIDTTPFASLLKNLGTLFGLGLALNSSMY
RESCKGKLSKWLPFRLSSIVASLVLLHVFDSLKPPSQVELVFYVLSFCKSAVVPLA
SVSVIPYC**LAL**GQPHKKSL (SEQ ID NO: 64,829)

[00820] The cDNA encoding the above listed proteins were cloned into expression cassette and transfected into HEK293T cells; Figure 98 demonstrates that while Q347X variant of the enzyme has virtually no activity, Δ346-347 and Δ347-348 variants may have residual phosphatase activity about 10% of the wildtype protein.

[00821] These studies demonstrate that G6PC protein with a deletion of the amino acids (346-347 or 347-348) had 10% of wildtype activity (i.e. higher than nonsense mutation Q347X).

Example 105 – Restoration of the G6PC activity by knock-in of cDNA or minigene

[00822] G6PC can be knocked-in in one of the following loci: ApoC3 chr11:116829908-116833071; Angptl3 chr1:62,597,487-62,606,305 ; Serpina1 chr14:94376747-94390692 ; Lp(a) chr6:160531483-160664259; Pcsk9 chr1:55,039,475-55,064,852; FIX chrX:139,530,736-139,563,458; ALB chr4:73,404,254-73,421,411; TTR chr18:31,591,766-31,599,023; TF chr3:133,661,997-133,779,005; Gys2 chr12:21,536,188-21,604,857; AAVS1(PPP1R12C) chr19:55,090,912-55,117,599; HGD chr3:120,628,167-120,682,570; CCR5 chr3:46,370,854-46,376,206; ASGR2 chr17:7,101,322-7,114,310; G6PC 17:42,900,796-42,914,432. Briefly, one or two gRNAs targeting one of these loci, more specifically exon 1 or exon 2 or intron 1.

[00823] The DNA donors are schematically represented in Figures 99A-99C, where examples of 3'UTR and polyadenylation signal are listed below:

>mouse a-Globin 3'UTR

AGCTGCCTTCTGCGGGGCTTGCCTTCTGGCCATGCCCTTCTTCTCTCCCTTGC ACCTGTACCTCTTGGTCTTTGAATAAAGCCTGAGTAGGAAG (SEQ ID NO: 64,830)

>human a-Globin 3'UTR

GCTGGAGCCTCGGTGGCCATGCTTCTTGCCCCTTGGGCCTCCCCCCAGCCCC TCCTCCCCTTCCTGCACCCGTACCCCCGTGGTCTTTGAATAAAGTCTGAGTGG GCGGC (SEQ ID NO: 64,831)

>human G6PC 3'UTR (synthetic short)

GAGATGTGGAGTCTTCGGTGTTTAAAGTCAACAACCATGCCAGGGATTGAGGA GGACTACTATTTGAAGCAATGGGCACCAAGTGAAATAAAGTCTTGTTAATTACT ATATTTTAGATGCA (SEQ ID NO: 64,832)

>polyadenylation signal b-Globin

AATAAAGGAAATTTATTTTCATTGCAATAGTGTGTTGGAATTTTTTGTGTCTCTC A (SEQ ID NO: 64,833)

>polyadenylation signal SV40

TTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTC ACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATC AATGTATCTTAT (SEQ ID NO: 64,834)

[00824] These studies demonstrate that left homology arm and right homology arm will be specific for each locus, including G6PC. One or two gRNAs targeting the above mentioned loci will be co-delivered with donor encoded by AAV.

[00826] Note Regarding Illustrative Embodiments

[00827] While the present disclosure provides descriptions of various specific embodiments for the purpose of illustrating various aspects of the present invention and/or its potential applications, it is understood that variations and modifications will occur to those skilled in the art. Accordingly, the invention or inventions described herein should be understood to be at least as broad as they are claimed, and not as more narrowly defined by particular illustrative embodiments provided herein.

[00828] Any patent, publication, or other disclosure material identified herein is incorporated by reference into this specification in its entirety unless otherwise indicated, but only to the extent that the incorporated material does not conflict with existing descriptions, definitions, statements, or other disclosure material expressly set forth in this specification. As such, and to the extent necessary, the express disclosure as set forth in this specification supersedes any conflicting material incorporated by reference. Any material, or portion thereof, that is said to be incorporated by reference into this specification, but which conflicts with existing definitions, statements, or other disclosure material set forth herein, is only incorporated to the extent that no conflict arises between that incorporated material and the existing disclosure material. Applicants reserve the right to amend this specification to expressly recite any subject matter, or portion thereof, incorporated by reference herein.

Claims

What is claimed is:

1. A method for editing the glucose-6-phosphatase, catalytic (G6PC) gene in a human cell by genome editing, the method comprising the step of: introducing into the human cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction, or modulation of expression of function of one or more exons within or near or affecting the expression or function of the G6PC gene and results in restoration of glucose-6-phosphatase (G6Pase) protein activity.

2. A method for inserting a G6PC gene in a human cell by genome editing, the method comprising introducing into the human cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near a safe harbor locus that results in a permanent insertion of the G6PC gene, and results in restoration of G6Pase protein activity.

3. An *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a), the method comprising the steps of:
i) creating a patient specific induced pluripotent stem cell (iPSC) , or editing within or near a safe harbor locus of the iPSC;
ii) editing within or near a glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the G6PC gene of the iPSC;
iii) differentiating the genome edited iPSC into a hepatocyte; and
iv) implanting the hepatocyte into the patient.

4. The method of claim 3, wherein the creating step comprises:
a) isolating a somatic cell from the patient; and

b) introducing a set of pluripotency-associated genes into the somatic cell to induce the somatic cell to become a pluripotent stem cell.

5. The method of claim 4, wherein the somatic cell is a fibroblast.

6. The method of claim 4, wherein the set of pluripotency-associated genes is one or more of the genes selected from the group consisting of OCT4, SOX2, KLF4, Lin28, NANOG and cMYC.

7. The method of any one of claims 3-6, wherein the editing step comprises introducing into the iPSC one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus and results in restoration of glucose-6-phosphatase (G6Pase) protein activity.

8. The method of claim 7, wherein the safe harbor locus is selected from the group consisting of AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR.

9. The method of any one of claims 3-8, wherein the differentiating step comprises one or more of the following to differentiate the genome edited iPSC into a hepatocyte: contacting the genome edited iPSC with one or more of activin, B27 supplement, FGF4, HGF, BMP2, BMP4, Oncostatin M, Dexametason.

10. The method of any one of claims 3-9, wherein the implanting step comprises implanting the hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

11. An *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a), the method comprising the steps of:
i) performing a biopsy of the patient's liver;
ii) isolating a liver specific progenitor cell or primary hepatocyte;
iii) editing within or near the glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the G6PC gene of the progenitor cell or primary hepatocyte or editing within or near a safe harbor locus of the progenitor cell or primary hepatocyte; and
iv) implanting the genome-edited progenitor cell or primary hepatocyte into the patient.

12. The method of claim 11, wherein the isolating step comprises: perfusion of fresh liver tissues with digestion enzymes, cell differential centrifugation, cell culturing, or combinations thereof.

13. The method of any one of claims 11-12, wherein the editing step comprises introducing into the progenitor cell or primary hepatocyte one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor that results in a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus and restoration of glucose-6-phosphatase (G6Pase) protein activity.

14. The method of claim 13, wherein the safe harbor locus is selected from the group consisting of AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR.

15. The method of any one of claims 11-14, wherein the implanting step comprises implanting the genome-edited progenitor cell or primary hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

16. An *ex vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a), the method comprising the steps of:
i) performing a biopsy of the patient's bone marrow;
ii) isolating a mesenchymal stem cell from the patient;
iii) editing within or near the glucose-6-phosphatase, catalytic (G6PC) gene or other DNA sequences that encode regulatory elements of the G6PC gene of the mesenchymal stem cell or editing within or near a safe harbor locus of the mesenchymal stem cell;
iv) differentiating the genome-edited mesenchymal stem cell into a hepatocyte; and
v) implanting the hepatocyte into the patient.

17. The method of claim 16, wherein the mesenchymal stem cell is isolated from the patient's bone marrow or peripheral blood.

18. The method of claim 16, wherein the isolating step comprises: aspiration of bone marrow and isolation of mesenchymal cells by density centrifugation using Percoll™.

19. The method of any one of claims 16-18, wherein the editing step comprises introducing into the mesenchymal stem cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus and restoration of glucose-6-phosphatase (G6Pase) protein activity.

20. The method of claim 19, wherein the safe harbor locus is selected from the group consisting of AAVS1 (PPP1R12C), ALB, Angptl3, ApoC3, ASGR2, CCR5, FIX (F9), Gys2, HGD, Lp(a), Pcsk9, Serpina1, TF, and TTR.

21. The method of any one of claims 16-19, wherein the differentiating step comprises one or more of the following to differentiate the genome edited mesenchymal stem cell into a hepatocyte: contacting the genome edited stem cell with one or more of insulin, transferrin, FGF4, HGF, or bile acids.

22. The method of any one of claims 16-21, wherein the implanting step comprises implanting the hepatocyte into the patient by transplantation, local injection, or systemic infusion, or combinations thereof.

23. An *in vivo* method for treating a patient with Glycogen Storage Disease type 1a (GSD1a), the method comprising the step of editing the glucose-6-phosphatase, catalytic (G6PC) gene in a cell of the patient, or other DNA sequences that encode regulatory elements of the G6PC gene, or editing within or near a safe harbor locus in a cell of the patient.

24. The method of claim 23, wherein the editing step comprises introducing into the cell one or more deoxyribonucleic acid (DNA) endonucleases to effect one or more single-strand breaks (SSBs) or double-strand breaks (DSBs) within or near the G6PC gene other DNA sequences that encode regulatory elements of the G6PC gene that results in a permanent insertion, correction, or modulation of expression or function of one or more exons within or near or affecting the expression or function of the G6PC gene or within or near a safe harbor locus that results in a permanent insertion of the G6PC gene and restoration of glucose-6-phosphatase (G6Pase) protein activity.

25. The method of any one of claims 1, 2, 7, 13, 19, or 24, wherein the one or more DNA endonucleases is a Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8, Cas9 (also known as Csn1 and Csx12), Cas100, Csy1, Csy2, Csy3, Cse1, Cse2, Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx10, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, or Cpf1 endonuclease; or a homolog

thereof, recombination of the naturally occurring molecule, codon-optimized, or modified version thereof, and combinations thereof.

26. The method of claim 25, wherein the method comprises introducing into the cell one or more polynucleotides encoding the one or more DNA endonucleases.

27. The method of claim 25, wherein the method comprises introducing into the cell one or more ribonucleic acids (RNAs) encoding the one or more DNA endonucleases.

28. The method of any one of claims 26 or 27, wherein the one or more polynucleotides or one or more RNAs is one or more modified polynucleotides or one or more modified RNAs.

29. The method of claim 26, wherein the DNA endonuclease is a protein or polypeptide.

30. The method of any one of the preceding claims, wherein the method further comprises introducing into the cell one or more guide ribonucleic acids (gRNAs).

31. The method of claim 30, wherein the one or more gRNAs are single-molecule guide RNA (sgRNAs).

32. The method of any one of claims 30-31, wherein the one or more gRNAs or one or more sgRNAs is one or more modified gRNAs or one or more modified sgRNAs.

33. The method of any one of claims 30-32, wherein the one or more DNA endonucleases is pre-complexed with one or more gRNAs or one or more sgRNAs.

34. The method of any one of the preceding claims, wherein the method further comprises introducing into the cell a polynucleotide donor template comprising at least a portion of the wild-type G6PC gene or cDNA.

35. The method of claim 34, wherein the at least a portion of the wild-type G6PC gene or cDNA is exon 1, exon 2, exon 3, exon 4, exon 5, intronic regions, fragments or combinations thereof, the entire G6PC gene, DNA sequences that encode wild-type regulatory elements of the G6PC gene, or cDNA.

36. The method of any one of claims 34-35, wherein the donor template is either a single or double stranded polynucleotide.

37. The method of any one of claims 34-36, wherein the donor template has homologous arms to the 17q21 region.

38. The method of any one of claims 1, 2, 7, 13, 19, or 24, wherein the method further comprises introducing into the cell one guide ribonucleic acid (gRNA) and a polynucleotide donor template comprising at least a portion of the wild-type G6PC gene, and wherein the one or more DNA endonucleases is one or more Cas9 endonucleases that effect one single-strand break (SSB) or double-strand break (DSB) at a DSB locus within or near the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor locus that facilitates insertion of a new sequence from the polynucleotide donor template into the chromosomal DNA at the locus or safe harbor locus that results in a permanent insertion or correction of a part of the chromosomal DNA of the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene proximal to the locus or safe harbor locus and restoration of G6Pase protein activity, and wherein the gRNA comprises a spacer sequence that is complementary to a segment of the locus or safe harbor locus.

39. The method of claim 38, wherein proximal means nucleotides both upstream and downstream of the locus or safe harbor locus.

40. The method of any one of claims 1, 2, 7, 13, 19, or 24, wherein the method further comprises introducing into the cell two guide ribonucleic acid (gRNAs) and a polynucleotide donor template comprising at least a portion of the wild-type G6PC gene, and wherein the one or more DNA endonucleases is two or more Cas9 or Cpf1 endonucleases that effect a pair of single-strand breaks (SSBs) or double-strand breaks (DSBs), the first at a 5' locus and the second at a 3' locus, within the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor locus that facilitates insertion of a new sequence from the polynucleotide donor template into the chromosomal DNA between the 5' locus and the 3' locus that results in permanent correction of the chromosomal DNA between the 5' locus and the 3' locus within the G6PC gene or other DNA sequences that encode regulatory elements of the G6PC gene or within or near a safe harbor locus and restoration of G6Pase protein activity, and wherein the first guide RNA comprises a spacer sequence that is complementary to a segment of the 5' locus and the second guide RNA comprises a spacer sequence that is complementary to a segment of the 3' locus.

41. The method of any one of claims 38-40, wherein the one or two gRNAs are one or two single-molecule guide RNA (sgRNAs).

42. The method of any one of claims 38-41, wherein the one or two gRNAs or one or two sgRNAs is one or two modified gRNA or one or two modified sgRNA.

43. The method of any one of claims 38-42, wherein the one or more DNA endonucleases is pre-complexed with one or two gRNAs or one or two sgRNAs.

44. The method of any one of claims 38-43, wherein the at least a portion of the wild-type G6PC gene or cDNA is exon 1, exon 2, exon 3, exon 4, exon 5, intronic regions, fragments or combinations thereof, the entire G6PC gene, DNA sequences that encode wild-type regulatory elements of the G6PC gene, or cDNA.

45. The method of any one of claims 38-44, wherein the donor template is either a single or double stranded polynucleotide.

46. The method of any one of claims 38-45, wherein the donor template has homologous arms to the 17q21 region.

47. The method of claim 3644, wherein the SSB, DSB, or 5' DSB and 3' DSB are in the first, second, third, fourth, fifth exon or intron of the G6PC gene.

48. The method of any one of claims 1, 2, 7, 13, 19, 24, 30-33, or 38-41, wherein the gRNA or sgRNA is directed to one or more of the following pathological variants: rs80356479, rs80356486, rs606231368, rs80356488, rs587776757, rs104894565, rs104894566, rs1801175, rs1801176, rs104894567, rs104894571, rs80356482, rs80356483, rs104894563, rs367727229, rs387906505, rs104894568, rs104894569, rs80356487, rs764920787, rs80356485, rs780226142, rs80356484.

49. The method of any one of claims 1, 2, 7, 13, 19 or 24-48, wherein the insertion or correction is by homology directed repair (HDR).

50. The method of any one of claims 1, 2, 7, 13, 19 or 24-49, wherein the Cas9 mRNA, gRNA, and donor template are either each formulated into separate lipid nanoparticles or all co-formulated into a lipid nanoparticle.

51. The method of any one of claims 1, 2, 7, 13, 19 or 24-49, wherein the Cas9 or Cpf1 mRNA is formulated into a lipid nanoparticle, and both the gRNA and donor template are delivered to the cell by a viral vector.

52. The method of claim 51, wherein the viral vector is an adeno-associated virus (AAV).

53. The method of claim 52, wherein the AAV vector is an AAV6 vector.

54. The method of any one of claims 1, 2, 7, 13, 19 or 24-49, wherein the Cas9 or Cpf1 mRNA, gRNA and a donor template are either each formulated into separate exosomes or all co-formulated into an exosome.

55. The method of any one of claims 1, 2, 7, 13, 19 or 24-49, wherein the Cas9 or Cpf1 mRNA is formulated into a lipid nanoparticle, and the gRNA is delivered to the cell by electroporation and donor template is delivered to the cell by a viral vector.

56. The method of claim 55, wherein the viral vector is an adeno-associated virus (AAV) vector.

57. The method of claim 56, wherein the AAV vector is an AAV6 vector.

58. The method of any one of the preceding claims, wherein the G6PC gene is located on Chromosome 17: 42,900,796 - 42,914,432 (Genome Reference Consortium – GRCh38/hg38).

59. The method of any one of claims 1, 2, 7, 13, 19 or 24-49, wherein the restoration of G6Pase protein activity is compared to wild-type or normal G6Pase protein activity.

60. The method of claim 1, wherein the human cell is a liver cell.

61. The method of claim 23, wherein the cell is a liver cell.

62. The method of any one of claims 1, 2, 7, 13, 19 or 24-49, wherein the G6PC gene is operably linked to an exogenous promoter that drives expression of the G6PC gene.

63. The method of any one of claims 1, 2, 7, 13, 19 or 24-49, wherein the one or more SSBs or DSBs occurs at a location immediately 3' to an endogenous promoter locus.

64. One or more guide ribonucleic acids (gRNAs) or editing a G6PC gene in a cell from a patient with Glycogen Storage Disease type 1a (GSD1a), the one or more gRNAs comprising a spacer sequence selected from the group consisting of the nucleic acid sequences in Figures 1-90 for editing the glucose-6-phosphatase, catalytic gene in a cell from a patient with Glycogen Storage Disease type 1a.

65. The one or more gRNAs of claim 64, wherein the one or more gRNAs are one or more single-molecule guide RNAs (sgRNAs).

66. The one or more gRNAs or sgRNAs of claim 64 or 65, wherein the one or more gRNAs or one or more sgRNAs is one or more modified gRNA or one or more modified sgRNA.

67. The one or more gRNAs or sgRNAs of claims 63-65, wherein the cell is a liver cell.

DEMANDE OU BREVET VOLUMINEUX

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Figure 1

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 1	TGGCGATATCTAGGTAGCCA	CAG	chr19	55112666	55112685	55112682	+
SEQ ID NO 2	GGCGATATCTAGGTAGCCAC	AGG	chr19	55112667	55112686	55112683	+
SEQ ID NO 3	CGATATCTAGGTAGCCACAG	GAG	chr19	55112669	55112688	55112685	+
SEQ ID NO 4	GATATCTAGGTAGCCACAGG	AGG	chr19	55112670	55112689	55112686	+
SEQ ID NO 5	ATCTAGGTAGCCACAGGAGG	CGG	chr19	55112673	55112692	55112689	+
SEQ ID NO 6	CCACAGGAGGCGGCCACGTG	CAG	chr19	55112683	55112702	55112699	+
SEQ ID NO 7	CAGGAGGCGGCCACGTGCAG	TGG	chr19	55112686	55112705	55112702	+
SEQ ID NO 8	CGGCCACGTGCAGTGGCGTC	CAG	chr19	55112693	55112712	55112709	+
SEQ ID NO 9	TCCAGCCCTCGTTGTCTGCC	TGG	chr19	55112711	55112730	55112727	+
SEQ ID NO 10	CTCGTTGTCTGCCTGGTTCA	CAG	chr19	55112718	55112737	55112734	+
SEQ ID NO 11	GTTGTCTGCCTGGTTCACAG	TGG	chr19	55112721	55112740	55112737	+
SEQ ID NO 12	CAGTGGCGCCCTGCTCCACC	AAG	chr19	55112738	55112757	55112754	+
SEQ ID NO 13	TGGCGCCCTGCTCCACCAAG	AAG	chr19	55112741	55112760	55112757	+
SEQ ID NO 14	ACCAAGAAGCGCACCACCTC	CAG	chr19	55112755	55112774	55112771	+
SEQ ID NO 15	CCAAGAAGCGCACCACCTCC	AGG	chr19	55112756	55112775	55112772	+
SEQ ID NO 16	CCTCCAGGTTCTCATCAATG	CAG	chr19	55112771	55112790	55112787	+
SEQ ID NO 17	CTCCAGGTTCTCATCAATGC	AGG	chr19	55112772	55112791	55112788	+
SEQ ID NO 18	GGTTCTCATCAATGCAGGCC	TGG	chr19	55112777	55112796	55112793	+
SEQ ID NO 19	GTTCTCATCAATGCAGGCCT	GGG	chr19	55112778	55112797	55112794	+
SEQ ID NO 20	TTCTCATCAATGCAGGCCTG	GGG	chr19	55112779	55112798	55112795	+
SEQ ID NO 21	TCTCATCAATGCAGGCCTGG	GGG	chr19	55112780	55112799	55112796	+
SEQ ID NO 22	CATCAATGCAGGCCTGGGGG	TGG	chr19	55112783	55112802	55112799	+
SEQ ID NO 23	ATCAATGCAGGCCTGGGGGT	GGG	chr19	55112784	55112803	55112800	+
SEQ ID NO 24	GCAGGCCTGGGGGTGGGAAA	CAG	chr19	55112790	55112809	55112806	+
SEQ ID NO 25	TGGGGGTGGGAAACAGCCGT	CAG	chr19	55112797	55112816	55112813	+
SEQ ID NO 26	GCCGTCAGCCGCACCTACCC	CAG	chr19	55112812	55112831	55112828	+
SEQ ID NO 27	AGCCGCACCTACCCCAGCCA	CGG	chr19	55112818	55112837	55112834	+
SEQ ID NO 28	CTACCCCAGCCACGGTGTCC	CAG	chr19	55112826	55112845	55112842	+
SEQ ID NO 29	CCCAGCCACGGTGTCCCAGC	AAG	chr19	55112830	55112849	55112846	+
SEQ ID NO 30	GCCACGGTGTCCCAGCAAGT	CGG	chr19	55112834	55112853	55112850	+
SEQ ID NO 31	CCACGGTGTCCCAGCAAGTC	GGG	chr19	55112835	55112854	55112851	+
SEQ ID NO 32	GTCCCAGCAAGTCGGGACTC	CAG	chr19	55112842	55112861	55112858	+
SEQ ID NO 33	CCCAGCAAGTCGGGACTCCA	GAG	chr19	55112844	55112863	55112860	+
SEQ ID NO 34	CCAGCAAGTCGGGACTCCAG	AGG	chr19	55112845	55112864	55112861	+
SEQ ID NO 35	CAGCAAGTCGGGACTCCAGA	GGG	chr19	55112846	55112865	55112862	+
SEQ ID NO 36	GCAAGTCGGGACTCCAGAGG	GAG	chr19	55112848	55112867	55112864	+
SEQ ID NO 37	TCCAGAGGGAGCCACGAAAA	CAG	chr19	55112860	55112879	55112876	+
SEQ ID NO 38	GGGAGCCACGAAAACAGATC	CAG	chr19	55112866	55112885	55112882	+
SEQ ID NO 39	GGAGCCACGAAAACAGATCC	AGG	chr19	55112867	55112886	55112883	+
SEQ ID NO 40	GAGCCACGAAAACAGATCCA	GGG	chr19	55112868	55112887	55112884	+
SEQ ID NO 41	CGAAAACAGATCCAGGGACA	CGG	chr19	55112874	55112893	55112890	+
SEQ ID NO 42	CAGATCCAGGGACACGGTGC	TAG	chr19	55112880	55112899	55112896	+
SEQ ID NO 43	AGATCCAGGGACACGGTGCT	AGG	chr19	55112881	55112900	55112897	+
SEQ ID NO 44	CCAGGGACACGGTGCTAGGA	CAG	chr19	55112885	55112904	55112901	+
SEQ ID NO 45	GGGACACGGTGCTAGGACAG	TGG	chr19	55112888	55112907	55112904	+
SEQ ID NO 46	GGACACGGTGCTAGGACAGT	GGG	chr19	55112889	55112908	55112905	+
SEQ ID NO 47	GACACGGTGCTAGGACAGTG	GGG	chr19	55112890	55112909	55112906	+
SEQ ID NO 48	CAGTGGGGAAAATGACCCAA	CAG	chr19	55112905	55112924	55112921	+

SEQ ID NO 49	GAAAATGACCCAACAGCCTC	TGG	chr19	55112912	55112931	55112928	+
SEQ ID NO 50	ACCCAACAGCCTCTGGCCAC	TGG	chr19	55112919	55112938	55112935	+
SEQ ID NO 51	CCTCTGGCCACTGGCTGTTT	AAG	chr19	55112928	55112947	55112944	+
SEQ ID NO 52	CTGGCTGTTTAAGATACGCC	TGG	chr19	55112938	55112957	55112954	+
SEQ ID NO 53	TTAAGATACGCCTGGTTGCC	CAG	chr19	55112946	55112965	55112962	+
SEQ ID NO 54	AGATACGCCTGGTTGCCCAG	TGG	chr19	55112949	55112968	55112965	+
SEQ ID NO 55	ACGCCTGGTTGCCCAGTGGT	CAG	chr19	55112953	55112972	55112969	+
SEQ ID NO 56	CGCCTGGTTGCCCAGTGGTC	AGG	chr19	55112954	55112973	55112970	+
SEQ ID NO 57	TGGTTGCCCAGTGGTCAGGC	CGG	chr19	55112958	55112977	55112974	+
SEQ ID NO 58	TGCCCAGTGGTCAGGCCGGC	CAG	chr19	55112962	55112981	55112978	+
SEQ ID NO 59	GCCCAGTGGTCAGGCCGGCC	AGG	chr19	55112963	55112982	55112979	+
SEQ ID NO 60	GGTCAGGCCGGCCAGGCCTT	CAG	chr19	55112970	55112989	55112986	+
SEQ ID NO 61	CCGGCCAGGCCTTCAGTGCT	CAG	chr19	55112977	55112996	55112993	+
SEQ ID NO 62	GCCAGGCCTTCAGTGCTCAG	TGG	chr19	55112980	55112999	55112996	+
SEQ ID NO 63	GTGCTCAGTGGAAACCACGA	AAG	chr19	55112992	55113011	55113008	+
SEQ ID NO 64	TGCTCAGTGGAAACCACGAA	AGG	chr19	55112993	55113012	55113009	+
SEQ ID NO 65	GGAAACCACGAAAGGACTCC	TGG	chr19	55113001	55113020	55113017	+
SEQ ID NO 66	GACTCCTGGCTATCTGCAAA	CAG	chr19	55113015	55113034	55113031	+
SEQ ID NO 67	ACTCCTGGCTATCTGCAAAC	AGG	chr19	55113016	55113035	55113032	+
SEQ ID NO 68	CCTGGCTATCTGCAAACAGG	AAG	chr19	55113019	55113038	55113035	+
SEQ ID NO 69	ATCTGCAAACAGGAAGTGAA	CGG	chr19	55113026	55113045	55113042	+
SEQ ID NO 70	TCTGCAAACAGGAAGTGAAC	GGG	chr19	55113027	55113046	55113043	+
SEQ ID NO 71	CTGCAAACAGGAAGTGAACG	GGG	chr19	55113028	55113047	55113044	+
SEQ ID NO 72	CAAACAGGAAGTGAACGGGG	AAG	chr19	55113031	55113050	55113047	+
SEQ ID NO 73	AAACAGGAAGTGAACGGGGA	AGG	chr19	55113032	55113051	55113048	+
SEQ ID NO 74	AACAGGAAGTGAACGGGGAA	GGG	chr19	55113033	55113052	55113049	+
SEQ ID NO 75	CAGGAAGTGAACGGGGAAGG	GAG	chr19	55113035	55113054	55113051	+
SEQ ID NO 76	AGGAAGTGAACGGGGAAGGG	AGG	chr19	55113036	55113055	55113052	+
SEQ ID NO 77	GGAAGTGAACGGGGAAGGGA	GGG	chr19	55113037	55113056	55113053	+
SEQ ID NO 78	GAAGTGAACGGGGAAGGGAG	GGG	chr19	55113038	55113057	55113054	+
SEQ ID NO 79	AAGTGAACGGGGAAGGGAGG	GGG	chr19	55113039	55113058	55113055	+
SEQ ID NO 80	AAGGGAGGGGGCTTCTCATC	TGG	chr19	55113051	55113070	55113067	+
SEQ ID NO 81	AGGGAGGGGGCTTCTCATCT	GGG	chr19	55113052	55113071	55113068	+
SEQ ID NO 82	GGGGGCTTCTCATCTGGGTG	CGG	chr19	55113057	55113076	55113073	+
SEQ ID NO 83	GGGGCTTCTCATCTGGGTGC	GGG	chr19	55113058	55113077	55113074	+
SEQ ID NO 84	CTGGGTGCGGGAACCCCACA	TGG	chr19	55113070	55113089	55113086	+
SEQ ID NO 85	GAACCCCACATGGTACCTGT	TAG	chr19	55113080	55113099	55113096	+
SEQ ID NO 86	CACATGGTACCTGTTAGACA	CGG	chr19	55113086	55113105	55113102	+
SEQ ID NO 87	AAAACCCCCGTCACCACCCA	CAG	chr19	55113110	55113129	55113126	+
SEQ ID NO 88	AAACCCCCGTCACCACCCAC	AGG	chr19	55113111	55113130	55113127	+
SEQ ID NO 89	CCCCCGTCACCACCCACAGG	TGG	chr19	55113114	55113133	55113130	+
SEQ ID NO 90	CCACCCACAGGTGGCGCTTC	CAG	chr19	55113123	55113142	55113139	+
SEQ ID NO 91	CAGGTGGCGCTTCCAGTGCT	CAG	chr19	55113130	55113149	55113146	+
SEQ ID NO 92	GGCGCTTCCAGTGCTCAGAC	TAG	chr19	55113135	55113154	55113151	+
SEQ ID NO 93	GCGCTTCCAGTGCTCAGACT	AGG	chr19	55113136	55113155	55113152	+
SEQ ID NO 94	CGCTTCCAGTGCTCAGACTA	GGG	chr19	55113137	55113156	55113153	+
SEQ ID NO 95	TTCCAGTGCTCAGACTAGGG	AAG	chr19	55113140	55113159	55113156	+
SEQ ID NO 96	CCAGTGCTCAGACTAGGGAA	GAG	chr19	55113142	55113161	55113158	+
SEQ ID NO 97	CAGTGCTCAGACTAGGGAAG	AGG	chr19	55113143	55113162	55113159	+

SEQ ID NO 98	TCAGACTAGGGAAGAGGTTC	CAG	chr19	55113149	55113168	55113165	+
SEQ ID NO 99	GGTTCCAGCCCCTCCTCCTT	CAG	chr19	55113164	55113183	55113180	+
SEQ ID NO 100	TTCCAGCCCCTCCTCCTTCA	GAG	chr19	55113166	55113185	55113182	+
SEQ ID NO 101	AGCCCCTCCTCCTTCAGAGC	CAG	chr19	55113170	55113189	55113186	+
SEQ ID NO 102	GCCCCTCCTCCTTCAGAGCC	AGG	chr19	55113171	55113190	55113187	+
SEQ ID NO 103	CCCTCCTCCTTCAGAGCCAG	GAG	chr19	55113173	55113192	55113189	+
SEQ ID NO 104	TCCTTCAGAGCCAGGAGTCC	TGG	chr19	55113179	55113198	55113195	+
SEQ ID NO 105	GAGCCAGGAGTCCTGGCCCC	CAG	chr19	55113186	55113205	55113202	+
SEQ ID NO 106	AGCCCCTCCTGCCTTAAACC	CAG	chr19	55113207	55113226	55113223	+
SEQ ID NO 107	CCTCCTGCCTTAAACCCAGC	CAG	chr19	55113211	55113230	55113227	+
SEQ ID NO 108	CTCCTGCCTTAAACCCAGCC	AGG	chr19	55113212	55113231	55113228	+
SEQ ID NO 109	AAACCCAGCCAGGTCCTTCC	AAG	chr19	55113222	55113241	55113238	+
SEQ ID NO 110	AACCCAGCCAGGTCCTTCCA	AGG	chr19	55113223	55113242	55113239	+
SEQ ID NO 111	ACCCAGCCAGGTCCTTCCAA	GGG	chr19	55113224	55113243	55113240	+
SEQ ID NO 112	GCCAGGTCCTTCCAAGGGTC	AAG	chr19	55113229	55113248	55113245	+
SEQ ID NO 113	GTCCTTCCAAGGGTCAAGCT	CGG	chr19	55113234	55113253	55113250	+
SEQ ID NO 114	GTCAAGCTCGGAAACCACCC	CAG	chr19	55113246	55113265	55113262	+
SEQ ID NO 115	AAGCTCGGAAACCACCCCAG	CAG	chr19	55113249	55113268	55113265	+
SEQ ID NO 116	CCACCCCAGCAGATACTCTG	CAG	chr19	55113260	55113279	55113276	+
SEQ ID NO 117	CACCCCAGCAGATACTCTGC	AGG	chr19	55113261	55113280	55113277	+
SEQ ID NO 118	GCAGATACTCTGCAGGAACG	AAG	chr19	55113268	55113287	55113284	+
SEQ ID NO 119	ACTCTGCAGGAACGAAGCCG	TGG	chr19	55113274	55113293	55113290	+
SEQ ID NO 120	CTCTGCAGGAACGAAGCCGT	GGG	chr19	55113275	55113294	55113291	+
SEQ ID NO 121	CAGGAACGAAGCCGTGGGCC	CAG	chr19	55113280	55113299	55113296	+
SEQ ID NO 122	AGGAACGAAGCCGTGGGCCC	AGG	chr19	55113281	55113300	55113297	+
SEQ ID NO 123	GGAACGAAGCCGTGGGCCCA	GGG	chr19	55113282	55113301	55113298	+
SEQ ID NO 124	GCCGTGGGCCCAGGGCTATG	CAG	chr19	55113290	55113309	55113306	+
SEQ ID NO 125	CCGTGGGCCCAGGGCTATGC	AGG	chr19	55113291	55113310	55113307	+
SEQ ID NO 126	CGTGGGCCCAGGGCTATGCA	GGG	chr19	55113292	55113311	55113308	+
SEQ ID NO 127	GGGCCCAGGGCTATGCAGGG	TGG	chr19	55113295	55113314	55113311	+
SEQ ID NO 128	GCCCAGGGCTATGCAGGGTG	GAG	chr19	55113297	55113316	55113313	+
SEQ ID NO 129	CCCAGGGCTATGCAGGGTGG	AGG	chr19	55113298	55113317	55113314	+
SEQ ID NO 130	AGGGCTATGCAGGGTGGAGG	AAG	chr19	55113301	55113320	55113317	+
SEQ ID NO 131	GGGCTATGCAGGGTGGAGGA	AGG	chr19	55113302	55113321	55113318	+
SEQ ID NO 132	GGAGGAAGGCCACCCTGTGC	TGG	chr19	55113316	55113335	55113332	+
SEQ ID NO 133	GAGGAAGGCCACCCTGTGCT	GGG	chr19	55113317	55113336	55113333	+
SEQ ID NO 134	AAGGCCACCCTGTGCTGGGA	CAG	chr19	55113321	55113340	55113337	+
SEQ ID NO 135	ACCCTGTGCTGGGACAGACT	CAG	chr19	55113327	55113346	55113343	+
SEQ ID NO 136	CCCTGTGCTGGGACAGACTC	AGG	chr19	55113328	55113347	55113344	+
SEQ ID NO 137	CCTGTGCTGGGACAGACTCA	GGG	chr19	55113329	55113348	55113345	+
SEQ ID NO 138	CTGTGCTGGGACAGACTCAG	GGG	chr19	55113330	55113349	55113346	+
SEQ ID NO 139	CTGGGACAGACTCAGGGGCC	TGG	chr19	55113335	55113354	55113351	+
SEQ ID NO 140	TGGGACAGACTCAGGGGCCT	GGG	chr19	55113336	55113355	55113352	+
SEQ ID NO 141	GACAGACTCAGGGGCCTGGG	CGG	chr19	55113339	55113358	55113355	+
SEQ ID NO 142	ACAGACTCAGGGGCCTGGGC	GGG	chr19	55113340	55113359	55113356	+
SEQ ID NO 143	AGGGGCCTGGGCGGGACTCC	CAG	chr19	55113348	55113367	55113364	+
SEQ ID NO 144	GGGCCTGGGCGGGACTCCCA	GAG	chr19	55113350	55113369	55113366	+
SEQ ID NO 145	GGCCTGGGCGGGACTCCCAG	AGG	chr19	55113351	55113370	55113367	+
SEQ ID NO 146	GCCTGGGCGGGACTCCCAGA	GGG	chr19	55113352	55113371	55113368	+

SEQ ID NO 147	CCTGGGCGGGACTCCCAGAG	GGG	chr19	55113353	55113372	55113369	+
SEQ ID NO 148	GGCGGGACTCCCAGAGGGGT	GAG	chr19	55113357	55113376	55113373	+
SEQ ID NO 149	GGACTCCCAGAGGGGTGAGA	CAG	chr19	55113361	55113380	55113377	+
SEQ ID NO 150	CAGCTGCACACCTGTGTGCC	TGG	chr19	55113381	55113400	55113397	+
SEQ ID NO 151	AGCTGCACACCTGTGTGCCT	GGG	chr19	55113382	55113401	55113398	+
SEQ ID NO 152	ACACCTGTGTGCCTGGGCCC	CAG	chr19	55113388	55113407	55113404	+
SEQ ID NO 153	CACCTGTGTGCCTGGGCCCC	AGG	chr19	55113389	55113408	55113405	+
SEQ ID NO 154	GGCCCCAGGCTGTCACACTC	CAG	chr19	55113403	55113422	55113419	+
SEQ ID NO 155	CTGTCACACTCCAGTTCACT	GAG	chr19	55113412	55113431	55113428	+
SEQ ID NO 156	TGTCACACTCCAGTTCACTG	AGG	chr19	55113413	55113432	55113429	+
SEQ ID NO 157	TCACTGAGGCCCCCTCTGCA	CGG	chr19	55113427	55113446	55113443	+
SEQ ID NO 158	CACTGAGGCCCCCTCTGCAC	GGG	chr19	55113428	55113447	55113444	+
SEQ ID NO 159	ACTGAGGCCCCCTCTGCACG	GGG	chr19	55113429	55113448	55113445	+
SEQ ID NO 160	CCCCTCTGCACGGGGCCCTG	CAG	chr19	55113437	55113456	55113453	+
SEQ ID NO 161	TCTGCACGGGGCCCTGCAGC	CAG	chr19	55113441	55113460	55113457	+
SEQ ID NO 162	CTGCACGGGGCCCTGCAGCC	AGG	chr19	55113442	55113461	55113458	+
SEQ ID NO 163	TGCACGGGGCCCTGCAGCCA	GGG	chr19	55113443	55113462	55113459	+
SEQ ID NO 164	GCACGGGGCCCTGCAGCCAG	GGG	chr19	55113444	55113463	55113460	+
SEQ ID NO 165	CCTGCAGCCAGGGGCTGACA	CGG	chr19	55113453	55113472	55113469	+
SEQ ID NO 166	CTGCAGCCAGGGGCTGACAC	GGG	chr19	55113454	55113473	55113470	+
SEQ ID NO 167	ACCGTTTCTCATTCTTCCCT	TAG	chr19	55113479	55113498	55113495	+
SEQ ID NO 168	CCGTTTCTCATTCTTCCCTT	AGG	chr19	55113480	55113499	55113496	+
SEQ ID NO 169	CGTTTCTCATTCTTCCCTTA	GGG	chr19	55113481	55113500	55113497	+
SEQ ID NO 170	GTTTCTCATTCTTCCCTTAG	GGG	chr19	55113482	55113501	55113498	+
SEQ ID NO 171	TCCCTTAGGGGTCCAAAACT	TGG	chr19	55113494	55113513	55113510	+
SEQ ID NO 172	CCCTTAGGGGTCCAAAACTT	GGG	chr19	55113495	55113514	55113511	+
SEQ ID NO 173	CCTTAGGGGTCCAAAACTTG	GGG	chr19	55113496	55113515	55113512	+
SEQ ID NO 174	CTTAGGGGTCCAAAACTTGG	GGG	chr19	55113497	55113516	55113513	+
SEQ ID NO 175	TTAGGGGTCCAAAACTTGGG	GGG	chr19	55113498	55113517	55113514	+
SEQ ID NO 176	TCCAAAACTTGGGGGGACAA	AAG	chr19	55113505	55113524	55113521	+
SEQ ID NO 177	ACTTGGGGGGACAAAAGCCG	AAG	chr19	55113511	55113530	55113527	+
SEQ ID NO 178	GGGGGACAAAAGCCGAAGTC	CAG	chr19	55113516	55113535	55113532	+
SEQ ID NO 179	GGGGACAAAAGCCGAAGTCC	AGG	chr19	55113517	55113536	55113533	+
SEQ ID NO 180	GGGACAAAAGCCGAAGTCCA	GGG	chr19	55113518	55113537	55113534	+
SEQ ID NO 181	GGACAAAAGCCGAAGTCCAG	GGG	chr19	55113519	55113538	55113535	+
SEQ ID NO 182	GACAAAAGCCGAAGTCCAGG	GGG	chr19	55113520	55113539	55113536	+
SEQ ID NO 183	AAAGCCGAAGTCCAGGGGGT	CGG	chr19	55113524	55113543	55113540	+
SEQ ID NO 184	AGCCGAAGTCCAGGGGGTCG	GAG	chr19	55113526	55113545	55113542	+
SEQ ID NO 185	GCCGAAGTCCAGGGGGTCGG	AGG	chr19	55113527	55113546	55113543	+
SEQ ID NO 186	CGAAGTCCAGGGGGTCGGAG	GAG	chr19	55113529	55113548	55113545	+
SEQ ID NO 187	GAAGTCCAGGGGGTCGGAGG	AGG	chr19	55113530	55113549	55113546	+
SEQ ID NO 188	AAGTCCAGGGGGTCGGAGGA	GGG	chr19	55113531	55113550	55113547	+
SEQ ID NO 189	GTCGGAGGAGGGACTTGCCC	CAG	chr19	55113542	55113561	55113558	+
SEQ ID NO 190	TCGGAGGAGGGACTTGCCCC	AGG	chr19	55113543	55113562	55113559	+
SEQ ID NO 191	GGGACTTGCCCCAGGCCTTG	TGG	chr19	55113551	55113570	55113567	+
SEQ ID NO 192	GCCCCAGGCCTTGTGGACAC	TGG	chr19	55113558	55113577	55113574	+
SEQ ID NO 193	CCCCAGGCCTTGTGGACACT	GGG	chr19	55113559	55113578	55113575	+
SEQ ID NO 194	CAGGCCTTGTGGACACTGGG	TGG	chr19	55113562	55113581	55113578	+
SEQ ID NO 195	AGGCCTTGTGGACACTGGGT	GGG	chr19	55113563	55113582	55113579	+

SEQ ID NO 196	TGTGGACACTGGGTGGGCTC	CGG	chr19	55113569	55113588	55113585	+
SEQ ID NO 197	GTGGACACTGGGTGGGCTCC	GGG	chr19	55113570	55113589	55113586	+
SEQ ID NO 198	GTGGGCTCCGGGACCTGAAC	TGG	chr19	55113581	55113600	55113597	+
SEQ ID NO 199	GGGCTCCGGGACCTGAACTG	GAG	chr19	55113583	55113602	55113599	+
SEQ ID NO 200	CCGGGACCTGAACTGGAGCT	GAG	chr19	55113588	55113607	55113604	+
SEQ ID NO 201	CGGGACCTGAACTGGAGCTG	AGG	chr19	55113589	55113608	55113605	+
SEQ ID NO 202	GACCTGAACTGGAGCTGAGG	AAG	chr19	55113592	55113611	55113608	+
SEQ ID NO 203	ACCTGAACTGGAGCTGAGGA	AGG	chr19	55113593	55113612	55113609	+
SEQ ID NO 204	CTGAACTGGAGCTGAGGAAG	GAG	chr19	55113595	55113614	55113611	+
SEQ ID NO 205	CTGGAGCTGAGGAAGGAGTG	AAG	chr19	55113600	55113619	55113616	+
SEQ ID NO 206	AAGGAGTGAAGCTAAACTCC	TAG	chr19	55113612	55113631	55113628	+
SEQ ID NO 207	AAGCTAAACTCCTAGATCCA	CGG	chr19	55113620	55113639	55113636	+
SEQ ID NO 208	AGCTAAACTCCTAGATCCAC	GGG	chr19	55113621	55113640	55113637	+
SEQ ID NO 209	CACGGGATAAATTACCCCCC	AAG	chr19	55113638	55113657	55113654	+
SEQ ID NO 210	CCAAGTCCCTCACCTCTCCA	AAG	chr19	55113656	55113675	55113672	+
SEQ ID NO 211	CCTCTCCAAAGCTGCCCATC	TGG	chr19	55113668	55113687	55113684	+
SEQ ID NO 212	TCTCCAAAGCTGCCCATCTG	GAG	chr19	55113670	55113689	55113686	+
SEQ ID NO 213	CTCCAAAGCTGCCCATCTGG	AGG	chr19	55113671	55113690	55113687	+
SEQ ID NO 214	CCAAAGCTGCCCATCTGGAG	GAG	chr19	55113673	55113692	55113689	+
SEQ ID NO 215	CAAAGCTGCCCATCTGGAGG	AGG	chr19	55113674	55113693	55113690	+
SEQ ID NO 216	AGCTGCCCATCTGGAGGAGG	CGG	chr19	55113677	55113696	55113693	+
SEQ ID NO 217	GCTGCCCATCTGGAGGAGGC	GGG	chr19	55113678	55113697	55113694	+
SEQ ID NO 218	TGCCCATCTGGAGGAGGCGG	GAG	chr19	55113680	55113699	55113696	+
SEQ ID NO 219	GCCCATCTGGAGGAGGCGGG	AGG	chr19	55113681	55113700	55113697	+
SEQ ID NO 220	CCCATCTGGAGGAGGCGGGA	GGG	chr19	55113682	55113701	55113698	+
SEQ ID NO 221	CATCTGGAGGAGGCGGGAGG	GAG	chr19	55113684	55113703	55113700	+
SEQ ID NO 222	AGGAGGCGGGAGGGAGCTAC	GAG	chr19	55113691	55113710	55113707	+
SEQ ID NO 223	GGAGGCGGGAGGGAGCTACG	AGG	chr19	55113692	55113711	55113708	+
SEQ ID NO 224	GAGGCGGGAGGGAGCTACGA	GGG	chr19	55113693	55113712	55113709	+
SEQ ID NO 225	GGGAGGGAGCTACGAGGGCC	AAG	chr19	55113698	55113717	55113714	+
SEQ ID NO 226	GAGGGAGCTACGAGGGCCAA	GAG	chr19	55113700	55113719	55113716	+
SEQ ID NO 227	GCTACGAGGGCCAAGAGCAT	GAG	chr19	55113706	55113725	55113722	+
SEQ ID NO 228	CTACGAGGGCCAAGAGCATG	AGG	chr19	55113707	55113726	55113723	+
SEQ ID NO 229	GGGCCAAGAGCATGAGGTCA	TGG	chr19	55113713	55113732	55113729	+
SEQ ID NO 230	AGCATGAGGTCATGGAAACT	CGG	chr19	55113721	55113740	55113737	+
SEQ ID NO 231	GCATGAGGTCATGGAAACTC	GGG	chr19	55113722	55113741	55113738	+
SEQ ID NO 232	TCATGGAAACTCGGGCTGTG	AAG	chr19	55113730	55113749	55113746	+
SEQ ID NO 233	CATGGAAACTCGGGCTGTGA	AGG	chr19	55113731	55113750	55113747	+
SEQ ID NO 234	ATGGAAACTCGGGCTGTGAA	GGG	chr19	55113732	55113751	55113748	+
SEQ ID NO 235	TGGAAACTCGGGCTGTGAAG	GGG	chr19	55113733	55113752	55113749	+
SEQ ID NO 236	TGAAGGGGCCGCACGTGCCC	TGG	chr19	55113748	55113767	55113764	+
SEQ ID NO 237	GAAGGGGCCGCACGTGCCCT	GGG	chr19	55113749	55113768	55113765	+
SEQ ID NO 238	GGCCGCACGTGCCCTGGGAA	CGG	chr19	55113754	55113773	55113770	+
SEQ ID NO 239	GCCGCACGTGCCCTGGGAAC	GGG	chr19	55113755	55113774	55113771	+
SEQ ID NO 240	CCCTGGGAACGGGATGAACT	CGG	chr19	55113765	55113784	55113781	+
SEQ ID NO 241	TCGGCTCGTTTATTTCCACC	CAG	chr19	55113784	55113803	55113800	+
SEQ ID NO 242	TTATTTCCACCCAGTTGTCA	TGG	chr19	55113793	55113812	55113809	+
SEQ ID NO 243	CCACCCAGTTGTCATGGCGA	TAG	chr19	55113799	55113818	55113815	+
SEQ ID NO 244	CACCCAGTTGTCATGGCGAT	AGG	chr19	55113800	55113819	55113816	+

SEQ ID NO 245	ACCCAGTTGTCATGGCGATA	GGG	chr19	55113801	55113820	55113817	+
SEQ ID NO 246	CCCAGTTGTCATGGCGATAG	GGG	chr19	55113802	55113821	55113818	+
SEQ ID NO 247	CAGTTGTCATGGCGATAGGG	GAG	chr19	55113804	55113823	55113820	+
SEQ ID NO 248	AGTTGTCATGGCGATAGGGG	AGG	chr19	55113805	55113824	55113821	+
SEQ ID NO 249	GTTGTCATGGCGATAGGGGA	GGG	chr19	55113806	55113825	55113822	+
SEQ ID NO 250	TTGTCATGGCGATAGGGGAG	GGG	chr19	55113807	55113826	55113823	+
SEQ ID NO 251	TGTCATGGCGATAGGGGAGG	GGG	chr19	55113808	55113827	55113824	+
SEQ ID NO 252	GTCATGGCGATAGGGGAGGG	GGG	chr19	55113809	55113828	55113825	+
SEQ ID NO 253	TGGCGATAGGGGAGGGGGGC	AAG	chr19	55113813	55113832	55113829	+
SEQ ID NO 254	GGCGATAGGGGAGGGGGGCA	AGG	chr19	55113814	55113833	55113830	+
SEQ ID NO 255	CGATAGGGGAGGGGGGCAAG	GAG	chr19	55113816	55113835	55113832	+
SEQ ID NO 256	ATAGGGGAGGGGGGCAAGGA	GAG	chr19	55113818	55113837	55113834	+
SEQ ID NO 257	GAGGGGGGCAAGGAGAGCAA	TGG	chr19	55113824	55113843	55113840	+
SEQ ID NO 258	AGGGGGGCAAGGAGAGCAAT	GGG	chr19	55113825	55113844	55113841	+
SEQ ID NO 259	GCAATGGGCCTTTCCCTTTC	AAG	chr19	55113840	55113859	55113856	+
SEQ ID NO 260	CAATGGGCCTTTCCCTTTCA	AGG	chr19	55113841	55113860	55113857	+
SEQ ID NO 261	TTCCCTTTCAAGGACCTGCC	CAG	chr19	55113851	55113870	55113867	+
SEQ ID NO 262	TTTCAAGGACCTGCCCAGTA	CAG	chr19	55113856	55113875	55113872	+
SEQ ID NO 263	TTCAAGGACCTGCCCAGTAC	AGG	chr19	55113857	55113876	55113873	+
SEQ ID NO 264	CAGTACAGGCATCCCTGTGA	AAG	chr19	55113871	55113890	55113887	+
SEQ ID NO 265	CATCCCTGTGAAAGATGCCT	GAG	chr19	55113880	55113899	55113896	+
SEQ ID NO 266	ATCCCTGTGAAAGATGCCTG	AGG	chr19	55113881	55113900	55113897	+
SEQ ID NO 267	TGTGAAAGATGCCTGAGGCC	TGG	chr19	55113886	55113905	55113902	+
SEQ ID NO 268	GTGAAAGATGCCTGAGGCCT	GGG	chr19	55113887	55113906	55113903	+
SEQ ID NO 269	GATGCCTGAGGCCTGGGCAC	CAG	chr19	55113893	55113912	55113909	+
SEQ ID NO 270	ATGCCTGAGGCCTGGGCACC	AGG	chr19	55113894	55113913	55113910	+
SEQ ID NO 271	TGCCTGAGGCCTGGGCACCA	GGG	chr19	55113895	55113914	55113911	+
SEQ ID NO 272	GGCCTGGGCACCAGGGACTC	CAG	chr19	55113902	55113921	55113918	+
SEQ ID NO 273	CCTGGGCACCAGGGACTCCA	GAG	chr19	55113904	55113923	55113920	+
SEQ ID NO 274	GCACCAGGGACTCCAGAGTC	CAG	chr19	55113909	55113928	55113925	+
SEQ ID NO 275	CACCAGGGACTCCAGAGTCC	AGG	chr19	55113910	55113929	55113926	+
SEQ ID NO 276	CAACCCCTCCCCATTCAACC	CAG	chr19	55113935	55113954	55113951	+
SEQ ID NO 277	AACCCCTCCCCATTCAACCC	AGG	chr19	55113936	55113955	55113952	+
SEQ ID NO 278	CCCCTCCCCATTCAACCCAG	GAG	chr19	55113938	55113957	55113954	+
SEQ ID NO 279	CCCTCCCCATTCAACCCAGG	AGG	chr19	55113939	55113958	55113955	+
SEQ ID NO 280	CCCCATTCAACCCAGGAGGC	CAG	chr19	55113943	55113962	55113959	+
SEQ ID NO 281	CCCATTCAACCCAGGAGGCC	AGG	chr19	55113944	55113963	55113960	+
SEQ ID NO 282	CAACCCAGGAGGCCAGGCCC	CAG	chr19	55113950	55113969	55113966	+
SEQ ID NO 283	GGCCCCAGCCCTTCCGCCCT	CAG	chr19	55113965	55113984	55113981	+
SEQ ID NO 284	AGCCCTTCCGCCCTCAGATG	AAG	chr19	55113971	55113990	55113987	+
SEQ ID NO 285	GCCCTTCCGCCCTCAGATGA	AGG	chr19	55113972	55113991	55113988	+
SEQ ID NO 286	CCTTCCGCCCTCAGATGAAG	GAG	chr19	55113974	55113993	55113990	+
SEQ ID NO 287	CGCCCTCAGATGAAGGAGTC	CAG	chr19	55113979	55113998	55113995	+
SEQ ID NO 288	GCCCTCAGATGAAGGAGTCC	AGG	chr19	55113980	55113999	55113996	+
SEQ ID NO 289	GATGAAGGAGTCCAGGCCCC	CAG	chr19	55113987	55114006	55114003	+
SEQ ID NO 290	GCCCCCAGCCTCTCCCCATT	CAG	chr19	55114002	55114021	55114018	+
SEQ ID NO 291	AGCCTCTCCCCATTCAGACC	CAG	chr19	55114008	55114027	55114024	+
SEQ ID NO 292	GCCTCTCCCCATTCAGACCC	AGG	chr19	55114009	55114028	55114025	+
SEQ ID NO 293	CCTCTCCCCATTCAGACCCA	GGG	chr19	55114010	55114029	55114026	+

SEQ ID NO 294	CTCTCCCCATTCAGACCCAG	GGG	chr19	55114011	55114030	55114027	+
SEQ ID NO 295	CCCATTCAGACCCAGGGGTC	CAG	chr19	55114016	55114035	55114032	+
SEQ ID NO 296	CCATTCAGACCCAGGGGTCC	AGG	chr19	55114017	55114036	55114033	+
SEQ ID NO 297	CAGACCCAGGGGTCCAGGCC	CAG	chr19	55114022	55114041	55114038	+
SEQ ID NO 298	AGGCCCAGCCCCGCCTCCCT	AAG	chr19	55114037	55114056	55114053	+
SEQ ID NO 299	AGCCCCGCCTCCCTAAGACC	CAG	chr19	55114043	55114062	55114059	+
SEQ ID NO 300	CCCGCCTCCCTAAGACCCAG	AAG	chr19	55114046	55114065	55114062	+
SEQ ID NO 301	CTCCCTAAGACCCAGAAGTC	CAG	chr19	55114051	55114070	55114067	+
SEQ ID NO 302	TCCCTAAGACCCAGAAGTCC	AGG	chr19	55114052	55114071	55114068	+
SEQ ID NO 303	GACCCAGAAGTCCAGGCCCC	CAG	chr19	55114059	55114078	55114075	+
SEQ ID NO 304	GCCCCCAGCCCCTCCTCCCT	CAG	chr19	55114074	55114093	55114090	+
SEQ ID NO 305	CCCTCCTCCCTCAGACCCAC	GAG	chr19	55114083	55114102	55114099	+
SEQ ID NO 306	CTCCCTCAGACCCACGAGTC	CAG	chr19	55114088	55114107	55114104	+
SEQ ID NO 307	TCCCTCAGACCCACGAGTCC	AGG	chr19	55114089	55114108	55114105	+
SEQ ID NO 308	AGACCCACGAGTCCAGGCCC	CAG	chr19	55114095	55114114	55114111	+
SEQ ID NO 309	GGCCCCAGCCCCTCCTCCCT	CGG	chr19	55114110	55114129	55114126	+
SEQ ID NO 310	AGCCCCTCCTCCCTCGGACC	CAG	chr19	55114116	55114135	55114132	+
SEQ ID NO 311	GCCCCTCCTCCCTCGGACCC	AGG	chr19	55114117	55114136	55114133	+
SEQ ID NO 312	CCCTCCTCCCTCGGACCCAG	GAG	chr19	55114119	55114138	55114135	+
SEQ ID NO 313	CTCCCTCGGACCCAGGAGTC	CAG	chr19	55114124	55114143	55114140	+
SEQ ID NO 314	TCCCTCGGACCCAGGAGTCC	AGG	chr19	55114125	55114144	55114141	+
SEQ ID NO 315	GACCCAGGAGTCCAGGCCCC	CAG	chr19	55114132	55114151	55114148	+
SEQ ID NO 316	GCCCCCAGTCCCTCCACCCT	CAG	chr19	55114147	55114166	55114163	+
SEQ ID NO 317	AGTCCCTCCACCCTCAGACC	CAG	chr19	55114153	55114172	55114169	+
SEQ ID NO 318	GTCCCTCCACCCTCAGACCC	AGG	chr19	55114154	55114173	55114170	+
SEQ ID NO 319	CCCTCCACCCTCAGACCCAG	GAG	chr19	55114156	55114175	55114172	+
SEQ ID NO 320	CACCCTCAGACCCAGGAGTC	CAG	chr19	55114161	55114180	55114177	+
SEQ ID NO 321	ACCCTCAGACCCAGGAGTCC	AGG	chr19	55114162	55114181	55114178	+
SEQ ID NO 322	AGACCCAGGAGTCCAGGCCC	CAG	chr19	55114168	55114187	55114184	+
SEQ ID NO 323	GGCCCCAGCCCCTCCTCCCT	CGG	chr19	55114183	55114202	55114199	+
SEQ ID NO 324	AGCCCCTCCTCCCTCGGACC	CAG	chr19	55114189	55114208	55114205	+
SEQ ID NO 325	GCCCCTCCTCCCTCGGACCC	AGG	chr19	55114190	55114209	55114206	+
SEQ ID NO 326	CCCTCCTCCCTCGGACCCAG	GAG	chr19	55114192	55114211	55114208	+
SEQ ID NO 327	CTCCCTCGGACCCAGGAGTC	CAG	chr19	55114197	55114216	55114213	+
SEQ ID NO 328	TCCCTCGGACCCAGGAGTCC	AGG	chr19	55114198	55114217	55114214	+
SEQ ID NO 329	GGACCCAGGAGTCCAGGCCC	CAG	chr19	55114204	55114223	55114220	+
SEQ ID NO 330	AGCCCCTCCTCTCTCAAACC	CAG	chr19	55114225	55114244	55114241	+
SEQ ID NO 331	GCCCCTCCTCTCTCAAACCC	AGG	chr19	55114226	55114245	55114242	+
SEQ ID NO 332	CCCTCCTCTCTCAAACCCAG	GAG	chr19	55114228	55114247	55114244	+
SEQ ID NO 333	CTCTCTCAAACCCAGGAGCC	CAG	chr19	55114233	55114252	55114249	+
SEQ ID NO 334	TCTCTCAAACCCAGGAGCCC	AGG	chr19	55114234	55114253	55114250	+
SEQ ID NO 335	AACCCAGGAGCCCAGGCCCC	CAG	chr19	55114241	55114260	55114257	+
SEQ ID NO 336	GCCCCCAGCTCTTCTCTGTT	CAG	chr19	55114256	55114275	55114272	+
SEQ ID NO 337	GCTCTTCTCTGTTCAGCCCT	AAG	chr19	55114263	55114282	55114279	+
SEQ ID NO 338	CTGTTCAGCCCTAAGAATCC	TGG	chr19	55114271	55114290	55114287	+
SEQ ID NO 339	AGCCCTAAGAATCCTGGCTC	CAG	chr19	55114277	55114296	55114293	+
SEQ ID NO 340	GGCTCCAGCCCCTCCTACTC	TAG	chr19	55114292	55114311	55114308	+
SEQ ID NO 341	TACTCTAGCCCCCAACCCCC	TAG	chr19	55114307	55114326	55114323	+
SEQ ID NO 342	CCCCCAACCCCCTAGCCACT	AAG	chr19	55114315	55114334	55114331	+

SEQ ID NO 343	CCCCAACCCCCTAGCCACTA	AGG	chr19	55114316	55114335	55114332	+
SEQ ID NO 344	CCCCTAGCCACTAAGGCAAT	TGG	chr19	55114323	55114342	55114339	+
SEQ ID NO 345	CCCTAGCCACTAAGGCAATT	GGG	chr19	55114324	55114343	55114340	+
SEQ ID NO 346	CCTAGCCACTAAGGCAATTG	GGG	chr19	55114325	55114344	55114341	+
SEQ ID NO 347	CCACTAAGGCAATTGGGGTG	CAG	chr19	55114330	55114349	55114346	+
SEQ ID NO 348	CACTAAGGCAATTGGGGTGC	AGG	chr19	55114331	55114350	55114347	+
SEQ ID NO 349	AGGCAATTGGGGTGCAGGAA	TGG	chr19	55114336	55114355	55114352	+
SEQ ID NO 350	GGCAATTGGGGTGCAGGAAT	GGG	chr19	55114337	55114356	55114353	+
SEQ ID NO 351	GCAATTGGGGTGCAGGAATG	GGG	chr19	55114338	55114357	55114354	+
SEQ ID NO 352	CAATTGGGGTGCAGGAATGG	GGG	chr19	55114339	55114358	55114355	+
SEQ ID NO 353	TTGGGGTGCAGGAATGGGGG	CAG	chr19	55114342	55114361	55114358	+
SEQ ID NO 354	TGGGGTGCAGGAATGGGGGC	AGG	chr19	55114343	55114362	55114359	+
SEQ ID NO 355	GGGGTGCAGGAATGGGGGCA	GGG	chr19	55114344	55114363	55114360	+
SEQ ID NO 356	CAGGAATGGGGGCAGGGTAC	CAG	chr19	55114350	55114369	55114366	+
SEQ ID NO 357	GGCAGGGTACCAGCCTCACC	AAG	chr19	55114360	55114379	55114376	+
SEQ ID NO 358	AGGGTACCAGCCTCACCAAG	TGG	chr19	55114363	55114382	55114379	+
SEQ ID NO 359	AAGTGGTTGATAAACCCACG	TGG	chr19	55114380	55114399	55114396	+
SEQ ID NO 360	AGTGGTTGATAAACCCACGT	GGG	chr19	55114381	55114400	55114397	+
SEQ ID NO 361	GTGGTTGATAAACCCACGTG	GGG	chr19	55114382	55114401	55114398	+
SEQ ID NO 362	AAACCCACGTGGGGTACCCT	AAG	chr19	55114391	55114410	55114407	+
SEQ ID NO 363	CGTGGGGTACCCTAAGAACT	TGG	chr19	55114398	55114417	55114414	+
SEQ ID NO 364	GTGGGGTACCCTAAGAACTT	GGG	chr19	55114399	55114418	55114415	+
SEQ ID NO 365	GTACCCTAAGAACTTGGGAA	CAG	chr19	55114404	55114423	55114420	+
SEQ ID NO 366	TAAGAACTTGGGAACAGCCA	CAG	chr19	55114410	55114429	55114426	+
SEQ ID NO 367	GAACTTGGGAACAGCCACAG	CAG	chr19	55114413	55114432	55114429	+
SEQ ID NO 368	AACTTGGGAACAGCCACAGC	AGG	chr19	55114414	55114433	55114430	+
SEQ ID NO 369	ACTTGGGAACAGCCACAGCA	GGG	chr19	55114415	55114434	55114431	+
SEQ ID NO 370	CTTGGGAACAGCCACAGCAG	GGG	chr19	55114416	55114435	55114432	+
SEQ ID NO 371	TTGGGAACAGCCACAGCAGG	GGG	chr19	55114417	55114436	55114433	+
SEQ ID NO 372	TGGGAACAGCCACAGCAGGG	GGG	chr19	55114418	55114437	55114434	+
SEQ ID NO 373	CACAGCAGGGGGGCGATGCT	TGG	chr19	55114428	55114447	55114444	+
SEQ ID NO 374	ACAGCAGGGGGGCGATGCTT	GGG	chr19	55114429	55114448	55114445	+
SEQ ID NO 375	CAGCAGGGGGGCGATGCTTG	GGG	chr19	55114430	55114449	55114446	+
SEQ ID NO 376	GCGATGCTTGGGGACCTGCC	TGG	chr19	55114440	55114459	55114456	+
SEQ ID NO 377	GATGCTTGGGGACCTGCCTG	GAG	chr19	55114442	55114461	55114458	+
SEQ ID NO 378	GCTTGGGGACCTGCCTGGAG	AAG	chr19	55114445	55114464	55114461	+
SEQ ID NO 379	CTTGGGGACCTGCCTGGAGA	AGG	chr19	55114446	55114465	55114462	+
SEQ ID NO 380	GACCTGCCTGGAGAAGGATG	CAG	chr19	55114452	55114471	55114468	+
SEQ ID NO 381	ACCTGCCTGGAGAAGGATGC	AGG	chr19	55114453	55114472	55114469	+
SEQ ID NO 382	CCTGGAGAAGGATGCAGGAC	GAG	chr19	55114458	55114477	55114474	+
SEQ ID NO 383	AGGATGCAGGACGAGAAACA	CAG	chr19	55114466	55114485	55114482	+
SEQ ID NO 384	CAGGACGAGAAACACAGCCC	CAG	chr19	55114472	55114491	55114488	+
SEQ ID NO 385	AGGACGAGAAACACAGCCCC	AGG	chr19	55114473	55114492	55114489	+
SEQ ID NO 386	ACGAGAAACACAGCCCCAGG	TGG	chr19	55114476	55114495	55114492	+
SEQ ID NO 387	GAGAAACACAGCCCCAGGTG	GAG	chr19	55114478	55114497	55114494	+
SEQ ID NO 388	ACAGCCCCAGGTGGAGAAAC	TGG	chr19	55114485	55114504	55114501	+
SEQ ID NO 389	CCCCAGGTGGAGAAACTGGC	CGG	chr19	55114489	55114508	55114505	+
SEQ ID NO 390	CCCAGGTGGAGAAACTGGCC	GGG	chr19	55114490	55114509	55114506	+
SEQ ID NO 391	GGAGAAACTGGCCGGGAATC	AAG	chr19	55114497	55114516	55114513	+

SEQ ID NO 392	AGAAACTGGCCGGGAATCAA	GAG	chr19	55114499	55114518	55114515	+
SEQ ID NO 393	GCCGGGAATCAAGAGTCACC	CAG	chr19	55114507	55114526	55114523	+
SEQ ID NO 394	CGGGAATCAAGAGTCACCCA	GAG	chr19	55114509	55114528	55114525	+
SEQ ID NO 395	AATCAAGAGTCACCCAGAGA	CAG	chr19	55114513	55114532	55114529	+
SEQ ID NO 396	ACCAACCATCCCTGTTTTCC	TAG	chr19	55114538	55114557	55114554	+
SEQ ID NO 397	CCAACCATCCCTGTTTTCCT	AGG	chr19	55114539	55114558	55114555	+
SEQ ID NO 398	ATCCCTGTTTTCCTAGGACT	GAG	chr19	55114545	55114564	55114561	+
SEQ ID NO 399	TCCCTGTTTTCCTAGGACTG	AGG	chr19	55114546	55114565	55114562	+
SEQ ID NO 400	CCCTGTTTTCCTAGGACTGA	GGG	chr19	55114547	55114566	55114563	+
SEQ ID NO 401	TTTCCTAGGACTGAGGGTTT	CAG	chr19	55114553	55114572	55114569	+
SEQ ID NO 402	GAGGGTTTCAGTGCTAAAAC	TAG	chr19	55114565	55114584	55114581	+
SEQ ID NO 403	AGGGTTTCAGTGCTAAAACT	AGG	chr19	55114566	55114585	55114582	+
SEQ ID NO 404	GTGCTAAAACTAGGCTGTCC	TGG	chr19	55114575	55114594	55114591	+
SEQ ID NO 405	TGCTAAAACTAGGCTGTCCT	GGG	chr19	55114576	55114595	55114592	+
SEQ ID NO 406	ACTAGGCTGTCCTGGGCAAA	CAG	chr19	55114583	55114602	55114599	+
SEQ ID NO 407	CTGTCCTGGGCAAACAGCAT	AAG	chr19	55114589	55114608	55114605	+
SEQ ID NO 408	CCTGGGCAAACAGCATAAGC	TGG	chr19	55114593	55114612	55114609	+
SEQ ID NO 409	TAAGCTGGTCACCCCACACC	CAG	chr19	55114608	55114627	55114624	+
SEQ ID NO 410	ACCCAGACCTGACCCAAACC	CAG	chr19	55114625	55114644	55114641	+
SEQ ID NO 411	AACCCAGCTCCCCTGCTTCT	TGG	chr19	55114641	55114660	55114657	+
SEQ ID NO 412	GCTTCTTGGCCACGTAACCT	GAG	chr19	55114655	55114674	55114671	+
SEQ ID NO 413	TCTTGGCCACGTAACCTGAG	AAG	chr19	55114658	55114677	55114674	+
SEQ ID NO 414	CTTGGCCACGTAACCTGAGA	AGG	chr19	55114659	55114678	55114675	+
SEQ ID NO 415	TTGGCCACGTAACCTGAGAA	GGG	chr19	55114660	55114679	55114676	+
SEQ ID NO 416	AATCCCTCCTCTCTGAACCC	CAG	chr19	55114683	55114702	55114699	+
SEQ ID NO 417	CCCAGCCCACCCCAATGCTC	CAG	chr19	55114701	55114720	55114717	+
SEQ ID NO 418	CCAGCCCACCCCAATGCTCC	AGG	chr19	55114702	55114721	55114718	+
SEQ ID NO 419	CCCCAATGCTCCAGGCCTCC	TGG	chr19	55114710	55114729	55114726	+
SEQ ID NO 420	CCCAATGCTCCAGGCCTCCT	GGG	chr19	55114711	55114730	55114727	+
SEQ ID NO 421	AGGCCTCCTGGGATACCCCG	AAG	chr19	55114722	55114741	55114738	+
SEQ ID NO 422	GCCTCCTGGGATACCCCGAA	GAG	chr19	55114724	55114743	55114740	+
SEQ ID NO 423	CCTGGGATACCCCGAAGAGT	GAG	chr19	55114728	55114747	55114744	+
SEQ ID NO 424	CCCCGAAGAGTGAGTTTGCC	AAG	chr19	55114737	55114756	55114753	+
SEQ ID NO 425	CGAAGAGTGAGTTTGCCAAG	CAG	chr19	55114740	55114759	55114756	+
SEQ ID NO 426	TTTGCCAAGCAGTCACCCCA	CAG	chr19	55114751	55114770	55114767	+
SEQ ID NO 427	CCAAGCAGTCACCCCACAGT	TGG	chr19	55114755	55114774	55114771	+
SEQ ID NO 428	AAGCAGTCACCCCACAGTTG	GAG	chr19	55114757	55114776	55114773	+
SEQ ID NO 429	AGCAGTCACCCCACAGTTGG	AGG	chr19	55114758	55114777	55114774	+
SEQ ID NO 430	CAGTCACCCCACAGTTGGAG	GAG	chr19	55114760	55114779	55114776	+
SEQ ID NO 431	TTGGAGGAGAATCCACCCAA	AAG	chr19	55114774	55114793	55114790	+
SEQ ID NO 432	TGGAGGAGAATCCACCCAAA	AGG	chr19	55114775	55114794	55114791	+
SEQ ID NO 433	AGGAGAATCCACCCAAAAGG	CAG	chr19	55114778	55114797	55114794	+
SEQ ID NO 434	AATCCACCCAAAAGGCAGCC	TGG	chr19	55114783	55114802	55114799	+
SEQ ID NO 435	CCACCCAAAAGGCAGCCTGG	TAG	chr19	55114786	55114805	55114802	+
SEQ ID NO 436	CCAAAAGGCAGCCTGGTAGA	CAG	chr19	55114790	55114809	55114806	+
SEQ ID NO 437	CAAAAGGCAGCCTGGTAGAC	AGG	chr19	55114791	55114810	55114807	+
SEQ ID NO 438	AAAAGGCAGCCTGGTAGACA	GGG	chr19	55114792	55114811	55114808	+
SEQ ID NO 439	GGCAGCCTGGTAGACAGGGC	TGG	chr19	55114796	55114815	55114812	+
SEQ ID NO 440	GCAGCCTGGTAGACAGGGCT	GGG	chr19	55114797	55114816	55114813	+

SEQ ID NO 441	CAGCCTGGTAGACAGGGCTG	GGG	chr19	55114798	55114817	55114814	+
SEQ ID NO 442	CCTGGTAGACAGGGCTGGGG	TGG	chr19	55114801	55114820	55114817	+
SEQ ID NO 443	AGGGCTGGGGTGGCCTCTCG	TGG	chr19	55114811	55114830	55114827	+
SEQ ID NO 444	GGGCTGGGGTGGCCTCTCGT	GGG	chr19	55114812	55114831	55114828	+
SEQ ID NO 445	GGCTGGGGTGGCCTCTCGTG	GGG	chr19	55114813	55114832	55114829	+
SEQ ID NO 446	GGGTGGCCTCTCGTGGGGTC	CAG	chr19	55114818	55114837	55114834	+
SEQ ID NO 447	GGTGGCCTCTCGTGGGGTCC	AGG	chr19	55114819	55114838	55114835	+
SEQ ID NO 448	CCTCTCGTGGGGTCCAGGCC	AAG	chr19	55114824	55114843	55114840	+
SEQ ID NO 449	CTCGTGGGGTCCAGGCCAAG	TAG	chr19	55114827	55114846	55114843	+
SEQ ID NO 450	TCGTGGGGTCCAGGCCAAGT	AGG	chr19	55114828	55114847	55114844	+
SEQ ID NO 451	TGGGGTCCAGGCCAAGTAGG	TGG	chr19	55114831	55114850	55114847	+
SEQ ID NO 452	TCCAGGCCAAGTAGGTGGCC	TGG	chr19	55114836	55114855	55114852	+
SEQ ID NO 453	CCAGGCCAAGTAGGTGGCCT	GGG	chr19	55114837	55114856	55114853	+
SEQ ID NO 454	CAGGCCAAGTAGGTGGCCTG	GGG	chr19	55114838	55114857	55114854	+
SEQ ID NO 455	AGTAGGTGGCCTGGGGCCTC	TGG	chr19	55114845	55114864	55114861	+
SEQ ID NO 456	GTAGGTGGCCTGGGGCCTCT	GGG	chr19	55114846	55114865	55114862	+
SEQ ID NO 457	TAGGTGGCCTGGGGCCTCTG	GGG	chr19	55114847	55114866	55114863	+
SEQ ID NO 458	AGGTGGCCTGGGGCCTCTGG	GGG	chr19	55114848	55114867	55114864	+
SEQ ID NO 459	CCTGGGGCCTCTGGGGGATG	CAG	chr19	55114854	55114873	55114870	+
SEQ ID NO 460	CTGGGGCCTCTGGGGGATGC	AGG	chr19	55114855	55114874	55114871	+
SEQ ID NO 461	TGGGGCCTCTGGGGGATGCA	GGG	chr19	55114856	55114875	55114872	+
SEQ ID NO 462	GGGGCCTCTGGGGGATGCAG	GGG	chr19	55114857	55114876	55114873	+
SEQ ID NO 463	GCCTCTGGGGGATGCAGGGG	AAG	chr19	55114860	55114879	55114876	+
SEQ ID NO 464	CCTCTGGGGGATGCAGGGGA	AGG	chr19	55114861	55114880	55114877	+
SEQ ID NO 465	CTCTGGGGGATGCAGGGGAA	GGG	chr19	55114862	55114881	55114878	+
SEQ ID NO 466	TCTGGGGGATGCAGGGGAAG	GGG	chr19	55114863	55114882	55114879	+
SEQ ID NO 467	CTGGGGGATGCAGGGGAAGG	GGG	chr19	55114864	55114883	55114880	+
SEQ ID NO 468	GATGCAGGGGAAGGGGGATG	CAG	chr19	55114870	55114889	55114886	+
SEQ ID NO 469	ATGCAGGGGAAGGGGGATGC	AGG	chr19	55114871	55114890	55114887	+
SEQ ID NO 470	TGCAGGGGAAGGGGGATGCA	GGG	chr19	55114872	55114891	55114888	+
SEQ ID NO 471	GCAGGGGAAGGGGGATGCAG	GGG	chr19	55114873	55114892	55114889	+
SEQ ID NO 472	GGAAGGGGGATGCAGGGGAA	CGG	chr19	55114878	55114897	55114894	+
SEQ ID NO 473	GAAGGGGGATGCAGGGGAAC	GGG	chr19	55114879	55114898	55114895	+
SEQ ID NO 474	AAGGGGGATGCAGGGGAACG	GGG	chr19	55114880	55114899	55114896	+
SEQ ID NO 475	GATGCAGGGGAACGGGGATG	CAG	chr19	55114886	55114905	55114902	+
SEQ ID NO 476	ATGCAGGGGAACGGGGATGC	AGG	chr19	55114887	55114906	55114903	+
SEQ ID NO 477	TGCAGGGGAACGGGGATGCA	GGG	chr19	55114888	55114907	55114904	+
SEQ ID NO 478	GCAGGGGAACGGGGATGCAG	GGG	chr19	55114889	55114908	55114905	+
SEQ ID NO 479	GGAACGGGGATGCAGGGGAA	CGG	chr19	55114894	55114913	55114910	+
SEQ ID NO 480	GAACGGGGATGCAGGGGAAC	GGG	chr19	55114895	55114914	55114911	+
SEQ ID NO 481	AACGGGGATGCAGGGGAACG	GGG	chr19	55114896	55114915	55114912	+
SEQ ID NO 482	GGATGCAGGGGAACGGGGCT	CAG	chr19	55114901	55114920	55114917	+
SEQ ID NO 483	GGGGAACGGGGCTCAGTCTG	AAG	chr19	55114908	55114927	55114924	+
SEQ ID NO 484	GGAACGGGGCTCAGTCTGAA	GAG	chr19	55114910	55114929	55114926	+
SEQ ID NO 485	ACGGGGCTCAGTCTGAAGAG	CAG	chr19	55114913	55114932	55114929	+
SEQ ID NO 486	GGGGCTCAGTCTGAAGAGCA	GAG	chr19	55114915	55114934	55114931	+
SEQ ID NO 487	CTCAGTCTGAAGAGCAGAGC	CAG	chr19	55114919	55114938	55114935	+
SEQ ID NO 488	TCAGTCTGAAGAGCAGAGCC	AGG	chr19	55114920	55114939	55114936	+
SEQ ID NO 489	AGCAGAGCCAGGAACCCCTG	TAG	chr19	55114931	55114950	55114947	+

SEQ ID NO 490	GCAGAGCCAGGAACCCCTGT	AGG	chr19	55114932	55114951	55114948	+
SEQ ID NO 491	CAGAGCCAGGAACCCCTGTA	GGG	chr19	55114933	55114952	55114949	+
SEQ ID NO 492	AGCCAGGAACCCCTGTAGGG	AAG	chr19	55114936	55114955	55114952	+
SEQ ID NO 493	GCCAGGAACCCCTGTAGGGA	AGG	chr19	55114937	55114956	55114953	+
SEQ ID NO 494	CCAGGAACCCCTGTAGGGAA	GGG	chr19	55114938	55114957	55114954	+
SEQ ID NO 495	CAGGAACCCCTGTAGGGAAG	GGG	chr19	55114939	55114958	55114955	+
SEQ ID NO 496	GAACCCCTGTAGGGAAGGGG	CAG	chr19	55114942	55114961	55114958	+
SEQ ID NO 497	AACCCCTGTAGGGAAGGGGC	AGG	chr19	55114943	55114962	55114959	+
SEQ ID NO 498	CCCCTGTAGGGAAGGGGCAG	GAG	chr19	55114945	55114964	55114961	+
SEQ ID NO 499	CCTGTAGGGAAGGGGCAGGA	GAG	chr19	55114947	55114966	55114963	+
SEQ ID NO 500	TAGGGAAGGGGCAGGAGAGC	CAG	chr19	55114951	55114970	55114967	+
SEQ ID NO 501	AGGGAAGGGGCAGGAGAGCC	AGG	chr19	55114952	55114971	55114968	+
SEQ ID NO 502	GGGAAGGGGCAGGAGAGCCA	GGG	chr19	55114953	55114972	55114969	+
SEQ ID NO 503	GGAAGGGGCAGGAGAGCCAG	GGG	chr19	55114954	55114973	55114970	+
SEQ ID NO 504	GGCAGGAGAGCCAGGGGCAT	GAG	chr19	55114960	55114979	55114976	+
SEQ ID NO 505	GGAGAGCCAGGGGCATGAGA	TGG	chr19	55114964	55114983	55114980	+
SEQ ID NO 506	GAGCCAGGGGCATGAGATGG	TGG	chr19	55114967	55114986	55114983	+
SEQ ID NO 507	AGGGGCATGAGATGGTGGAC	GAG	chr19	55114972	55114991	55114988	+
SEQ ID NO 508	GGGGCATGAGATGGTGGACG	AGG	chr19	55114973	55114992	55114989	+
SEQ ID NO 509	GCATGAGATGGTGGACGAGG	AAG	chr19	55114976	55114995	55114992	+
SEQ ID NO 510	CATGAGATGGTGGACGAGGA	AGG	chr19	55114977	55114996	55114993	+
SEQ ID NO 511	ATGAGATGGTGGACGAGGAA	GGG	chr19	55114978	55114997	55114994	+
SEQ ID NO 512	TGAGATGGTGGACGAGGAAG	GGG	chr19	55114979	55114998	55114995	+
SEQ ID NO 513	GAGATGGTGGACGAGGAAGG	GGG	chr19	55114980	55114999	55114996	+
SEQ ID NO 514	TGGTGGACGAGGAAGGGGGA	CAG	chr19	55114984	55115003	55115000	+
SEQ ID NO 515	GGTGGACGAGGAAGGGGGAC	AGG	chr19	55114985	55115004	55115001	+
SEQ ID NO 516	GTGGACGAGGAAGGGGGACA	GGG	chr19	55114986	55115005	55115002	+
SEQ ID NO 517	GACGAGGAAGGGGGACAGGG	AAG	chr19	55114989	55115008	55115005	+
SEQ ID NO 518	GAAGGGGGACAGGGAAGCCT	GAG	chr19	55114995	55115014	55115011	+
SEQ ID NO 519	GGAAGCCTGAGCGCCTCTCC	TGG	chr19	55115007	55115026	55115023	+
SEQ ID NO 520	GAAGCCTGAGCGCCTCTCCT	GGG	chr19	55115008	55115027	55115024	+
SEQ ID NO 521	GCGCCTCTCCTGGGCTTGCC	AAG	chr19	55115017	55115036	55115033	+
SEQ ID NO 522	CGCCTCTCCTGGGCTTGCCA	AGG	chr19	55115018	55115037	55115034	+
SEQ ID NO 523	GCTTGCCAAGGACTCAAACC	CAG	chr19	55115030	55115049	55115046	+
SEQ ID NO 524	TGCCAAGGACTCAAACCCAG	AAG	chr19	55115033	55115052	55115049	+
SEQ ID NO 525	AGGACTCAAACCCAGAAGCC	CAG	chr19	55115038	55115057	55115054	+
SEQ ID NO 526	GACTCAAACCCAGAAGCCCA	GAG	chr19	55115040	55115059	55115056	+
SEQ ID NO 527	TCAAACCCAGAAGCCCAGAG	CAG	chr19	55115043	55115062	55115059	+
SEQ ID NO 528	CAAACCCAGAAGCCCAGAGC	AGG	chr19	55115044	55115063	55115060	+
SEQ ID NO 529	AAACCCAGAAGCCCAGAGCA	GGG	chr19	55115045	55115064	55115061	+
SEQ ID NO 530	AGAAGCCCAGAGCAGGGCCT	TAG	chr19	55115051	55115070	55115067	+
SEQ ID NO 531	GAAGCCCAGAGCAGGGCCTT	AGG	chr19	55115052	55115071	55115068	+
SEQ ID NO 532	AAGCCCAGAGCAGGGCCTTA	GGG	chr19	55115053	55115072	55115069	+
SEQ ID NO 533	CCCAGAGCAGGGCCTTAGGG	AAG	chr19	55115056	55115075	55115072	+
SEQ ID NO 534	AGAGCAGGGCCTTAGGGAAG	CGG	chr19	55115059	55115078	55115075	+
SEQ ID NO 535	GAGCAGGGCCTTAGGGAAGC	GGG	chr19	55115060	55115079	55115076	+
SEQ ID NO 536	AGGGAAGCGGGACCCTGCTC	TGG	chr19	55115072	55115091	55115088	+
SEQ ID NO 537	GGGAAGCGGGACCCTGCTCT	GGG	chr19	55115073	55115092	55115089	+
SEQ ID NO 538	AAGCGGGACCCTGCTCTGGG	CGG	chr19	55115076	55115095	55115092	+

SEQ ID NO 539	GCGGGACCCTGCTCTGGGCG	GAG	chr19	55115078	55115097	55115094	+
SEQ ID NO 540	CGGGACCCTGCTCTGGGCGG	AGG	chr19	55115079	55115098	55115095	+
SEQ ID NO 541	CTGGGCGGAGGAATATGTCC	CAG	chr19	55115091	55115110	55115107	+
SEQ ID NO 542	GCGGAGGAATATGTCCCAGA	TAG	chr19	55115095	55115114	55115111	+
SEQ ID NO 543	GAATATGTCCCAGATAGCAC	TGG	chr19	55115101	55115120	55115117	+
SEQ ID NO 544	AATATGTCCCAGATAGCACT	GGG	chr19	55115102	55115121	55115118	+
SEQ ID NO 545	ATATGTCCCAGATAGCACTG	GGG	chr19	55115103	55115122	55115119	+
SEQ ID NO 546	GATAGCACTGGGGACTCTTT	AAG	chr19	55115113	55115132	55115129	+
SEQ ID NO 547	ATAGCACTGGGGACTCTTTA	AGG	chr19	55115114	55115133	55115130	+
SEQ ID NO 548	CACTGGGGACTCTTTAAGGA	AAG	chr19	55115118	55115137	55115134	+
SEQ ID NO 549	TGGGGACTCTTTAAGGAAAG	AAG	chr19	55115121	55115140	55115137	+
SEQ ID NO 550	GGGGACTCTTTAAGGAAAGA	AGG	chr19	55115122	55115141	55115138	+
SEQ ID NO 551	ACTCTTTAAGGAAAGAAGGA	TGG	chr19	55115126	55115145	55115142	+
SEQ ID NO 552	TCTTTAAGGAAAGAAGGATG	GAG	chr19	55115128	55115147	55115144	+
SEQ ID NO 553	TAAGGAAAGAAGGATGGAGA	AAG	chr19	55115132	55115151	55115148	+
SEQ ID NO 554	AGGAAAGAAGGATGGAGAAA	GAG	chr19	55115134	55115153	55115150	+
SEQ ID NO 555	AAGAAGGATGGAGAAAGAGA	AAG	chr19	55115138	55115157	55115154	+
SEQ ID NO 556	AGAAGGATGGAGAAAGAGAA	AGG	chr19	55115139	55115158	55115155	+
SEQ ID NO 557	GAAGGATGGAGAAAGAGAAA	GGG	chr19	55115140	55115159	55115156	+
SEQ ID NO 558	AGGATGGAGAAAGAGAAAGG	GAG	chr19	55115142	55115161	55115158	+
SEQ ID NO 559	ATGGAGAAAGAGAAAGGGAG	TAG	chr19	55115145	55115164	55115161	+
SEQ ID NO 560	GGAGAAAGAGAAAGGGAGTA	GAG	chr19	55115147	55115166	55115163	+
SEQ ID NO 561	GAGAAAGAGAAAGGGAGTAG	AGG	chr19	55115148	55115167	55115164	+
SEQ ID NO 562	AAAGAGAAAGGGAGTAGAGG	CGG	chr19	55115151	55115170	55115167	+
SEQ ID NO 563	GAGTAGAGGCGGCCACGACC	TGG	chr19	55115162	55115181	55115178	+
SEQ ID NO 564	GCCACGACCTGGTGAACACC	TAG	chr19	55115173	55115192	55115189	+
SEQ ID NO 565	CCACGACCTGGTGAACACCT	AGG	chr19	55115174	55115193	55115190	+
SEQ ID NO 566	TAGGACGCACCATTCTCACA	AAG	chr19	55115193	55115212	55115209	+
SEQ ID NO 567	AGGACGCACCATTCTCACAA	AGG	chr19	55115194	55115213	55115210	+
SEQ ID NO 568	GGACGCACCATTCTCACAAA	GGG	chr19	55115195	55115214	55115211	+
SEQ ID NO 569	ACGCACCATTCTCACAAAGG	GAG	chr19	55115197	55115216	55115213	+
SEQ ID NO 570	CACAAAGGGAGTTTTCCACA	CGG	chr19	55115209	55115228	55115225	+
SEQ ID NO 571	GGACACCCCCCTCCTCACCA	CAG	chr19	55115230	55115249	55115246	+
SEQ ID NO 572	CCTCCTCACCACAGCCCTGC	CAG	chr19	55115239	55115258	55115255	+
SEQ ID NO 573	CTCCTCACCACAGCCCTGCC	AGG	chr19	55115240	55115259	55115256	+
SEQ ID NO 574	TCACCACAGCCCTGCCAGGA	CGG	chr19	55115244	55115263	55115260	+
SEQ ID NO 575	CACCACAGCCCTGCCAGGAC	GGG	chr19	55115245	55115264	55115261	+
SEQ ID NO 576	ACCACAGCCCTGCCAGGACG	GGG	chr19	55115246	55115265	55115262	+
SEQ ID NO 577	CAGCCCTGCCAGGACGGGGC	TGG	chr19	55115250	55115269	55115266	+
SEQ ID NO 578	GCCAGGACGGGGCTGGCTAC	TGG	chr19	55115257	55115276	55115273	+
SEQ ID NO 579	TGGCTACTGGCCTTATCTCA	CAG	chr19	55115270	55115289	55115286	+
SEQ ID NO 580	GGCTACTGGCCTTATCTCAC	AGG	chr19	55115271	55115290	55115287	+
SEQ ID NO 581	TCACAGGTAAAACTGACGCA	CGG	chr19	55115287	55115306	55115303	+
SEQ ID NO 582	ACAGGTAAAACTGACGCACG	GAG	chr19	55115289	55115308	55115305	+
SEQ ID NO 583	CAGGTAAAACTGACGCACGG	AGG	chr19	55115290	55115309	55115306	+
SEQ ID NO 584	CACGGAGGAACAATATAAAT	TGG	chr19	55115305	55115324	55115321	+
SEQ ID NO 585	ACGGAGGAACAATATAAATT	GGG	chr19	55115306	55115325	55115322	+
SEQ ID NO 586	CGGAGGAACAATATAAATTG	GGG	chr19	55115307	55115326	55115323	+
SEQ ID NO 587	GAACAATATAAATTGGGGAC	TAG	chr19	55115312	55115331	55115328	+

SEQ ID NO 588	AATATAAATTGGGGACTAGA	AAG	chr19	55115316	55115335	55115332	+
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SEQ ID NO 590	AATTGGGGACTAGAAAGGTG	AAG	chr19	55115322	55115341	55115338	+
SEQ ID NO 591	TTGGGGACTAGAAAGGTGAA	GAG	chr19	55115324	55115343	55115340	+
SEQ ID NO 592	ACTAGAAAGGTGAAGAGCCA	AAG	chr19	55115330	55115349	55115346	+
SEQ ID NO 593	GAAAGGTGAAGAGCCAAAGT	TAG	chr19	55115334	55115353	55115350	+
SEQ ID NO 594	GAAGAGCCAAAGTTAGAACT	CAG	chr19	55115341	55115360	55115357	+
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SEQ ID NO 596	TTCCAAACTGCTTCTCCTCT	TGG	chr19	55115388	55115407	55115404	+
SEQ ID NO 597	TCCAAACTGCTTCTCCTCTT	GGG	chr19	55115389	55115408	55115405	+
SEQ ID NO 598	AAACTGCTTCTCCTCTTGGG	AAG	chr19	55115392	55115411	55115408	+
SEQ ID NO 599	CTTCTCCTCTTGGGAAGTGT	AAG	chr19	55115398	55115417	55115414	+
SEQ ID NO 600	TTCTCCTCTTGGGAAGTGTA	AGG	chr19	55115399	55115418	55115415	+
SEQ ID NO 601	TCCTCTTGGGAAGTGTAAGG	AAG	chr19	55115402	55115421	55115418	+
SEQ ID NO 602	TGGGAAGTGTAAGGAAGCTG	CAG	chr19	55115408	55115427	55115424	+
SEQ ID NO 603	GTGTAAGGAAGCTGCAGCAC	CAG	chr19	55115414	55115433	55115430	+
SEQ ID NO 604	TGTAAGGAAGCTGCAGCACC	AGG	chr19	55115415	55115434	55115431	+
SEQ ID NO 605	GGAAGCTGCAGCACCAGGAT	CAG	chr19	55115420	55115439	55115436	+
SEQ ID NO 606	CCAGGATCAGTGAAACGCAC	CAG	chr19	55115433	55115452	55115449	+
SEQ ID NO 607	GATCAGTGAAACGCACCAGA	CGG	chr19	55115437	55115456	55115453	+
SEQ ID NO 608	AACGCACCAGACGGCCGCGT	CAG	chr19	55115446	55115465	55115462	+
SEQ ID NO 609	CGCACCAGACGGCCGCGTCA	GAG	chr19	55115448	55115467	55115464	+
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SEQ ID NO 611	ACGGCCGCGTCAGAGCAGCT	CAG	chr19	55115456	55115475	55115472	+
SEQ ID NO 612	CGGCCGCGTCAGAGCAGCTC	AGG	chr19	55115457	55115476	55115473	+
SEQ ID NO 613	CGTCAGAGCAGCTCAGGTTC	TGG	chr19	55115463	55115482	55115479	+
SEQ ID NO 614	GTCAGAGCAGCTCAGGTTCT	GGG	chr19	55115464	55115483	55115480	+
SEQ ID NO 615	CAGAGCAGCTCAGGTTCTGG	GAG	chr19	55115466	55115485	55115482	+
SEQ ID NO 616	GAGCAGCTCAGGTTCTGGGA	GAG	chr19	55115468	55115487	55115484	+
SEQ ID NO 617	AGCAGCTCAGGTTCTGGGAG	AGG	chr19	55115469	55115488	55115485	+
SEQ ID NO 618	GCAGCTCAGGTTCTGGGAGA	GGG	chr19	55115470	55115489	55115486	+
SEQ ID NO 619	GCTCAGGTTCTGGGAGAGGG	TAG	chr19	55115473	55115492	55115489	+
SEQ ID NO 620	GGTTCTGGGAGAGGGTAGCG	CAG	chr19	55115478	55115497	55115494	+
SEQ ID NO 621	GTTCTGGGAGAGGGTAGCGC	AGG	chr19	55115479	55115498	55115495	+
SEQ ID NO 622	TTCTGGGAGAGGGTAGCGCA	GGG	chr19	55115480	55115499	55115496	+
SEQ ID NO 623	TGGGAGAGGGTAGCGCAGGG	TGG	chr19	55115483	55115502	55115499	+
SEQ ID NO 624	GGTAGCGCAGGGTGGCCACT	GAG	chr19	55115491	55115510	55115507	+
SEQ ID NO 625	GCAGGGTGGCCACTGAGAAC	CGG	chr19	55115497	55115516	55115513	+
SEQ ID NO 626	CAGGGTGGCCACTGAGAACC	GGG	chr19	55115498	55115517	55115514	+
SEQ ID NO 627	GGTGGCCACTGAGAACCGGG	CAG	chr19	55115501	55115520	55115517	+
SEQ ID NO 628	GTGGCCACTGAGAACCGGGC	AGG	chr19	55115502	55115521	55115518	+
SEQ ID NO 629	CTTCCCTCCCACCCCCTGCC	AAG	chr19	55115539	55115558	55115555	+
SEQ ID NO 630	CCCTGCCAAGCTCTCCCTCC	CAG	chr19	55115552	55115571	55115568	+
SEQ ID NO 631	CCTGCCAAGCTCTCCCTCCC	AGG	chr19	55115553	55115572	55115569	+
SEQ ID NO 632	CTCCCTCCCAGGATCCTCTC	TGG	chr19	55115564	55115583	55115580	+
SEQ ID NO 633	ATCCTCTCTGGCTCCATCGT	AAG	chr19	55115576	55115595	55115592	+
SEQ ID NO 634	GCTCCATCGTAAGCAAACCT	TAG	chr19	55115586	55115605	55115602	+
SEQ ID NO 635	TCCATCGTAAGCAAACCTTA	GAG	chr19	55115588	55115607	55115604	+
SEQ ID NO 636	CCATCGTAAGCAAACCTTAG	AGG	chr19	55115589	55115608	55115605	+

SEQ ID NO 637	TAAGCAAACCTTAGAGGTTC	TGG	chr19	55115595	55115614	55115611	+
SEQ ID NO 638	CAAACCTTAGAGGTTCTGGC	AAG	chr19	55115599	55115618	55115615	+
SEQ ID NO 639	AAACCTTAGAGGTTCTGGCA	AGG	chr19	55115600	55115619	55115616	+
SEQ ID NO 640	ACCTTAGAGGTTCTGGCAAG	GAG	chr19	55115602	55115621	55115618	+
SEQ ID NO 641	CTTAGAGGTTCTGGCAAGGA	GAG	chr19	55115604	55115623	55115620	+
SEQ ID NO 642	TAGAGGTTCTGGCAAGGAGA	GAG	chr19	55115606	55115625	55115622	+
SEQ ID NO 643	GGTTCTGGCAAGGAGAGAGA	TGG	chr19	55115610	55115629	55115626	+
SEQ ID NO 644	GGCAAGGAGAGAGATGGCTC	CAG	chr19	55115616	55115635	55115632	+
SEQ ID NO 645	GCAAGGAGAGAGATGGCTCC	AGG	chr19	55115617	55115636	55115633	+
SEQ ID NO 646	AGAGAGATGGCTCCAGGAAA	TGG	chr19	55115623	55115642	55115639	+
SEQ ID NO 647	GAGAGATGGCTCCAGGAAAT	GGG	chr19	55115624	55115643	55115640	+
SEQ ID NO 648	AGAGATGGCTCCAGGAAATG	GGG	chr19	55115625	55115644	55115641	+
SEQ ID NO 649	GAGATGGCTCCAGGAAATGG	GGG	chr19	55115626	55115645	55115642	+
SEQ ID NO 650	AGGAAATGGGGGTGTGTCAC	CAG	chr19	55115637	55115656	55115653	+
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SEQ ID NO 652	TGGGGGTGTGTCACCAGATA	AGG	chr19	55115643	55115662	55115659	+
SEQ ID NO 653	CAGATAAGGAATCTGCCTAA	CAG	chr19	55115657	55115676	55115673	+
SEQ ID NO 654	AGATAAGGAATCTGCCTAAC	AGG	chr19	55115658	55115677	55115674	+
SEQ ID NO 655	ATAAGGAATCTGCCTAACAG	GAG	chr19	55115660	55115679	55115676	+
SEQ ID NO 656	TAAGGAATCTGCCTAACAGG	AGG	chr19	55115661	55115680	55115677	+
SEQ ID NO 657	GGAATCTGCCTAACAGGAGG	TGG	chr19	55115664	55115683	55115680	+
SEQ ID NO 658	GAATCTGCCTAACAGGAGGT	GGG	chr19	55115665	55115684	55115681	+
SEQ ID NO 659	AATCTGCCTAACAGGAGGTG	GGG	chr19	55115666	55115685	55115682	+
SEQ ID NO 660	ATCTGCCTAACAGGAGGTGG	GGG	chr19	55115667	55115686	55115683	+
SEQ ID NO 661	GCCTAACAGGAGGTGGGGGT	TAG	chr19	55115671	55115690	55115687	+
SEQ ID NO 662	GTGGGGGTTAGACCCAATAT	CAG	chr19	55115683	55115702	55115699	+
SEQ ID NO 663	TGGGGGTTAGACCCAATATC	AGG	chr19	55115684	55115703	55115700	+
SEQ ID NO 664	GGGGTTAGACCCAATATCAG	GAG	chr19	55115686	55115705	55115702	+
SEQ ID NO 665	TAGACCCAATATCAGGAGAC	TAG	chr19	55115691	55115710	55115707	+
SEQ ID NO 666	AGACCCAATATCAGGAGACT	AGG	chr19	55115692	55115711	55115708	+
SEQ ID NO 667	CCCAATATCAGGAGACTAGG	AAG	chr19	55115695	55115714	55115711	+
SEQ ID NO 668	CCAATATCAGGAGACTAGGA	AGG	chr19	55115696	55115715	55115712	+
SEQ ID NO 669	AATATCAGGAGACTAGGAAG	GAG	chr19	55115698	55115717	55115714	+
SEQ ID NO 670	ATATCAGGAGACTAGGAAGG	AGG	chr19	55115699	55115718	55115715	+
SEQ ID NO 671	ATCAGGAGACTAGGAAGGAG	GAG	chr19	55115701	55115720	55115717	+
SEQ ID NO 672	TCAGGAGACTAGGAAGGAGG	AGG	chr19	55115702	55115721	55115718	+
SEQ ID NO 673	GACTAGGAAGGAGGAGGCCT	AAG	chr19	55115708	55115727	55115724	+
SEQ ID NO 674	ACTAGGAAGGAGGAGGCCTA	AGG	chr19	55115709	55115728	55115725	+
SEQ ID NO 675	GGAAGGAGGAGGCCTAAGGA	TGG	chr19	55115713	55115732	55115729	+
SEQ ID NO 676	GAAGGAGGAGGCCTAAGGAT	GGG	chr19	55115714	55115733	55115730	+
SEQ ID NO 677	AAGGAGGAGGCCTAAGGATG	GGG	chr19	55115715	55115734	55115731	+
SEQ ID NO 678	TCTGTCACCAATCCTGTCCC	TAG	chr19	55115742	55115761	55115758	+
SEQ ID NO 679	GTCACCAATCCTGTCCCTAG	TGG	chr19	55115745	55115764	55115761	+
SEQ ID NO 680	TGTCCCTAGTGGCCCCACTG	TGG	chr19	55115756	55115775	55115772	+
SEQ ID NO 681	GTCCCTAGTGGCCCCACTGT	GGG	chr19	55115757	55115776	55115773	+
SEQ ID NO 682	TCCCTAGTGGCCCCACTGTG	GGG	chr19	55115758	55115777	55115774	+
SEQ ID NO 683	CTAGTGGCCCCACTGTGGGG	TGG	chr19	55115761	55115780	55115777	+
SEQ ID NO 684	AGTGGCCCCACTGTGGGGTG	GAG	chr19	55115763	55115782	55115779	+
SEQ ID NO 685	GTGGCCCCACTGTGGGGTGG	AGG	chr19	55115764	55115783	55115780	+

SEQ ID NO 686	TGGCCCCACTGTGGGGTGGA	GGG	chr19	55115765	55115784	55115781	+
SEQ ID NO 687	GGCCCCACTGTGGGGTGGAG	GGG	chr19	55115766	55115785	55115782	+
SEQ ID NO 688	CCACTGTGGGGTGGAGGGGA	CAG	chr19	55115770	55115789	55115786	+
SEQ ID NO 689	GGGGTGGAGGGGACAGATAA	AAG	chr19	55115777	55115796	55115793	+
SEQ ID NO 690	AGGGGACAGATAAAAGTACC	CAG	chr19	55115784	55115803	55115800	+
SEQ ID NO 691	CAGATAAAAGTACCCAGAAC	CAG	chr19	55115790	55115809	55115806	+
SEQ ID NO 692	GATAAAAGTACCCAGAACCA	GAG	chr19	55115792	55115811	55115808	+
SEQ ID NO 693	AGAACCAGAGCCACATTAAC	CGG	chr19	55115805	55115824	55115821	+
SEQ ID NO 694	AGAGCCACATTAACCGGCCC	TGG	chr19	55115811	55115830	55115827	+
SEQ ID NO 695	GAGCCACATTAACCGGCCCT	GGG	chr19	55115812	55115831	55115828	+
SEQ ID NO 696	TTAACCGGCCCTGGGAATAT	AAG	chr19	55115820	55115839	55115836	+
SEQ ID NO 697	TAACCGGCCCTGGGAATATA	AGG	chr19	55115821	55115840	55115837	+
SEQ ID NO 698	CCGGCCCTGGGAATATAAGG	TGG	chr19	55115824	55115843	55115840	+
SEQ ID NO 699	CTGGGAATATAAGGTGGTCC	CAG	chr19	55115830	55115849	55115846	+
SEQ ID NO 700	AATATAAGGTGGTCCCAGCT	CGG	chr19	55115835	55115854	55115851	+
SEQ ID NO 701	ATATAAGGTGGTCCCAGCTC	GGG	chr19	55115836	55115855	55115852	+
SEQ ID NO 702	TATAAGGTGGTCCCAGCTCG	GGG	chr19	55115837	55115856	55115853	+
SEQ ID NO 703	GTGGTCCCAGCTCGGGGACA	CAG	chr19	55115843	55115862	55115859	+
SEQ ID NO 704	TGGTCCCAGCTCGGGGACAC	AGG	chr19	55115844	55115863	55115860	+
SEQ ID NO 705	GCTCGGGGACACAGGATCCC	TGG	chr19	55115852	55115871	55115868	+
SEQ ID NO 706	TCGGGGACACAGGATCCCTG	GAG	chr19	55115854	55115873	55115870	+
SEQ ID NO 707	CGGGGACACAGGATCCCTGG	AGG	chr19	55115855	55115874	55115871	+
SEQ ID NO 708	GGACACAGGATCCCTGGAGG	CAG	chr19	55115858	55115877	55115874	+
SEQ ID NO 709	GCAGCAAACATGCTGTCCTG	AAG	chr19	55115877	55115896	55115893	+
SEQ ID NO 710	GCAAACATGCTGTCCTGAAG	TGG	chr19	55115880	55115899	55115896	+
SEQ ID NO 711	ATGCTGTCCTGAAGTGGACA	TAG	chr19	55115886	55115905	55115902	+
SEQ ID NO 712	TGCTGTCCTGAAGTGGACAT	AGG	chr19	55115887	55115906	55115903	+
SEQ ID NO 713	GCTGTCCTGAAGTGGACATA	GGG	chr19	55115888	55115907	55115904	+
SEQ ID NO 714	CTGTCCTGAAGTGGACATAG	GGG	chr19	55115889	55115908	55115905	+
SEQ ID NO 715	CTGAAGTGGACATAGGGGCC	CGG	chr19	55115894	55115913	55115910	+
SEQ ID NO 716	TGAAGTGGACATAGGGGCCC	GGG	chr19	55115895	55115914	55115911	+
SEQ ID NO 717	GTGGACATAGGGGCCCGGGT	TGG	chr19	55115899	55115918	55115915	+
SEQ ID NO 718	GGACATAGGGGCCCGGGTTG	GAG	chr19	55115901	55115920	55115917	+
SEQ ID NO 719	GACATAGGGGCCCGGGTTGG	AGG	chr19	55115902	55115921	55115918	+
SEQ ID NO 720	ATAGGGGCCCGGGTTGGAGG	AAG	chr19	55115905	55115924	55115921	+
SEQ ID NO 721	GGGGCCCGGGTTGGAGGAAG	AAG	chr19	55115908	55115927	55115924	+
SEQ ID NO 722	CCGGGTTGGAGGAAGAAGAC	TAG	chr19	55115913	55115932	55115929	+
SEQ ID NO 723	TTGGAGGAAGAAGACTAGCT	GAG	chr19	55115918	55115937	55115934	+
SEQ ID NO 724	AAGAAGACTAGCTGAGCTCT	CGG	chr19	55115925	55115944	55115941	+
SEQ ID NO 725	TAGCTGAGCTCTCGGACCCC	TGG	chr19	55115933	55115952	55115949	+
SEQ ID NO 726	CTGAGCTCTCGGACCCCTGG	AAG	chr19	55115936	55115955	55115952	+
SEQ ID NO 727	ACCCCTGGAAGATGCCATGA	CAG	chr19	55115948	55115967	55115964	+
SEQ ID NO 728	CCCCTGGAAGATGCCATGAC	AGG	chr19	55115949	55115968	55115965	+
SEQ ID NO 729	CCCTGGAAGATGCCATGACA	GGG	chr19	55115950	55115969	55115966	+
SEQ ID NO 730	CCTGGAAGATGCCATGACAG	GGG	chr19	55115951	55115970	55115967	+
SEQ ID NO 731	CTGGAAGATGCCATGACAGG	GGG	chr19	55115952	55115971	55115968	+
SEQ ID NO 732	AAGATGCCATGACAGGGGGC	TGG	chr19	55115956	55115975	55115972	+
SEQ ID NO 733	ATGCCATGACAGGGGGCTGG	AAG	chr19	55115959	55115978	55115975	+
SEQ ID NO 734	GCCATGACAGGGGGCTGGAA	GAG	chr19	55115961	55115980	55115977	+

SEQ ID NO 735	TGACAGGGGGCTGGAAGAGC	TAG	chr19	55115965	55115984	55115981	+
SEQ ID NO 736	GGGGGCTGGAAGAGCTAGCA	CAG	chr19	55115970	55115989	55115986	+
SEQ ID NO 737	CTGGAAGAGCTAGCACAGAC	TAG	chr19	55115975	55115994	55115991	+
SEQ ID NO 738	GGAAGAGCTAGCACAGACTA	GAG	chr19	55115977	55115996	55115993	+
SEQ ID NO 739	AAGAGCTAGCACAGACTAGA	GAG	chr19	55115979	55115998	55115995	+
SEQ ID NO 740	AGAGCTAGCACAGACTAGAG	AGG	chr19	55115980	55115999	55115996	+
SEQ ID NO 741	CTAGCACAGACTAGAGAGGT	AAG	chr19	55115984	55116003	55116000	+
SEQ ID NO 742	TAGCACAGACTAGAGAGGTA	AGG	chr19	55115985	55116004	55116001	+
SEQ ID NO 743	AGCACAGACTAGAGAGGTAA	GGG	chr19	55115986	55116005	55116002	+
SEQ ID NO 744	GCACAGACTAGAGAGGTAAG	GGG	chr19	55115987	55116006	55116003	+
SEQ ID NO 745	CACAGACTAGAGAGGTAAGG	GGG	chr19	55115988	55116007	55116004	+
SEQ ID NO 746	ACAGACTAGAGAGGTAAGGG	GGG	chr19	55115989	55116008	55116005	+
SEQ ID NO 747	GACTAGAGAGGTAAGGGGGG	TAG	chr19	55115992	55116011	55116008	+
SEQ ID NO 748	ACTAGAGAGGTAAGGGGGGT	AGG	chr19	55115993	55116012	55116009	+
SEQ ID NO 749	CTAGAGAGGTAAGGGGGGTA	GGG	chr19	55115994	55116013	55116010	+
SEQ ID NO 750	TAGAGAGGTAAGGGGGGTAG	GGG	chr19	55115995	55116014	55116011	+
SEQ ID NO 751	GAGAGGTAAGGGGGGTAGGG	GAG	chr19	55115997	55116016	55116013	+
SEQ ID NO 752	TAGGGGAGCTGCCCAAATGA	AAG	chr19	55116012	55116031	55116028	+
SEQ ID NO 753	AGGGGAGCTGCCCAAATGAA	AGG	chr19	55116013	55116032	55116029	+
SEQ ID NO 754	GGGAGCTGCCCAAATGAAAG	GAG	chr19	55116015	55116034	55116031	+
SEQ ID NO 755	GCTGCCCAAATGAAAGGAGT	GAG	chr19	55116019	55116038	55116035	+
SEQ ID NO 756	TGCCCAAATGAAAGGAGTGA	GAG	chr19	55116021	55116040	55116037	+
SEQ ID NO 757	GCCCAAATGAAAGGAGTGAG	AGG	chr19	55116022	55116041	55116038	+
SEQ ID NO 758	TGAGAGGTGACCCGAATCCA	CAG	chr19	55116038	55116057	55116054	+
SEQ ID NO 759	GAGAGGTGACCCGAATCCAC	AGG	chr19	55116039	55116058	55116055	+
SEQ ID NO 760	GAGGTGACCCGAATCCACAG	GAG	chr19	55116041	55116060	55116057	+
SEQ ID NO 761	GACCCGAATCCACAGGAGAA	CGG	chr19	55116046	55116065	55116062	+
SEQ ID NO 762	ACCCGAATCCACAGGAGAAC	GGG	chr19	55116047	55116066	55116063	+
SEQ ID NO 763	CCCGAATCCACAGGAGAACG	GGG	chr19	55116048	55116067	55116064	+
SEQ ID NO 764	CCACAGGAGAACGGGGTGTC	CAG	chr19	55116055	55116074	55116071	+
SEQ ID NO 765	CACAGGAGAACGGGGTGTCC	AGG	chr19	55116056	55116075	55116072	+
SEQ ID NO 766	GAGAACGGGGTGTCCAGGCA	AAG	chr19	55116061	55116080	55116077	+
SEQ ID NO 767	ACGGGGTGTCCAGGCAAAGA	AAG	chr19	55116065	55116084	55116081	+
SEQ ID NO 768	GGTGTCCAGGCAAAGAAAGC	AAG	chr19	55116069	55116088	55116085	+
SEQ ID NO 769	TGTCCAGGCAAAGAAAGCAA	GAG	chr19	55116071	55116090	55116087	+
SEQ ID NO 770	GTCCAGGCAAAGAAAGCAAG	AGG	chr19	55116072	55116091	55116088	+
SEQ ID NO 771	AGGCAAAGAAAGCAAGAGGA	TGG	chr19	55116076	55116095	55116092	+
SEQ ID NO 772	GCAAAGAAAGCAAGAGGATG	GAG	chr19	55116078	55116097	55116094	+
SEQ ID NO 773	AAAGAAAGCAAGAGGATGGA	GAG	chr19	55116080	55116099	55116096	+
SEQ ID NO 774	AAGAAAGCAAGAGGATGGAG	AGG	chr19	55116081	55116100	55116097	+
SEQ ID NO 775	AAAGCAAGAGGATGGAGAGG	TGG	chr19	55116084	55116103	55116100	+
SEQ ID NO 776	AGAGGATGGAGAGGTGGCTA	AAG	chr19	55116090	55116109	55116106	+
SEQ ID NO 777	GATGGAGAGGTGGCTAAAGC	CAG	chr19	55116094	55116113	55116110	+
SEQ ID NO 778	ATGGAGAGGTGGCTAAAGCC	AGG	chr19	55116095	55116114	55116111	+
SEQ ID NO 779	TGGAGAGGTGGCTAAAGCCA	GGG	chr19	55116096	55116115	55116112	+
SEQ ID NO 780	GAGAGGTGGCTAAAGCCAGG	GAG	chr19	55116098	55116117	55116114	+
SEQ ID NO 781	GGTGGCTAAAGCCAGGGAGA	CGG	chr19	55116102	55116121	55116118	+
SEQ ID NO 782	GTGGCTAAAGCCAGGGAGAC	GGG	chr19	55116103	55116122	55116119	+
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SEQ ID NO 784	GCCAGGGAGACGGGGTACTT	TGG	chr19	55116112	55116131	55116128	+
SEQ ID NO 785	CCAGGGAGACGGGGTACTTT	GGG	chr19	55116113	55116132	55116129	+
SEQ ID NO 786	CAGGGAGACGGGGTACTTTG	GGG	chr19	55116114	55116133	55116130	+
SEQ ID NO 787	CGGGGTACTTTGGGGTTGTC	CAG	chr19	55116122	55116141	55116138	+
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SEQ ID NO 789	CCAGAAAAACGGTGATGATG	CAG	chr19	55116141	55116160	55116157	+
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SEQ ID NO 791	CGGTGATGATGCAGGCCTAC	AAG	chr19	55116150	55116169	55116166	+
SEQ ID NO 792	TGATGATGCAGGCCTACAAG	AAG	chr19	55116153	55116172	55116169	+
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SEQ ID NO 794	ATGATGCAGGCCTACAAGAA	GGG	chr19	55116155	55116174	55116171	+
SEQ ID NO 795	TGATGCAGGCCTACAAGAAG	GGG	chr19	55116156	55116175	55116172	+
SEQ ID NO 796	ATGCAGGCCTACAAGAAGGG	GAG	chr19	55116158	55116177	55116174	+
SEQ ID NO 797	TGCAGGCCTACAAGAAGGGG	AGG	chr19	55116159	55116178	55116175	+
SEQ ID NO 798	AGGCCTACAAGAAGGGGAGG	CGG	chr19	55116162	55116181	55116178	+
SEQ ID NO 799	GGCCTACAAGAAGGGGAGGC	GGG	chr19	55116163	55116182	55116179	+
SEQ ID NO 800	AAGAAGGGGAGGCGGGACGC	AAG	chr19	55116170	55116189	55116186	+
SEQ ID NO 801	AGAAGGGGAGGCGGGACGCA	AGG	chr19	55116171	55116190	55116187	+
SEQ ID NO 802	GAAGGGGAGGCGGGACGCAA	GGG	chr19	55116172	55116191	55116188	+
SEQ ID NO 803	AGGGGAGGCGGGACGCAAGG	GAG	chr19	55116174	55116193	55116190	+
SEQ ID NO 804	GACGCAAGGGAGACATCCGT	CGG	chr19	55116185	55116204	55116201	+
SEQ ID NO 805	CGCAAGGGAGACATCCGTCG	GAG	chr19	55116187	55116206	55116203	+
SEQ ID NO 806	AAGGGAGACATCCGTCGGAG	AAG	chr19	55116190	55116209	55116206	+
SEQ ID NO 807	AGGGAGACATCCGTCGGAGA	AGG	chr19	55116191	55116210	55116207	+
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SEQ ID NO 809	AGAAGGCCATCCTAAGAAAC	GAG	chr19	55116208	55116227	55116224	+
SEQ ID NO 810	AAGGCCATCCTAAGAAACGA	GAG	chr19	55116210	55116229	55116226	+
SEQ ID NO 811	CCATCCTAAGAAACGAGAGA	TGG	chr19	55116214	55116233	55116230	+
SEQ ID NO 812	CTAAGAAACGAGAGATGGCA	CAG	chr19	55116219	55116238	55116235	+
SEQ ID NO 813	TAAGAAACGAGAGATGGCAC	AGG	chr19	55116220	55116239	55116236	+
SEQ ID NO 814	ACGAGAGATGGCACAGGCCC	CAG	chr19	55116226	55116245	55116242	+
SEQ ID NO 815	AGAGATGGCACAGGCCCCAG	AAG	chr19	55116229	55116248	55116245	+
SEQ ID NO 816	GAGATGGCACAGGCCCCAGA	AGG	chr19	55116230	55116249	55116246	+
SEQ ID NO 817	GATGGCACAGGCCCCAGAAG	GAG	chr19	55116232	55116251	55116248	+
SEQ ID NO 818	GGCACAGGCCCCAGAAGGAG	AAG	chr19	55116235	55116254	55116251	+
SEQ ID NO 819	GCACAGGCCCCAGAAGGAGA	AGG	chr19	55116236	55116255	55116252	+
SEQ ID NO 820	GGCCCCAGAAGGAGAAGGAA	AAG	chr19	55116241	55116260	55116257	+
SEQ ID NO 821	GCCCCAGAAGGAGAAGGAAA	AGG	chr19	55116242	55116261	55116258	+
SEQ ID NO 822	CCCCAGAAGGAGAAGGAAAA	GGG	chr19	55116243	55116262	55116259	+
SEQ ID NO 823	AGGAGAAGGAAAAGGGAACC	CAG	chr19	55116250	55116269	55116266	+
SEQ ID NO 824	GAAGGAAAAGGGAACCCAGC	GAG	chr19	55116254	55116273	55116270	+
SEQ ID NO 825	AAAAGGGAACCCAGCGAGTG	AAG	chr19	55116259	55116278	55116275	+
SEQ ID NO 826	GGGAACCCAGCGAGTGAAGA	CGG	chr19	55116263	55116282	55116279	+
SEQ ID NO 827	CCCAGCGAGTGAAGACGGCA	TGG	chr19	55116268	55116287	55116284	+
SEQ ID NO 828	CCAGCGAGTGAAGACGGCAT	GGG	chr19	55116269	55116288	55116285	+
SEQ ID NO 829	CAGCGAGTGAAGACGGCATG	GGG	chr19	55116270	55116289	55116286	+
SEQ ID NO 830	GAGTGAAGACGGCATGGGGT	TGG	chr19	55116274	55116293	55116290	+
SEQ ID NO 831	AGTGAAGACGGCATGGGGTT	GGG	chr19	55116275	55116294	55116291	+
SEQ ID NO 832	AAGACGGCATGGGGTTGGGT	GAG	chr19	55116279	55116298	55116295	+

SEQ ID NO 833	AGACGGCATGGGGTTGGGTG	AGG	chr19	55116280	55116299	55116296	+
SEQ ID NO 834	GACGGCATGGGGTTGGGTGA	GGG	chr19	55116281	55116300	55116297	+
SEQ ID NO 835	CGGCATGGGGTTGGGTGAGG	GAG	chr19	55116283	55116302	55116299	+
SEQ ID NO 836	GGCATGGGGTTGGGTGAGGG	AGG	chr19	55116284	55116303	55116300	+
SEQ ID NO 837	CATGGGGTTGGGTGAGGGAG	GAG	chr19	55116286	55116305	55116302	+
SEQ ID NO 838	TGGGGTTGGGTGAGGGAGGA	GAG	chr19	55116288	55116307	55116304	+
SEQ ID NO 839	GGTGAGGGAGGAGAGATGCC	CGG	chr19	55116296	55116315	55116312	+
SEQ ID NO 840	TGAGGGAGGAGAGATGCCCG	GAG	chr19	55116298	55116317	55116314	+
SEQ ID NO 841	AGGGAGGAGAGATGCCCGGA	GAG	chr19	55116300	55116319	55116316	+
SEQ ID NO 842	GGGAGGAGAGATGCCCGGAG	AGG	chr19	55116301	55116320	55116317	+
SEQ ID NO 843	AGAGATGCCCGGAGAGGACC	CAG	chr19	55116307	55116326	55116323	+
SEQ ID NO 844	GCCCGGAGAGGACCCAGACA	CGG	chr19	55116313	55116332	55116329	+
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SEQ ID NO 846	CCGGAGAGGACCCAGACACG	GGG	chr19	55116315	55116334	55116331	+
SEQ ID NO 847	GGAGAGGACCCAGACACGGG	GAG	chr19	55116317	55116336	55116333	+
SEQ ID NO 848	GAGAGGACCCAGACACGGGG	AGG	chr19	55116318	55116337	55116334	+
SEQ ID NO 849	AGACACGGGGAGGATCCGCT	CAG	chr19	55116328	55116347	55116344	+
SEQ ID NO 850	ACACGGGGAGGATCCGCTCA	GAG	chr19	55116330	55116349	55116346	+
SEQ ID NO 851	CACGGGGAGGATCCGCTCAG	AGG	chr19	55116331	55116350	55116347	+
SEQ ID NO 852	TCCGCTCAGAGGACATCACG	TGG	chr19	55116342	55116361	55116358	+
SEQ ID NO 853	TCAGAGGACATCACGTGGTG	CAG	chr19	55116347	55116366	55116363	+
SEQ ID NO 854	ACATCACGTGGTGCAGCGCC	GAG	chr19	55116354	55116373	55116370	+
SEQ ID NO 855	TCACGTGGTGCAGCGCCGAG	AAG	chr19	55116357	55116376	55116373	+
SEQ ID NO 856	CACGTGGTGCAGCGCCGAGA	AGG	chr19	55116358	55116377	55116374	+
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SEQ ID NO 858	GCGCCGAGAAGGAAGTGCTC	CGG	chr19	55116369	55116388	55116385	+
SEQ ID NO 859	CGAGAAGGAAGTGCTCCGGA	AAG	chr19	55116373	55116392	55116389	+
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SEQ ID NO 863	CCGGAAAGAGCATCCTTGGG	CAG	chr19	55116388	55116407	55116404	+
SEQ ID NO 864	AGCATCCTTGGGCAGCAACA	CAG	chr19	55116396	55116415	55116412	+
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SEQ ID NO 866	CCTTGGGCAGCAACACAGCA	GAG	chr19	55116401	55116420	55116417	+
SEQ ID NO 867	TTGGGCAGCAACACAGCAGA	GAG	chr19	55116403	55116422	55116419	+
SEQ ID NO 868	GCAGCAACACAGCAGAGAGC	AAG	chr19	55116407	55116426	55116423	+
SEQ ID NO 869	CAGCAACACAGCAGAGAGCA	AGG	chr19	55116408	55116427	55116424	+
SEQ ID NO 870	AGCAACACAGCAGAGAGCAA	GGG	chr19	55116409	55116428	55116425	+
SEQ ID NO 871	GCAACACAGCAGAGAGCAAG	GGG	chr19	55116410	55116429	55116426	+
SEQ ID NO 872	ACACAGCAGAGAGCAAGGGG	AAG	chr19	55116413	55116432	55116429	+
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SEQ ID NO 874	CAGCAGAGAGCAAGGGGAAG	AGG	chr19	55116416	55116435	55116432	+
SEQ ID NO 875	AGCAGAGAGCAAGGGGAAGA	GGG	chr19	55116417	55116436	55116433	+
SEQ ID NO 876	CAGAGAGCAAGGGGAAGAGG	GAG	chr19	55116419	55116438	55116435	+
SEQ ID NO 877	AGAGCAAGGGGAAGAGGGAG	TGG	chr19	55116422	55116441	55116438	+
SEQ ID NO 878	AGCAAGGGGAAGAGGGAGTG	GAG	chr19	55116424	55116443	55116440	+
SEQ ID NO 879	GCAAGGGGAAGAGGGAGTGG	AGG	chr19	55116425	55116444	55116441	+
SEQ ID NO 880	AGGGGAAGAGGGAGTGGAGG	AAG	chr19	55116428	55116447	55116444	+
SEQ ID NO 881	GAAGAGGGAGTGGAGGAAGA	CGG	chr19	55116432	55116451	55116448	+

SEQ ID NO 882	GTGGAGGAAGACGGAACCTG	AAG	chr19	55116441	55116460	55116457	+
SEQ ID NO 883	TGGAGGAAGACGGAACCTGA	AGG	chr19	55116442	55116461	55116458	+
SEQ ID NO 884	GAGGAAGACGGAACCTGAAG	GAG	chr19	55116444	55116463	55116460	+
SEQ ID NO 885	AGGAAGACGGAACCTGAAGG	AGG	chr19	55116445	55116464	55116461	+
SEQ ID NO 886	AAGACGGAACCTGAAGGAGG	CGG	chr19	55116448	55116467	55116464	+
SEQ ID NO 887	ACGGAACCTGAAGGAGGCGG	CAG	chr19	55116451	55116470	55116467	+
SEQ ID NO 888	CGGAACCTGAAGGAGGCGGC	AGG	chr19	55116452	55116471	55116468	+
SEQ ID NO 889	GGAACCTGAAGGAGGCGGCA	GGG	chr19	55116453	55116472	55116469	+
SEQ ID NO 890	ACCTGAAGGAGGCGGCAGGG	AAG	chr19	55116456	55116475	55116472	+
SEQ ID NO 891	CCTGAAGGAGGCGGCAGGGA	AGG	chr19	55116457	55116476	55116473	+
SEQ ID NO 892	GGAGGCGGCAGGGAAGGATC	TGG	chr19	55116463	55116482	55116479	+
SEQ ID NO 893	GAGGCGGCAGGGAAGGATCT	GGG	chr19	55116464	55116483	55116480	+
SEQ ID NO 894	CGGCAGGGAAGGATCTGGGC	CAG	chr19	55116468	55116487	55116484	+
SEQ ID NO 895	GGAAGGATCTGGGCCAGCCG	TAG	chr19	55116474	55116493	55116490	+
SEQ ID NO 896	AAGGATCTGGGCCAGCCGTA	GAG	chr19	55116476	55116495	55116492	+
SEQ ID NO 897	AGGATCTGGGCCAGCCGTAG	AGG	chr19	55116477	55116496	55116493	+
SEQ ID NO 898	GGCCAGCCGTAGAGGTGACC	CAG	chr19	55116485	55116504	55116501	+
SEQ ID NO 899	GCCAGCCGTAGAGGTGACCC	AGG	chr19	55116486	55116505	55116502	+
SEQ ID NO 900	GTAGAGGTGACCCAGGCCAC	AAG	chr19	55116493	55116512	55116509	+
SEQ ID NO 901	GTGACCCAGGCCACAAGCTG	CAG	chr19	55116499	55116518	55116515	+
SEQ ID NO 902	CCCAGGCCACAAGCTGCAGA	CAG	chr19	55116503	55116522	55116519	+
SEQ ID NO 903	GGCCACAAGCTGCAGACAGA	AAG	chr19	55116507	55116526	55116523	+
SEQ ID NO 904	CACAAGCTGCAGACAGAAAG	CGG	chr19	55116510	55116529	55116526	+
SEQ ID NO 905	GCTGCAGACAGAAAGCGGCA	CAG	chr19	55116515	55116534	55116531	+
SEQ ID NO 906	CTGCAGACAGAAAGCGGCAC	AGG	chr19	55116516	55116535	55116532	+
SEQ ID NO 907	GACAGAAAGCGGCACAGGCC	CAG	chr19	55116521	55116540	55116537	+
SEQ ID NO 908	ACAGAAAGCGGCACAGGCCC	AGG	chr19	55116522	55116541	55116538	+
SEQ ID NO 909	CAGAAAGCGGCACAGGCCCA	GGG	chr19	55116523	55116542	55116539	+
SEQ ID NO 910	AGAAAGCGGCACAGGCCCAG	GGG	chr19	55116524	55116543	55116540	+
SEQ ID NO 911	AAAGCGGCACAGGCCCAGGG	GAG	chr19	55116526	55116545	55116542	+
SEQ ID NO 912	AGCGGCACAGGCCCAGGGGA	GAG	chr19	55116528	55116547	55116544	+
SEQ ID NO 913	CAGGCCCAGGGGAGAGAATG	CAG	chr19	55116535	55116554	55116551	+
SEQ ID NO 914	AGGCCCAGGGGAGAGAATGC	AGG	chr19	55116536	55116555	55116552	+
SEQ ID NO 915	CCAGGGGAGAGAATGCAGGT	CAG	chr19	55116540	55116559	55116556	+
SEQ ID NO 916	AGGGGAGAGAATGCAGGTCA	GAG	chr19	55116542	55116561	55116558	+
SEQ ID NO 917	GAGAGAATGCAGGTCAGAGA	AAG	chr19	55116546	55116565	55116562	+
SEQ ID NO 918	AGAATGCAGGTCAGAGAAAG	CAG	chr19	55116549	55116568	55116565	+
SEQ ID NO 919	GAATGCAGGTCAGAGAAAGC	AGG	chr19	55116550	55116569	55116566	+
SEQ ID NO 920	CAGAGAAAGCAGGACCTGCC	TGG	chr19	55116560	55116579	55116576	+
SEQ ID NO 921	AGAGAAAGCAGGACCTGCCT	GGG	chr19	55116561	55116580	55116577	+
SEQ ID NO 922	GAAAGCAGGACCTGCCTGGG	AAG	chr19	55116564	55116583	55116580	+
SEQ ID NO 923	AAAGCAGGACCTGCCTGGGA	AGG	chr19	55116565	55116584	55116581	+
SEQ ID NO 924	AAGCAGGACCTGCCTGGGAA	GGG	chr19	55116566	55116585	55116582	+
SEQ ID NO 925	AGCAGGACCTGCCTGGGAAG	GGG	chr19	55116567	55116586	55116583	+
SEQ ID NO 926	ACCTGCCTGGGAAGGGGAAA	CAG	chr19	55116573	55116592	55116589	+
SEQ ID NO 927	TGCCTGGGAAGGGGAAACAG	TGG	chr19	55116576	55116595	55116592	+
SEQ ID NO 928	GCCTGGGAAGGGGAAACAGT	GGG	chr19	55116577	55116596	55116593	+
SEQ ID NO 929	GGGAAGGGGAAACAGTGGGC	CAG	chr19	55116581	55116600	55116597	+
SEQ ID NO 930	GAAGGGGAAACAGTGGGCCA	GAG	chr19	55116583	55116602	55116599	+

SEQ ID NO 931	AAGGGGAAACAGTGGGCCAG	AGG	chr19	55116584	55116603	55116600	+
SEQ ID NO 932	GGGAAACAGTGGGCCAGAGG	CGG	chr19	55116587	55116606	55116603	+
SEQ ID NO 933	ACAGTGGGCCAGAGGCGGCG	CAG	chr19	55116592	55116611	55116608	+
SEQ ID NO 934	GTGGGCCAGAGGCGGCGCAG	AAG	chr19	55116595	55116614	55116611	+
SEQ ID NO 935	GCCAGAGGCGGCGCAGAAGC	CAG	chr19	55116599	55116618	55116615	+
SEQ ID NO 936	AGAGGCGGCGCAGAAGCCAG	TAG	chr19	55116602	55116621	55116618	+
SEQ ID NO 937	AGGCGGCGCAGAAGCCAGTA	GAG	chr19	55116604	55116623	55116620	+
SEQ ID NO 938	GCAGAAGCCAGTAGAGCTCA	AAG	chr19	55116611	55116630	55116627	+
SEQ ID NO 939	GAAGCCAGTAGAGCTCAAAG	TGG	chr19	55116614	55116633	55116630	+
SEQ ID NO 940	CAGTAGAGCTCAAAGTGGTC	CGG	chr19	55116619	55116638	55116635	+
SEQ ID NO 941	AGCTCAAAGTGGTCCGGACT	CAG	chr19	55116625	55116644	55116641	+
SEQ ID NO 942	GCTCAAAGTGGTCCGGACTC	AGG	chr19	55116626	55116645	55116642	+
SEQ ID NO 943	TCAAAGTGGTCCGGACTCAG	GAG	chr19	55116628	55116647	55116644	+
SEQ ID NO 944	AAAGTGGTCCGGACTCAGGA	GAG	chr19	55116630	55116649	55116646	+
SEQ ID NO 945	AGTGGTCCGGACTCAGGAGA	GAG	chr19	55116632	55116651	55116648	+
SEQ ID NO 946	GTCCGGACTCAGGAGAGAGA	CGG	chr19	55116636	55116655	55116652	+
SEQ ID NO 947	CGGACTCAGGAGAGAGACGG	CAG	chr19	55116639	55116658	55116655	+
SEQ ID NO 948	CAGGAGAGAGACGGCAGCGT	TAG	chr19	55116645	55116664	55116661	+
SEQ ID NO 949	GGAGAGAGACGGCAGCGTTA	GAG	chr19	55116647	55116666	55116663	+
SEQ ID NO 950	GAGAGAGACGGCAGCGTTAG	AGG	chr19	55116648	55116667	55116664	+
SEQ ID NO 951	AGAGAGACGGCAGCGTTAGA	GGG	chr19	55116649	55116668	55116665	+
SEQ ID NO 952	GAGACGGCAGCGTTAGAGGG	CAG	chr19	55116652	55116671	55116668	+
SEQ ID NO 953	GACGGCAGCGTTAGAGGGCA	GAG	chr19	55116654	55116673	55116670	+
SEQ ID NO 954	AGCGTTAGAGGGCAGAGTTC	CGG	chr19	55116660	55116679	55116676	+
SEQ ID NO 955	GTTAGAGGGCAGAGTTCCGG	CGG	chr19	55116663	55116682	55116679	+
SEQ ID NO 956	AGGGCAGAGTTCCGGCGGCA	CAG	chr19	55116668	55116687	55116684	+
SEQ ID NO 957	CAGAGTTCCGGCGGCACAGC	AAG	chr19	55116672	55116691	55116688	+
SEQ ID NO 958	AGAGTTCCGGCGGCACAGCA	AGG	chr19	55116673	55116692	55116689	+
SEQ ID NO 959	GAGTTCCGGCGGCACAGCAA	GGG	chr19	55116674	55116693	55116690	+
SEQ ID NO 960	GGCGGCACAGCAAGGGCACT	CGG	chr19	55116681	55116700	55116697	+
SEQ ID NO 961	GCGGCACAGCAAGGGCACTC	GGG	chr19	55116682	55116701	55116698	+
SEQ ID NO 962	CGGCACAGCAAGGGCACTCG	GGG	chr19	55116683	55116702	55116699	+
SEQ ID NO 963	GGCACAGCAAGGGCACTCGG	GGG	chr19	55116684	55116703	55116700	+
SEQ ID NO 964	CAGCAAGGGCACTCGGGGGC	GAG	chr19	55116688	55116707	55116704	+
SEQ ID NO 965	GCAAGGGCACTCGGGGGCGA	GAG	chr19	55116690	55116709	55116706	+
SEQ ID NO 966	CAAGGGCACTCGGGGGCGAG	AGG	chr19	55116691	55116710	55116707	+
SEQ ID NO 967	AGGGCACTCGGGGGCGAGAG	GAG	chr19	55116693	55116712	55116709	+
SEQ ID NO 968	GGGCACTCGGGGGCGAGAGG	AGG	chr19	55116694	55116713	55116710	+
SEQ ID NO 969	GGCACTCGGGGGCGAGAGGA	GGG	chr19	55116695	55116714	55116711	+
SEQ ID NO 970	ACTCGGGGGCGAGAGGAGGG	CAG	chr19	55116698	55116717	55116714	+
SEQ ID NO 971	GGCGAGAGGAGGGCAGCGCA	AAG	chr19	55116705	55116724	55116721	+
SEQ ID NO 972	AGGGCAGCGCAAAGTGACAA	TGG	chr19	55116714	55116733	55116730	+
SEQ ID NO 973	CAGCGCAAAGTGACAATGGC	CAG	chr19	55116718	55116737	55116734	+
SEQ ID NO 974	AGCGCAAAGTGACAATGGCC	AGG	chr19	55116719	55116738	55116735	+
SEQ ID NO 975	GCGCAAAGTGACAATGGCCA	GGG	chr19	55116720	55116739	55116736	+
SEQ ID NO 976	AAAGTGACAATGGCCAGGGC	CAG	chr19	55116724	55116743	55116740	+
SEQ ID NO 977	AAGTGACAATGGCCAGGGCC	AGG	chr19	55116725	55116744	55116741	+
SEQ ID NO 978	TGACAATGGCCAGGGCCAGG	CAG	chr19	55116728	55116747	55116744	+
SEQ ID NO 979	AATGGCCAGGGCCAGGCAGA	TAG	chr19	55116732	55116751	55116748	+

SEQ ID NO 980	CCAGGGCCAGGCAGATAGAC	CAG	chr19	55116737	55116756	55116753	+
SEQ ID NO 981	CCAGGCAGATAGACCAGACT	GAG	chr19	55116743	55116762	55116759	+
SEQ ID NO 982	AGATAGACCAGACTGAGCTA	TGG	chr19	55116749	55116768	55116765	+
SEQ ID NO 983	GATAGACCAGACTGAGCTAT	GGG	chr19	55116750	55116769	55116766	+
SEQ ID NO 984	TAGACCAGACTGAGCTATGG	GAG	chr19	55116752	55116771	55116768	+
SEQ ID NO 985	CCAGACTGAGCTATGGGAGC	TGG	chr19	55116756	55116775	55116772	+
SEQ ID NO 986	CTGAGCTATGGGAGCTGGCT	CAG	chr19	55116761	55116780	55116777	+
SEQ ID NO 987	TGAGCTATGGGAGCTGGCTC	AGG	chr19	55116762	55116781	55116778	+
SEQ ID NO 988	TATGGGAGCTGGCTCAGGTT	CAG	chr19	55116767	55116786	55116783	+
SEQ ID NO 989	ATGGGAGCTGGCTCAGGTTC	AGG	chr19	55116768	55116787	55116784	+
SEQ ID NO 990	GGGAGCTGGCTCAGGTTCAG	GAG	chr19	55116770	55116789	55116786	+
SEQ ID NO 991	GAGCTGGCTCAGGTTCAGGA	GAG	chr19	55116772	55116791	55116788	+
SEQ ID NO 992	AGCTGGCTCAGGTTCAGGAG	AGG	chr19	55116773	55116792	55116789	+
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SEQ ID NO 994	GGCTCAGGTTCAGGAGAGGG	CAG	chr19	55116777	55116796	55116793	+
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SEQ ID NO 996	CTCAGGTTCAGGAGAGGGCA	GGG	chr19	55116779	55116798	55116795	+
SEQ ID NO 997	AGGTTCAGGAGAGGGCAGGG	CAG	chr19	55116782	55116801	55116798	+
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SEQ ID NO 999	GTTCAGGAGAGGGCAGGGCA	GGG	chr19	55116784	55116803	55116800	+
SEQ ID NO 1000	CAGGAGAGGGCAGGGCAGGG	AAG	chr19	55116787	55116806	55116803	+
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SEQ ID NO 1004	GCAGGGAAGGAGACAAAGTC	CAG	chr19	55116801	55116820	55116817	+
SEQ ID NO 1005	CAGGGAAGGAGACAAAGTCC	AGG	chr19	55116802	55116821	55116818	+
SEQ ID NO 1006	AAGGAGACAAAGTCCAGGAC	CGG	chr19	55116807	55116826	55116823	+
SEQ ID NO 1007	AGACAAAGTCCAGGACCGGC	TGG	chr19	55116811	55116830	55116827	+
SEQ ID NO 1008	ACAAAGTCCAGGACCGGCTG	GAG	chr19	55116813	55116832	55116829	+
SEQ ID NO 1009	CAAAGTCCAGGACCGGCTGG	AGG	chr19	55116814	55116833	55116830	+
SEQ ID NO 1010	AAAGTCCAGGACCGGCTGGA	GGG	chr19	55116815	55116834	55116831	+
SEQ ID NO 1011	AAGTCCAGGACCGGCTGGAG	GGG	chr19	55116816	55116835	55116832	+
SEQ ID NO 1012	CGGCTGGAGGGGCTCAACAT	CGG	chr19	55116827	55116846	55116843	+
SEQ ID NO 1013	CTGGAGGGGCTCAACATCGG	AAG	chr19	55116830	55116849	55116846	+
SEQ ID NO 1014	GGAGGGGCTCAACATCGGAA	GAG	chr19	55116832	55116851	55116848	+
SEQ ID NO 1015	GAGGGGCTCAACATCGGAAG	AGG	chr19	55116833	55116852	55116849	+
SEQ ID NO 1016	AGGGGCTCAACATCGGAAGA	GGG	chr19	55116834	55116853	55116850	+
SEQ ID NO 1017	GGGGCTCAACATCGGAAGAG	GGG	chr19	55116835	55116854	55116851	+
SEQ ID NO 1018	GCTCAACATCGGAAGAGGGG	AAG	chr19	55116838	55116857	55116854	+
SEQ ID NO 1019	ACATCGGAAGAGGGGAAGTC	GAG	chr19	55116843	55116862	55116859	+
SEQ ID NO 1020	CATCGGAAGAGGGGAAGTCG	AGG	chr19	55116844	55116863	55116860	+
SEQ ID NO 1021	ATCGGAAGAGGGGAAGTCGA	GGG	chr19	55116845	55116864	55116861	+
SEQ ID NO 1022	CGGAAGAGGGGAAGTCGAGG	GAG	chr19	55116847	55116866	55116863	+
SEQ ID NO 1023	GGAAGAGGGGAAGTCGAGGG	AGG	chr19	55116848	55116867	55116864	+
SEQ ID NO 1024	GAAGAGGGGAAGTCGAGGGA	GGG	chr19	55116849	55116868	55116865	+
SEQ ID NO 1025	AGGGGAAGTCGAGGGAGGGA	TGG	chr19	55116853	55116872	55116869	+
SEQ ID NO 1026	GAAGTCGAGGGAGGGATGGT	AAG	chr19	55116857	55116876	55116873	+
SEQ ID NO 1027	AAGTCGAGGGAGGGATGGTA	AGG	chr19	55116858	55116877	55116874	+
SEQ ID NO 1028	GTCGAGGGAGGGATGGTAAG	GAG	chr19	55116860	55116879	55116876	+

SEQ ID NO 1029	TCGAGGGAGGGATGGTAAGG	AGG	chr19	55116861	55116880	55116877	+
SEQ ID NO 1030	GGATGGTAAGGAGGACTGCA	TGG	chr19	55116870	55116889	55116886	+
SEQ ID NO 1031	GATGGTAAGGAGGACTGCAT	GGG	chr19	55116871	55116890	55116887	+
SEQ ID NO 1032	GTAAGGAGGACTGCATGGGT	CAG	chr19	55116875	55116894	55116891	+
SEQ ID NO 1033	GAGGACTGCATGGGTCAGCA	CAG	chr19	55116880	55116899	55116896	+
SEQ ID NO 1034	AGGACTGCATGGGTCAGCAC	AGG	chr19	55116881	55116900	55116897	+
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SEQ ID NO 1037	CAGCACAGGCTGCCAAAGCC	AGG	chr19	55116895	55116914	55116911	+
SEQ ID NO 1038	AGCACAGGCTGCCAAAGCCA	GGG	chr19	55116896	55116915	55116912	+
SEQ ID NO 1039	CAGGCTGCCAAAGCCAGGGC	CAG	chr19	55116900	55116919	55116916	+
SEQ ID NO 1040	GCCAAAGCCAGGGCCAGTTA	AAG	chr19	55116906	55116925	55116922	+
SEQ ID NO 1041	CAGTTAAAGCGACTCCAATG	CGG	chr19	55116920	55116939	55116936	+
SEQ ID NO 1042	TTAAAGCGACTCCAATGCGG	AAG	chr19	55116923	55116942	55116939	+
SEQ ID NO 1043	AAAGCGACTCCAATGCGGAA	GAG	chr19	55116925	55116944	55116941	+
SEQ ID NO 1044	AGCGACTCCAATGCGGAAGA	GAG	chr19	55116927	55116946	55116943	+
SEQ ID NO 1045	GACTCCAATGCGGAAGAGAG	TAG	chr19	55116930	55116949	55116946	+
SEQ ID NO 1046	ACTCCAATGCGGAAGAGAGT	AGG	chr19	55116931	55116950	55116947	+
SEQ ID NO 1047	ATGCGGAAGAGAGTAGGTCG	AAG	chr19	55116937	55116956	55116953	+
SEQ ID NO 1048	TGCGGAAGAGAGTAGGTCGA	AGG	chr19	55116938	55116957	55116954	+
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SEQ ID NO 1050	CGGAAGAGAGTAGGTCGAAG	GGG	chr19	55116940	55116959	55116956	+
SEQ ID NO 1051	GAGAGTAGGTCGAAGGGGAA	TGG	chr19	55116945	55116964	55116961	+
SEQ ID NO 1052	GTAGGTCGAAGGGGAATGGT	AAG	chr19	55116949	55116968	55116965	+
SEQ ID NO 1053	TAGGTCGAAGGGGAATGGTA	AGG	chr19	55116950	55116969	55116966	+
SEQ ID NO 1054	GGTCGAAGGGGAATGGTAAG	GAG	chr19	55116952	55116971	55116968	+
SEQ ID NO 1055	GTCGAAGGGGAATGGTAAGG	AGG	chr19	55116953	55116972	55116969	+
SEQ ID NO 1056	AGGGGAATGGTAAGGAGGCC	TGG	chr19	55116958	55116977	55116974	+
SEQ ID NO 1057	GGGGAATGGTAAGGAGGCCT	GGG	chr19	55116959	55116978	55116975	+
SEQ ID NO 1058	GGGAATGGTAAGGAGGCCTG	GGG	chr19	55116960	55116979	55116976	+
SEQ ID NO 1059	AATGGTAAGGAGGCCTGGGG	CAG	chr19	55116963	55116982	55116979	+
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SEQ ID NO 1061	TAAGGAGGCCTGGGGCAGAG	TGG	chr19	55116968	55116987	55116984	+
SEQ ID NO 1062	GAGGCCTGGGGCAGAGTGGT	CAG	chr19	55116972	55116991	55116988	+
SEQ ID NO 1063	CTGGGGCAGAGTGGTCAGCA	CAG	chr19	55116977	55116996	55116993	+
SEQ ID NO 1064	GGGGCAGAGTGGTCAGCACA	GAG	chr19	55116979	55116998	55116995	+
SEQ ID NO 1065	GCAGAGTGGTCAGCACAGAG	TGG	chr19	55116982	55117001	55116998	+
SEQ ID NO 1066	GTGGTCAGCACAGAGTGGCT	AAG	chr19	55116987	55117006	55117003	+
SEQ ID NO 1067	CAGCACAGAGTGGCTAAGCC	CAG	chr19	55116992	55117011	55117008	+
SEQ ID NO 1068	AGCACAGAGTGGCTAAGCCC	AGG	chr19	55116993	55117012	55117009	+
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SEQ ID NO 1072	AAGCCCAGGGCCAGTTGAAG	CGG	chr19	55117007	55117026	55117023	+
SEQ ID NO 1073	CAGTTGAAGCGGCTCCAATT	CGG	chr19	55117018	55117037	55117034	+
SEQ ID NO 1074	TTGAAGCGGCTCCAATTCGG	AAG	chr19	55117021	55117040	55117037	+
SEQ ID NO 1075	AAGCGGCTCCAATTCGGAAG	TGG	chr19	55117024	55117043	55117040	+
SEQ ID NO 1076	AGCGGCTCCAATTCGGAAGT	GGG	chr19	55117025	55117044	55117041	+
SEQ ID NO 1077	GCGGCTCCAATTCGGAAGTG	GGG	chr19	55117026	55117045	55117042	+

SEQ ID NO 1078	GCTCCAATTCGGAAGTGGGG	TGG	chr19	55117029	55117048	55117045	+
SEQ ID NO 1079	ATTCGGAAGTGGGGTGGTCG	AAG	chr19	55117035	55117054	55117051	+
SEQ ID NO 1080	TTCGGAAGTGGGGTGGTCGA	AGG	chr19	55117036	55117055	55117052	+
SEQ ID NO 1081	TCGGAAGTGGGGTGGTCGAA	GGG	chr19	55117037	55117056	55117053	+
SEQ ID NO 1082	CGGAAGTGGGGTGGTCGAAG	GGG	chr19	55117038	55117057	55117054	+
SEQ ID NO 1083	GTGGGGTGGTCGAAGGGGAA	TGG	chr19	55117043	55117062	55117059	+
SEQ ID NO 1084	GGTGGTCGAAGGGGAATGGT	AAG	chr19	55117047	55117066	55117063	+
SEQ ID NO 1085	GTGGTCGAAGGGGAATGGTA	AGG	chr19	55117048	55117067	55117064	+
SEQ ID NO 1086	TGGTCGAAGGGGAATGGTAA	GGG	chr19	55117049	55117068	55117065	+
SEQ ID NO 1087	GGTCGAAGGGGAATGGTAAG	GGG	chr19	55117050	55117069	55117066	+
SEQ ID NO 1088	GTCGAAGGGGAATGGTAAGG	GGG	chr19	55117051	55117070	55117067	+
SEQ ID NO 1089	AGGGGAATGGTAAGGGGGAC	TGG	chr19	55117056	55117075	55117072	+
SEQ ID NO 1090	GGGGAATGGTAAGGGGGACT	GGG	chr19	55117057	55117076	55117073	+
SEQ ID NO 1091	AATGGTAAGGGGGACTGGGA	CGG	chr19	55117061	55117080	55117077	+
SEQ ID NO 1092	ATGGTAAGGGGGACTGGGAC	GGG	chr19	55117062	55117081	55117078	+
SEQ ID NO 1093	TGGTAAGGGGGACTGGGACG	GGG	chr19	55117063	55117082	55117079	+
SEQ ID NO 1094	GGGGGACTGGGACGGGGTGT	CAG	chr19	55117069	55117088	55117085	+
SEQ ID NO 1095	ACTGGGACGGGGTGTCAGCA	TAG	chr19	55117074	55117093	55117090	+
SEQ ID NO 1096	CTGGGACGGGGTGTCAGCAT	AGG	chr19	55117075	55117094	55117091	+
SEQ ID NO 1097	TGGGACGGGGTGTCAGCATA	GGG	chr19	55117076	55117095	55117092	+
SEQ ID NO 1098	GACGGGGTGTCAGCATAGGG	TGG	chr19	55117079	55117098	55117095	+
SEQ ID NO 1099	GGTGTCAGCATAGGGTGGCA	AAG	chr19	55117084	55117103	55117100	+
SEQ ID NO 1100	CAGCATAGGGTGGCAAAGCC	CAG	chr19	55117089	55117108	55117105	+
SEQ ID NO 1101	AGCATAGGGTGGCAAAGCCC	AGG	chr19	55117090	55117109	55117106	+
SEQ ID NO 1102	GCATAGGGTGGCAAAGCCCA	GGG	chr19	55117091	55117110	55117107	+
SEQ ID NO 1103	AGGGTGGCAAAGCCCAGGGC	CAG	chr19	55117095	55117114	55117111	+
SEQ ID NO 1104	GGGTGGCAAAGCCCAGGGCC	AGG	chr19	55117096	55117115	55117112	+
SEQ ID NO 1105	AAGCCCAGGGCCAGGAACGA	CGG	chr19	55117104	55117123	55117120	+
SEQ ID NO 1106	AGCCCAGGGCCAGGAACGAC	GGG	chr19	55117105	55117124	55117121	+
SEQ ID NO 1107	GCCCAGGGCCAGGAACGACG	GGG	chr19	55117106	55117125	55117122	+
SEQ ID NO 1108	CAGGGCCAGGAACGACGGGG	CGG	chr19	55117109	55117128	55117125	+
SEQ ID NO 1109	CAGGAACGACGGGGCGGATC	GAG	chr19	55117115	55117134	55117131	+
SEQ ID NO 1110	ACGACGGGGCGGATCGAGAC	TGG	chr19	55117120	55117139	55117136	+
SEQ ID NO 1111	GGGCGGATCGAGACTGGCAA	CGG	chr19	55117126	55117145	55117142	+
SEQ ID NO 1112	GGCGGATCGAGACTGGCAAC	GGG	chr19	55117127	55117146	55117143	+
SEQ ID NO 1113	GCGGATCGAGACTGGCAACG	GGG	chr19	55117128	55117147	55117144	+
SEQ ID NO 1114	GATCGAGACTGGCAACGGGG	AAG	chr19	55117131	55117150	55117147	+
SEQ ID NO 1115	ATCGAGACTGGCAACGGGGA	AGG	chr19	55117132	55117151	55117148	+
SEQ ID NO 1116	CGAGACTGGCAACGGGGAAG	GAG	chr19	55117134	55117153	55117150	+
SEQ ID NO 1117	GAGACTGGCAACGGGGAAGG	AGG	chr19	55117135	55117154	55117151	+
SEQ ID NO 1118	AACGGGGAAGGAGGATGCCC	CAG	chr19	55117144	55117163	55117160	+
SEQ ID NO 1119	ACGGGGAAGGAGGATGCCCC	AGG	chr19	55117145	55117164	55117161	+
SEQ ID NO 1120	GGGAAGGAGGATGCCCCAGG	TGG	chr19	55117148	55117167	55117164	+
SEQ ID NO 1121	GGAGGATGCCCCAGGTGGCG	CAG	chr19	55117153	55117172	55117169	+
SEQ ID NO 1122	GGATGCCCCAGGTGGCGCAG	CAG	chr19	55117156	55117175	55117172	+
SEQ ID NO 1123	ATGCCCCAGGTGGCGCAGCA	GAG	chr19	55117158	55117177	55117174	+
SEQ ID NO 1124	TGCCCCAGGTGGCGCAGCAG	AGG	chr19	55117159	55117178	55117175	+
SEQ ID NO 1125	GCCCCAGGTGGCGCAGCAGA	GGG	chr19	55117160	55117179	55117176	+
SEQ ID NO 1126	CCAGGTGGCGCAGCAGAGGG	TGG	chr19	55117163	55117182	55117179	+

SEQ ID NO 1127	GGCGCAGCAGAGGGTGGACC	TGG	chr19	55117169	55117188	55117185	+
SEQ ID NO 1128	GCAGAGGGTGGACCTGGCCC	CGG	chr19	55117175	55117194	55117191	+
SEQ ID NO 1129	CAGAGGGTGGACCTGGCCCC	GGG	chr19	55117176	55117195	55117192	+
SEQ ID NO 1130	GAGGGTGGACCTGGCCCCGG	GAG	chr19	55117178	55117197	55117194	+
SEQ ID NO 1131	GACCTGGCCCCGGGAGACGC	CGG	chr19	55117185	55117204	55117201	+
SEQ ID NO 1132	ACCTGGCCCCGGGAGACGCC	GGG	chr19	55117186	55117205	55117202	+
SEQ ID NO 1133	TGGCCCCGGGAGACGCCGGG	CGG	chr19	55117189	55117208	55117205	+
SEQ ID NO 1134	GGCCCCGGGAGACGCCGGGC	GGG	chr19	55117190	55117209	55117206	+
SEQ ID NO 1135	GCCCCGGGAGACGCCGGGCG	GGG	chr19	55117191	55117210	55117207	+
SEQ ID NO 1136	CCCCGGGAGACGCCGGGCGG	GGG	chr19	55117192	55117211	55117208	+
SEQ ID NO 1137	CCCGGGAGACGCCGGGCGGG	GGG	chr19	55117193	55117212	55117209	+
SEQ ID NO 1138	CCGGGCGGGGGGCGCTGACC	TGG	chr19	55117204	55117223	55117220	+
SEQ ID NO 1139	CGGGGGGCGCTGACCTGGTG	CAG	chr19	55117209	55117228	55117225	+
SEQ ID NO 1140	GGGGGGCGCTGACCTGGTGC	AGG	chr19	55117210	55117229	55117226	+
SEQ ID NO 1141	GGGGGCGCTGACCTGGTGCA	GGG	chr19	55117211	55117230	55117227	+
SEQ ID NO 1142	GTGCAGGGCGCTGATACCGT	CGG	chr19	55117226	55117245	55117242	+
SEQ ID NO 1143	GGCGCTGATACCGTCGGCGT	TGG	chr19	55117232	55117251	55117248	+
SEQ ID NO 1144	GCTGATACCGTCGGCGTTGG	TGG	chr19	55117235	55117254	55117251	+
SEQ ID NO 1145	TGATACCGTCGGCGTTGGTG	GAG	chr19	55117237	55117256	55117253	+
SEQ ID NO 1146	CCGTCGGCGTTGGTGGAGTC	CAG	chr19	55117242	55117261	55117258	+
SEQ ID NO 1147	GGCGTTGGTGGAGTCCAGCA	CGG	chr19	55117247	55117266	55117263	+
SEQ ID NO 1148	TGGTGGAGTCCAGCACGGCG	CGG	chr19	55117252	55117271	55117268	+
SEQ ID NO 1149	GGTGGAGTCCAGCACGGCGC	GGG	chr19	55117253	55117272	55117269	+
SEQ ID NO 1150	GGAGTCCAGCACGGCGCGGG	CGG	chr19	55117256	55117275	55117272	+
SEQ ID NO 1151	GAGTCCAGCACGGCGCGGGC	GGG	chr19	55117257	55117276	55117273	+
SEQ ID NO 1152	TCCAGCACGGCGCGGGCGGG	CGG	chr19	55117260	55117279	55117276	+
SEQ ID NO 1153	AGCACGGCGCGGGCGGGCGG	CGG	chr19	55117263	55117282	55117279	+
SEQ ID NO 1154	GGCGCGGGCGGGCGGCGGCG	CGG	chr19	55117268	55117287	55117284	+
SEQ ID NO 1155	GCGGGCGGGCGGCGGCGCGG	CGG	chr19	55117271	55117290	55117287	+
SEQ ID NO 1156	CGGGCGGGCGGCGGCGCGGC	GGG	chr19	55117272	55117291	55117288	+
SEQ ID NO 1157	GGGCGGGCGGCGGCGCGGCG	GGG	chr19	55117273	55117292	55117289	+
SEQ ID NO 1158	GGCGGCGGCGCGGCGGGGTC	GAG	chr19	55117278	55117297	55117294	+
SEQ ID NO 1159	CGGCGCGGCGGGGTCGAGCT	CGG	chr19	55117283	55117302	55117299	+
SEQ ID NO 1160	GGCGGGGTCGAGCTCGGCGC	CGG	chr19	55117289	55117308	55117305	+
SEQ ID NO 1161	GCGGGGTCGAGCTCGGCGCC	GGG	chr19	55117290	55117309	55117306	+
SEQ ID NO 1162	CGGGGTCGAGCTCGGCGCCG	GGG	chr19	55117291	55117310	55117307	+
SEQ ID NO 1163	GTCGAGCTCGGCGCCGGGGC	CAG	chr19	55117295	55117314	55117311	+
SEQ ID NO 1164	TCGAGCTCGGCGCCGGGGCC	AGG	chr19	55117296	55117315	55117312	+
SEQ ID NO 1165	CGAGCTCGGCGCCGGGGCCA	GGG	chr19	55117297	55117316	55117313	+
SEQ ID NO 1166	CTCGGCGCCGGGGCCAGGGT	CGG	chr19	55117301	55117320	55117317	+
SEQ ID NO 1167	GGCGCCGGGGCCAGGGTCGG	CGG	chr19	55117304	55117323	55117320	+
SEQ ID NO 1168	GGGCCAGGGTCGGCGGCGCG	CAG	chr19	55117311	55117330	55117327	+
SEQ ID NO 1169	GGGTCGGCGGCGCGCAGCAT	CAG	chr19	55117317	55117336	55117333	+
SEQ ID NO 1170	AGCATCAGACGCGCCTCGTC	CAG	chr19	55117332	55117351	55117348	+
SEQ ID NO 1171	GCATCAGACGCGCCTCGTCC	AGG	chr19	55117333	55117352	55117349	+
SEQ ID NO 1172	CGTCCAGGTCGCCGCCCGCA	CAG	chr19	55117348	55117367	55117364	+
SEQ ID NO 1173	GTCCAGGTCGCCGCCCGCAC	AGG	chr19	55117349	55117368	55117365	+
SEQ ID NO 1174	TCGCCGCCCGCACAGGCCGC	CAG	chr19	55117356	55117375	55117372	+
SEQ ID NO 1175	CGCCGCCCGCACAGGCCGCC	AGG	chr19	55117357	55117376	55117373	+

SEQ ID NO 1176	CGCACAGGCCGCCAGGAACT	CGG	chr19	55117364	55117383	55117380	+
SEQ ID NO 1177	ACAGGCCGCCAGGAACTCGG	CGG	chr19	55117367	55117386	55117383	+
SEQ ID NO 1178	GGAACTCGGCGGCGCGCTCG	AAG	chr19	55117378	55117397	55117394	+
SEQ ID NO 1179	ACTCGGCGGCGCGCTCGAAG	CGG	chr19	55117381	55117400	55117397	+
SEQ ID NO 1180	GGCGGCGCGCTCGAAGCGGA	CGG	chr19	55117385	55117404	55117401	+
SEQ ID NO 1181	CGCGCTCGAAGCGGACGGTG	CGG	chr19	55117390	55117409	55117406	+
SEQ ID NO 1182	GCGCTCGAAGCGGACGGTGC	GGG	chr19	55117391	55117410	55117407	+
SEQ ID NO 1183	CGAAGCGGACGGTGCGGGCG	CGG	chr19	55117396	55117415	55117412	+
SEQ ID NO 1184	GGTGCGGGCGCGGCGCTCTC	CGG	chr19	55117406	55117425	55117422	+
SEQ ID NO 1185	GTGCGGGCGCGGCGCTCTCC	GGG	chr19	55117407	55117426	55117423	+
SEQ ID NO 1186	TGCGGGCGCGGCGCTCTCCG	GGG	chr19	55117408	55117427	55117424	+
SEQ ID NO 1187	GGCGCGGCGCTCTCCGGGGC	CAG	chr19	55117412	55117431	55117428	+
SEQ ID NO 1188	GCGCGGCGCTCTCCGGGGCC	AGG	chr19	55117413	55117432	55117429	+
SEQ ID NO 1189	GCGCTCTCCGGGGCCAGGCT	CGG	chr19	55117418	55117437	55117434	+
SEQ ID NO 1190	GCCCGCGCCCCCCACTGCCG	CAG	chr19	55117446	55117465	55117462	+
SEQ ID NO 1191	GCTGCTCCCGTCGCCGCTCC	CGG	chr19	55117468	55117487	55117484	+
SEQ ID NO 1192	CTGCTCCCGTCGCCGCTCCC	GGG	chr19	55117469	55117488	55117485	+
SEQ ID NO 1193	CTCCCGTCGCCGCTCCCGGG	CAG	chr19	55117472	55117491	55117488	+
SEQ ID NO 1194	GCAGCCGCCGCCGCCGCCCC	CGG	chr19	55117491	55117510	55117507	+
SEQ ID NO 1195	CAGCCGCCGCCGCCGCCCCC	GGG	chr19	55117492	55117511	55117508	+
SEQ ID NO 1196	CGCCGCCGCCGCCCCCGGGC	CAG	chr19	55117496	55117515	55117512	+
SEQ ID NO 1197	GCCGCCCCCGGGCCAGCCGC	CGG	chr19	55117503	55117522	55117519	+
SEQ ID NO 1198	CCGCCCCCGGGCCAGCCGCC	GGG	chr19	55117504	55117523	55117520	+
SEQ ID NO 1199	AGCCGCCGGGCCATCCTCTC	CGG	chr19	55117517	55117536	55117533	+
SEQ ID NO 1200	CATCGCACCGCCCGCCCGCC	CAG	chr19	55117541	55117560	55117557	+
SEQ ID NO 1201	GCACCGCCCGCCCGCCCAGC	GAG	chr19	55117545	55117564	55117561	+
SEQ ID NO 1202	CGCCCGCCCGCCCAGCGAGC	GAG	chr19	55117549	55117568	55117565	+
SEQ ID NO 1203	CGCCCGCCCAGCGAGCGAGC	GAG	chr19	55117553	55117572	55117569	+
SEQ ID NO 1204	CCAGCGAGCGAGCGAGCGCC	GAG	chr19	55117560	55117579	55117576	+
SEQ ID NO 1205	TGGTGGCGGCGGTTGGGGCT	CGG	chr19	55117581	55117600	55117584	-
SEQ ID NO 1206	CTCGGCGCTCGCTCGCTCGC	TGG	chr19	55117563	55117582	55117566	-
SEQ ID NO 1207	TCGGCGCTCGCTCGCTCGCT	GGG	chr19	55117562	55117581	55117565	-
SEQ ID NO 1208	GCGCTCGCTCGCTCGCTGGG	CGG	chr19	55117559	55117578	55117562	-
SEQ ID NO 1209	CGCTCGCTCGCTCGCTGGGC	GGG	chr19	55117558	55117577	55117561	-
SEQ ID NO 1210	TCGCTCGCTCGCTGGGCGGG	CGG	chr19	55117555	55117574	55117558	-
SEQ ID NO 1211	CGCTCGCTCGCTGGGCGGGC	GGG	chr19	55117554	55117573	55117557	-
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SEQ ID NO 1213	CGGGCGGGCGGTGCGATGTC	CGG	chr19	55117539	55117558	55117542	-
SEQ ID NO 1214	GGCGGGCGGTGCGATGTCCG	GAG	chr19	55117537	55117556	55117540	-
SEQ ID NO 1215	CGGGCGGTGCGATGTCCGGA	GAG	chr19	55117535	55117554	55117538	-
SEQ ID NO 1216	GGGCGGTGCGATGTCCGGAG	AGG	chr19	55117534	55117553	55117537	-
SEQ ID NO 1217	GGTGCGATGTCCGGAGAGGA	TGG	chr19	55117530	55117549	55117533	-
SEQ ID NO 1218	GATGTCCGGAGAGGATGGCC	CGG	chr19	55117525	55117544	55117528	-
SEQ ID NO 1219	GTCCGGAGAGGATGGCCCGG	CGG	chr19	55117522	55117541	55117525	-
SEQ ID NO 1220	GGAGAGGATGGCCCGGCGGC	TGG	chr19	55117518	55117537	55117521	-
SEQ ID NO 1221	GGATGGCCCGGCGGCTGGCC	CGG	chr19	55117513	55117532	55117516	-
SEQ ID NO 1222	GATGGCCCGGCGGCTGGCCC	GGG	chr19	55117512	55117531	55117515	-
SEQ ID NO 1223	ATGGCCCGGCGGCTGGCCCG	GGG	chr19	55117511	55117530	55117514	-
SEQ ID NO 1224	TGGCCCGGCGGCTGGCCCGG	GGG	chr19	55117510	55117529	55117513	-

SEQ ID NO 1225	CCCGGCGGCTGGCCCGGGGG	CGG	chr19	55117507	55117526	55117510	-
SEQ ID NO 1226	GGCGGCTGGCCCGGGGGCGG	CGG	chr19	55117504	55117523	55117507	-
SEQ ID NO 1227	GGCTGGCCCGGGGGCGGCGG	CGG	chr19	55117501	55117520	55117504	-
SEQ ID NO 1228	TGGCCCGGGGGCGGCGGCGG	CGG	chr19	55117498	55117517	55117501	-
SEQ ID NO 1229	GGGCGGCGGCGGCGGCTGCC	CGG	chr19	55117490	55117509	55117493	-
SEQ ID NO 1230	GGCGGCGGCGGCGGCTGCCC	GGG	chr19	55117489	55117508	55117492	-
SEQ ID NO 1231	CGGCGGCGGCGGCTGCCCGG	GAG	chr19	55117487	55117506	55117490	-
SEQ ID NO 1232	CGGCGGCGGCTGCCCGGGAG	CGG	chr19	55117484	55117503	55117487	-
SEQ ID NO 1233	CGGCTGCCCGGGAGCGGCGA	CGG	chr19	55117478	55117497	55117481	-
SEQ ID NO 1234	GGCTGCCCGGGAGCGGCGAC	GGG	chr19	55117477	55117496	55117480	-
SEQ ID NO 1235	CTGCCCGGGAGCGGCGACGG	GAG	chr19	55117475	55117494	55117478	-
SEQ ID NO 1236	CCCGGGAGCGGCGACGGGAG	CAG	chr19	55117472	55117491	55117475	-
SEQ ID NO 1237	AGCGGCGACGGGAGCAGCTG	CGG	chr19	55117466	55117485	55117469	-
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SEQ ID NO 1239	GACGGGAGCAGCTGCGGCAG	TGG	chr19	55117460	55117479	55117463	-
SEQ ID NO 1240	ACGGGAGCAGCTGCGGCAGT	GGG	chr19	55117459	55117478	55117462	-
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SEQ ID NO 1247	CGGCAGTGGGGGGCGCGGGC	GGG	chr19	55117446	55117465	55117449	-
SEQ ID NO 1248	GGGGGGCGCGGGCGGGCGCC	GAG	chr19	55117439	55117458	55117442	-
SEQ ID NO 1249	GCGCGGGCGGGCGCCGAGCC	TGG	chr19	55117434	55117453	55117437	-
SEQ ID NO 1250	GCGGGCGCCGAGCCTGGCCC	CGG	chr19	55117428	55117447	55117431	-
SEQ ID NO 1251	GGGCGCCGAGCCTGGCCCCG	GAG	chr19	55117426	55117445	55117429	-
SEQ ID NO 1252	GCGCCGAGCCTGGCCCCGGA	GAG	chr19	55117424	55117443	55117427	-
SEQ ID NO 1253	GCGCCCGCACCGTCCGCTTC	GAG	chr19	55117397	55117416	55117400	-
SEQ ID NO 1254	TCCGCTTCGAGCGCGCCGCC	GAG	chr19	55117385	55117404	55117388	-
SEQ ID NO 1255	CGAGCGCGCCGCCGAGTTCC	TGG	chr19	55117378	55117397	55117381	-
SEQ ID NO 1256	GCGCGCCGCCGAGTTCCTGG	CGG	chr19	55117375	55117394	55117378	-
SEQ ID NO 1257	CGAGTTCCTGGCGGCCTGTG	CGG	chr19	55117366	55117385	55117369	-
SEQ ID NO 1258	GAGTTCCTGGCGGCCTGTGC	GGG	chr19	55117365	55117384	55117368	-
SEQ ID NO 1259	TTCCTGGCGGCCTGTGCGGG	CGG	chr19	55117362	55117381	55117365	-
SEQ ID NO 1260	GGCCTGTGCGGGCGGCGACC	TGG	chr19	55117354	55117373	55117357	-
SEQ ID NO 1261	GTGCGGGCGGCGACCTGGAC	GAG	chr19	55117349	55117368	55117352	-
SEQ ID NO 1262	TGCGGGCGGCGACCTGGACG	AGG	chr19	55117348	55117367	55117351	-
SEQ ID NO 1263	ATGCTGCGCGCCGCCGACCC	TGG	chr19	55117317	55117336	55117320	-
SEQ ID NO 1264	CGCGCCGCCGACCCTGGCCC	CGG	chr19	55117311	55117330	55117314	-
SEQ ID NO 1265	CCGACCCTGGCCCCGGCGCC	GAG	chr19	55117304	55117323	55117307	-
SEQ ID NO 1266	GCCGCCCGCCCGCGCCGTGC	TGG	chr19	55117264	55117283	55117267	-
SEQ ID NO 1267	CTGGACTCCACCAACGCCGA	CGG	chr19	55117245	55117264	55117248	-
SEQ ID NO 1268	TCCACCAACGCCGACGGTAT	CAG	chr19	55117239	55117258	55117242	-
SEQ ID NO 1269	ACGGTATCAGCGCCCTGCAC	CAG	chr19	55117226	55117245	55117229	-
SEQ ID NO 1270	CGGTATCAGCGCCCTGCACC	AGG	chr19	55117225	55117244	55117228	-
SEQ ID NO 1271	ATCAGCGCCCTGCACCAGGT	CAG	chr19	55117221	55117240	55117224	-
SEQ ID NO 1272	CCAGGTCAGCGCCCCCCGCC	CGG	chr19	55117207	55117226	55117210	-
SEQ ID NO 1273	GCCCCCCGCCCGGCGTCTCC	CGG	chr19	55117197	55117216	55117200	-

SEQ ID NO 1274	CCCCCCGCCCGGCGTCTCCC	GGG	chr19	55117196	55117215	55117199	-
SEQ ID NO 1275	CCCCCGCCCGGCGTCTCCCG	GGG	chr19	55117195	55117214	55117198	-
SEQ ID NO 1276	CGCCCGGCGTCTCCCGGGGC	CAG	chr19	55117191	55117210	55117194	-
SEQ ID NO 1277	GCCCGGCGTCTCCCGGGGCC	AGG	chr19	55117190	55117209	55117193	-
SEQ ID NO 1278	CCACCCTCTGCTGCGCCACC	TGG	chr19	55117166	55117185	55117169	-
SEQ ID NO 1279	CACCCTCTGCTGCGCCACCT	GGG	chr19	55117165	55117184	55117168	-
SEQ ID NO 1280	ACCCTCTGCTGCGCCACCTG	GGG	chr19	55117164	55117183	55117167	-
SEQ ID NO 1281	GCATCCTCCTTCCCCGTTGC	CAG	chr19	55117142	55117161	55117145	-
SEQ ID NO 1282	TCGATCCGCCCCGTCGTTCC	TGG	chr19	55117117	55117136	55117120	-
SEQ ID NO 1283	CGCCCCGTCGTTCCTGGCCC	TGG	chr19	55117111	55117130	55117114	-
SEQ ID NO 1284	GCCCCGTCGTTCCTGGCCCT	GGG	chr19	55117110	55117129	55117113	-
SEQ ID NO 1285	CCTATGCTGACACCCCGTCC	CAG	chr19	55117078	55117097	55117081	-
SEQ ID NO 1286	CGACCACCCCACTTCCGAAT	TGG	chr19	55117035	55117054	55117038	-
SEQ ID NO 1287	ACCACCCCACTTCCGAATTG	GAG	chr19	55117033	55117052	55117036	-
SEQ ID NO 1288	CGAATTGGAGCCGCTTCAAC	TGG	chr19	55117020	55117039	55117023	-
SEQ ID NO 1289	GGAGCCGCTTCAACTGGCCC	TGG	chr19	55117014	55117033	55117017	-
SEQ ID NO 1290	GAGCCGCTTCAACTGGCCCT	GGG	chr19	55117013	55117032	55117016	-
SEQ ID NO 1291	GCTTCAACTGGCCCTGGGCT	TAG	chr19	55117008	55117027	55117011	-
SEQ ID NO 1292	CTGTGCTGACCACTCTGCCC	CAG	chr19	55116980	55116999	55116983	-
SEQ ID NO 1293	TGTGCTGACCACTCTGCCCC	AGG	chr19	55116979	55116998	55116982	-
SEQ ID NO 1294	CGACCTACTCTCTTCCGCAT	TGG	chr19	55116937	55116956	55116940	-
SEQ ID NO 1295	ACCTACTCTCTTCCGCATTG	GAG	chr19	55116935	55116954	55116938	-
SEQ ID NO 1296	CGCATTGGAGTCGCTTTAAC	TGG	chr19	55116922	55116941	55116925	-
SEQ ID NO 1297	GGAGTCGCTTTAACTGGCCC	TGG	chr19	55116916	55116935	55116919	-
SEQ ID NO 1298	GCTTTAACTGGCCCTGGCTT	TGG	chr19	55116910	55116929	55116913	-
SEQ ID NO 1299	TTAACTGGCCCTGGCTTTGG	CAG	chr19	55116907	55116926	55116910	-
SEQ ID NO 1300	GCAGCCTGTGCTGACCCATG	CAG	chr19	55116888	55116907	55116891	-
SEQ ID NO 1301	ACTTCCCCTCTTCCGATGTT	GAG	chr19	55116842	55116861	55116845	-
SEQ ID NO 1302	CTTCCGATGTTGAGCCCCTC	CAG	chr19	55116833	55116852	55116836	-
SEQ ID NO 1303	CGATGTTGAGCCCCTCCAGC	CGG	chr19	55116829	55116848	55116832	-
SEQ ID NO 1304	TGAGCCCCTCCAGCCGGTCC	TGG	chr19	55116823	55116842	55116826	-
SEQ ID NO 1305	CCCTGCCCTCTCCTGAACCT	GAG	chr19	55116782	55116801	55116785	-
SEQ ID NO 1306	GCCCTCTCCTGAACCTGAGC	CAG	chr19	55116778	55116797	55116781	-
SEQ ID NO 1307	TGAACCTGAGCCAGCTCCCA	TAG	chr19	55116769	55116788	55116772	-
SEQ ID NO 1308	CTGAGCCAGCTCCCATAGCT	CAG	chr19	55116764	55116783	55116767	-
SEQ ID NO 1309	CCAGCTCCCATAGCTCAGTC	TGG	chr19	55116759	55116778	55116762	-
SEQ ID NO 1310	CTCAGTCTGGTCTATCTGCC	TGG	chr19	55116746	55116765	55116749	-
SEQ ID NO 1311	CTGGTCTATCTGCCTGGCCC	TGG	chr19	55116740	55116759	55116743	-
SEQ ID NO 1312	GCTGCCCTCCTCTCGCCCCC	GAG	chr19	55116702	55116721	55116705	-
SEQ ID NO 1313	GAGTGCCCTTGCTGTGCCGC	CGG	chr19	55116682	55116701	55116685	-
SEQ ID NO 1314	AACGCTGCCGTCTCTCTCCT	GAG	chr19	55116646	55116665	55116649	-
SEQ ID NO 1315	TGCCGTCTCTCTCCTGAGTC	CGG	chr19	55116641	55116660	55116644	-
SEQ ID NO 1316	TCCTGAGTCCGGACCACTTT	GAG	chr19	55116630	55116649	55116633	-
SEQ ID NO 1317	CGGACCACTTTGAGCTCTAC	TGG	chr19	55116621	55116640	55116624	-
SEQ ID NO 1318	ACTGGCTTCTGCGCCGCCTC	TGG	chr19	55116603	55116622	55116606	-
SEQ ID NO 1319	GGCCCACTGTTTCCCCTTCC	CAG	chr19	55116582	55116601	55116585	-
SEQ ID NO 1320	GCCCACTGTTTCCCCTTCCC	AGG	chr19	55116581	55116600	55116584	-
SEQ ID NO 1321	CACTGTTTCCCCTTCCCAGG	CAG	chr19	55116578	55116597	55116581	-
SEQ ID NO 1322	ACTGTTTCCCCTTCCCAGGC	AGG	chr19	55116577	55116596	55116580	-

SEQ ID NO 1323	CTGACCTGCATTCTCTCCCC	TGG	chr19	55116543	55116562	55116546	-
SEQ ID NO 1324	TGACCTGCATTCTCTCCCCT	GGG	chr19	55116542	55116561	55116545	-
SEQ ID NO 1325	CCTGTGCCGCTTTCTGTCTG	CAG	chr19	55116519	55116538	55116522	-
SEQ ID NO 1326	CGCTTTCTGTCTGCAGCTTG	TGG	chr19	55116512	55116531	55116515	-
SEQ ID NO 1327	TCTGTCTGCAGCTTGTGGCC	TGG	chr19	55116507	55116526	55116510	-
SEQ ID NO 1328	CTGTCTGCAGCTTGTGGCCT	GGG	chr19	55116506	55116525	55116509	-
SEQ ID NO 1329	TGTGGCCTGGGTCACCTCTA	CGG	chr19	55116494	55116513	55116497	-
SEQ ID NO 1330	GCCTGGGTCACCTCTACGGC	TGG	chr19	55116490	55116509	55116493	-
SEQ ID NO 1331	GGTCACCTCTACGGCTGGCC	CAG	chr19	55116485	55116504	55116488	-
SEQ ID NO 1332	TCCTTCCCTGCCGCCTCCTT	CAG	chr19	55116461	55116480	55116464	-
SEQ ID NO 1333	CCTTCCCTGCCGCCTCCTTC	AGG	chr19	55116460	55116479	55116463	-
SEQ ID NO 1334	TCTCTGCTGTGTTGCTGCCC	AAG	chr19	55116405	55116424	55116408	-
SEQ ID NO 1335	CTCTGCTGTGTTGCTGCCCA	AGG	chr19	55116404	55116423	55116407	-
SEQ ID NO 1336	CTGCCCAAGGATGCTCTTTC	CGG	chr19	55116391	55116410	55116394	-
SEQ ID NO 1337	GCCCAAGGATGCTCTTTCCG	GAG	chr19	55116389	55116408	55116392	-
SEQ ID NO 1338	TTTCCGGAGCACTTCCTTCT	CGG	chr19	55116375	55116394	55116378	-
SEQ ID NO 1339	TGCACCACGTGATGTCCTCT	GAG	chr19	55116349	55116368	55116352	-
SEQ ID NO 1340	ACCACGTGATGTCCTCTGAG	CGG	chr19	55116346	55116365	55116349	-
SEQ ID NO 1341	GAGCGGATCCTCCCCGTGTC	TGG	chr19	55116329	55116348	55116332	-
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SEQ ID NO 1343	CCCCGTGTCTGGGTCCTCTC	CGG	chr19	55116318	55116337	55116321	-
SEQ ID NO 1344	CCCGTGTCTGGGTCCTCTCC	GGG	chr19	55116317	55116336	55116320	-
SEQ ID NO 1345	CCCATGCCGTCTTCACTCGC	TGG	chr19	55116272	55116291	55116275	-
SEQ ID NO 1346	CCATGCCGTCTTCACTCGCT	GGG	chr19	55116271	55116290	55116274	-
SEQ ID NO 1347	TTCCCTTTTCCTTCTCCTTC	TGG	chr19	55116248	55116267	55116251	-
SEQ ID NO 1348	TCCCTTTTCCTTCTCCTTCT	GGG	chr19	55116247	55116266	55116250	-
SEQ ID NO 1349	CCCTTTTCCTTCTCCTTCTG	GGG	chr19	55116246	55116265	55116249	-
SEQ ID NO 1350	CTGTGCCATCTCTCGTTTCT	TAG	chr19	55116222	55116241	55116225	-
SEQ ID NO 1351	TGTGCCATCTCTCGTTTCTT	AGG	chr19	55116221	55116240	55116224	-
SEQ ID NO 1352	CCATCTCTCGTTTCTTAGGA	TGG	chr19	55116217	55116236	55116220	-
SEQ ID NO 1353	CTTAGGATGGCCTTCTCCGA	CGG	chr19	55116204	55116223	55116207	-
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SEQ ID NO 1359	GTACCCCGTCTCCCTGGCTT	TAG	chr19	55116110	55116129	55116113	-
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SEQ ID NO 1362	ACCCCGTTCTCCTGTGGATT	CGG	chr19	55116052	55116071	55116055	-
SEQ ID NO 1363	CCCCGTTCTCCTGTGGATTC	GGG	chr19	55116051	55116070	55116054	-
SEQ ID NO 1364	CACCTCTCACTCCTTTCATT	TGG	chr19	55116027	55116046	55116030	-
SEQ ID NO 1365	ACCTCTCACTCCTTTCATTT	GGG	chr19	55116026	55116045	55116029	-
SEQ ID NO 1366	TCTCACTCCTTTCATTTGGG	CAG	chr19	55116023	55116042	55116026	-
SEQ ID NO 1367	CCCTACCCCCCTTACCTCTC	TAG	chr19	55115997	55116016	55116000	-
SEQ ID NO 1368	CTTACCTCTCTAGTCTGTGC	TAG	chr19	55115987	55116006	55115990	-
SEQ ID NO 1369	CTAGTCTGTGCTAGCTCTTC	CAG	chr19	55115978	55115997	55115981	-
SEQ ID NO 1370	GCTCTTCCAGCCCCCTGTCA	TGG	chr19	55115965	55115984	55115968	-
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SEQ ID NO 1374	CCTGTCATGGCATCTTCCAG	GGG	chr19	55115952	55115971	55115955	-
SEQ ID NO 1375	ATGGCATCTTCCAGGGGTCC	GAG	chr19	55115946	55115965	55115949	-
SEQ ID NO 1376	GGCATCTTCCAGGGGTCCGA	GAG	chr19	55115944	55115963	55115947	-
SEQ ID NO 1377	CTTCCAGGGGTCCGAGAGCT	CAG	chr19	55115939	55115958	55115942	-
SEQ ID NO 1378	CAGGGGTCCGAGAGCTCAGC	TAG	chr19	55115935	55115954	55115938	-
SEQ ID NO 1379	CTAGTCTTCTTCCTCCAACC	CGG	chr19	55115916	55115935	55115919	-
SEQ ID NO 1380	TAGTCTTCTTCCTCCAACCC	GGG	chr19	55115915	55115934	55115918	-
SEQ ID NO 1381	CCGGGCCCCTATGTCCACTT	CAG	chr19	55115897	55115916	55115900	-
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SEQ ID NO 1384	GACAGCATGTTTGCTGCCTC	CAG	chr19	55115874	55115893	55115877	-
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SEQ ID NO 1389	GGATCCTGTGTCCCCGAGCT	GGG	chr19	55115851	55115870	55115854	-
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SEQ ID NO 1391	TGGGACCACCTTATATTCCC	AGG	chr19	55115832	55115851	55115835	-
SEQ ID NO 1392	GGGACCACCTTATATTCCCA	GGG	chr19	55115831	55115850	55115834	-
SEQ ID NO 1393	CCACCTTATATTCCCAGGGC	CGG	chr19	55115827	55115846	55115830	-
SEQ ID NO 1394	ATTCCCAGGGCCGGTTAATG	TGG	chr19	55115818	55115837	55115821	-
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SEQ ID NO 1396	GGTTAATGTGGCTCTGGTTC	TGG	chr19	55115806	55115825	55115809	-
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SEQ ID NO 1410	TGACAGAAAAGCCCCATCCT	TAG	chr19	55115729	55115748	55115732	-
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SEQ ID NO 1413	CCTTCCTAGTCTCCTGATAT	TGG	chr19	55115699	55115718	55115702	-
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SEQ ID NO 1506	TCCATCCTTCTTTCCTTAAA	GAG	chr19	55115130	55115149	55115133	-
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SEQ ID NO 1513	CATATTCCTCCGCCCAGAGC	AGG	chr19	55115088	55115107	55115091	-
SEQ ID NO 1514	ATATTCCTCCGCCCAGAGCA	GGG	chr19	55115087	55115106	55115090	-
SEQ ID NO 1515	GAGCAGGGTCCCGCTTCCCT	AAG	chr19	55115072	55115091	55115075	-
SEQ ID NO 1516	AGCAGGGTCCCGCTTCCCTA	AGG	chr19	55115071	55115090	55115074	-
SEQ ID NO 1517	GCTTCCCTAAGGCCCTGCTC	TGG	chr19	55115060	55115079	55115063	-
SEQ ID NO 1518	CTTCCCTAAGGCCCTGCTCT	GGG	chr19	55115059	55115078	55115062	-

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SEQ ID NO 1523	TCTGGGTTTGAGTCCTTGGC	AAG	chr19	55115034	55115053	55115037	-
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SEQ ID NO 1525	TTTGAGTCCTTGGCAAGCCC	AGG	chr19	55115028	55115047	55115031	-
SEQ ID NO 1526	TGAGTCCTTGGCAAGCCCAG	GAG	chr19	55115026	55115045	55115029	-
SEQ ID NO 1527	AGTCCTTGGCAAGCCCAGGA	GAG	chr19	55115024	55115043	55115027	-
SEQ ID NO 1528	GTCCTTGGCAAGCCCAGGAG	AGG	chr19	55115023	55115042	55115026	-
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SEQ ID NO 1542	CCTGCATCCCCCAGAGGCCC	CAG	chr19	55114858	55114877	55114861	-
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SEQ ID NO 1546	CTACTTGGCCTGGACCCCAC	GAG	chr19	55114830	55114849	55114833	-
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SEQ ID NO 1549	GACCCCACGAGAGGCCACCC	CAG	chr19	55114818	55114837	55114821	-
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SEQ ID NO 1735	GGGGCTGGGGCCTGGACTCG	TGG	chr19	55114102	55114121	55114105	-
SEQ ID NO 1736	GGGCTGGGGCCTGGACTCGT	GGG	chr19	55114101	55114120	55114104	-
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SEQ ID NO 1738	GGCCTGGACTCGTGGGTCTG	AGG	chr19	55114094	55114113	55114097	-
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SEQ ID NO 1747	GGTCTGAGGGAGGAGGGGCT	GGG	chr19	55114080	55114099	55114083	-
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SEQ ID NO 1753	GGGCCTGGACTTCTGGGTCT	TAG	chr19	55114058	55114077	55114061	-
SEQ ID NO 1754	GGCCTGGACTTCTGGGTCTT	AGG	chr19	55114057	55114076	55114060	-
SEQ ID NO 1755	GCCTGGACTTCTGGGTCTTA	GGG	chr19	55114056	55114075	55114059	-
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SEQ ID NO 1760	TTCTGGGTCTTAGGGAGGCG	GGG	chr19	55114048	55114067	55114051	-
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SEQ ID NO 1762	GGTCTTAGGGAGGCGGGGCT	GGG	chr19	55114043	55114062	55114046	-
SEQ ID NO 1763	TAGGGAGGCGGGGCTGGGCC	TGG	chr19	55114038	55114057	55114041	-

SEQ ID NO 1764	CGGGGCTGGGCCTGGACCCC	TGG	chr19	55114030	55114049	55114033	-
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SEQ ID NO 1766	CCTGGACCCCTGGGTCTGAA	TGG	chr19	55114020	55114039	55114023	-
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SEQ ID NO 1769	GACCCCTGGGTCTGAATGGG	GAG	chr19	55114016	55114035	55114019	-
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SEQ ID NO 1798	GGGTTGAATGGGGAGGGGTT	GGG	chr19	55113936	55113955	55113939	-
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SEQ ID NO 1801	GGGGTTGGGCCTGGACTCTG	GAG	chr19	55113922	55113941	55113925	-
SEQ ID NO 1802	GGCCTGGACTCTGGAGTCCC	TGG	chr19	55113915	55113934	55113918	-
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SEQ ID NO 1804	CTCTGGAGTCCCTGGTGCCC	AGG	chr19	55113907	55113926	55113910	-
SEQ ID NO 1805	AGTCCCTGGTGCCCAGGCCT	CAG	chr19	55113901	55113920	55113904	-
SEQ ID NO 1806	GTCCCTGGTGCCCAGGCCTC	AGG	chr19	55113900	55113919	55113903	-
SEQ ID NO 1807	CAGGCCTCAGGCATCTTTCA	CAG	chr19	55113888	55113907	55113891	-
SEQ ID NO 1808	AGGCCTCAGGCATCTTTCAC	AGG	chr19	55113887	55113906	55113890	-
SEQ ID NO 1809	GGCCTCAGGCATCTTTCACA	GGG	chr19	55113886	55113905	55113889	-
SEQ ID NO 1810	TTTCACAGGGATGCCTGTAC	TGG	chr19	55113873	55113892	55113876	-
SEQ ID NO 1811	TTCACAGGGATGCCTGTACT	GGG	chr19	55113872	55113891	55113875	-
SEQ ID NO 1812	ACAGGGATGCCTGTACTGGG	CAG	chr19	55113869	55113888	55113872	-

SEQ ID NO 1813	CAGGGATGCCTGTACTGGGC	AGG	chr19	55113868	55113887	55113871	-
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SEQ ID NO 1815	GTACTGGGCAGGTCCTTGAA	AGG	chr19	55113857	55113876	55113860	-
SEQ ID NO 1816	TACTGGGCAGGTCCTTGAAA	GGG	chr19	55113856	55113875	55113859	-
SEQ ID NO 1817	GGGCAGGTCCTTGAAAGGGA	AAG	chr19	55113852	55113871	55113855	-
SEQ ID NO 1818	GGCAGGTCCTTGAAAGGGAA	AGG	chr19	55113851	55113870	55113854	-
SEQ ID NO 1819	TCCCCTATCGCCATGACAAC	TGG	chr19	55113806	55113825	55113809	-
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SEQ ID NO 1822	ACAACTGGGTGGAAATAAAC	GAG	chr19	55113791	55113810	55113794	-
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SEQ ID NO 1828	GGGCACGTGCGGCCCCTTCA	CAG	chr19	55113748	55113767	55113751	-
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SEQ ID NO 1831	CCTCATGCTCTTGGCCCTCG	TAG	chr19	55113710	55113729	55113713	-
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SEQ ID NO 1937	GGTTTAAGGCAGGAGGGGCT	GGG	chr19	55113207	55113226	55113210	-
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SEQ ID NO 1939	TTTAAGGCAGGAGGGGCTGG	GGG	chr19	55113205	55113224	55113208	-
SEQ ID NO 1940	AGGCAGGAGGGGCTGGGGGC	CAG	chr19	55113201	55113220	55113204	-
SEQ ID NO 1941	GGCAGGAGGGGCTGGGGGCC	AGG	chr19	55113200	55113219	55113203	-
SEQ ID NO 1942	GGGCTGGGGGCCAGGACTCC	TGG	chr19	55113192	55113211	55113195	-
SEQ ID NO 1943	GGCCAGGACTCCTGGCTCTG	AAG	chr19	55113184	55113203	55113187	-
SEQ ID NO 1944	GCCAGGACTCCTGGCTCTGA	AGG	chr19	55113183	55113202	55113186	-
SEQ ID NO 1945	CAGGACTCCTGGCTCTGAAG	GAG	chr19	55113181	55113200	55113184	-
SEQ ID NO 1946	AGGACTCCTGGCTCTGAAGG	AGG	chr19	55113180	55113199	55113183	-
SEQ ID NO 1947	GACTCCTGGCTCTGAAGGAG	GAG	chr19	55113178	55113197	55113181	-
SEQ ID NO 1948	ACTCCTGGCTCTGAAGGAGG	AGG	chr19	55113177	55113196	55113180	-
SEQ ID NO 1949	CTCCTGGCTCTGAAGGAGGA	GGG	chr19	55113176	55113195	55113179	-
SEQ ID NO 1950	TCCTGGCTCTGAAGGAGGAG	GGG	chr19	55113175	55113194	55113178	-
SEQ ID NO 1951	GGCTCTGAAGGAGGAGGGGC	TGG	chr19	55113171	55113190	55113174	-
SEQ ID NO 1952	AGGGGCTGGAACCTCTTCCC	TAG	chr19	55113157	55113176	55113160	-
SEQ ID NO 1953	TGGAACCTCTTCCCTAGTCT	GAG	chr19	55113151	55113170	55113154	-
SEQ ID NO 1954	CTCTTCCCTAGTCTGAGCAC	TGG	chr19	55113145	55113164	55113148	-
SEQ ID NO 1955	TTCCCTAGTCTGAGCACTGG	AAG	chr19	55113142	55113161	55113145	-
SEQ ID NO 1956	AGCACTGGAAGCGCCACCTG	TGG	chr19	55113130	55113149	55113133	-
SEQ ID NO 1957	GCACTGGAAGCGCCACCTGT	GGG	chr19	55113129	55113148	55113132	-
SEQ ID NO 1958	CTGGAAGCGCCACCTGTGGG	TGG	chr19	55113126	55113145	55113129	-
SEQ ID NO 1959	GCGCCACCTGTGGGTGGTGA	CGG	chr19	55113120	55113139	55113123	-

SEQ ID NO 1960	CGCCACCTGTGGGTGGTGAC	GGG	chr19	55113119	55113138	55113122	-
SEQ ID NO 1961	GCCACCTGTGGGTGGTGACG	GGG	chr19	55113118	55113137	55113121	-
SEQ ID NO 1962	CCACCTGTGGGTGGTGACGG	GGG	chr19	55113117	55113136	55113120	-
SEQ ID NO 1963	GGGGGTTTTGCCGTGTCTAA	CAG	chr19	55113099	55113118	55113102	-
SEQ ID NO 1964	GGGGTTTTGCCGTGTCTAAC	AGG	chr19	55113098	55113117	55113101	-
SEQ ID NO 1965	CGTGTCTAACAGGTACCATG	TGG	chr19	55113088	55113107	55113091	-
SEQ ID NO 1966	GTGTCTAACAGGTACCATGT	GGG	chr19	55113087	55113106	55113090	-
SEQ ID NO 1967	TGTCTAACAGGTACCATGTG	GGG	chr19	55113086	55113105	55113089	-
SEQ ID NO 1968	CCATGTGGGGTTCCCGCACC	CAG	chr19	55113073	55113092	55113076	-
SEQ ID NO 1969	TGGGGTTCCCGCACCCAGAT	GAG	chr19	55113068	55113087	55113071	-
SEQ ID NO 1970	GGTTCCCGCACCCAGATGAG	AAG	chr19	55113065	55113084	55113068	-
SEQ ID NO 1971	CCCCGTTCACTTCCTGTTTG	CAG	chr19	55113031	55113050	55113034	-
SEQ ID NO 1972	GTTCACTTCCTGTTTGCAGA	TAG	chr19	55113027	55113046	55113030	-
SEQ ID NO 1973	ACTTCCTGTTTGCAGATAGC	CAG	chr19	55113023	55113042	55113026	-
SEQ ID NO 1974	CTTCCTGTTTGCAGATAGCC	AGG	chr19	55113022	55113041	55113025	-
SEQ ID NO 1975	TCCTGTTTGCAGATAGCCAG	GAG	chr19	55113020	55113039	55113023	-
SEQ ID NO 1976	GATAGCCAGGAGTCCTTTCG	TGG	chr19	55113009	55113028	55113012	-
SEQ ID NO 1977	GTCCTTTCGTGGTTTCCACT	GAG	chr19	55112998	55113017	55113001	-
SEQ ID NO 1978	GTGGTTTCCACTGAGCACTG	AAG	chr19	55112990	55113009	55112993	-
SEQ ID NO 1979	TGGTTTCCACTGAGCACTGA	AGG	chr19	55112989	55113008	55112992	-
SEQ ID NO 1980	TCCACTGAGCACTGAAGGCC	TGG	chr19	55112984	55113003	55112987	-
SEQ ID NO 1981	CTGAGCACTGAAGGCCTGGC	CGG	chr19	55112980	55112999	55112983	-
SEQ ID NO 1982	GGCCTGGCCGGCCTGACCAC	TGG	chr19	55112968	55112987	55112971	-
SEQ ID NO 1983	GCCTGGCCGGCCTGACCACT	GGG	chr19	55112967	55112986	55112970	-
SEQ ID NO 1984	CGGCCTGACCACTGGGCAAC	CAG	chr19	55112960	55112979	55112963	-
SEQ ID NO 1985	GGCCTGACCACTGGGCAACC	AGG	chr19	55112959	55112978	55112962	-
SEQ ID NO 1986	GCAACCAGGCGTATCTTAAA	CAG	chr19	55112945	55112964	55112948	-
SEQ ID NO 1987	CCAGGCGTATCTTAAACAGC	CAG	chr19	55112941	55112960	55112944	-
SEQ ID NO 1988	GGCGTATCTTAAACAGCCAG	TGG	chr19	55112938	55112957	55112941	-
SEQ ID NO 1989	TATCTTAAACAGCCAGTGGC	CAG	chr19	55112934	55112953	55112937	-
SEQ ID NO 1990	TCTTAAACAGCCAGTGGCCA	GAG	chr19	55112932	55112951	55112935	-
SEQ ID NO 1991	CTTAAACAGCCAGTGGCCAG	AGG	chr19	55112931	55112950	55112934	-
SEQ ID NO 1992	AGCCAGTGGCCAGAGGCTGT	TGG	chr19	55112924	55112943	55112927	-
SEQ ID NO 1993	GCCAGTGGCCAGAGGCTGTT	GGG	chr19	55112923	55112942	55112926	-
SEQ ID NO 1994	GGTCATTTTCCCCACTGTCC	TAG	chr19	55112902	55112921	55112905	-
SEQ ID NO 1995	CTGTCCTAGCACCGTGTCCC	TGG	chr19	55112888	55112907	55112891	-
SEQ ID NO 1996	TGTCCCTGGATCTGTTTTCG	TGG	chr19	55112874	55112893	55112877	-
SEQ ID NO 1997	TCTGTTTTCGTGGCTCCCTC	TGG	chr19	55112864	55112883	55112867	-
SEQ ID NO 1998	TGTTTTCGTGGCTCCCTCTG	GAG	chr19	55112862	55112881	55112865	-
SEQ ID NO 1999	CCTCTGGAGTCCCGACTTGC	TGG	chr19	55112848	55112867	55112851	-
SEQ ID NO 2000	CTCTGGAGTCCCGACTTGCT	GGG	chr19	55112847	55112866	55112850	-
SEQ ID NO 2001	CCCGACTTGCTGGGACACCG	TGG	chr19	55112838	55112857	55112841	-
SEQ ID NO 2002	ACTTGCTGGGACACCGTGGC	TGG	chr19	55112834	55112853	55112837	-
SEQ ID NO 2003	CTTGCTGGGACACCGTGGCT	GGG	chr19	55112833	55112852	55112836	-
SEQ ID NO 2004	TTGCTGGGACACCGTGGCTG	GGG	chr19	55112832	55112851	55112835	-
SEQ ID NO 2005	CTGGGACACCGTGGCTGGGG	TAG	chr19	55112829	55112848	55112832	-
SEQ ID NO 2006	TGGGACACCGTGGCTGGGGT	AGG	chr19	55112828	55112847	55112831	-
SEQ ID NO 2007	CACCGTGGCTGGGGTAGGTG	CGG	chr19	55112823	55112842	55112826	-
SEQ ID NO 2008	GCTGGGGTAGGTGCGGCTGA	CGG	chr19	55112816	55112835	55112819	-

SEQ ID NO 2009	TGACGGCTGTTTCCCACCCC	CAG	chr19	55112799	55112818	55112802	-
SEQ ID NO 2010	GACGGCTGTTTCCCACCCCC	AGG	chr19	55112798	55112817	55112801	-
SEQ ID NO 2011	ACCCCCAGGCCTGCATTGAT	GAG	chr19	55112784	55112803	55112787	-
SEQ ID NO 2012	GGCCTGCATTGATGAGAACC	TGG	chr19	55112777	55112796	55112780	-
SEQ ID NO 2013	CCTGCATTGATGAGAACCTG	GAG	chr19	55112775	55112794	55112778	-
SEQ ID NO 2014	CTGCATTGATGAGAACCTGG	AGG	chr19	55112774	55112793	55112777	-
SEQ ID NO 2015	CATTGATGAGAACCTGGAGG	TGG	chr19	55112771	55112790	55112774	-
SEQ ID NO 2016	CCTGGAGGTGGTGCGCTTCT	TGG	chr19	55112759	55112778	55112762	-
SEQ ID NO 2017	GGAGGTGGTGCGCTTCTTGG	TGG	chr19	55112756	55112775	55112759	-
SEQ ID NO 2018	AGGTGGTGCGCTTCTTGGTG	GAG	chr19	55112754	55112773	55112757	-
SEQ ID NO 2019	TGGTGCGCTTCTTGGTGGAG	CAG	chr19	55112751	55112770	55112754	-
SEQ ID NO 2020	GGTGCGCTTCTTGGTGGAGC	AGG	chr19	55112750	55112769	55112753	-
SEQ ID NO 2021	GTGCGCTTCTTGGTGGAGCA	GGG	chr19	55112749	55112768	55112752	-
SEQ ID NO 2022	AGCAGGGCGCCACTGTGAAC	CAG	chr19	55112733	55112752	55112736	-
SEQ ID NO 2023	GCAGGGCGCCACTGTGAACC	AGG	chr19	55112732	55112751	55112735	-
SEQ ID NO 2024	GGGCGCCACTGTGAACCAGG	CAG	chr19	55112729	55112748	55112732	-
SEQ ID NO 2025	CTGTGAACCAGGCAGACAAC	GAG	chr19	55112721	55112740	55112724	-
SEQ ID NO 2026	TGTGAACCAGGCAGACAACG	AGG	chr19	55112720	55112739	55112723	-
SEQ ID NO 2027	GTGAACCAGGCAGACAACGA	GGG	chr19	55112719	55112738	55112722	-
SEQ ID NO 2028	ACCAGGCAGACAACGAGGGC	TGG	chr19	55112715	55112734	55112718	-
SEQ ID NO 2029	GGGCTGGACGCCACTGCACG	TGG	chr19	55112699	55112718	55112702	-
SEQ ID NO 2030	CTGCACGTGGCCGCCTCCTG	TGG	chr19	55112686	55112705	55112689	-
SEQ ID NO 2031	GGCCGCCTCCTGTGGCTACC	TAG	chr19	55112678	55112697	55112681	-
SEQ ID NO 2032	TGTGGCTACCTAGATATCGC	CAG	chr19	55112668	55112687	55112671	-

Figure 2

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 2033	GTTCTCATCAATGCAGGCCT	GGGGGT	chr19	55112778	55112797	55112794	+
SEQ ID NO 2034	GAAGGGAGGGGGCTTCTCAT	CTGGGT	chr19	55113050	55113069	55113066	+
SEQ ID NO 2035	GCCCCTCCTCCTTCAGAGCC	AGGAGT	chr19	55113171	55113190	55113187	+
SEQ ID NO 2036	AAACCCAGCCAGGTCCTTCC	AAGGGT	chr19	55113222	55113241	55113238	+
SEQ ID NO 2037	GCCGTGGGCCCAGGGCTATG	CAGGGT	chr19	55113290	55113309	55113306	+
SEQ ID NO 2038	GGCCTGGGCGGGACTCCCAG	AGGGGT	chr19	55113351	55113370	55113367	+
SEQ ID NO 2039	CCGTTTCTCATTCTTCCCTT	AGGGGT	chr19	55113480	55113499	55113496	+
SEQ ID NO 2040	GGGACAAAAGCCGAAGTCCA	GGGGGT	chr19	55113518	55113537	55113534	+
SEQ ID NO 2041	TGCCCCAGGCCTTGTGGACA	CTGGGT	chr19	55113557	55113576	55113573	+
SEQ ID NO 2042	ACCTGAACTGGAGCTGAGGA	AGGAGT	chr19	55113593	55113612	55113609	+
SEQ ID NO 2043	AAGCTAAACTCCTAGATCCA	CGGGAT	chr19	55113620	55113639	55113636	+
SEQ ID NO 2044	GGCCGCACGTGCCCTGGGAA	CGGGAT	chr19	55113754	55113773	55113770	+
SEQ ID NO 2045	GGCCTGGGCACCAGGGACTC	CAGAGT	chr19	55113902	55113921	55113918	+
SEQ ID NO 2046	GCCCTTCCGCCCTCAGATGA	AGGAGT	chr19	55113972	55113991	55113988	+
SEQ ID NO 2047	GCCTCTCCCCATTCAGACCC	AGGGGT	chr19	55114009	55114028	55114025	+
SEQ ID NO 2048	GCCCCTCCTCCCTCAGACCC	ACGAGT	chr19	55114081	55114100	55114097	+
SEQ ID NO 2049	GCCCCTCCTCCCTCGGACCC	AGGAGT	chr19	55114117	55114136	55114133	+
SEQ ID NO 2050	GTCCCTCCACCCTCAGACCC	AGGAGT	chr19	55114154	55114173	55114170	+
SEQ ID NO 2051	GCCCCTCCTCCCTCGGACCC	AGGAGT	chr19	55114190	55114209	55114206	+
SEQ ID NO 2052	GCTCTTCTCTGTTCAGCCCT	AAGAAT	chr19	55114263	55114282	55114279	+
SEQ ID NO 2053	CCCCTAGCCACTAAGGCAAT	TGGGGT	chr19	55114323	55114342	55114339	+
SEQ ID NO 2054	CACTAAGGCAATTGGGGTGC	AGGAAT	chr19	55114331	55114350	55114347	+
SEQ ID NO 2055	TTGGGGTGCAGGAATGGGGG	CAGGGT	chr19	55114342	55114361	55114358	+
SEQ ID NO 2056	AAGTGGTTGATAAACCCACG	TGGGGT	chr19	55114380	55114399	55114396	+
SEQ ID NO 2057	GCTTGGGGACCTGCCTGGAG	AAGGAT	chr19	55114445	55114464	55114461	+
SEQ ID NO 2058	CCCAGGTGGAGAAACTGGCC	GGGAAT	chr19	55114490	55114509	55114506	+
SEQ ID NO 2059	GGAGAAACTGGCCGGGAATC	AAGAGT	chr19	55114497	55114516	55114513	+
SEQ ID NO 2060	ATCCCTGTTTTCCTAGGACT	GAGGGT	chr19	55114545	55114564	55114561	+
SEQ ID NO 2061	TTGGCCACGTAACCTGAGAA	GGGAAT	chr19	55114660	55114679	55114676	+
SEQ ID NO 2062	CCCCAATGCTCCAGGCCTCC	TGGGAT	chr19	55114710	55114729	55114726	+
SEQ ID NO 2063	AGGCCTCCTGGGATACCCCG	AAGAGT	chr19	55114722	55114741	55114738	+
SEQ ID NO 2064	CTCCTGGGATACCCCGAAGA	GTGAGT	chr19	55114726	55114745	55114742	+
SEQ ID NO 2065	CAGTCACCCCACAGTTGGAG	GAGAAT	chr19	55114760	55114779	55114776	+
SEQ ID NO 2066	GGCAGCCTGGTAGACAGGGC	TGGGGT	chr19	55114796	55114815	55114812	+
SEQ ID NO 2067	AGGGCTGGGGTGGCCTCTCG	TGGGGT	chr19	55114811	55114830	55114827	+
SEQ ID NO 2068	TAGGTGGCCTGGGGCCTCTG	GGGGAT	chr19	55114847	55114866	55114863	+
SEQ ID NO 2069	TCTGGGGGATGCAGGGGAAG	GGGGAT	chr19	55114863	55114882	55114879	+
SEQ ID NO 2070	GAAGGGGGATGCAGGGGAAC	GGGGAT	chr19	55114879	55114898	55114895	+
SEQ ID NO 2071	CGGGACCCTGCTCTGGGCGG	AGGAAT	chr19	55115079	55115098	55115095	+
SEQ ID NO 2072	TGGGGACTCTTTAAGGAAAG	AAGGAT	chr19	55115121	55115140	55115137	+
SEQ ID NO 2073	GAAGGATGGAGAAAGAGAAA	GGGAGT	chr19	55115140	55115159	55115156	+
SEQ ID NO 2074	GGACGCACCATTCTCACAAA	GGGAGT	chr19	55115195	55115214	55115211	+
SEQ ID NO 2075	GTGTAAGGAAGCTGCAGCAC	CAGGAT	chr19	55115414	55115433	55115430	+
SEQ ID NO 2076	GAGCAGCTCAGGTTCTGGGA	GAGGGT	chr19	55115468	55115487	55115484	+
SEQ ID NO 2077	GGTTCTGGGAGAGGGTAGCG	CAGGGT	chr19	55115478	55115497	55115494	+
SEQ ID NO 2078	CCCTGCCAAGCTCTCCCTCC	CAGGAT	chr19	55115552	55115571	55115568	+
SEQ ID NO 2079	GAGAGATGGCTCCAGGAAAT	GGGGGT	chr19	55115624	55115643	55115640	+
SEQ ID NO 2080	TGGGGGTGTGTCACCAGATA	AGGAAT	chr19	55115643	55115662	55115659	+

SEQ ID NO 2081	GAATCTGCCTAACAGGAGGT	GGGGGT	chr19	55115665	55115684	55115681	+
SEQ ID NO 2082	GACTAGGAAGGAGGAGGCCT	AAGGAT	chr19	55115708	55115727	55115724	+
SEQ ID NO 2083	TGTCCCTAGTGGCCCCACTG	TGGGGT	chr19	55115756	55115775	55115772	+
SEQ ID NO 2084	GAGCCACATTAACCGGCCCT	GGGAAT	chr19	55115812	55115831	55115828	+
SEQ ID NO 2085	GTGGTCCCAGCTCGGGGACA	CAGGAT	chr19	55115843	55115862	55115859	+
SEQ ID NO 2086	CCTGAAGTGGACATAGGGGC	CCGGGT	chr19	55115893	55115912	55115909	+
SEQ ID NO 2087	GCACAGACTAGAGAGGTAAG	GGGGGT	chr19	55115987	55116006	55116003	+
SEQ ID NO 2088	AGGGGAGCTGCCCAAATGAA	AGGAGT	chr19	55116013	55116032	55116029	+
SEQ ID NO 2089	TGAAAGGAGTGAGAGGTGAC	CCGAAT	chr19	55116029	55116048	55116045	+
SEQ ID NO 2090	GACCCGAATCCACAGGAGAA	CGGGGT	chr19	55116046	55116065	55116062	+
SEQ ID NO 2091	TGTCCAGGCAAAGAAAGCAA	GAGGAT	chr19	55116071	55116090	55116087	+
SEQ ID NO 2092	GGTGGCTAAAGCCAGGGAGA	CGGGGT	chr19	55116102	55116121	55116118	+
SEQ ID NO 2093	GCCAGGGAGACGGGGTACTT	TGGGGT	chr19	55116112	55116131	55116128	+
SEQ ID NO 2094	GAGAAGGAAAAGGGAACCCA	GCGAGT	chr19	55116252	55116271	55116268	+
SEQ ID NO 2095	CCCAGCGAGTGAAGACGGCA	TGGGGT	chr19	55116268	55116287	55116284	+
SEQ ID NO 2096	CGAGTGAAGACGGCATGGGG	TTGGGT	chr19	55116273	55116292	55116289	+
SEQ ID NO 2097	GGAGAGGACCCAGACACGGG	GAGGAT	chr19	55116317	55116336	55116333	+
SEQ ID NO 2098	AGCAGAGAGCAAGGGGAAGA	GGGAGT	chr19	55116417	55116436	55116433	+
SEQ ID NO 2099	ACCTGAAGGAGGCGGCAGGG	AAGGAT	chr19	55116456	55116475	55116472	+
SEQ ID NO 2100	AGCGGCACAGGCCCAGGGGA	GAGAAT	chr19	55116528	55116547	55116544	+
SEQ ID NO 2101	GAGACGGCAGCGTTAGAGGG	CAGAGT	chr19	55116652	55116671	55116668	+
SEQ ID NO 2102	GGAAGAGGGGAAGTCGAGGG	AGGGAT	chr19	55116848	55116867	55116864	+
SEQ ID NO 2103	GGGATGGTAAGGAGGACTGC	ATGGGT	chr19	55116869	55116888	55116885	+
SEQ ID NO 2104	AAAGCGACTCCAATGCGGAA	GAGAGT	chr19	55116925	55116944	55116941	+
SEQ ID NO 2105	CGGAAGAGAGTAGGTCGAAG	GGGAAT	chr19	55116940	55116959	55116956	+
SEQ ID NO 2106	AATGGTAAGGAGGCCTGGGG	CAGAGT	chr19	55116963	55116982	55116979	+
SEQ ID NO 2107	CTGGGGCAGAGTGGTCAGCA	CAGAGT	chr19	55116977	55116996	55116993	+
SEQ ID NO 2108	AAGCGGCTCCAATTCGGAAG	TGGGGT	chr19	55117024	55117043	55117040	+
SEQ ID NO 2109	CGGAAGTGGGGTGGTCGAAG	GGGAAT	chr19	55117038	55117057	55117054	+
SEQ ID NO 2110	AATGGTAAGGGGGGACTGGGA	CGGGGT	chr19	55117061	55117080	55117077	+
SEQ ID NO 2111	ACTGGGACGGGGTGTCAGCA	TAGGGT	chr19	55117074	55117093	55117090	+
SEQ ID NO 2112	CCAGGGCCAGGAACGACGGG	GCGGAT	chr19	55117108	55117127	55117124	+
SEQ ID NO 2113	CGAGACTGGCAACGGGGAAG	GAGGAT	chr19	55117134	55117153	55117150	+
SEQ ID NO 2114	ATGCCCCAGGTGGCGCAGCA	GAGGGT	chr19	55117158	55117177	55117174	+
SEQ ID NO 2115	GCTGATACCGTCGGCGTTGG	TGGAGT	chr19	55117235	55117254	55117251	+
SEQ ID NO 2116	GCGGGCGGGCGGCGGCGCGG	CGGGGT	chr19	55117271	55117290	55117287	+
SEQ ID NO 2117	GTCGAGCTCGGCGCCGGGGC	CAGGGT	chr19	55117295	55117314	55117311	+
SEQ ID NO 2118	CGGGCGGTGCGATGTCCGGA	GAGGAT	chr19	55117535	55117554	55117538	-
SEQ ID NO 2119	CGTCCGCTTCGAGCGCGCCG	CCGAGT	chr19	55117387	55117406	55117390	-
SEQ ID NO 2120	CCCCTTCGACCACCCCACTT	CCGAAT	chr19	55117041	55117060	55117044	-
SEQ ID NO 2121	CGACCTACTCTCTTCCGCAT	TGGAGT	chr19	55116937	55116956	55116940	-
SEQ ID NO 2122	GCGCTGCCCTCCTCTCGCCC	CCGAGT	chr19	55116704	55116723	55116707	-
SEQ ID NO 2123	CTAACGCTGCCGTCTCTCTC	CTGAGT	chr19	55116648	55116667	55116651	-
SEQ ID NO 2124	TTCTGTCTGCAGCTTGTGGC	CTGGGT	chr19	55116508	55116527	55116511	-
SEQ ID NO 2125	TCTCTGCTGTGTTGCTGCCC	AAGGAT	chr19	55116405	55116424	55116408	-
SEQ ID NO 2126	CACCACGTGATGTCCTCTGA	GCGGAT	chr19	55116347	55116366	55116350	-
SEQ ID NO 2127	TGAGCGGATCCTCCCCGTGT	CTGGGT	chr19	55116330	55116349	55116333	-
SEQ ID NO 2128	CCCCATGCCGTCTTCACTCG	CTGGGT	chr19	55116273	55116292	55116276	-
SEQ ID NO 2129	CTGTGCCATCTCTCGTTTCT	TAGGAT	chr19	55116222	55116241	55116225	-

SEQ ID NO 2130	TCTTAGGATGGCCTTCTCCG	ACGGAT	chr19	55116205	55116224	55116208 -
SEQ ID NO 2131	CCTGGACACCCCGTTCTCCT	GTGGAT	chr19	55116059	55116078	55116062 -
SEQ ID NO 2132	CACCCCGTTCTCCTGTGGAT	TCGGGT	chr19	55116053	55116072	55116056 -
SEQ ID NO 2133	CCCCTGTCATGGCATCTTCC	AGGGGT	chr19	55115954	55115973	55115957 -
SEQ ID NO 2134	ACAGCATGTTTGCTGCCTCC	AGGGAT	chr19	55115873	55115892	55115876 -
SEQ ID NO 2135	CGGTTAATGTGGCTCTGGTT	CTGGGT	chr19	55115807	55115826	55115810 -
SEQ ID NO 2136	CACAGTGGGGCCACTAGGGA	CAGGAT	chr19	55115758	55115777	55115761 -
SEQ ID NO 2137	TCCTTCCTAGTCTCCTGATA	TTGGGT	chr19	55115700	55115719	55115703 -
SEQ ID NO 2138	TTGCTTACGATGGAGCCAGA	GAGGAT	chr19	55115582	55115601	55115585 -
SEQ ID NO 2139	CTGGGAGGGAGAGCTTGGCA	GGGGGT	chr19	55115555	55115574	55115558 -
SEQ ID NO 2140	CAGGGGGTGGGAGGGAAGGG	GGGGAT	chr19	55115537	55115556	55115540 -
SEQ ID NO 2141	GCAGTTTGGAAAAACAAAAT	CAGAAT	chr19	55115379	55115398	55115382 -
SEQ ID NO 2142	AAAATCAGAATAAGTTGGTC	CTGAGT	chr19	55115364	55115383	55115367 -
SEQ ID NO 2143	GGCAGGGCTGTGGTGAGGAG	GGGGGT	chr19	55115240	55115259	55115243 -
SEQ ID NO 2144	GTGTGGAAAACTCCCTTTGT	GAGAAT	chr19	55115210	55115229	55115213 -
SEQ ID NO 2145	TCTCCATCCTTCTTTCCTTA	AAGAGT	chr19	55115132	55115151	55115135 -
SEQ ID NO 2146	ACATATTCCTCCGCCCAGAG	CAGGGT	chr19	55115089	55115108	55115092 -
SEQ ID NO 2147	TAAGGCCCTGCTCTGGGCTT	CTGGGT	chr19	55115053	55115072	55115056 -
SEQ ID NO 2148	CCTGCTCTGGGCTTCTGGGT	TTGAGT	chr19	55115047	55115066	55115050 -
SEQ ID NO 2149	CTCTCCTGCCCCTTCCCTAC	AGGGGT	chr19	55114950	55114969	55114953 -
SEQ ID NO 2150	CCTGTCTACCAGGCTGCCTT	TTGGGT	chr19	55114794	55114813	55114797 -
SEQ ID NO 2151	TCTACCAGGCTGCCTTTTGG	GTGGAT	chr19	55114790	55114809	55114793 -
SEQ ID NO 2152	GGTGGATTCTCCTCCAACTG	TGGGGT	chr19	55114771	55114790	55114774 -
SEQ ID NO 2153	TGCTTGGCAAACTCACTCTT	CGGGGT	chr19	55114742	55114761	55114745 -
SEQ ID NO 2154	TCCCAGGAGGCCTGGAGCAT	TGGGGT	chr19	55114715	55114734	55114718 -
SEQ ID NO 2155	CCTGGAGCATTGGGGTGGGC	TGGGGT	chr19	55114705	55114724	55114708 -
SEQ ID NO 2156	TGGGCTGGGGTTCAGAGAGG	AGGGAT	chr19	55114690	55114709	55114693 -
SEQ ID NO 2157	GTGGCCAAGAAGCAGGGGAG	CTGGGT	chr19	55114648	55114667	55114651 -
SEQ ID NO 2158	AAGAAGCAGGGGAGCTGGGT	TTGGGT	chr19	55114642	55114661	55114645 -
SEQ ID NO 2159	GAGCTGGGTTTGGGTCAGGT	CTGGGT	chr19	55114631	55114650	55114634 -
SEQ ID NO 2160	GTTTGGGTCAGGTCTGGGTG	TGGGGT	chr19	55114624	55114643	55114627 -
SEQ ID NO 2161	ACCCTCAGTCCTAGGAAAAC	AGGGAT	chr19	55114551	55114570	55114554 -
SEQ ID NO 2162	GGGATGGTTGGTCACTGTCT	CTGGGT	chr19	55114530	55114549	55114533 -
SEQ ID NO 2163	TGTGGCTGTTCCCAAGTTCT	TAGGGT	chr19	55114412	55114431	55114415 -
SEQ ID NO 2164	AAGTTCTTAGGGTACCCCAC	GTGGGT	chr19	55114399	55114418	55114402 -
SEQ ID NO 2165	CCCAATTGCCTTAGTGGCTA	GGGGGT	chr19	55114327	55114346	55114330 -
SEQ ID NO 2166	GTGGCTAGGGGGTTGGGGGC	TAGAGT	chr19	55114314	55114333	55114317 -
SEQ ID NO 2167	AGAGTAGGAGGGGCTGGAGC	CAGGAT	chr19	55114293	55114312	55114296 -
SEQ ID NO 2168	AGAGCTGGGGGCCTGGGCTC	CTGGGT	chr19	55114248	55114267	55114251 -
SEQ ID NO 2169	AGGGGCTGGGGCCTGGACTC	CTGGGT	chr19	55114212	55114231	55114215 -
SEQ ID NO 2170	AGGGGCTGGGGCCTGGACTC	CTGGGT	chr19	55114176	55114195	55114179 -
SEQ ID NO 2171	GGGCCTGGACTCCTGGGTCT	GAGGGT	chr19	55114168	55114187	55114171 -
SEQ ID NO 2172	GGGACTGGGGGCCTGGACTC	CTGGGT	chr19	55114139	55114158	55114142 -
SEQ ID NO 2173	AGGGGCTGGGGCCTGGACTC	GTGGGT	chr19	55114103	55114122	55114106 -
SEQ ID NO 2174	GGGGCTGGGGGCCTGGACTT	CTGGGT	chr19	55114066	55114085	55114069 -
SEQ ID NO 2175	GCGGGGCTGGGCCTGGACCC	CTGGGT	chr19	55114031	55114050	55114034 -
SEQ ID NO 2176	CTGGGCCTGGACCCCTGGGT	CTGAAT	chr19	55114025	55114044	55114028 -
SEQ ID NO 2177	AAGGGCTGGGGCCTGGCCTC	CTGGGT	chr19	55113958	55113977	55113961 -
SEQ ID NO 2178	CTGGGGCCTGGCCTCCTGGG	TTGAAT	chr19	55113953	55113972	55113956 -

SEQ ID NO 2179	GCCTCCTGGGTTGAATGGGG	AGGGGT	chr19	55113943	55113962	55113946 -
SEQ ID NO 2180	GAGGGGTTGGGCCTGGACTC	TGGAGT	chr19	55113924	55113943	55113927 -
SEQ ID NO 2181	AGGCCTCAGGCATCTTTCAC	AGGGAT	chr19	55113887	55113906	55113890 -
SEQ ID NO 2182	CTCCCCTATCGCCATGACAA	CTGGGT	chr19	55113807	55113826	55113810 -
SEQ ID NO 2183	ACTGGGTGGAAATAAACGAG	CCGAGT	chr19	55113788	55113807	55113791 -
SEQ ID NO 2184	ACGTGCGGCCCCTTCACAGC	CCGAGT	chr19	55113744	55113763	55113747 -
SEQ ID NO 2185	TTGGAGAGGTGAGGGACTTG	GGGGGT	chr19	55113657	55113676	55113660 -
SEQ ID NO 2186	CTTGGGGGGTAATTTATCCC	GTGGAT	chr19	55113641	55113660	55113644 -
SEQ ID NO 2187	GTAATTTATCCCGTGGATCT	AGGAGT	chr19	55113633	55113652	55113636 -
SEQ ID NO 2188	AAGTTTTGGACCCCTAAGGG	AAGAAT	chr19	55113495	55113514	55113498 -
SEQ ID NO 2189	CAGAGGGGGCCTCAGTGAAC	TGGAGT	chr19	55113425	55113444	55113428 -
SEQ ID NO 2190	TGCAGCTGTCTCACCCCTCT	GGGAGT	chr19	55113369	55113388	55113372 -
SEQ ID NO 2191	TGGGAGTCCCGCCCAGGCCC	CTGAGT	chr19	55113350	55113369	55113353 -
SEQ ID NO 2192	CCCCTGAGTCTGTCCCAGCA	CAGGGT	chr19	55113333	55113352	55113336 -
SEQ ID NO 2193	GGCCCACGGCTTCGTTCCTG	CAGAGT	chr19	55113280	55113299	55113283 -
SEQ ID NO 2194	CGTTCCTGCAGAGTATCTGC	TGGGGT	chr19	55113268	55113287	55113271 -
SEQ ID NO 2195	TGACCCTTGGAAGGACCTGG	CTGGGT	chr19	55113230	55113249	55113233 -
SEQ ID NO 2196	GAGCACTGGAAGCGCCACCT	GTGGGT	chr19	55113131	55113150	55113134 -
SEQ ID NO 2197	CGCCACCTGTGGGTGGTGAC	GGGGGT	chr19	55113119	55113138	55113122 -
SEQ ID NO 2198	CGTGTCTAACAGGTACCATG	TGGGGT	chr19	55113088	55113107	55113091 -
SEQ ID NO 2199	CTTCCTGTTTGCAGATAGCC	AGGAGT	chr19	55113022	55113041	55113025 -
SEQ ID NO 2200	CAGCCAGTGGCCAGAGGCTG	TTGGGT	chr19	55112925	55112944	55112928 -
SEQ ID NO 2201	ACTGTCCTAGCACCGTGTCC	CTGGAT	chr19	55112889	55112908	55112892 -
SEQ ID NO 2202	TCTGTTTTCGTGGCTCCCTC	TGGAGT	chr19	55112864	55112883	55112867 -
SEQ ID NO 2203	ACTTGCTGGGACACCGTGGC	TGGGGT	chr19	55112834	55112853	55112837 -

Figure 3

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 2204	AGCTCTTCTCTGTTCAGCCC	TAAGAAT	chr19	55114262	55114281	55114278	+
SEQ ID NO 2205	GCCTGGAGAAGGATGCAGGA	CGAGAAA	chr19	55114457	55114476	55114473	+
SEQ ID NO 2206	CGAGAAACACAGCCCCAGGT	GGAGAAA	chr19	55114477	55114496	55114493	+
SEQ ID NO 2207	GCAGTCACCCCACAGTTGGA	GGAGAAT	chr19	55114759	55114778	55114775	+
SEQ ID NO 2208	CTCTTTAAGGAAAGAAGGAT	GGAGAAA	chr19	55115127	55115146	55115143	+
SEQ ID NO 2209	AAGGAAAGAAGGATGGAGAA	AGAGAAA	chr19	55115133	55115152	55115149	+
SEQ ID NO 2210	GGAACAATATAAATTGGGGA	CTAGAAA	chr19	55115311	55115330	55115327	+
SEQ ID NO 2211	GGAGAACGGGGTGTCCAGGC	AAAGAAA	chr19	55116060	55116079	55116076	+
SEQ ID NO 2212	ACGGGGTACTTTGGGGTTGT	CCAGAAA	chr19	55116121	55116140	55116137	+
SEQ ID NO 2213	TCCGTCGGAGAAGGCCATCC	TAAGAAA	chr19	55116200	55116219	55116216	+
SEQ ID NO 2214	ACCCAGGCCACAAGCTGCAG	ACAGAAA	chr19	55116502	55116521	55116518	+
SEQ ID NO 2215	AAGCGGCACAGGCCCAGGGG	AGAGAAT	chr19	55116527	55116546	55116543	+
SEQ ID NO 2216	CAGGGGAGAGAATGCAGGTC	AGAGAAA	chr19	55116541	55116560	55116557	+
SEQ ID NO 2217	CACTAGGGACAGGATTGGTG	ACAGAAA	chr19	55115747	55115766	55115750	-
SEQ ID NO 2218	AGCAGTTTGGAAAAACAAAA	TCAGAAT	chr19	55115380	55115399	55115383	-
SEQ ID NO 2219	CGTGTGGAAAACTCCCTTTG	TGAGAAT	chr19	55115211	55115230	55115214	-
SEQ ID NO 2220	CAAGTTTTGGACCCCTAAGG	GAAGAAT	chr19	55113496	55113515	55113499	-
SEQ ID NO 2221	TTGGACCCCTAAGGGAAGAA	TGAGAAA	chr19	55113490	55113509	55113493	-

Figure 4

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 2222	GGGACTCCAGAGGGAGCCAC	GAAAAC	chr19	55112855	55112874	55112871	+
SEQ ID NO 2223	ATGGTACCTGTTAGACACGG	CAAAAC	chr19	55113089	55113108	55113105	+
SEQ ID NO 2224	TCATTCTTCCCTTAGGGGTC	CAAAAC	chr19	55113487	55113506	55113503	+
SEQ ID NO 2225	AGGACTGAGGGTTTCAGTGC	TAAAAC	chr19	55114559	55114578	55114575	+
SEQ ID NO 2226	TACTGGCCTTATCTCACAGG	TAAAAC	chr19	55115274	55115293	55115290	+
SEQ ID NO 2227	GGTACTTTGGGGTTGTCCAG	AAAAAC	chr19	55116125	55116144	55116141	+
SEQ ID NO 2228	CAAGAGGAGAAGCAGTTTGG	AAAAAC	chr19	55115390	55115409	55115393	-
SEQ ID NO 2229	AGGAGGGGGGTGTCCGTGTG	GAAAAC	chr19	55115225	55115244	55115228	-
SEQ ID NO 2230	ACTGAAACCCTCAGTCCTAG	GAAAAC	chr19	55114557	55114576	55114560	-

Figure 5

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 2231	CCCAACAGCCTCTGGCCACT	GGCTGTTT	chr19	55112920	55112939	55112936	+
SEQ ID NO 2232	GGAAGTGAACGGGGAAGGGA	GGGGGCTT	chr19	55113037	55113056	55113053	+
SEQ ID NO 2233	CCCCCGTCACCACCCACAGG	TGGCGCTT	chr19	55113114	55113133	55113130	+
SEQ ID NO 2234	AGCCAGGGGCTGACACGGGC	CACCGTTT	chr19	55113458	55113477	55113474	+
SEQ ID NO 2235	CTGGGAACGGGATGAACTCG	GCTCGTTT	chr19	55113767	55113786	55113783	+
SEQ ID NO 2236	GAACAGCCACAGCAGGGGGG	CGATGCTT	chr19	55114421	55114440	55114437	+
SEQ ID NO 2237	CAGAGACAGTGACCAACCAT	CCCTGTTT	chr19	55114527	55114546	55114543	+
SEQ ID NO 2238	ATCCCTGTTTTCCTAGGACT	GAGGGTTT	chr19	55114545	55114564	55114561	+
SEQ ID NO 2239	ACCTGACCCAAACCCAGCTC	CCCTGCTT	chr19	55114631	55114650	55114647	+
SEQ ID NO 2240	CTCCTGGGATACCCCGAAGA	GTGAGTTT	chr19	55114726	55114745	55114742	+
SEQ ID NO 2241	GGGAAGCCTGAGCGCCTCTC	CTGGGCTT	chr19	55115006	55115025	55115022	+
SEQ ID NO 2242	GGACGCACCATTCTCACAAA	GGGAGTTT	chr19	55115195	55115214	55115211	+
SEQ ID NO 2243	TAGAACTCAGGACCAACTTA	TTCTGATT	chr19	55115354	55115373	55115370	+
SEQ ID NO 2244	TCAGGACCAACTTATTCTGA	TTTTGTTT	chr19	55115360	55115379	55115376	+
SEQ ID NO 2245	ATTCTGATTTTGTTTTTCCA	AACTGCTT	chr19	55115373	55115392	55115389	+
SEQ ID NO 2246	GGAAGGAGGAGGCCTAAGGA	TGGGGCTT	chr19	55115713	55115732	55115729	+
SEQ ID NO 2247	GAGAGCGCCGCGCCCGCACC	GTCCGCTT	chr19	55117406	55117425	55117409	-
SEQ ID NO 2248	CCGCCCCGTCGTTCCTGGCC	CTGGGCTT	chr19	55117112	55117131	55117115	-
SEQ ID NO 2249	CCACCCCACTTCCGAATTGG	AGCCGCTT	chr19	55117032	55117051	55117035	-
SEQ ID NO 2250	TGGAGCCGCTTCAACTGGCC	CTGGGCTT	chr19	55117015	55117034	55117018	-
SEQ ID NO 2251	CCTACTCTCTTCCGCATTGG	AGTCGCTT	chr19	55116934	55116953	55116937	-
SEQ ID NO 2252	TTGGAGTCGCTTTAACTGGC	CCTGGCTT	chr19	55116918	55116937	55116921	-
SEQ ID NO 2253	TCCGGACCACTTTGAGCTCT	ACTGGCTT	chr19	55116623	55116642	55116626	-
SEQ ID NO 2254	CTTCTGCGCCGCCTCTGGCC	CACTGTTT	chr19	55116598	55116617	55116601	-
SEQ ID NO 2255	GTTTCCCCTTCCCAGGCAGG	TCCTGCTT	chr19	55116574	55116593	55116577	-
SEQ ID NO 2256	CATTCTCTCCCCTGGGCCTG	TGCCGCTT	chr19	55116535	55116554	55116538	-
SEQ ID NO 2257	GGCCTGTGCCGCTTTCTGTC	TGCAGCTT	chr19	55116521	55116540	55116524	-
SEQ ID NO 2258	CTTCTGGGGCCTGTGCCATC	TCTCGTTT	chr19	55116232	55116251	55116235	-
SEQ ID NO 2259	TTCTTGTAGGCCTGCATCAT	CACCGTTT	chr19	55116155	55116174	55116158	-
SEQ ID NO 2260	ACCCCAAAGTACCCCGTCTC	CCTGGCTT	chr19	55116118	55116137	55116121	-
SEQ ID NO 2261	CTTTAGCCACCTCTCCATCC	TCTTGCTT	chr19	55116093	55116112	55116096	-
SEQ ID NO 2262	GCCTGGACACCCCGTTCTCC	TGTGGATT	chr19	55116060	55116079	55116063	-
SEQ ID NO 2263	CCTATGTCCACTTCAGGACA	GCATGTTT	chr19	55115890	55115909	55115893	-
SEQ ID NO 2264	CCACAGTGGGGCCACTAGGG	ACAGGATT	chr19	55115759	55115778	55115762	-
SEQ ID NO 2265	CTAACCCCCACCTCCTGTTA	GGCAGATT	chr19	55115674	55115693	55115677	-
SEQ ID NO 2266	TCTCTCCTTGCCAGAACCTC	TAAGGTTT	chr19	55115608	55115627	55115611	-
SEQ ID NO 2267	TCCTTGCCAGAACCTCTAAG	GTTTGCTT	chr19	55115604	55115623	55115607	-
SEQ ID NO 2268	CCAGAGAGGATCCTGGGAGG	GAGAGCTT	chr19	55115567	55115586	55115570	-
SEQ ID NO 2269	TGCTCTGACGCGGCCGTCTG	GTGCGTTT	chr19	55115453	55115472	55115456	-
SEQ ID NO 2270	CGTTTCACTGATCCTGGTGC	TGCAGCTT	chr19	55115430	55115449	55115433	-
SEQ ID NO 2271	TTACACTTCCCAAGAGGAGA	AGCAGTTT	chr19	55115400	55115419	55115403	-
SEQ ID NO 2272	TTTATATTGTTCCTCCGTGC	GTCAGTTT	chr19	55115304	55115323	55115307	-
SEQ ID NO 2273	TTCCTCCGCCCAGAGCAGGG	TCCCGCTT	chr19	55115084	55115103	55115087	-
SEQ ID NO 2274	CGCTTCCCTAAGGCCCTGCT	CTGGGCTT	chr19	55115061	55115080	55115064	-
SEQ ID NO 2275	TAAGGCCCTGCTCTGGGCTT	CTGGGTTT	chr19	55115053	55115072	55115056	-
SEQ ID NO 2276	GGCAAGCCCAGGAGAGGCGC	TCAGGCTT	chr19	55115017	55115036	55115020	-
SEQ ID NO 2277	GTCTACCAGGCTGCCTTTTG	GGTGGATT	chr19	55114791	55114810	55114794	-
SEQ ID NO 2278	TTCTCCTCCAACTGTGGGGT	GACTGCTT	chr19	55114765	55114784	55114768	-

SEQ ID NO 2279	GTGGGCTGGGGTTCAGAGAG	GAGGGATT	chr19	55114691	55114710	55114694 -
SEQ ID NO 2280	GTGGCCAAGAAGCAGGGGAG	CTGGGTTT	chr19	55114648	55114667	55114651 -
SEQ ID NO 2281	TCAGGTCTGGGTGTGGGGTG	ACCAGCTT	chr19	55114617	55114636	55114620 -
SEQ ID NO 2282	GGTGTGGGGTGACCAGCTTA	TGCTGTTT	chr19	55114608	55114627	55114611 -
SEQ ID NO 2283	ATGCTGTTTGCCCAGGACAG	CCTAGTTT	chr19	55114589	55114608	55114592 -
SEQ ID NO 2284	GGTCACTGTCTCTGGGTGAC	TCTTGATT	chr19	55114521	55114540	55114524 -
SEQ ID NO 2285	TGGGTGACTCTTGATTCCCG	GCCAGTTT	chr19	55114509	55114528	55114512 -
SEQ ID NO 2286	GCCAGTTTCTCCACCTGGGG	CTGTGTTT	chr19	55114489	55114508	55114492 -
SEQ ID NO 2287	AAGTTCTTAGGGTACCCCAC	GTGGGTTT	chr19	55114399	55114418	55114402 -
SEQ ID NO 2288	TAGAGTAGGAGGGGCTGGAG	CCAGGATT	chr19	55114294	55114313	55114297 -
SEQ ID NO 2289	AGAGCTGGGGGCCTGGGCTC	CTGGGTTT	chr19	55114248	55114267	55114251 -
SEQ ID NO 2290	ACGTGCGGCCCCTTCACAGC	CCGAGTTT	chr19	55113744	55113763	55113747 -
SEQ ID NO 2291	CCTCCCGCCTCCTCCAGATG	GGCAGCTT	chr19	55113684	55113703	55113687 -
SEQ ID NO 2292	GTAATTTATCCCGTGGATCT	AGGAGTTT	chr19	55113633	55113652	55113636 -
SEQ ID NO 2293	TTATCCCGTGGATCTAGGAG	TTTAGCTT	chr19	55113628	55113647	55113631 -
SEQ ID NO 2294	CCTCCTCCGACCCCCTGGAC	TTCGGCTT	chr19	55113533	55113552	55113536 -
SEQ ID NO 2295	GGACTTCGGCTTTTGTCCCC	CCAAGTTT	chr19	55113517	55113536	55113520 -
SEQ ID NO 2296	ACCCTGCATAGCCCTGGGCC	CACGGCTT	chr19	55113296	55113315	55113299 -
SEQ ID NO 2297	TCCTGCAGAGTATCTGCTGG	GGTGGTTT	chr19	55113265	55113284	55113268 -
SEQ ID NO 2298	AGTATCTGCTGGGGTGGTTT	CCGAGCTT	chr19	55113257	55113276	55113260 -
SEQ ID NO 2299	TGACCCTTGGAAGGACCTGG	CTGGGTTT	chr19	55113230	55113249	55113233 -
SEQ ID NO 2300	CGCCACCTGTGGGTGGTGAC	GGGGGTTT	chr19	55113119	55113138	55113122 -
SEQ ID NO 2301	CCCTCCCTTCCCCGTTCACT	TCCTGTTT	chr19	55113040	55113059	55113043 -
SEQ ID NO 2302	CAGATAGCCAGGAGTCCTTT	CGTGGTTT	chr19	55113011	55113030	55113014 -
SEQ ID NO 2303	TCCTAGCACCGTGTCCCTGG	ATCTGTTT	chr19	55112885	55112904	55112888 -
SEQ ID NO 2304	CTGGGGTAGGTGCGGCTGAC	GGCTGTTT	chr19	55112815	55112834	55112818 -
SEQ ID NO 2305	TTGATGAGAACCTGGAGGTG	GTGCGCTT	chr19	55112769	55112788	55112772 -

Figure 6

#	Sequence	PAM	Chr	Start	End	Cut site 1 (5' of)	Cut site 2 (5' of)	Str
SEQ ID NO 2306	GCGATATCTAGGTAGCCACAGG	CTG	chr19	55112668	55112689	55112685	55112690	+
SEQ ID NO 2307	GGTAGCCACAGGAGGCGGCCAC	CTA	chr19	55112678	55112699	55112695	55112700	+
SEQ ID NO 2308	GTTGTCTGCCTGGTTCACAGTG	CTC	chr19	55112721	55112742	55112738	55112743	+
SEQ ID NO 2309	TCTGCCTGGTTCACAGTGGCGC	TTG	chr19	55112725	55112746	55112742	55112747	+
SEQ ID NO 2310	CCTGGTTCACAGTGGCGCCCTG	CTG	chr19	55112729	55112750	55112746	55112751	+
SEQ ID NO 2311	GTTCACAGTGGCGCCCTGCTCC	CTG	chr19	55112733	55112754	55112750	55112755	+
SEQ ID NO 2312	ACAGTGGCGCCCTGCTCCACCA	TTC	chr19	55112737	55112758	55112754	55112759	+
SEQ ID NO 2313	CTCCACCAAGAAGCGCACCACC	CTG	chr19	55112751	55112772	55112768	55112773	+
SEQ ID NO 2314	CACCAAGAAGCGCACCACCTCC	CTC	chr19	55112754	55112775	55112771	55112776	+
SEQ ID NO 2315	CAGGTTCTCATCAATGCAGGCC	CTC	chr19	55112775	55112796	55112792	55112797	+
SEQ ID NO 2316	TCATCAATGCAGGCCTGGGGGT	TTC	chr19	55112782	55112803	55112799	55112804	+
SEQ ID NO 2317	ATCAATGCAGGCCTGGGGGTGG	CTC	chr19	55112784	55112805	55112801	55112806	+
SEQ ID NO 2318	GGGGTGGGAAACAGCCGTCAGC	CTG	chr19	55112799	55112820	55112816	55112821	+
SEQ ID NO 2319	CCCCAGCCACGGTGTCCCAGCA	CTA	chr19	55112829	55112850	55112846	55112851	+
SEQ ID NO 2320	CAGAGGGAGCCACGAAAACAGA	CTC	chr19	55112862	55112883	55112879	55112884	+
SEQ ID NO 2321	GGACAGTGGGGAAAATGACCCA	CTA	chr19	55112902	55112923	55112919	55112924	+
SEQ ID NO 2322	TGGCCACTGGCTGTTTAAGATA	CTC	chr19	55112932	55112953	55112949	55112954	+
SEQ ID NO 2323	GCCACTGGCTGTTTAAGATACG	CTG	chr19	55112934	55112955	55112951	55112956	+
SEQ ID NO 2324	GCTGTTTAAGATACGCCTGGTT	CTG	chr19	55112941	55112962	55112958	55112963	+
SEQ ID NO 2325	TTTAAGATACGCCTGGTTGCCC	CTG	chr19	55112945	55112966	55112962	55112967	+
SEQ ID NO 2326	AAGATACGCCTGGTTGCCCAGT	TTT	chr19	55112948	55112969	55112965	55112970	+
SEQ ID NO 2327	AGATACGCCTGGTTGCCCAGTG	TTA	chr19	55112949	55112970	55112966	55112971	+
SEQ ID NO 2328	GTTGCCCAGTGGTCAGGCCGGC	CTG	chr19	55112960	55112981	55112977	55112982	+
SEQ ID NO 2329	CCCAGTGGTCAGGCCGGCCAGG	TTG	chr19	55112964	55112985	55112981	55112986	+
SEQ ID NO 2330	CAGTGCTCAGTGGAAACCACGA	CTT	chr19	55112990	55113011	55113007	55113012	+
SEQ ID NO 2331	AGTGCTCAGTGGAAACCACGAA	TTC	chr19	55112991	55113012	55113008	55113013	+
SEQ ID NO 2332	AGTGGAAACCACGAAAGGACTC	CTC	chr19	55112998	55113019	55113015	55113020	+
SEQ ID NO 2333	CTGGCTATCTGCAAACAGGAAG	CTC	chr19	55113020	55113041	55113037	55113042	+
SEQ ID NO 2334	GCTATCTGCAAACAGGAAGTGA	CTG	chr19	55113023	55113044	55113040	55113045	+
SEQ ID NO 2335	TCTGCAAACAGGAAGTGAACGG	CTA	chr19	55113027	55113048	55113044	55113049	+
SEQ ID NO 2336	CAAACAGGAAGTGAACGGGGAA	CTG	chr19	55113031	55113052	55113048	55113053	+
SEQ ID NO 2337	CTCATCTGGGTGCGGGAACCCC	CTT	chr19	55113065	55113086	55113082	55113087	+
SEQ ID NO 2338	TCATCTGGGTGCGGGAACCCCA	TTC	chr19	55113066	55113087	55113083	55113088	+
SEQ ID NO 2339	ATCTGGGTGCGGGAACCCCACA	CTC	chr19	55113068	55113089	55113085	55113090	+
SEQ ID NO 2340	GGTGCGGGAACCCCACATGGTA	CTG	chr19	55113073	55113094	55113090	55113095	+
SEQ ID NO 2341	TTAGACACGGCAAAACCCCCGT	CTG	chr19	55113099	55113120	55113116	55113121	+
SEQ ID NO 2342	GACACGGCAAAACCCCCGTCAC	TTA	chr19	55113102	55113123	55113119	55113124	+
SEQ ID NO 2343	CCAGTGCTCAGACTAGGGAAGA	CTT	chr19	55113142	55113163	55113159	55113164	+
SEQ ID NO 2344	CAGTGCTCAGACTAGGGAAGAG	TTC	chr19	55113143	55113164	55113160	55113165	+
SEQ ID NO 2345	AGACTAGGGAAGAGGTTCCAGC	CTC	chr19	55113151	55113172	55113168	55113173	+
SEQ ID NO 2346	GGGAAGAGGTTCCAGCCCCTCC	CTA	chr19	55113157	55113178	55113174	55113179	+
SEQ ID NO 2347	CAGCCCCTCCTCCTTCAGAGCC	TTC	chr19	55113169	55113190	55113186	55113191	+
SEQ ID NO 2348	CTCCTTCAGAGCCAGGAGTCCT	CTC	chr19	55113178	55113199	55113195	55113200	+
SEQ ID NO 2349	CTTCAGAGCCAGGAGTCCTGGC	CTC	chr19	55113181	55113202	55113198	55113203	+
SEQ ID NO 2350	CAGAGCCAGGAGTCCTGGCCCC	CTT	chr19	55113184	55113205	55113201	55113206	+
SEQ ID NO 2351	AGAGCCAGGAGTCCTGGCCCCC	TTC	chr19	55113185	55113206	55113202	55113207	+
SEQ ID NO 2352	GCCCCCAGCCCCTCCTGCCTTA	CTG	chr19	55113201	55113222	55113218	55113223	+
SEQ ID NO 2353	CTGCCTTAAACCCAGCCAGGTC	CTC	chr19	55113215	55113236	55113232	55113237	+
SEQ ID NO 2354	CCTTAAACCCAGCCAGGTCCTT	CTG	chr19	55113218	55113239	55113235	55113240	+
SEQ ID NO 2355	AAACCCAGCCAGGTCCTTCCAA	CTT	chr19	55113222	55113243	55113239	55113244	+
SEQ ID NO 2356	AACCCAGCCAGGTCCTTCCAAG	TTA	chr19	55113223	55113244	55113240	55113245	+
SEQ ID NO 2357	CCAAGGGTCAAGCTCGGAAACC	CTT	chr19	55113240	55113261	55113257	55113262	+
SEQ ID NO 2358	CAAGGGTCAAGCTCGGAAACCA	TTC	chr19	55113241	55113262	55113258	55113263	+
SEQ ID NO 2359	GGAAACCACCCCAGCAGATACT	CTC	chr19	55113255	55113276	55113272	55113277	+
SEQ ID NO 2360	TGCAGGAACGAAGCCGTGGGCC	CTC	chr19	55113278	55113299	55113295	55113300	+
SEQ ID NO 2361	CAGGAACGAAGCCGTGGGCCCA	CTG	chr19	55113280	55113301	55113297	55113302	+
SEQ ID NO 2362	TGCAGGGTGGAGGAAGGCCACC	CTA	chr19	55113308	55113329	55113325	55113330	+
SEQ ID NO 2363	TGCTGGGACAGACTCAGGGGCC	CTG	chr19	55113333	55113354	55113350	55113355	+

SEQ ID NO 2364	GGACAGACTCAGGGGCCTGGGC	CTG	chr19	55113338	55113359	55113355	55113360	+
SEQ ID NO 2365	AGGGGCCTGGGCGGGACTCCCA	CTC	chr19	55113348	55113369	55113365	55113370	+
SEQ ID NO 2366	GGCGGGACTCCCAGAGGGGTGA	CTG	chr19	55113357	55113378	55113374	55113379	+
SEQ ID NO 2367	CCAGAGGGGTGAGACAGCTGCA	CTC	chr19	55113367	55113388	55113384	55113389	+
SEQ ID NO 2368	CACACCTGTGTGCCTGGGCCCC	CTG	chr19	55113387	55113408	55113404	55113409	+
SEQ ID NO 2369	TGTGCCTGGGCCCCAGGCTGTC	CTG	chr19	55113395	55113416	55113412	55113417	+
SEQ ID NO 2370	GGCCCCAGGCTGTCACACTCCA	CTG	chr19	55113403	55113424	55113420	55113425	+
SEQ ID NO 2371	TCACACTCCAGTTCACTGAGGC	CTG	chr19	55113415	55113436	55113432	55113437	+
SEQ ID NO 2372	CAGTTCACTGAGGCCCCCTCTG	CTC	chr19	55113423	55113444	55113440	55113445	+
SEQ ID NO 2373	ACTGAGGCCCCCTCTGCACGGG	TTC	chr19	55113429	55113450	55113446	55113451	+
SEQ ID NO 2374	AGGCCCCCTCTGCACGGGGCCC	CTG	chr19	55113433	55113454	55113450	55113455	+
SEQ ID NO 2375	TGCACGGGGCCCTGCAGCCAGG	CTC	chr19	55113443	55113464	55113460	55113465	+
SEQ ID NO 2376	CACGGGGCCCTGCAGCCAGGGG	CTG	chr19	55113445	55113466	55113462	55113467	+
SEQ ID NO 2377	CAGCCAGGGGCTGACACGGGCC	CTG	chr19	55113457	55113478	55113474	55113479	+
SEQ ID NO 2378	ACACGGGCCACCGTTTCTCATT	CTG	chr19	55113470	55113491	55113487	55113492	+
SEQ ID NO 2379	CTCATTCTTCCCTTAGGGGTCC	TTT	chr19	55113486	55113507	55113503	55113508	+
SEQ ID NO 2380	TCATTCTTCCCTTAGGGGTCCA	TTC	chr19	55113487	55113508	55113504	55113509	+
SEQ ID NO 2381	ATTCTTCCCTTAGGGGTCCAAA	CTC	chr19	55113489	55113510	55113506	55113511	+
SEQ ID NO 2382	TTCCCTTAGGGGTCCAAAACTT	TTC	chr19	55113493	55113514	55113510	55113515	+
SEQ ID NO 2383	CCCTTAGGGGTCCAAAACTTGG	CTT	chr19	55113495	55113516	55113512	55113517	+
SEQ ID NO 2384	CCTTAGGGGTCCAAAACTTGGG	TTC	chr19	55113496	55113517	55113513	55113518	+
SEQ ID NO 2385	AGGGGTCCAAAACTTGGGGGGA	CTT	chr19	55113500	55113521	55113517	55113522	+
SEQ ID NO 2386	GGGGTCCAAAACTTGGGGGGAC	TTA	chr19	55113501	55113522	55113518	55113523	+
SEQ ID NO 2387	GGGGGGACAAAAGCCGAAGTCC	CTT	chr19	55113515	55113536	55113532	55113537	+
SEQ ID NO 2388	GGGGGACAAAAGCCGAAGTCCA	TTG	chr19	55113516	55113537	55113533	55113538	+
SEQ ID NO 2389	GCCCCAGGCCTTGTGGACACTG	CTT	chr19	55113558	55113579	55113575	55113580	+
SEQ ID NO 2390	CCCCAGGCCTTGTGGACACTGG	TTG	chr19	55113559	55113580	55113576	55113581	+
SEQ ID NO 2391	GTGGACACTGGGTGGGCTCCGG	CTT	chr19	55113570	55113591	55113587	55113592	+
SEQ ID NO 2392	TGGACACTGGGTGGGCTCCGGG	TTG	chr19	55113571	55113592	55113588	55113593	+
SEQ ID NO 2393	GGTGGGCTCCGGGACCTGAACT	CTG	chr19	55113580	55113601	55113597	55113602	+
SEQ ID NO 2394	CGGGACCTGAACTGGAGCTGAG	CTC	chr19	55113589	55113610	55113606	55113611	+
SEQ ID NO 2395	AACTGGAGCTGAGGAAGGAGTG	CTG	chr19	55113598	55113619	55113615	55113620	+
SEQ ID NO 2396	GAGCTGAGGAAGGAGTGAAGCT	CTG	chr19	55113603	55113624	55113620	55113625	+
SEQ ID NO 2397	AGGAAGGAGTGAAGCTAAACTC	CTG	chr19	55113609	55113630	55113626	55113631	+
SEQ ID NO 2398	AACTCCTAGATCCACGGGATAA	CTA	chr19	55113626	55113647	55113643	55113648	+
SEQ ID NO 2399	CTAGATCCACGGGATAAATTAC	CTC	chr19	55113631	55113652	55113648	55113653	+
SEQ ID NO 2400	GATCCACGGGATAAATTACCCC	CTA	chr19	55113634	55113655	55113651	55113656	+
SEQ ID NO 2401	CCCCCCAAGTCCCTCACCTCTC	TTA	chr19	55113652	55113673	55113669	55113674	+
SEQ ID NO 2402	ACCTCTCCAAAGCTGCCCATCT	CTC	chr19	55113667	55113688	55113684	55113689	+
SEQ ID NO 2403	TCCAAAGCTGCCCATCTGGAGG	CTC	chr19	55113672	55113693	55113689	55113694	+
SEQ ID NO 2404	CAAAGCTGCCCATCTGGAGGAG	CTC	chr19	55113674	55113695	55113691	55113696	+
SEQ ID NO 2405	CCCATCTGGAGGAGGCGGGAGG	CTG	chr19	55113682	55113703	55113699	55113704	+
SEQ ID NO 2406	GAGGAGGCGGGAGGGAGCTACG	CTG	chr19	55113690	55113711	55113707	55113712	+
SEQ ID NO 2407	CGAGGGCCAAGAGCATGAGGTC	CTA	chr19	55113710	55113731	55113727	55113732	+
SEQ ID NO 2408	GGGCTGTGAAGGGGCCGCACGT	CTC	chr19	55113742	55113763	55113759	55113764	+
SEQ ID NO 2409	TGAAGGGGCCGCACGTGCCCTG	CTG	chr19	55113748	55113769	55113765	55113770	+
SEQ ID NO 2410	GGAACGGGATGAACTCGGCTCG	CTG	chr19	55113770	55113791	55113787	55113792	+
SEQ ID NO 2411	GGCTCGTTTATTTCCACCCAGT	CTC	chr19	55113786	55113807	55113803	55113808	+
SEQ ID NO 2412	GTTTATTTCCACCCAGTTGTCA	CTC	chr19	55113791	55113812	55113808	55113813	+
SEQ ID NO 2413	ATTTCCACCCAGTTGTCATGGC	TTT	chr19	55113795	55113816	55113812	55113817	+
SEQ ID NO 2414	TTTCCACCCAGTTGTCATGGCG	TTA	chr19	55113796	55113817	55113813	55113818	+
SEQ ID NO 2415	CCACCCAGTTGTCATGGCGATA	TTT	chr19	55113799	55113820	55113816	55113821	+
SEQ ID NO 2416	CACCCAGTTGTCATGGCGATAG	TTC	chr19	55113800	55113821	55113817	55113822	+
SEQ ID NO 2417	TCATGGCGATAGGGGAGGGGGG	TTG	chr19	55113810	55113831	55113827	55113832	+
SEQ ID NO 2418	TCCCTTTCAAGGACCTGCCCAG	CTT	chr19	55113852	55113873	55113869	55113874	+
SEQ ID NO 2419	CCCTTTCAAGGACCTGCCCAGT	TTT	chr19	55113853	55113874	55113870	55113875	+
SEQ ID NO 2420	CCTTTCAAGGACCTGCCCAGTA	TTC	chr19	55113854	55113875	55113871	55113876	+
SEQ ID NO 2421	TCAAGGACCTGCCCAGTACAGG	CTT	chr19	55113858	55113879	55113875	55113880	+
SEQ ID NO 2422	CAAGGACCTGCCCAGTACAGGC	TTT	chr19	55113859	55113880	55113876	55113881	+

SEQ ID NO 2423	AAGGACCTGCCCAGTACAGGCA	TTC	chr19	55113860	55113881	55113877	55113882	+
SEQ ID NO 2424	CCCAGTACAGGCATCCCTGTGA	CTG	chr19	55113869	55113890	55113886	55113891	+
SEQ ID NO 2425	TGAAAGATGCCTGAGGCCTGGG	CTG	chr19	55113888	55113909	55113905	55113910	+
SEQ ID NO 2426	AGGCCTGGGCACCAGGGACTCC	CTG	chr19	55113901	55113922	55113918	55113923	+
SEQ ID NO 2427	GGCACCAGGGACTCCAGAGTCC	CTG	chr19	55113908	55113929	55113925	55113930	+
SEQ ID NO 2428	CAGAGTCCAGGCCCAACCCCTC	CTC	chr19	55113922	55113943	55113939	55113944	+
SEQ ID NO 2429	CCCATTCAACCCAGGAGGCCAG	CTC	chr19	55113944	55113965	55113961	55113966	+
SEQ ID NO 2430	AACCCAGGAGGCCAGGCCCCAG	TTC	chr19	55113951	55113972	55113968	55113973	+
SEQ ID NO 2431	CCGCCCTCAGATGAAGGAGTCC	CTT	chr19	55113978	55113999	55113995	55114000	+
SEQ ID NO 2432	CGCCCTCAGATGAAGGAGTCCA	TTC	chr19	55113979	55114000	55113996	55114001	+
SEQ ID NO 2433	AGATGAAGGAGTCCAGGCCCCC	CTC	chr19	55113986	55114007	55114003	55114008	+
SEQ ID NO 2434	TCCCCATTCAGACCCAGGGGTC	CTC	chr19	55114014	55114035	55114031	55114036	+
SEQ ID NO 2435	CCCATTCAGACCCAGGGGTCCA	CTC	chr19	55114016	55114037	55114033	55114038	+
SEQ ID NO 2436	AGACCCAGGGGTCCAGGCCCAG	TTC	chr19	55114023	55114044	55114040	55114045	+
SEQ ID NO 2437	CCTAAGACCCAGAAGTCCAGGC	CTC	chr19	55114054	55114075	55114071	55114076	+
SEQ ID NO 2438	AGACCCAGAAGTCCAGGCCCCC	CTA	chr19	55114058	55114079	55114075	55114080	+
SEQ ID NO 2439	CTCCCTCAGACCCACGAGTCCA	CTC	chr19	55114088	55114109	55114105	55114110	+
SEQ ID NO 2440	CCTCAGACCCACGAGTCCAGGC	CTC	chr19	55114091	55114112	55114108	55114113	+
SEQ ID NO 2441	AGACCCACGAGTCCAGGCCCCA	CTC	chr19	55114095	55114116	55114112	55114117	+
SEQ ID NO 2442	CTCCCTCGGACCCAGGAGTCCA	CTC	chr19	55114124	55114145	55114141	55114146	+
SEQ ID NO 2443	CCTCGGACCCAGGAGTCCAGGC	CTC	chr19	55114127	55114148	55114144	55114149	+
SEQ ID NO 2444	GGACCCAGGAGTCCAGGCCCCC	CTC	chr19	55114131	55114152	55114148	55114153	+
SEQ ID NO 2445	CACCCTCAGACCCAGGAGTCCA	CTC	chr19	55114161	55114182	55114178	55114183	+
SEQ ID NO 2446	AGACCCAGGAGTCCAGGCCCCA	CTC	chr19	55114168	55114189	55114185	55114190	+
SEQ ID NO 2447	CTCCCTCGGACCCAGGAGTCCA	CTC	chr19	55114197	55114218	55114214	55114219	+
SEQ ID NO 2448	CCTCGGACCCAGGAGTCCAGGC	CTC	chr19	55114200	55114221	55114217	55114222	+
SEQ ID NO 2449	GGACCCAGGAGTCCAGGCCCCA	CTC	chr19	55114204	55114225	55114221	55114226	+
SEQ ID NO 2450	CTCTCTCAAACCCAGGAGCCCA	CTC	chr19	55114233	55114254	55114250	55114255	+
SEQ ID NO 2451	TCTCAAACCCAGGAGCCCAGGC	CTC	chr19	55114236	55114257	55114253	55114258	+
SEQ ID NO 2452	TCAAACCCAGGAGCCCAGGCCC	CTC	chr19	55114238	55114259	55114255	55114260	+
SEQ ID NO 2453	AAACCCAGGAGCCCAGGCCCCC	CTC	chr19	55114240	55114261	55114257	55114262	+
SEQ ID NO 2454	TTCTCTGTTCAGCCCTAAGAAT	CTC	chr19	55114267	55114288	55114284	55114289	+
SEQ ID NO 2455	CTCTGTTCAGCCCTAAGAATCC	CTT	chr19	55114269	55114290	55114286	55114291	+
SEQ ID NO 2456	TCTGTTCAGCCCTAAGAATCCT	TTC	chr19	55114270	55114291	55114287	55114292	+
SEQ ID NO 2457	TGTTCAGCCCTAAGAATCCTGG	CTC	chr19	55114272	55114293	55114289	55114294	+
SEQ ID NO 2458	TTCAGCCCTAAGAATCCTGGCT	CTG	chr19	55114274	55114295	55114291	55114296	+
SEQ ID NO 2459	AGCCCTAAGAATCCTGGCTCCA	TTC	chr19	55114277	55114298	55114294	55114299	+
SEQ ID NO 2460	AGAATCCTGGCTCCAGCCCCTC	CTA	chr19	55114284	55114305	55114301	55114306	+
SEQ ID NO 2461	GCTCCAGCCCCTCCTACTCTAG	CTG	chr19	55114293	55114314	55114310	55114315	+
SEQ ID NO 2462	CAGCCCCTCCTACTCTAGCCCC	CTC	chr19	55114297	55114318	55114314	55114319	+
SEQ ID NO 2463	CTACTCTAGCCCCCAACCCCCT	CTC	chr19	55114306	55114327	55114323	55114328	+
SEQ ID NO 2464	CTCTAGCCCCCAACCCCCTAGC	CTA	chr19	55114309	55114330	55114326	55114331	+
SEQ ID NO 2465	TAGCCCCCAACCCCCTAGCCAC	CTC	chr19	55114312	55114333	55114329	55114334	+
SEQ ID NO 2466	GCCCCCAACCCCCTAGCCACTA	CTA	chr19	55114314	55114335	55114331	55114336	+
SEQ ID NO 2467	GCCACTAAGGCAATTGGGGTGC	CTA	chr19	55114329	55114350	55114346	55114351	+
SEQ ID NO 2468	AGGCAATTGGGGTGCAGGAATG	CTA	chr19	55114336	55114357	55114353	55114358	+
SEQ ID NO 2469	GGGTGCAGGAATGGGGGCAGGG	TTG	chr19	55114345	55114366	55114362	55114367	+
SEQ ID NO 2470	ACCAAGTGGTTGATAAACCCAC	CTC	chr19	55114377	55114398	55114394	55114399	+
SEQ ID NO 2471	ATAAACCCACGTGGGGTACCCT	TTG	chr19	55114389	55114410	55114406	55114411	+
SEQ ID NO 2472	AGAACTTGGGAACAGCCACAGC	CTA	chr19	55114412	55114433	55114429	55114434	+
SEQ ID NO 2473	GGGAACAGCCACAGCAGGGGGG	CTT	chr19	55114419	55114440	55114436	55114441	+
SEQ ID NO 2474	GGAACAGCCACAGCAGGGGGGC	TTG	chr19	55114420	55114441	55114437	55114442	+
SEQ ID NO 2475	GGGGACCTGCCTGGAGAAGGAT	CTT	chr19	55114449	55114470	55114466	55114471	+
SEQ ID NO 2476	GGGACCTGCCTGGAGAAGGATG	TTG	chr19	55114450	55114471	55114467	55114472	+
SEQ ID NO 2477	CCTGGAGAAGGATGCAGGACGA	CTG	chr19	55114458	55114479	55114475	55114480	+
SEQ ID NO 2478	GAGAAGGATGCAGGACGAGAAA	CTG	chr19	55114462	55114483	55114479	55114484	+
SEQ ID NO 2479	GCCGGGAATCAAGAGTCACCCA	CTG	chr19	55114507	55114528	55114524	55114529	+
SEQ ID NO 2480	TTTTCCTAGGACTGAGGGTTTC	CTG	chr19	55114552	55114573	55114569	55114574	+
SEQ ID NO 2481	TCCTAGGACTGAGGGTTTCAGT	TTT	chr19	55114555	55114576	55114572	55114577	+

SEQ ID NO 2482	CCTAGGACTGAGGGTTTCAGTG	TTT	chr19	55114556	55114577	55114573	55114578	+
SEQ ID NO 2483	CTAGGACTGAGGGTTTCAGTGC	TTC	chr19	55114557	55114578	55114574	55114579	+
SEQ ID NO 2484	GGACTGAGGGTTTCAGTGCTAA	CTA	chr19	55114560	55114581	55114577	55114582	+
SEQ ID NO 2485	AGGGTTTCAGTGCTAAAACTAG	CTG	chr19	55114566	55114587	55114583	55114588	+
SEQ ID NO 2486	CAGTGCTAAAACTAGGCTGTCC	TTT	chr19	55114573	55114594	55114590	55114595	+
SEQ ID NO 2487	AGTGCTAAAACTAGGCTGTCCT	TTC	chr19	55114574	55114595	55114591	55114596	+
SEQ ID NO 2488	AAACTAGGCTGTCCTGGGCAAA	CTA	chr19	55114581	55114602	55114598	55114603	+
SEQ ID NO 2489	GGCTGTCCTGGGCAAACAGCAT	CTA	chr19	55114587	55114608	55114604	55114609	+
SEQ ID NO 2490	TCCTGGGCAAACAGCATAAGCT	CTG	chr19	55114592	55114613	55114609	55114614	+
SEQ ID NO 2491	GGCAAACAGCATAAGCTGGTCA	CTG	chr19	55114597	55114618	55114614	55114619	+
SEQ ID NO 2492	GTCACCCCACACCCAGACCTGA	CTG	chr19	55114615	55114636	55114632	55114637	+
SEQ ID NO 2493	ACCCAAACCCAGCTCCCCTGCT	CTG	chr19	55114636	55114657	55114653	55114658	+
SEQ ID NO 2494	CCCTGCTTCTTGGCCACGTAAC	CTC	chr19	55114651	55114672	55114668	55114673	+
SEQ ID NO 2495	CTTCTTGGCCACGTAACCTGAG	CTG	chr19	55114656	55114677	55114673	55114678	+
SEQ ID NO 2496	CTTGGCCACGTAACCTGAGAAG	CTT	chr19	55114659	55114680	55114676	55114681	+
SEQ ID NO 2497	TTGGCCACGTAACCTGAGAAGG	TTC	chr19	55114660	55114681	55114677	55114682	+
SEQ ID NO 2498	GGCCACGTAACCTGAGAAGGGA	CTT	chr19	55114662	55114683	55114679	55114684	+
SEQ ID NO 2499	GCCACGTAACCTGAGAAGGGAA	TTG	chr19	55114663	55114684	55114680	55114685	+
SEQ ID NO 2500	AGAAGGGAATCCCTCCTCTCTG	CTG	chr19	55114676	55114697	55114693	55114698	+
SEQ ID NO 2501	CTCTCTGAACCCCAGCCCACCC	CTC	chr19	55114691	55114712	55114708	55114713	+
SEQ ID NO 2502	TCTGAACCCCAGCCCACCCCAA	CTC	chr19	55114694	55114715	55114711	55114716	+
SEQ ID NO 2503	TGAACCCCAGCCCACCCCAATG	CTC	chr19	55114696	55114717	55114713	55114718	+
SEQ ID NO 2504	AACCCCAGCCCACCCCAATGCT	CTG	chr19	55114698	55114719	55114715	55114720	+
SEQ ID NO 2505	CAGGCCTCCTGGGATACCCCGA	CTC	chr19	55114721	55114742	55114738	55114743	+
SEQ ID NO 2506	CTGGGATACCCCGAAGAGTGAG	CTC	chr19	55114729	55114750	55114746	55114751	+
SEQ ID NO 2507	GGATACCCCGAAGAGTGAGTTT	CTG	chr19	55114732	55114753	55114749	55114754	+
SEQ ID NO 2508	GCCAAGCAGTCACCCCACAGTT	TTT	chr19	55114754	55114775	55114771	55114776	+
SEQ ID NO 2509	CCAAGCAGTCACCCCACAGTTG	TTG	chr19	55114755	55114776	55114772	55114777	+
SEQ ID NO 2510	GAGGAGAATCCACCCAAAAGGC	TTG	chr19	55114777	55114798	55114794	55114799	+
SEQ ID NO 2511	GTAGACAGGGCTGGGGTGGCCT	CTG	chr19	55114805	55114826	55114822	55114827	+
SEQ ID NO 2512	GGGTGGCCTCTCGTGGGGTCCA	CTG	chr19	55114818	55114839	55114835	55114840	+
SEQ ID NO 2513	TCGTGGGGTCCAGGCCAAGTAG	CTC	chr19	55114828	55114849	55114845	55114850	+
SEQ ID NO 2514	GTGGGGTCCAGGCCAAGTAGGT	CTC	chr19	55114830	55114851	55114847	55114852	+
SEQ ID NO 2515	GGGCCTCTGGGGGATGCAGGGG	CTG	chr19	55114858	55114879	55114875	55114880	+
SEQ ID NO 2516	TGGGGGATGCAGGGGAAGGGGG	CTC	chr19	55114865	55114886	55114882	55114887	+
SEQ ID NO 2517	GGGGATGCAGGGGAAGGGGGAT	CTG	chr19	55114867	55114888	55114884	55114889	+
SEQ ID NO 2518	AGTCTGAAGAGCAGAGCCAGGA	CTC	chr19	55114922	55114943	55114939	55114944	+
SEQ ID NO 2519	AAGAGCAGAGCCAGGAACCCCT	CTG	chr19	55114928	55114949	55114945	55114950	+
SEQ ID NO 2520	TAGGGAAGGGGCAGGAGAGCCA	CTG	chr19	55114951	55114972	55114968	55114973	+
SEQ ID NO 2521	AGCGCCTCTCCTGGGCTTGCCA	CTG	chr19	55115016	55115037	55115033	55115038	+
SEQ ID NO 2522	TCCTGGGCTTGCCAAGGACTCA	CTC	chr19	55115024	55115045	55115041	55115046	+
SEQ ID NO 2523	CTGGGCTTGCCAAGGACTCAAA	CTC	chr19	55115026	55115047	55115043	55115048	+
SEQ ID NO 2524	GGCTTGCCAAGGACTCAAACCC	CTG	chr19	55115029	55115050	55115046	55115051	+
SEQ ID NO 2525	GCCAAGGACTCAAACCCAGAAG	CTT	chr19	55115034	55115055	55115051	55115056	+
SEQ ID NO 2526	CCAAGGACTCAAACCCAGAAGC	TTG	chr19	55115035	55115056	55115052	55115057	+
SEQ ID NO 2527	AAACCCAGAAGCCCAGAGCAGG	CTC	chr19	55115045	55115066	55115062	55115067	+
SEQ ID NO 2528	AGGGAAGCGGGACCCTGCTCTG	CTT	chr19	55115072	55115093	55115089	55115094	+
SEQ ID NO 2529	GGGAAGCGGGACCCTGCTCTGG	TTA	chr19	55115073	55115094	55115090	55115095	+
SEQ ID NO 2530	CTCTGGGCGGAGGAATATGTCC	CTG	chr19	55115089	55115110	55115106	55115111	+
SEQ ID NO 2531	TGGGCGGAGGAATATGTCCCAG	CTC	chr19	55115092	55115113	55115109	55115114	+
SEQ ID NO 2532	GGCGGAGGAATATGTCCCAGAT	CTG	chr19	55115094	55115115	55115111	55115116	+
SEQ ID NO 2533	GGGACTCTTTAAGGAAAGAAGG	CTG	chr19	55115123	55115144	55115140	55115145	+
SEQ ID NO 2534	TTTAAGGAAAGAAGGATGGAGA	CTC	chr19	55115130	55115151	55115147	55115152	+
SEQ ID NO 2535	TAAGGAAAGAAGGATGGAGAAA	CTT	chr19	55115132	55115153	55115149	55115154	+
SEQ ID NO 2536	AAGGAAAGAAGGATGGAGAAAG	TTT	chr19	55115133	55115154	55115150	55115155	+
SEQ ID NO 2537	AGGAAAGAAGGATGGAGAAAGA	TTA	chr19	55115134	55115155	55115151	55115156	+
SEQ ID NO 2538	GTGAACACCTAGGACGCACCAT	CTG	chr19	55115184	55115205	55115201	55115206	+
SEQ ID NO 2539	GGACGCACCATTCTCACAAAGG	CTA	chr19	55115195	55115216	55115212	55115217	+
SEQ ID NO 2540	TCACAAAGGGAGTTTTCCACAC	TTC	chr19	55115208	55115229	55115225	55115230	+

SEQ ID NO 2541	ACAAAGGGAGTTTTCCACACGG	CTC	chr19	55115210	55115231	55115227	55115232	+
SEQ ID NO 2542	TCCACACGGACACCCCCCTCCT	TTT	chr19	55115223	55115244	55115240	55115245	+
SEQ ID NO 2543	CCACACGGACACCCCCCTCCTC	TTT	chr19	55115224	55115245	55115241	55115246	+
SEQ ID NO 2544	CACACGGACACCCCCCTCCTCA	TTC	chr19	55115225	55115246	55115242	55115247	+
SEQ ID NO 2545	CTCACCACAGCCCTGCCAGGAC	CTC	chr19	55115243	55115264	55115260	55115265	+
SEQ ID NO 2546	ACCACAGCCCTGCCAGGACGGG	CTC	chr19	55115246	55115267	55115263	55115268	+
SEQ ID NO 2547	CCAGGACGGGGCTGGCTACTGG	CTG	chr19	55115258	55115279	55115275	55115280	+
SEQ ID NO 2548	GCTACTGGCCTTATCTCACAGG	CTG	chr19	55115272	55115293	55115289	55115294	+
SEQ ID NO 2549	CTGGCCTTATCTCACAGGTAAA	CTA	chr19	55115276	55115297	55115293	55115298	+
SEQ ID NO 2550	GCCTTATCTCACAGGTAAAACT	CTG	chr19	55115279	55115300	55115296	55115301	+
SEQ ID NO 2551	ATCTCACAGGTAAAACTGACGC	CTT	chr19	55115284	55115305	55115301	55115306	+
SEQ ID NO 2552	TCTCACAGGTAAAACTGACGCA	TTA	chr19	55115285	55115306	55115302	55115307	+
SEQ ID NO 2553	ACAGGTAAAACTGACGCACGGA	CTC	chr19	55115289	55115310	55115306	55115311	+
SEQ ID NO 2554	ACGCACGGAGGAACAATATAAA	CTG	chr19	55115302	55115323	55115319	55115324	+
SEQ ID NO 2555	GGGACTAGAAAGGTGAAGAGCC	TTG	chr19	55115327	55115348	55115344	55115349	+
SEQ ID NO 2556	GAAAGGTGAAGAGCCAAAGTTA	CTA	chr19	55115334	55115355	55115351	55115356	+
SEQ ID NO 2557	GAACTCAGGACCAACTTATTCT	TTA	chr19	55115356	55115377	55115373	55115378	+
SEQ ID NO 2558	AGGACCAACTTATTCTGATTTT	CTC	chr19	55115362	55115383	55115379	55115384	+
SEQ ID NO 2559	ATTCTGATTTTGTTTTTCCAAA	CTT	chr19	55115373	55115394	55115390	55115395	+
SEQ ID NO 2560	TTCTGATTTTGTTTTTCCAAAC	TTA	chr19	55115374	55115395	55115391	55115396	+
SEQ ID NO 2561	TGATTTTGTTTTTCCAAACTGC	TTC	chr19	55115377	55115398	55115394	55115399	+
SEQ ID NO 2562	ATTTTGTTTTTCCAAACTGCTT	CTG	chr19	55115379	55115400	55115396	55115401	+
SEQ ID NO 2563	TGTTTTTCCAAACTGCTTCTCC	TTT	chr19	55115383	55115404	55115400	55115405	+
SEQ ID NO 2564	GTTTTTCCAAACTGCTTCTCCT	TTT	chr19	55115384	55115405	55115401	55115406	+
SEQ ID NO 2565	TTTTTCCAAACTGCTTCTCCTC	TTG	chr19	55115385	55115406	55115402	55115407	+
SEQ ID NO 2566	TTCCAAACTGCTTCTCCTCTTG	TTT	chr19	55115388	55115409	55115405	55115410	+
SEQ ID NO 2567	TCCAAACTGCTTCTCCTCTTGG	TTT	chr19	55115389	55115410	55115406	55115411	+
SEQ ID NO 2568	CCAAACTGCTTCTCCTCTTGGG	TTT	chr19	55115390	55115411	55115407	55115412	+
SEQ ID NO 2569	CAAACTGCTTCTCCTCTTGGGA	TTC	chr19	55115391	55115412	55115408	55115413	+
SEQ ID NO 2570	CTTCTCCTCTTGGGAAGTGTAA	CTG	chr19	55115398	55115419	55115415	55115420	+
SEQ ID NO 2571	CTCCTCTTGGGAAGTGTAAGGA	CTT	chr19	55115401	55115422	55115418	55115423	+
SEQ ID NO 2572	TCCTCTTGGGAAGTGTAAGGAA	TTC	chr19	55115402	55115423	55115419	55115424	+
SEQ ID NO 2573	CTCTTGGGAAGTGTAAGGAAGC	CTC	chr19	55115404	55115425	55115421	55115426	+
SEQ ID NO 2574	TTGGGAAGTGTAAGGAAGCTGC	CTC	chr19	55115407	55115428	55115424	55115429	+
SEQ ID NO 2575	GGGAAGTGTAAGGAAGCTGCAG	CTT	chr19	55115409	55115430	55115426	55115431	+
SEQ ID NO 2576	GGAAGTGTAAGGAAGCTGCAGC	TTG	chr19	55115410	55115431	55115427	55115432	+
SEQ ID NO 2577	CAGCACCAGGATCAGTGAAACG	CTG	chr19	55115428	55115449	55115445	55115450	+
SEQ ID NO 2578	AGGTTCTGGGAGAGGGTAGCGC	CTC	chr19	55115477	55115498	55115494	55115499	+
SEQ ID NO 2579	TGGGAGAGGGTAGCGCAGGGTG	TTC	chr19	55115483	55115504	55115500	55115505	+
SEQ ID NO 2580	GGAGAGGGTAGCGCAGGGTGGC	CTG	chr19	55115485	55115506	55115502	55115507	+
SEQ ID NO 2581	AGAACCGGGCAGGTCACGCATC	CTG	chr19	55115512	55115533	55115529	55115534	+
SEQ ID NO 2582	CCCTCCCACCCCCTGCCAAGCT	CTT	chr19	55115542	55115563	55115559	55115564	+
SEQ ID NO 2583	CCTCCCACCCCCTGCCAAGCTC	TTC	chr19	55115543	55115564	55115560	55115565	+
SEQ ID NO 2584	CCACCCCCTGCCAAGCTCTCCC	CTC	chr19	55115547	55115568	55115564	55115569	+
SEQ ID NO 2585	CCAAGCTCTCCCTCCCAGGATC	CTG	chr19	55115557	55115578	55115574	55115579	+
SEQ ID NO 2586	TCCCTCCCAGGATCCTCTCTGG	CTC	chr19	55115565	55115586	55115582	55115587	+
SEQ ID NO 2587	CCTCCCAGGATCCTCTCTGGCT	CTC	chr19	55115567	55115588	55115584	55115589	+
SEQ ID NO 2588	CCAGGATCCTCTCTGGCTCCAT	CTC	chr19	55115571	55115592	55115588	55115593	+
SEQ ID NO 2589	TCTGGCTCCATCGTAAGCAAAC	CTC	chr19	55115582	55115603	55115599	55115604	+
SEQ ID NO 2590	TGGCTCCATCGTAAGCAAACCT	CTC	chr19	55115584	55115605	55115601	55115606	+
SEQ ID NO 2591	GCTCCATCGTAAGCAAACCTTA	CTG	chr19	55115586	55115607	55115603	55115608	+
SEQ ID NO 2592	CATCGTAAGCAAACCTTAGAGG	CTC	chr19	55115590	55115611	55115607	55115612	+
SEQ ID NO 2593	AGAGGTTCTGGCAAGGAGAGAG	CTT	chr19	55115607	55115628	55115624	55115629	+
SEQ ID NO 2594	GAGGTTCTGGCAAGGAGAGAGA	TTA	chr19	55115608	55115629	55115625	55115630	+
SEQ ID NO 2595	TGGCAAGGAGAGAGATGGCTCC	TTC	chr19	55115615	55115636	55115632	55115637	+
SEQ ID NO 2596	GCAAGGAGAGAGATGGCTCCAG	CTG	chr19	55115617	55115638	55115634	55115639	+
SEQ ID NO 2597	CAGGAAATGGGGGTGTGTCACC	CTC	chr19	55115636	55115657	55115653	55115658	+
SEQ ID NO 2598	CCTAACAGGAGGTGGGGGTTAG	CTG	chr19	55115672	55115693	55115689	55115694	+
SEQ ID NO 2599	ACAGGAGGTGGGGGTTAGACCC	CTA	chr19	55115676	55115697	55115693	55115698	+

SEQ ID NO 2600	GACCCAATATCAGGAGACTAGG	TTA	chr19	55115693	55115714	55115710	55115715	+
SEQ ID NO 2601	GGAAGGAGGAGGCCTAAGGATG	CTA	chr19	55115713	55115734	55115730	55115735	+
SEQ ID NO 2602	AGGATGGGGCTTTTCTGTCACC	CTA	chr19	55115729	55115750	55115746	55115751	+
SEQ ID NO 2603	TTCTGTCACCAATCCTGTCCCT	CTT	chr19	55115741	55115762	55115758	55115763	+
SEQ ID NO 2604	TCTGTCACCAATCCTGTCCCTA	TTT	chr19	55115742	55115763	55115759	55115764	+
SEQ ID NO 2605	CTGTCACCAATCCTGTCCCTAG	TTT	chr19	55115743	55115764	55115760	55115765	+
SEQ ID NO 2606	TGTCACCAATCCTGTCCCTAGT	TTC	chr19	55115744	55115765	55115761	55115766	+
SEQ ID NO 2607	TCACCAATCCTGTCCCTAGTGG	CTG	chr19	55115746	55115767	55115763	55115768	+
SEQ ID NO 2608	TCCCTAGTGGCCCCACTGTGGG	CTG	chr19	55115758	55115779	55115775	55115780	+
SEQ ID NO 2609	GTGGCCCCACTGTGGGGTGGAG	CTA	chr19	55115764	55115785	55115781	55115786	+
SEQ ID NO 2610	TGGGGTGGAGGGGACAGATAAA	CTG	chr19	55115776	55115797	55115793	55115798	+
SEQ ID NO 2611	ACCGGCCCTGGGAATATAAGGT	TTA	chr19	55115823	55115844	55115840	55115845	+
SEQ ID NO 2612	GGAATATAAGGTGGTCCCAGCT	CTG	chr19	55115833	55115854	55115850	55115855	+
SEQ ID NO 2613	GGGGACACAGGATCCCTGGAGG	CTC	chr19	55115856	55115877	55115873	55115878	+
SEQ ID NO 2614	GAGGCAGCAAACATGCTGTCCT	CTG	chr19	55115874	55115895	55115891	55115896	+
SEQ ID NO 2615	TCCTGAAGTGGACATAGGGGCC	CTG	chr19	55115892	55115913	55115909	55115914	+
SEQ ID NO 2616	AAGTGGACATAGGGGCCCGGGT	CTG	chr19	55115897	55115918	55115914	55115919	+
SEQ ID NO 2617	GAGGAAGAAGACTAGCTGAGCT	TTG	chr19	55115921	55115942	55115938	55115943	+
SEQ ID NO 2618	GCTGAGCTCTCGGACCCCTGGA	CTA	chr19	55115935	55115956	55115952	55115957	+
SEQ ID NO 2619	AGCTCTCGGACCCCTGGAAGAT	CTG	chr19	55115939	55115960	55115956	55115961	+
SEQ ID NO 2620	TCGGACCCCTGGAAGATGCCAT	CTC	chr19	55115944	55115965	55115961	55115966	+
SEQ ID NO 2621	GGACCCCTGGAAGATGCCATGA	CTC	chr19	55115946	55115967	55115963	55115968	+
SEQ ID NO 2622	GAAGATGCCATGACAGGGGGCT	CTG	chr19	55115955	55115976	55115972	55115977	+
SEQ ID NO 2623	GAAGAGCTAGCACAGACTAGAG	CTG	chr19	55115978	55115999	55115995	55116000	+
SEQ ID NO 2624	GCACAGACTAGAGAGGTAAGGG	CTA	chr19	55115987	55116008	55116004	55116009	+
SEQ ID NO 2625	GAGAGGTAAGGGGGGTAGGGGA	CTA	chr19	55115997	55116018	55116014	55116019	+
SEQ ID NO 2626	CCCAAATGAAAGGAGTGAGAGG	CTG	chr19	55116023	55116044	55116040	55116045	+
SEQ ID NO 2627	AAGCCAGGGAGACGGGGTACTT	CTA	chr19	55116110	55116131	55116127	55116132	+
SEQ ID NO 2628	TGGGGTTGTCCAGAAAAACGGT	CTT	chr19	55116132	55116153	55116149	55116154	+
SEQ ID NO 2629	GGGGTTGTCCAGAAAAACGGTG	TTT	chr19	55116133	55116154	55116150	55116155	+
SEQ ID NO 2630	GGGTTGTCCAGAAAAACGGTGA	TTG	chr19	55116134	55116155	55116151	55116156	+
SEQ ID NO 2631	TCCAGAAAAACGGTGATGATGC	TTG	chr19	55116140	55116161	55116157	55116162	+
SEQ ID NO 2632	CAAGAAGGGGAGGCGGGACGCA	CTA	chr19	55116169	55116190	55116186	55116191	+
SEQ ID NO 2633	AGAAACGAGAGATGGCACAGGC	CTA	chr19	55116222	55116243	55116239	55116244	+
SEQ ID NO 2634	GGTGAGGGAGGAGAGATGCCCG	TTG	chr19	55116296	55116317	55116313	55116318	+
SEQ ID NO 2635	AGAGGACATCACGTGGTGCAGC	CTC	chr19	55116349	55116370	55116366	55116371	+
SEQ ID NO 2636	CGGAAAGAGCATCCTTGGGCAG	CTC	chr19	55116389	55116410	55116406	55116411	+
SEQ ID NO 2637	GGGCAGCAACACAGCAGAGAGC	CTT	chr19	55116405	55116426	55116422	55116427	+
SEQ ID NO 2638	GGCAGCAACACAGCAGAGAGCA	TTG	chr19	55116406	55116427	55116423	55116428	+
SEQ ID NO 2639	AAGGAGGCGGCAGGGAAGGATC	CTG	chr19	55116461	55116482	55116478	55116483	+
SEQ ID NO 2640	GGCCAGCCGTAGAGGTGACCCA	CTG	chr19	55116485	55116506	55116502	55116507	+
SEQ ID NO 2641	CAGACAGAAAGCGGCACAGGCC	CTG	chr19	55116519	55116540	55116536	55116541	+
SEQ ID NO 2642	CCTGGGAAGGGGAAACAGTGGG	CTG	chr19	55116578	55116599	55116595	55116600	+
SEQ ID NO 2643	GGAAGGGGAAACAGTGGGCCAG	CTG	chr19	55116582	55116603	55116599	55116604	+
SEQ ID NO 2644	AAAGTGGTCCGGACTCAGGAGA	CTC	chr19	55116630	55116651	55116647	55116652	+
SEQ ID NO 2645	AGGAGAGAGACGGCAGCGTTAG	CTC	chr19	55116646	55116667	55116663	55116668	+
SEQ ID NO 2646	GAGGGCAGAGTTCCGGCGGCAC	TTA	chr19	55116667	55116688	55116684	55116689	+
SEQ ID NO 2647	CGGCGGCACAGCAAGGGCACTC	TTC	chr19	55116680	55116701	55116697	55116702	+
SEQ ID NO 2648	GGGGGCGAGAGGAGGGCAGCGC	CTC	chr19	55116702	55116723	55116719	55116724	+
SEQ ID NO 2649	AGCTATGGGAGCTGGCTCAGGT	CTG	chr19	55116764	55116785	55116781	55116786	+
SEQ ID NO 2650	TGGGAGCTGGCTCAGGTTCAGG	CTA	chr19	55116769	55116790	55116786	55116791	+
SEQ ID NO 2651	GCTCAGGTTCAGGAGAGGGCAG	CTG	chr19	55116778	55116799	55116795	55116800	+
SEQ ID NO 2652	AGGTTCAGGAGAGGGCAGGGCA	CTC	chr19	55116782	55116803	55116799	55116804	+
SEQ ID NO 2653	AGGAGAGGGCAGGGCAGGGAAG	TTC	chr19	55116788	55116809	55116805	55116810	+
SEQ ID NO 2654	GAGGGGCTCAACATCGGAAGAG	CTG	chr19	55116833	55116854	55116850	55116855	+
SEQ ID NO 2655	AACATCGGAAGAGGGGAAGTCG	CTC	chr19	55116842	55116863	55116859	55116864	+
SEQ ID NO 2656	CATGGGTCAGCACAGGCTGCCA	CTG	chr19	55116888	55116909	55116905	55116910	+
SEQ ID NO 2657	CCAAAGCCAGGGCCAGTTAAAG	CTG	chr19	55116907	55116928	55116924	55116929	+
SEQ ID NO 2658	AAGCGACTCCAATGCGGAAGAG	TTA	chr19	55116926	55116947	55116943	55116948	+

SEQ ID NO 2659	CAATGCGGAAGAGAGTAGGTCG	CTC	chr19	55116935	55116956	55116952	55116957	+
SEQ ID NO 2660	GGGCAGAGTGGTCAGCACAGAG	CTG	chr19	55116980	55117001	55116997	55117002	+
SEQ ID NO 2661	AGCCCAGGGCCAGTTGAAGCGG	CTA	chr19	55117008	55117029	55117025	55117030	+
SEQ ID NO 2662	AAGCGGCTCCAATTCGGAAGTG	TTG	chr19	55117024	55117045	55117041	55117046	+
SEQ ID NO 2663	CAATTCGGAAGTGGGGTGGTCG	CTC	chr19	55117033	55117054	55117050	55117055	+
SEQ ID NO 2664	GGAAGTGGGGTGGTCGAAGGGG	TTC	chr19	55117039	55117060	55117056	55117061	+
SEQ ID NO 2665	GGACGGGGTGTCAGCATAGGGT	CTG	chr19	55117078	55117099	55117095	55117100	+
SEQ ID NO 2666	GCAACGGGGAAGGAGGATGCCC	CTG	chr19	55117142	55117163	55117159	55117164	+
SEQ ID NO 2667	GCCCCGGGAGACGCCGGGCGGG	CTG	chr19	55117191	55117212	55117208	55117213	+
SEQ ID NO 2668	ACCTGGTGCAGGGCGCTGATAC	CTG	chr19	55117221	55117242	55117238	55117243	+
SEQ ID NO 2669	GTGCAGGGCGCTGATACCGTCG	CTG	chr19	55117226	55117247	55117243	55117248	+
SEQ ID NO 2670	ATACCGTCGGCGTTGGTGGAGT	CTG	chr19	55117239	55117260	55117256	55117261	+
SEQ ID NO 2671	GTGGAGTCCAGCACGGCGCGGG	TTG	chr19	55117254	55117275	55117271	55117276	+
SEQ ID NO 2672	GGCGCCGGGGCCAGGGTCGGCG	CTC	chr19	55117304	55117325	55117321	55117326	+
SEQ ID NO 2673	GTCCAGGTCGCCGCCCGCACAG	CTC	chr19	55117349	55117370	55117366	55117371	+
SEQ ID NO 2674	GGCGGCGCGCTCGAAGCGGACG	CTC	chr19	55117385	55117406	55117402	55117407	+
SEQ ID NO 2675	GAAGCGGACGGTGCGGGCGCGG	CTC	chr19	55117397	55117418	55117414	55117419	+
SEQ ID NO 2676	TCCGGGGCCAGGCTCGGCGCCC	CTC	chr19	55117424	55117445	55117441	55117446	+
SEQ ID NO 2677	CGGGGCCAGGCTCGGCGCCCGC	CTC	chr19	55117426	55117447	55117443	55117448	+
SEQ ID NO 2678	GGCGCCCGCCCGCGCCCCCCAC	CTC	chr19	55117439	55117460	55117456	55117461	+
SEQ ID NO 2679	CCGCAGCTGCTCCCGTCGCCGC	CTG	chr19	55117463	55117484	55117480	55117485	+
SEQ ID NO 2680	CTCCCGTCGCCGCTCCCGGGCA	CTG	chr19	55117472	55117493	55117489	55117494	+
SEQ ID NO 2681	CCGTCGCCGCTCCCGGGCAGCC	CTC	chr19	55117475	55117496	55117492	55117497	+
SEQ ID NO 2682	CCGGGCAGCCGCCGCCGCCGCC	CTC	chr19	55117487	55117508	55117504	55117509	+
SEQ ID NO 2683	TCCGGACATCGCACCGCCCGCC	CTC	chr19	55117535	55117556	55117552	55117557	+
SEQ ID NO 2684	CGGACATCGCACCGCCCGCCCG	CTC	chr19	55117537	55117558	55117554	55117559	+
SEQ ID NO 2685	GGGCTCGGCGCTCGCTCGCTCG	TTG	chr19	55117564	55117585	55117569	55117564	-
SEQ ID NO 2686	GGCGCTCGCTCGCTCGCTGGGC	CTC	chr19	55117558	55117579	55117563	55117558	-
SEQ ID NO 2687	GCTCGCTCGCTGGGCGGGCGGG	CTC	chr19	55117551	55117572	55117556	55117551	-
SEQ ID NO 2688	GCTCGCTGGGCGGGCGGGCGGT	CTC	chr19	55117547	55117568	55117552	55117547	-
SEQ ID NO 2689	GCTGGGCGGGCGGGCGGTGCGA	CTC	chr19	55117543	55117564	55117548	55117543	-
SEQ ID NO 2690	GGCGGGCGGGCGGTGCGATGTC	CTG	chr19	55117539	55117560	55117544	55117539	-
SEQ ID NO 2691	GCCCGGGGGCGGCGGCGGCGGC	CTG	chr19	55117494	55117515	55117499	55117494	-
SEQ ID NO 2692	CCCGGGAGCGGCGACGGGAGCA	CTG	chr19	55117470	55117491	55117475	55117470	-
SEQ ID NO 2693	CGGCAGTGGGGGGCGCGGGCGG	CTG	chr19	55117444	55117465	55117449	55117444	-
SEQ ID NO 2694	GCCCCGGAGAGCGCCGCGCCCG	CTG	chr19	55117410	55117431	55117415	55117410	-
SEQ ID NO 2695	CGAGCGCGCCGCCGAGTTCCTG	CTT	chr19	55117376	55117397	55117381	55117376	-
SEQ ID NO 2696	GAGCGCGCCGCCGAGTTCCTGG	TTC	chr19	55117375	55117396	55117380	55117375	-
SEQ ID NO 2697	CTGGCGGCCTGTGCGGGCGGCG	TTC	chr19	55117357	55117378	55117362	55117357	-
SEQ ID NO 2698	GCGGCCTGTGCGGGCGGCGACC	CTG	chr19	55117354	55117375	55117359	55117354	-
SEQ ID NO 2699	TGCGGGCGGCGACCTGGACGAG	CTG	chr19	55117346	55117367	55117351	55117346	-
SEQ ID NO 2700	GACGAGGCGCGTCTGATGCTGC	CTG	chr19	55117330	55117351	55117335	55117330	-
SEQ ID NO 2701	ATGCTGCGCGCCGCCGACCCTG	CTG	chr19	55117315	55117336	55117320	55117315	-
SEQ ID NO 2702	CGCGCCGCCGACCCTGGCCCCG	CTG	chr19	55117309	55117330	55117314	55117309	-
SEQ ID NO 2703	GCCCCGGCGCCGAGCTCGACCC	CTG	chr19	55117293	55117314	55117298	55117293	-
SEQ ID NO 2704	GACCCCGCCGCGCCGCCGCCCG	CTC	chr19	55117276	55117297	55117281	55117276	-
SEQ ID NO 2705	GACTCCACCAACGCCGACGGTA	CTG	chr19	55117240	55117261	55117245	55117240	-
SEQ ID NO 2706	CACCAACGCCGACGGTATCAGC	CTC	chr19	55117235	55117256	55117240	55117235	-
SEQ ID NO 2707	CACCAGGTCAGCGCCCCCCGCC	CTG	chr19	55117207	55117228	55117212	55117207	-
SEQ ID NO 2708	CCGGGGCCAGGTCCACCCTCTG	CTC	chr19	55117176	55117197	55117181	55117176	-
SEQ ID NO 2709	TGCTGCGCCACCTGGGGCATCC	CTC	chr19	55117156	55117177	55117161	55117156	-
SEQ ID NO 2710	CTGCGCCACCTGGGGCATCCTC	CTG	chr19	55117154	55117175	55117159	55117154	-
SEQ ID NO 2711	CGCCACCTGGGGCATCCTCCTT	CTG	chr19	55117151	55117172	55117156	55117151	-
SEQ ID NO 2712	GGGCATCCTCCTTCCCCGTTGC	CTG	chr19	55117142	55117163	55117147	55117142	-
SEQ ID NO 2713	CTTCCCCGTTGCCAGTCTCGAT	CTC	chr19	55117132	55117153	55117137	55117132	-
SEQ ID NO 2714	CCCCGTTGCCAGTCTCGATCCG	CTT	chr19	55117129	55117150	55117134	55117129	-
SEQ ID NO 2715	CCCGTTGCCAGTCTCGATCCGC	TTC	chr19	55117128	55117149	55117133	55117128	-
SEQ ID NO 2716	CCAGTCTCGATCCGCCCCGTCG	TTG	chr19	55117121	55117142	55117126	55117121	-
SEQ ID NO 2717	GATCCGCCCCGTCGTTCCTGGC	CTC	chr19	55117113	55117134	55117118	55117113	-

SEQ ID NO 2718	CTGGCCCTGGGCTTTGCCACCC	TTC	chr19	55117096	55117117	55117101	55117096	-
SEQ ID NO 2719	GCCCTGGGCTTTGCCACCCTAT	CTG	chr19	55117093	55117114	55117098	55117093	-
SEQ ID NO 2720	GGCTTTGCCACCCTATGCTGAC	CTG	chr19	55117087	55117108	55117092	55117087	-
SEQ ID NO 2721	TGCCACCCTATGCTGACACCCC	CTT	chr19	55117082	55117103	55117087	55117082	-
SEQ ID NO 2722	GCCACCCTATGCTGACACCCCG	TTT	chr19	55117081	55117102	55117086	55117081	-
SEQ ID NO 2723	CCACCCTATGCTGACACCCCGT	TTG	chr19	55117080	55117101	55117085	55117080	-
SEQ ID NO 2724	TGCTGACACCCCGTCCCAGTCC	CTA	chr19	55117072	55117093	55117077	55117072	-
SEQ ID NO 2725	ACACCCCGTCCCAGTCCCCCTT	CTG	chr19	55117067	55117088	55117072	55117067	-
SEQ ID NO 2726	ACCATTCCCCTTCGACCACCCC	CTT	chr19	55117045	55117066	55117050	55117045	-
SEQ ID NO 2727	CCATTCCCCTTCGACCACCCCA	TTA	chr19	55117044	55117065	55117049	55117044	-
SEQ ID NO 2728	CCCTTCGACCACCCCACTTCCG	TTC	chr19	55117038	55117059	55117043	55117038	-
SEQ ID NO 2729	CGACCACCCCACTTCCGAATTG	CTT	chr19	55117033	55117054	55117038	55117033	-
SEQ ID NO 2730	GACCACCCCACTTCCGAATTGG	TTC	chr19	55117032	55117053	55117037	55117032	-
SEQ ID NO 2731	CCGAATTGGAGCCGCTTCAACT	CTT	chr19	55117019	55117040	55117024	55117019	-
SEQ ID NO 2732	CGAATTGGAGCCGCTTCAACTG	TTC	chr19	55117018	55117039	55117023	55117018	-
SEQ ID NO 2733	GAGCCGCTTCAACTGGCCCTGG	TTG	chr19	55117011	55117032	55117016	55117011	-
SEQ ID NO 2734	CAACTGGCCCTGGGCTTAGCCA	CTT	chr19	55117002	55117023	55117007	55117002	-
SEQ ID NO 2735	AACTGGCCCTGGGCTTAGCCAC	TTC	chr19	55117001	55117022	55117006	55117001	-
SEQ ID NO 2736	GCCCTGGGCTTAGCCACTCTGT	CTG	chr19	55116996	55117017	55117001	55116996	-
SEQ ID NO 2737	GGCTTAGCCACTCTGTGCTGAC	CTG	chr19	55116990	55117011	55116995	55116990	-
SEQ ID NO 2738	AGCCACTCTGTGCTGACCACTC	CTT	chr19	55116985	55117006	55116990	55116985	-
SEQ ID NO 2739	GCCACTCTGTGCTGACCACTCT	TTA	chr19	55116984	55117005	55116989	55116984	-
SEQ ID NO 2740	TGTGCTGACCACTCTGCCCCAG	CTC	chr19	55116977	55116998	55116982	55116977	-
SEQ ID NO 2741	TGCTGACCACTCTGCCCCAGGC	CTG	chr19	55116975	55116996	55116980	55116975	-
SEQ ID NO 2742	ACCACTCTGCCCCAGGCCTCCT	CTG	chr19	55116970	55116991	55116975	55116970	-
SEQ ID NO 2743	TGCCCCAGGCCTCCTTACCATT	CTC	chr19	55116963	55116984	55116968	55116963	-
SEQ ID NO 2744	CCCCAGGCCTCCTTACCATTCC	CTG	chr19	55116961	55116982	55116966	55116961	-
SEQ ID NO 2745	CTTACCATTCCCCTTCGACCTA	CTC	chr19	55116950	55116971	55116955	55116950	-
SEQ ID NO 2746	ACCATTCCCCTTCGACCTACTC	CTT	chr19	55116947	55116968	55116952	55116947	-
SEQ ID NO 2747	CCATTCCCCTTCGACCTACTCT	TTA	chr19	55116946	55116967	55116951	55116946	-
SEQ ID NO 2748	CCCTTCGACCTACTCTCTTCCG	TTC	chr19	55116940	55116961	55116945	55116940	-
SEQ ID NO 2749	CGACCTACTCTCTTCCGCATTG	CTT	chr19	55116935	55116956	55116940	55116935	-
SEQ ID NO 2750	GACCTACTCTCTTCCGCATTGG	TTC	chr19	55116934	55116955	55116939	55116934	-
SEQ ID NO 2751	CTCTCTTCCGCATTGGAGTCGC	CTA	chr19	55116928	55116949	55116933	55116928	-
SEQ ID NO 2752	TCTTCCGCATTGGAGTCGCTTT	CTC	chr19	55116925	55116946	55116930	55116925	-
SEQ ID NO 2753	TTCCGCATTGGAGTCGCTTTAA	CTC	chr19	55116923	55116944	55116928	55116923	-
SEQ ID NO 2754	CCGCATTGGAGTCGCTTTAACT	CTT	chr19	55116921	55116942	55116926	55116921	-
SEQ ID NO 2755	CGCATTGGAGTCGCTTTAACTG	TTC	chr19	55116920	55116941	55116925	55116920	-
SEQ ID NO 2756	GAGTCGCTTTAACTGGCCCTGG	TTG	chr19	55116913	55116934	55116918	55116913	-
SEQ ID NO 2757	TAACTGGCCCTGGCTTTGGCAG	CTT	chr19	55116904	55116925	55116909	55116904	-
SEQ ID NO 2758	AACTGGCCCTGGCTTTGGCAGC	TTT	chr19	55116903	55116924	55116908	55116903	-
SEQ ID NO 2759	ACTGGCCCTGGCTTTGGCAGCC	TTA	chr19	55116902	55116923	55116907	55116902	-
SEQ ID NO 2760	GCCCTGGCTTTGGCAGCCTGTG	CTG	chr19	55116898	55116919	55116903	55116898	-
SEQ ID NO 2761	GCTTTGGCAGCCTGTGCTGACC	CTG	chr19	55116892	55116913	55116897	55116892	-
SEQ ID NO 2762	TGGCAGCCTGTGCTGACCCATG	CTT	chr19	55116888	55116909	55116893	55116888	-
SEQ ID NO 2763	GGCAGCCTGTGCTGACCCATGC	TTT	chr19	55116887	55116908	55116892	55116887	-
SEQ ID NO 2764	GCAGCCTGTGCTGACCCATGCA	TTG	chr19	55116886	55116907	55116891	55116886	-
SEQ ID NO 2765	TGCTGACCCATGCAGTCCTCCT	CTG	chr19	55116878	55116899	55116883	55116878	-
SEQ ID NO 2766	ACCCATGCAGTCCTCCTTACCA	CTG	chr19	55116873	55116894	55116878	55116873	-
SEQ ID NO 2767	CTTACCATCCCTCCCTCGACTT	CTC	chr19	55116858	55116879	55116863	55116858	-
SEQ ID NO 2768	ACCATCCCTCCCTCGACTTCCC	CTT	chr19	55116855	55116876	55116860	55116855	-
SEQ ID NO 2769	CCATCCCTCCCTCGACTTCCCC	TTA	chr19	55116854	55116875	55116859	55116854	-
SEQ ID NO 2770	CCTCGACTTCCCCTCTTCCGAT	CTC	chr19	55116845	55116866	55116850	55116845	-
SEQ ID NO 2771	GACTTCCCCTCTTCCGATGTTG	CTC	chr19	55116841	55116862	55116846	55116841	-
SEQ ID NO 2772	CCCCTCTTCCGATGTTGAGCCC	CTT	chr19	55116836	55116857	55116841	55116836	-
SEQ ID NO 2773	CCCTCTTCCGATGTTGAGCCCC	TTC	chr19	55116835	55116856	55116840	55116835	-
SEQ ID NO 2774	TTCCGATGTTGAGCCCCTCCAG	CTC	chr19	55116830	55116851	55116835	55116830	-
SEQ ID NO 2775	CCGATGTTGAGCCCCTCCAGCC	CTT	chr19	55116828	55116849	55116833	55116828	-
SEQ ID NO 2776	CGATGTTGAGCCCCTCCAGCCG	TTC	chr19	55116827	55116848	55116832	55116827	-

SEQ ID NO 2777	AGCCCCTCCAGCCGGTCCTGGA	TTG	chr19	55116819	55116840	55116824	55116819	-
SEQ ID NO 2778	CAGCCGGTCCTGGACTTTGTCT	CTC	chr19	55116811	55116832	55116816	55116811	-
SEQ ID NO 2779	GACTTTGTCTCCTTCCCTGCCC	CTG	chr19	55116799	55116820	55116804	55116799	-
SEQ ID NO 2780	TGTCTCCTTCCCTGCCCTGCCC	CTT	chr19	55116794	55116815	55116799	55116794	-
SEQ ID NO 2781	GTCTCCTTCCCTGCCCTGCCCT	TTT	chr19	55116793	55116814	55116798	55116793	-
SEQ ID NO 2782	TCTCCTTCCCTGCCCTGCCCTC	TTG	chr19	55116792	55116813	55116797	55116792	-
SEQ ID NO 2783	CTTCCCTGCCCTGCCCTCTCCT	CTC	chr19	55116788	55116809	55116793	55116788	-
SEQ ID NO 2784	CCCTGCCCTGCCCTCTCCTGAA	CTT	chr19	55116785	55116806	55116790	55116785	-
SEQ ID NO 2785	CCTGCCCTGCCCTCTCCTGAAC	TTC	chr19	55116784	55116805	55116789	55116784	-
SEQ ID NO 2786	CCCTGCCCTCTCCTGAACCTGA	CTG	chr19	55116780	55116801	55116785	55116780	-
SEQ ID NO 2787	CCCTCTCCTGAACCTGAGCCAG	CTG	chr19	55116775	55116796	55116780	55116775	-
SEQ ID NO 2788	TCCTGAACCTGAGCCAGCTCCC	CTC	chr19	55116770	55116791	55116775	55116770	-
SEQ ID NO 2789	CTGAACCTGAGCCAGCTCCCAT	CTC	chr19	55116768	55116789	55116773	55116768	-
SEQ ID NO 2790	AACCTGAGCCAGCTCCCATAGC	CTG	chr19	55116765	55116786	55116770	55116765	-
SEQ ID NO 2791	AGCCAGCTCCCATAGCTCAGTC	CTG	chr19	55116759	55116780	55116764	55116759	-
SEQ ID NO 2792	CCATAGCTCAGTCTGGTCTATC	CTC	chr19	55116750	55116771	55116755	55116750	-
SEQ ID NO 2793	AGTCTGGTCTATCTGCCTGGCC	CTC	chr19	55116741	55116762	55116746	55116741	-
SEQ ID NO 2794	GTCTATCTGCCTGGCCCTGGCC	CTG	chr19	55116735	55116756	55116740	55116735	-
SEQ ID NO 2795	TCTGCCTGGCCCTGGCCATTGT	CTA	chr19	55116730	55116751	55116735	55116730	-
SEQ ID NO 2796	CCTGGCCCTGGCCATTGTCACT	CTG	chr19	55116726	55116747	55116731	55116726	-
SEQ ID NO 2797	GCCCTGGCCATTGTCACTTTGC	CTG	chr19	55116722	55116743	55116727	55116722	-
SEQ ID NO 2798	GCCATTGTCACTTTGCGCTGCC	CTG	chr19	55116716	55116737	55116721	55116716	-
SEQ ID NO 2799	TCACTTTGCGCTGCCCTCCTCT	TTG	chr19	55116709	55116730	55116714	55116709	-
SEQ ID NO 2800	TGCGCTGCCCTCCTCTCGCCCC	CTT	chr19	55116703	55116724	55116708	55116703	-
SEQ ID NO 2801	GCGCTGCCCTCCTCTCGCCCCC	TTT	chr19	55116702	55116723	55116707	55116702	-
SEQ ID NO 2802	CGCTGCCCTCCTCTCGCCCCCG	TTG	chr19	55116701	55116722	55116706	55116701	-
SEQ ID NO 2803	CCCTCCTCTCGCCCCCGAGTGC	CTG	chr19	55116696	55116717	55116701	55116696	-
SEQ ID NO 2804	CTCTCGCCCCCGAGTGCCCTTG	CTC	chr19	55116691	55116712	55116696	55116691	-
SEQ ID NO 2805	TCGCCCCCGAGTGCCCTTGCTG	CTC	chr19	55116688	55116709	55116693	55116688	-
SEQ ID NO 2806	GCCCCCGAGTGCCCTTGCTGTG	CTC	chr19	55116686	55116707	55116691	55116686	-
SEQ ID NO 2807	GCTGTGCCGCCGGAACTCTGCC	CTT	chr19	55116670	55116691	55116675	55116670	-
SEQ ID NO 2808	CTGTGCCGCCGGAACTCTGCCC	TTG	chr19	55116669	55116690	55116674	55116669	-
SEQ ID NO 2809	TGCCGCCGGAACTCTGCCCTCT	CTG	chr19	55116666	55116687	55116671	55116666	-
SEQ ID NO 2810	TGCCCTCTAACGCTGCCGTCTC	CTC	chr19	55116652	55116673	55116657	55116652	-
SEQ ID NO 2811	CCCTCTAACGCTGCCGTCTCTC	CTG	chr19	55116650	55116671	55116655	55116650	-
SEQ ID NO 2812	TAACGCTGCCGTCTCTCTCCTG	CTC	chr19	55116645	55116666	55116650	55116645	-
SEQ ID NO 2813	ACGCTGCCGTCTCTCTCCTGAG	CTA	chr19	55116643	55116664	55116648	55116643	-
SEQ ID NO 2814	CCGTCTCTCTCCTGAGTCCGGA	CTG	chr19	55116637	55116658	55116642	55116637	-
SEQ ID NO 2815	TCTCCTGAGTCCGGACCACTTT	CTC	chr19	55116630	55116651	55116635	55116630	-
SEQ ID NO 2816	TCCTGAGTCCGGACCACTTTGA	CTC	chr19	55116628	55116649	55116633	55116628	-
SEQ ID NO 2817	CTGAGTCCGGACCACTTTGAGC	CTC	chr19	55116626	55116647	55116631	55116626	-
SEQ ID NO 2818	AGTCCGGACCACTTTGAGCTCT	CTG	chr19	55116623	55116644	55116628	55116623	-
SEQ ID NO 2819	TGAGCTCTACTGGCTTCTGCGC	CTT	chr19	55116609	55116630	55116614	55116609	-
SEQ ID NO 2820	GAGCTCTACTGGCTTCTGCGCC	TTT	chr19	55116608	55116629	55116613	55116608	-
SEQ ID NO 2821	AGCTCTACTGGCTTCTGCGCCG	TTG	chr19	55116607	55116628	55116612	55116607	-
SEQ ID NO 2822	TACTGGCTTCTGCGCCGCCTCT	CTC	chr19	55116602	55116623	55116607	55116602	-
SEQ ID NO 2823	CTGGCTTCTGCGCCGCCTCTGG	CTA	chr19	55116600	55116621	55116605	55116600	-
SEQ ID NO 2824	GCTTCTGCGCCGCCTCTGGCCC	CTG	chr19	55116597	55116618	55116602	55116597	-
SEQ ID NO 2825	CTGCGCCGCCTCTGGCCCACTG	CTT	chr19	55116593	55116614	55116598	55116593	-
SEQ ID NO 2826	TGCGCCGCCTCTGGCCCACTGT	TTC	chr19	55116592	55116613	55116597	55116592	-
SEQ ID NO 2827	CGCCGCCTCTGGCCCACTGTTT	CTG	chr19	55116590	55116611	55116595	55116590	-
SEQ ID NO 2828	TGGCCCACTGTTTCCCCTTCCC	CTC	chr19	55116581	55116602	55116586	55116581	-
SEQ ID NO 2829	GCCCACTGTTTCCCCTTCCCAG	CTG	chr19	55116579	55116600	55116584	55116579	-
SEQ ID NO 2830	TTTCCCCTTCCCAGGCAGGTCC	CTG	chr19	55116571	55116592	55116576	55116571	-
SEQ ID NO 2831	CCCCTTCCCAGGCAGGTCCTGC	TTT	chr19	55116568	55116589	55116573	55116568	-
SEQ ID NO 2832	CCCTTCCCAGGCAGGTCCTGCT	TTC	chr19	55116567	55116588	55116572	55116567	-
SEQ ID NO 2833	CCCAGGCAGGTCCTGCTTTCTC	CTT	chr19	55116562	55116583	55116567	55116562	-
SEQ ID NO 2834	CCAGGCAGGTCCTGCTTTCTCT	TTC	chr19	55116561	55116582	55116566	55116561	-
SEQ ID NO 2835	CTTTCTCTGACCTGCATTCTCT	CTG	chr19	55116547	55116568	55116552	55116547	-

SEQ ID NO 2836	TCTCTGACCTGCATTCTCTCCC	CTT	chr19	55116544	55116565	55116549	55116544	-
SEQ ID NO 2837	CTCTGACCTGCATTCTCTCCCC	TTT	chr19	55116543	55116564	55116548	55116543	-
SEQ ID NO 2838	TCTGACCTGCATTCTCTCCCCT	TTC	chr19	55116542	55116563	55116547	55116542	-
SEQ ID NO 2839	TGACCTGCATTCTCTCCCCTGG	CTC	chr19	55116540	55116561	55116545	55116540	-
SEQ ID NO 2840	ACCTGCATTCTCTCCCCTGGGC	CTG	chr19	55116538	55116559	55116543	55116538	-
SEQ ID NO 2841	CATTCTCTCCCCTGGGCCTGTG	CTG	chr19	55116533	55116554	55116538	55116533	-
SEQ ID NO 2842	TCTCCCCTGGGCCTGTGCCGCT	TTC	chr19	55116528	55116549	55116533	55116528	-
SEQ ID NO 2843	TCCCCTGGGCCTGTGCCGCTTT	CTC	chr19	55116526	55116547	55116531	55116526	-
SEQ ID NO 2844	CCCTGGGCCTGTGCCGCTTTCT	CTC	chr19	55116524	55116545	55116529	55116524	-
SEQ ID NO 2845	GGCCTGTGCCGCTTTCTGTCTG	CTG	chr19	55116519	55116540	55116524	55116519	-
SEQ ID NO 2846	TGCCGCTTTCTGTCTGCAGCTT	CTG	chr19	55116513	55116534	55116518	55116513	-
SEQ ID NO 2847	TCTGTCTGCAGCTTGTGGCCTG	CTT	chr19	55116505	55116526	55116510	55116505	-
SEQ ID NO 2848	CTGTCTGCAGCTTGTGGCCTGG	TTT	chr19	55116504	55116525	55116509	55116504	-
SEQ ID NO 2849	TGTCTGCAGCTTGTGGCCTGGG	TTC	chr19	55116503	55116524	55116508	55116503	-
SEQ ID NO 2850	TCTGCAGCTTGTGGCCTGGGTC	CTG	chr19	55116501	55116522	55116506	55116501	-
SEQ ID NO 2851	CAGCTTGTGGCCTGGGTCACCT	CTG	chr19	55116497	55116518	55116502	55116497	-
SEQ ID NO 2852	GTGGCCTGGGTCACCTCTACGG	CTT	chr19	55116491	55116512	55116496	55116491	-
SEQ ID NO 2853	TGGCCTGGGTCACCTCTACGGC	TTG	chr19	55116490	55116511	55116495	55116490	-
SEQ ID NO 2854	GGTCACCTCTACGGCTGGCCCA	CTG	chr19	55116483	55116504	55116488	55116483	-
SEQ ID NO 2855	TACGGCTGGCCCAGATCCTTCC	CTC	chr19	55116474	55116495	55116479	55116474	-
SEQ ID NO 2856	CGGCTGGCCCAGATCCTTCCCT	CTA	chr19	55116472	55116493	55116477	55116472	-
SEQ ID NO 2857	GCCCAGATCCTTCCCTGCCGCC	CTG	chr19	55116466	55116487	55116471	55116466	-
SEQ ID NO 2858	CCCTGCCGCCTCCTTCAGGTTC	CTT	chr19	55116454	55116475	55116459	55116454	-
SEQ ID NO 2859	CCTGCCGCCTCCTTCAGGTTCC	TTC	chr19	55116453	55116474	55116458	55116453	-
SEQ ID NO 2860	CCGCCTCCTTCAGGTTCCGTCT	CTG	chr19	55116449	55116470	55116454	55116449	-
SEQ ID NO 2861	CTTCAGGTTCCGTCTTCCTCCA	CTC	chr19	55116442	55116463	55116447	55116442	-
SEQ ID NO 2862	CAGGTTCCGTCTTCCTCCACTC	CTT	chr19	55116439	55116460	55116444	55116439	-
SEQ ID NO 2863	AGGTTCCGTCTTCCTCCACTCC	TTC	chr19	55116438	55116459	55116443	55116438	-
SEQ ID NO 2864	CGTCTTCCTCCACTCCCTCTTC	TTC	chr19	55116432	55116453	55116437	55116432	-
SEQ ID NO 2865	CCTCCACTCCCTCTTCCCCTTG	CTT	chr19	55116426	55116447	55116431	55116426	-
SEQ ID NO 2866	CTCCACTCCCTCTTCCCCTTGC	TTC	chr19	55116425	55116446	55116430	55116425	-
SEQ ID NO 2867	CACTCCCTCTTCCCCTTGCTCT	CTC	chr19	55116422	55116443	55116427	55116422	-
SEQ ID NO 2868	CCTCTTCCCCTTGCTCTCTGCT	CTC	chr19	55116417	55116438	55116422	55116417	-
SEQ ID NO 2869	TTCCCCTTGCTCTCTGCTGTGT	CTC	chr19	55116413	55116434	55116418	55116413	-
SEQ ID NO 2870	CCCCTTGCTCTCTGCTGTGTTG	CTT	chr19	55116411	55116432	55116416	55116411	-
SEQ ID NO 2871	CCCTTGCTCTCTGCTGTGTTGC	TTC	chr19	55116410	55116431	55116415	55116410	-
SEQ ID NO 2872	GCTCTCTGCTGTGTTGCTGCCC	CTT	chr19	55116405	55116426	55116410	55116405	-
SEQ ID NO 2873	CTCTCTGCTGTGTTGCTGCCCA	TTG	chr19	55116404	55116425	55116409	55116404	-
SEQ ID NO 2874	TCTGCTGTGTTGCTGCCCAAGG	CTC	chr19	55116401	55116422	55116406	55116401	-
SEQ ID NO 2875	TGCTGTGTTGCTGCCCAAGGAT	CTC	chr19	55116399	55116420	55116404	55116399	-
SEQ ID NO 2876	CTGTGTTGCTGCCCAAGGATGC	CTG	chr19	55116397	55116418	55116402	55116397	-
SEQ ID NO 2877	TGTTGCTGCCCAAGGATGCTCT	CTG	chr19	55116394	55116415	55116399	55116394	-
SEQ ID NO 2878	CTGCCCAAGGATGCTCTTTCCG	TTG	chr19	55116389	55116410	55116394	55116389	-
SEQ ID NO 2879	CCCAAGGATGCTCTTTCCGGAG	CTG	chr19	55116386	55116407	55116391	55116386	-
SEQ ID NO 2880	TTTCCGGAGCACTTCCTTCTCG	CTC	chr19	55116373	55116394	55116378	55116373	-
SEQ ID NO 2881	TCCGGAGCACTTCCTTCTCGGC	CTT	chr19	55116371	55116392	55116376	55116371	-
SEQ ID NO 2882	CCGGAGCACTTCCTTCTCGGCG	TTT	chr19	55116370	55116391	55116375	55116370	-
SEQ ID NO 2883	CGGAGCACTTCCTTCTCGGCGC	TTC	chr19	55116369	55116390	55116374	55116369	-
SEQ ID NO 2884	CCTTCTCGGCGCTGCACCACGT	CTT	chr19	55116359	55116380	55116364	55116359	-
SEQ ID NO 2885	CTTCTCGGCGCTGCACCACGTG	TTC	chr19	55116358	55116379	55116363	55116358	-
SEQ ID NO 2886	CTCGGCGCTGCACCACGTGATG	CTT	chr19	55116355	55116376	55116360	55116355	-
SEQ ID NO 2887	TCGGCGCTGCACCACGTGATGT	TTC	chr19	55116354	55116375	55116359	55116354	-
SEQ ID NO 2888	GGCGCTGCACCACGTGATGTCC	CTC	chr19	55116352	55116373	55116357	55116352	-
SEQ ID NO 2889	CACCACGTGATGTCCTCTGAGC	CTG	chr19	55116345	55116366	55116350	55116345	-
SEQ ID NO 2890	TGAGCGGATCCTCCCCGTGTCT	CTC	chr19	55116328	55116349	55116333	55116328	-
SEQ ID NO 2891	AGCGGATCCTCCCCGTGTCTGG	CTG	chr19	55116326	55116347	55116331	55116326	-
SEQ ID NO 2892	CCCGTGTCTGGGTCCTCTCCGG	CTC	chr19	55116315	55116336	55116320	55116315	-
SEQ ID NO 2893	GGTCCTCTCCGGGCATCTCTCC	CTG	chr19	55116305	55116326	55116310	55116305	-
SEQ ID NO 2894	TCCGGGCATCTCTCCTCCCTCA	CTC	chr19	55116298	55116319	55116303	55116298	-

SEQ ID NO 2895	CGGGCATCTCTCCTCCCTCACC	CTC	chr19	55116296	55116317	55116301	55116296	-
SEQ ID NO 2896	TCCTCCCTCACCCAACCCCATG	CTC	chr19	55116286	55116307	55116291	55116286	-
SEQ ID NO 2897	CTCCCTCACCCAACCCCATGCC	CTC	chr19	55116284	55116305	55116289	55116284	-
SEQ ID NO 2898	CCTCACCCAACCCCATGCCGTC	CTC	chr19	55116281	55116302	55116286	55116281	-
SEQ ID NO 2899	ACCCAACCCCATGCCGTCTTCA	CTC	chr19	55116277	55116298	55116282	55116277	-
SEQ ID NO 2900	CACTCGCTGGGTTCCCTTTTCC	CTT	chr19	55116257	55116278	55116262	55116257	-
SEQ ID NO 2901	ACTCGCTGGGTTCCCTTTTCCT	TTC	chr19	55116256	55116277	55116261	55116256	-
SEQ ID NO 2902	GCTGGGTTCCCTTTTCCTTCTC	CTC	chr19	55116252	55116273	55116257	55116252	-
SEQ ID NO 2903	GGTTCCCTTTTCCTTCTCCTTC	CTG	chr19	55116248	55116269	55116253	55116248	-
SEQ ID NO 2904	CCTTTTCCTTCTCCTTCTGGGG	TTC	chr19	55116243	55116264	55116248	55116243	-
SEQ ID NO 2905	TTCCTTCTCCTTCTGGGGCCTG	CTT	chr19	55116239	55116260	55116244	55116239	-
SEQ ID NO 2906	TCCTTCTCCTTCTGGGGCCTGT	TTT	chr19	55116238	55116259	55116243	55116238	-
SEQ ID NO 2907	CCTTCTCCTTCTGGGGCCTGTG	TTT	chr19	55116237	55116258	55116242	55116237	-
SEQ ID NO 2908	CTTCTCCTTCTGGGGCCTGTGC	TTC	chr19	55116236	55116257	55116241	55116236	-
SEQ ID NO 2909	CTCCTTCTGGGGCCTGTGCCAT	CTT	chr19	55116233	55116254	55116238	55116233	-
SEQ ID NO 2910	TCCTTCTGGGGCCTGTGCCATC	TTC	chr19	55116232	55116253	55116237	55116232	-
SEQ ID NO 2911	CTTCTGGGGCCTGTGCCATCTC	CTC	chr19	55116230	55116251	55116235	55116230	-
SEQ ID NO 2912	CTGGGGCCTGTGCCATCTCTCG	CTT	chr19	55116227	55116248	55116232	55116227	-
SEQ ID NO 2913	TGGGGCCTGTGCCATCTCTCGT	TTC	chr19	55116226	55116247	55116231	55116226	-
SEQ ID NO 2914	GGGCCTGTGCCATCTCTCGTTT	CTG	chr19	55116224	55116245	55116229	55116224	-
SEQ ID NO 2915	TGCCATCTCTCGTTTCTTAGGA	CTG	chr19	55116217	55116238	55116222	55116217	-
SEQ ID NO 2916	TCGTTTCTTAGGATGGCCTTCT	CTC	chr19	55116208	55116229	55116213	55116208	-
SEQ ID NO 2917	GTTTCTTAGGATGGCCTTCTCC	CTC	chr19	55116206	55116227	55116211	55116206	-
SEQ ID NO 2918	CTTAGGATGGCCTTCTCCGACG	TTT	chr19	55116202	55116223	55116207	55116202	-
SEQ ID NO 2919	TTAGGATGGCCTTCTCCGACGG	TTC	chr19	55116201	55116222	55116206	55116201	-
SEQ ID NO 2920	AGGATGGCCTTCTCCGACGGAT	CTT	chr19	55116199	55116220	55116204	55116199	-
SEQ ID NO 2921	GGATGGCCTTCTCCGACGGATG	TTA	chr19	55116198	55116219	55116203	55116198	-
SEQ ID NO 2922	CTCCGACGGATGTCTCCCTTGC	CTT	chr19	55116188	55116209	55116193	55116188	-
SEQ ID NO 2923	TCCGACGGATGTCTCCCTTGCG	TTC	chr19	55116187	55116208	55116192	55116187	-
SEQ ID NO 2924	CGACGGATGTCTCCCTTGCGTC	CTC	chr19	55116185	55116206	55116190	55116185	-
SEQ ID NO 2925	CCTTGCGTCCCGCCTCCCCTTC	CTC	chr19	55116172	55116193	55116177	55116172	-
SEQ ID NO 2926	GCGTCCCGCCTCCCCTTCTTGT	CTT	chr19	55116168	55116189	55116173	55116168	-
SEQ ID NO 2927	CGTCCCGCCTCCCCTTCTTGTA	TTG	chr19	55116167	55116188	55116172	55116167	-
SEQ ID NO 2928	CCCTTCTTGTAGGCCTGCATCA	CTC	chr19	55116156	55116177	55116161	55116156	-
SEQ ID NO 2929	CTTGTAGGCCTGCATCATCACC	CTT	chr19	55116151	55116172	55116156	55116151	-
SEQ ID NO 2930	TTGTAGGCCTGCATCATCACCG	TTC	chr19	55116150	55116171	55116155	55116150	-
SEQ ID NO 2931	GTAGGCCTGCATCATCACCGTT	CTT	chr19	55116148	55116169	55116153	55116148	-
SEQ ID NO 2932	TAGGCCTGCATCATCACCGTTT	TTG	chr19	55116147	55116168	55116152	55116147	-
SEQ ID NO 2933	CATCATCACCGTTTTTCTGGAC	CTG	chr19	55116139	55116160	55116144	55116139	-
SEQ ID NO 2934	TTCTGGACAACCCCAAAGTACC	TTT	chr19	55116125	55116146	55116130	55116125	-
SEQ ID NO 2935	TCTGGACAACCCCAAAGTACCC	TTT	chr19	55116124	55116145	55116129	55116124	-
SEQ ID NO 2936	CTGGACAACCCCAAAGTACCCC	TTT	chr19	55116123	55116144	55116128	55116123	-
SEQ ID NO 2937	TGGACAACCCCAAAGTACCCCG	TTC	chr19	55116122	55116143	55116127	55116122	-
SEQ ID NO 2938	GACAACCCCAAAGTACCCCGTC	CTG	chr19	55116120	55116141	55116125	55116120	-
SEQ ID NO 2939	CCTGGCTTTAGCCACCTCTCCA	CTC	chr19	55116096	55116117	55116101	55116096	-
SEQ ID NO 2940	GCTTTAGCCACCTCTCCATCCT	CTG	chr19	55116092	55116113	55116097	55116092	-
SEQ ID NO 2941	TAGCCACCTCTCCATCCTCTTG	CTT	chr19	55116088	55116109	55116093	55116088	-
SEQ ID NO 2942	AGCCACCTCTCCATCCTCTTGC	TTT	chr19	55116087	55116108	55116092	55116087	-
SEQ ID NO 2943	GCCACCTCTCCATCCTCTTGCT	TTA	chr19	55116086	55116107	55116091	55116086	-
SEQ ID NO 2944	TCCATCCTCTTGCTTTCTTTGC	CTC	chr19	55116078	55116099	55116083	55116078	-
SEQ ID NO 2945	CATCCTCTTGCTTTCTTTGCCT	CTC	chr19	55116076	55116097	55116081	55116076	-
SEQ ID NO 2946	TTGCTTTCTTTGCCTGGACACC	CTC	chr19	55116069	55116090	55116074	55116069	-
SEQ ID NO 2947	GCTTTCTTTGCCTGGACACCCC	CTT	chr19	55116067	55116088	55116072	55116067	-
SEQ ID NO 2948	CTTTCTTTGCCTGGACACCCCG	TTG	chr19	55116066	55116087	55116071	55116066	-
SEQ ID NO 2949	TCTTTGCCTGGACACCCCGTTC	CTT	chr19	55116063	55116084	55116068	55116063	-
SEQ ID NO 2950	CTTTGCCTGGACACCCCGTTCT	TTT	chr19	55116062	55116083	55116067	55116062	-
SEQ ID NO 2951	TTTGCCTGGACACCCCGTTCTC	TTC	chr19	55116061	55116082	55116066	55116061	-
SEQ ID NO 2952	TGCCTGGACACCCCGTTCTCCT	CTT	chr19	55116059	55116080	55116064	55116059	-
SEQ ID NO 2953	GCCTGGACACCCCGTTCTCCTG	TTT	chr19	55116058	55116079	55116063	55116058	-

SEQ ID NO 2954	CCTGGACACCCCGTTCTCCTGT	TTG	chr19	55116057	55116078	55116062	55116057	-
SEQ ID NO 2955	GACACCCCGTTCTCCTGTGGAT	CTG	chr19	55116053	55116074	55116058	55116053	-
SEQ ID NO 2956	TCCTGTGGATTCGGGTCACCTC	TTC	chr19	55116041	55116062	55116046	55116041	-
SEQ ID NO 2957	CTGTGGATTCGGGTCACCTCTC	CTC	chr19	55116039	55116060	55116044	55116039	-
SEQ ID NO 2958	TGGATTCGGGTCACCTCTCACT	CTG	chr19	55116036	55116057	55116041	55116036	-
SEQ ID NO 2959	GGGTCACCTCTCACTCCTTTCA	TTC	chr19	55116029	55116050	55116034	55116029	-
SEQ ID NO 2960	TCACTCCTTTCATTTGGGCAGC	CTC	chr19	55116019	55116040	55116024	55116019	-
SEQ ID NO 2961	ACTCCTTTCATTTGGGCAGCTC	CTC	chr19	55116017	55116038	55116022	55116017	-
SEQ ID NO 2962	CTTTCATTTGGGCAGCTCCCCT	CTC	chr19	55116013	55116034	55116018	55116013	-
SEQ ID NO 2963	TCATTTGGGCAGCTCCCCTACC	CTT	chr19	55116010	55116031	55116015	55116010	-
SEQ ID NO 2964	CATTTGGGCAGCTCCCCTACCC	TTT	chr19	55116009	55116030	55116014	55116009	-
SEQ ID NO 2965	ATTTGGGCAGCTCCCCTACCCC	TTC	chr19	55116008	55116029	55116013	55116008	-
SEQ ID NO 2966	GGGCAGCTCCCCTACCCCCCTT	TTT	chr19	55116004	55116025	55116009	55116004	-
SEQ ID NO 2967	GGCAGCTCCCCTACCCCCCTTA	TTG	chr19	55116003	55116024	55116008	55116003	-
SEQ ID NO 2968	CCCTACCCCCCTTACCTCTCTA	CTC	chr19	55115995	55116016	55116000	55115995	-
SEQ ID NO 2969	CCCCCCTTACCTCTCTAGTCTG	CTA	chr19	55115990	55116011	55115995	55115990	-
SEQ ID NO 2970	ACCTCTCTAGTCTGTGCTAGCT	CTT	chr19	55115982	55116003	55115987	55115982	-
SEQ ID NO 2971	CCTCTCTAGTCTGTGCTAGCTC	TTA	chr19	55115981	55116002	55115986	55115981	-
SEQ ID NO 2972	TCTAGTCTGTGCTAGCTCTTCC	CTC	chr19	55115977	55115998	55115982	55115977	-
SEQ ID NO 2973	TAGTCTGTGCTAGCTCTTCCAG	CTC	chr19	55115975	55115996	55115980	55115975	-
SEQ ID NO 2974	GTCTGTGCTAGCTCTTCCAGCC	CTA	chr19	55115973	55115994	55115978	55115973	-
SEQ ID NO 2975	TGCTAGCTCTTCCAGCCCCCTG	CTG	chr19	55115968	55115989	55115973	55115968	-
SEQ ID NO 2976	GCTCTTCCAGCCCCCTGTCATG	CTA	chr19	55115963	55115984	55115968	55115963	-
SEQ ID NO 2977	TTCCAGCCCCCTGTCATGGCAT	CTC	chr19	55115959	55115980	55115964	55115959	-
SEQ ID NO 2978	CCAGCCCCCTGTCATGGCATCT	CTT	chr19	55115957	55115978	55115962	55115957	-
SEQ ID NO 2979	CAGCCCCCTGTCATGGCATCTT	TTC	chr19	55115956	55115977	55115961	55115956	-
SEQ ID NO 2980	TCATGGCATCTTCCAGGGGTCC	CTG	chr19	55115946	55115967	55115951	55115946	-
SEQ ID NO 2981	CCAGGGGTCCGAGAGCTCAGCT	CTT	chr19	55115934	55115955	55115939	55115934	-
SEQ ID NO 2982	CAGGGGTCCGAGAGCTCAGCTA	TTC	chr19	55115933	55115954	55115938	55115933	-
SEQ ID NO 2983	AGCTAGTCTTCTTCCTCCAACC	CTC	chr19	55115916	55115937	55115921	55115916	-
SEQ ID NO 2984	GTCTTCTTCCTCCAACCCGGGC	CTA	chr19	55115911	55115932	55115916	55115911	-
SEQ ID NO 2985	CTTCCTCCAACCCGGGCCCCTA	CTT	chr19	55115906	55115927	55115911	55115906	-
SEQ ID NO 2986	TTCCTCCAACCCGGGCCCCTAT	TTC	chr19	55115905	55115926	55115910	55115905	-
SEQ ID NO 2987	CCTCCAACCCGGGCCCCTATGT	CTT	chr19	55115903	55115924	55115908	55115903	-
SEQ ID NO 2988	CTCCAACCCGGGCCCCTATGTC	TTC	chr19	55115902	55115923	55115907	55115902	-
SEQ ID NO 2989	CAACCCGGGCCCCTATGTCCAC	CTC	chr19	55115899	55115920	55115904	55115899	-
SEQ ID NO 2990	TGTCCACTTCAGGACAGCATGT	CTA	chr19	55115884	55115905	55115889	55115884	-
SEQ ID NO 2991	CAGGACAGCATGTTTGCTGCCT	CTT	chr19	55115875	55115896	55115880	55115875	-
SEQ ID NO 2992	AGGACAGCATGTTTGCTGCCTC	TTC	chr19	55115874	55115895	55115879	55115874	-
SEQ ID NO 2993	GCTGCCTCCAGGGATCCTGTGT	TTT	chr19	55115860	55115881	55115865	55115860	-
SEQ ID NO 2994	CTGCCTCCAGGGATCCTGTGTC	TTG	chr19	55115859	55115880	55115864	55115859	-
SEQ ID NO 2995	CCTCCAGGGATCCTGTGTCCCC	CTG	chr19	55115856	55115877	55115861	55115856	-
SEQ ID NO 2996	CAGGGATCCTGTGTCCCCGAGC	CTC	chr19	55115852	55115873	55115857	55115852	-
SEQ ID NO 2997	TGTCCCCGAGCTGGGACCACCT	CTG	chr19	55115841	55115862	55115846	55115841	-
SEQ ID NO 2998	GGACCACCTTATATTCCCAGGG	CTG	chr19	55115828	55115849	55115833	55115828	-
SEQ ID NO 2999	ATATTCCCAGGGCCGGTTAATG	CTT	chr19	55115818	55115839	55115823	55115818	-
SEQ ID NO 3000	TATTCCCAGGGCCGGTTAATGT	TTA	chr19	55115817	55115838	55115822	55115817	-
SEQ ID NO 3001	CCAGGGCCGGTTAATGTGGCTC	TTC	chr19	55115812	55115833	55115817	55115812	-
SEQ ID NO 3002	ATGTGGCTCTGGTTCTGGGTAC	TTA	chr19	55115799	55115820	55115804	55115799	-
SEQ ID NO 3003	TGGTTCTGGGTACTTTTATCTG	CTC	chr19	55115790	55115811	55115795	55115790	-
SEQ ID NO 3004	GTTCTGGGTACTTTTATCTGTC	CTG	chr19	55115788	55115809	55115793	55115788	-
SEQ ID NO 3005	TGGGTACTTTTATCTGTCCCCT	TTC	chr19	55115784	55115805	55115789	55115784	-
SEQ ID NO 3006	GGTACTTTTATCTGTCCCCTCC	CTG	chr19	55115782	55115803	55115787	55115782	-
SEQ ID NO 3007	TTATCTGTCCCCTCCACCCCAC	CTT	chr19	55115775	55115796	55115780	55115775	-
SEQ ID NO 3008	TATCTGTCCCCTCCACCCCACA	TTT	chr19	55115774	55115795	55115779	55115774	-
SEQ ID NO 3009	ATCTGTCCCCTCCACCCCACAG	TTT	chr19	55115773	55115794	55115778	55115773	-
SEQ ID NO 3010	TCTGTCCCCTCCACCCCACAGT	TTA	chr19	55115772	55115793	55115777	55115772	-
SEQ ID NO 3011	TCCCCTCCACCCCACAGTGGGG	CTG	chr19	55115768	55115789	55115773	55115768	-
SEQ ID NO 3012	CACCCCACAGTGGGGCCACTAG	CTC	chr19	55115761	55115782	55115766	55115761	-

SEQ ID NO 3013	GGGACAGGATTGGTGACAGAAA	CTA	chr19	55115740	55115761	55115745	55115740	-
SEQ ID NO 3014	GTGACAGAAAAGCCCCATCCTT	TTG	chr19	55115728	55115749	55115733	55115728	-
SEQ ID NO 3015	AGGCCTCCTCCTTCCTAGTCTC	CTT	chr19	55115706	55115727	55115711	55115706	-
SEQ ID NO 3016	GGCCTCCTCCTTCCTAGTCTCC	TTA	chr19	55115705	55115726	55115710	55115705	-
SEQ ID NO 3017	CTCCTTCCTAGTCTCCTGATAT	CTC	chr19	55115699	55115720	55115704	55115699	-
SEQ ID NO 3018	CTTCCTAGTCTCCTGATATTGG	CTC	chr19	55115696	55115717	55115701	55115696	-
SEQ ID NO 3019	CCTAGTCTCCTGATATTGGGTC	CTT	chr19	55115693	55115714	55115698	55115693	-
SEQ ID NO 3020	CTAGTCTCCTGATATTGGGTCT	TTC	chr19	55115692	55115713	55115697	55115692	-
SEQ ID NO 3021	GTCTCCTGATATTGGGTCTAAC	CTA	chr19	55115689	55115710	55115694	55115689	-
SEQ ID NO 3022	CTGATATTGGGTCTAACCCCCA	CTC	chr19	55115684	55115705	55115689	55115684	-
SEQ ID NO 3023	ATATTGGGTCTAACCCCCACCT	CTG	chr19	55115681	55115702	55115686	55115681	-
SEQ ID NO 3024	GGTCTAACCCCCACCTCCTGTT	TTG	chr19	55115675	55115696	55115680	55115675	-
SEQ ID NO 3025	ACCCCCACCTCCTGTTAGGCAG	CTA	chr19	55115669	55115690	55115674	55115669	-
SEQ ID NO 3026	CTGTTAGGCAGATTCCTTATCT	CTC	chr19	55115658	55115679	55115663	55115658	-
SEQ ID NO 3027	TTAGGCAGATTCCTTATCTGGT	CTG	chr19	55115655	55115676	55115660	55115655	-
SEQ ID NO 3028	GGCAGATTCCTTATCTGGTGAC	TTA	chr19	55115652	55115673	55115657	55115652	-
SEQ ID NO 3029	CTTATCTGGTGACACACCCCCA	TTC	chr19	55115643	55115664	55115648	55115643	-
SEQ ID NO 3030	ATCTGGTGACACACCCCCATTT	CTT	chr19	55115640	55115661	55115645	55115640	-
SEQ ID NO 3031	TCTGGTGACACACCCCCATTTC	TTA	chr19	55115639	55115660	55115644	55115639	-
SEQ ID NO 3032	GTGACACACCCCCATTTCCTGG	CTG	chr19	55115635	55115656	55115640	55115635	-
SEQ ID NO 3033	CCTGGAGCCATCTCTCTCCTTG	TTT	chr19	55115618	55115639	55115623	55115618	-
SEQ ID NO 3034	CTGGAGCCATCTCTCTCCTTGC	TTC	chr19	55115617	55115638	55115622	55115617	-
SEQ ID NO 3035	GAGCCATCTCTCTCCTTGCCAG	CTG	chr19	55115614	55115635	55115619	55115614	-
SEQ ID NO 3036	TCTCCTTGCCAGAACCTCTAAG	CTC	chr19	55115604	55115625	55115609	55115604	-
SEQ ID NO 3037	TCCTTGCCAGAACCTCTAAGGT	CTC	chr19	55115602	55115623	55115607	55115602	-
SEQ ID NO 3038	CTTGCCAGAACCTCTAAGGTTT	CTC	chr19	55115600	55115621	55115605	55115600	-
SEQ ID NO 3039	GCCAGAACCTCTAAGGTTTGCT	CTT	chr19	55115597	55115618	55115602	55115597	-
SEQ ID NO 3040	CCAGAACCTCTAAGGTTTGCTT	TTG	chr19	55115596	55115617	55115601	55115596	-
SEQ ID NO 3041	TAAGGTTTGCTTACGATGGAGC	CTC	chr19	55115586	55115607	55115591	55115586	-
SEQ ID NO 3042	AGGTTTGCTTACGATGGAGCCA	CTA	chr19	55115584	55115605	55115589	55115584	-
SEQ ID NO 3043	GCTTACGATGGAGCCAGAGAGG	TTT	chr19	55115578	55115599	55115583	55115578	-
SEQ ID NO 3044	CTTACGATGGAGCCAGAGAGGA	TTG	chr19	55115577	55115598	55115582	55115577	-
SEQ ID NO 3045	ACGATGGAGCCAGAGAGGATCC	CTT	chr19	55115574	55115595	55115579	55115574	-
SEQ ID NO 3046	CGATGGAGCCAGAGAGGATCCT	TTA	chr19	55115573	55115594	55115578	55115573	-
SEQ ID NO 3047	GGAGGGAGAGCTTGGCAGGGGG	CTG	chr19	55115550	55115571	55115555	55115550	-
SEQ ID NO 3048	GGCAGGGGGTGGGAGGGAAGGG	CTT	chr19	55115537	55115558	55115542	55115537	-
SEQ ID NO 3049	GCAGGGGGTGGGAGGGAAGGGG	TTG	chr19	55115536	55115557	55115541	55115536	-
SEQ ID NO 3050	CCCGGTTCTCAGTGGCCACCCT	CTG	chr19	55115499	55115520	55115504	55115499	-
SEQ ID NO 3051	TCAGTGGCCACCCTGCGCTACC	TTC	chr19	55115491	55115512	55115496	55115491	-
SEQ ID NO 3052	AGTGGCCACCCTGCGCTACCCT	CTC	chr19	55115489	55115510	55115494	55115489	-
SEQ ID NO 3053	CGCTACCCTCTCCCAGAACCTG	CTG	chr19	55115476	55115497	55115481	55115476	-
SEQ ID NO 3054	CCCTCTCCCAGAACCTGAGCTG	CTA	chr19	55115471	55115492	55115476	55115471	-
SEQ ID NO 3055	TCCCAGAACCTGAGCTGCTCTG	CTC	chr19	55115466	55115487	55115471	55115466	-
SEQ ID NO 3056	CCAGAACCTGAGCTGCTCTGAC	CTC	chr19	55115464	55115485	55115469	55115464	-
SEQ ID NO 3057	AGCTGCTCTGACGCGGCCGTCT	CTG	chr19	55115454	55115475	55115459	55115454	-
SEQ ID NO 3058	CTCTGACGCGGCCGTCTGGTGC	CTG	chr19	55115449	55115470	55115454	55115449	-
SEQ ID NO 3059	TGACGCGGCCGTCTGGTGCGTT	CTC	chr19	55115446	55115467	55115451	55115446	-
SEQ ID NO 3060	ACGCGGCCGTCTGGTGCGTTTC	CTG	chr19	55115444	55115465	55115449	55115444	-
SEQ ID NO 3061	GTGCGTTTCACTGATCCTGGTG	CTG	chr19	55115431	55115452	55115436	55115431	-
SEQ ID NO 3062	CACTGATCCTGGTGCTGCAGCT	TTT	chr19	55115423	55115444	55115428	55115423	-
SEQ ID NO 3063	ACTGATCCTGGTGCTGCAGCTT	TTC	chr19	55115422	55115443	55115427	55115422	-
SEQ ID NO 3064	ATCCTGGTGCTGCAGCTTCCTT	CTG	chr19	55115418	55115439	55115423	55115418	-
SEQ ID NO 3065	GTGCTGCAGCTTCCTTACACTT	CTG	chr19	55115412	55115433	55115417	55115412	-
SEQ ID NO 3066	CAGCTTCCTTACACTTCCCAAG	CTG	chr19	55115406	55115427	55115411	55115406	-
SEQ ID NO 3067	CCTTACACTTCCCAAGAGGAGA	CTT	chr19	55115400	55115421	55115405	55115400	-
SEQ ID NO 3068	CTTACACTTCCCAAGAGGAGAA	TTC	chr19	55115399	55115420	55115404	55115399	-
SEQ ID NO 3069	ACACTTCCCAAGAGGAGAAGCA	CTT	chr19	55115396	55115417	55115401	55115396	-
SEQ ID NO 3070	CACTTCCCAAGAGGAGAAGCAG	TTA	chr19	55115395	55115416	55115400	55115395	-
SEQ ID NO 3071	CCCAAGAGGAGAAGCAGTTTGG	CTT	chr19	55115390	55115411	55115395	55115390	-

SEQ ID NO 3072	CCAAGAGGAGAAGCAGTTTGGA	TTC	chr19	55115389	55115410	55115394	55115389	-
SEQ ID NO 3073	GGAAAAACAAAATCAGAATAAG	TTT	chr19	55115370	55115391	55115375	55115370	-
SEQ ID NO 3074	GAAAAACAAAATCAGAATAAGT	TTG	chr19	55115369	55115390	55115374	55115369	-
SEQ ID NO 3075	GTCCTGAGTTCTAACTTTGGCT	TTG	chr19	55115345	55115366	55115350	55115345	-
SEQ ID NO 3076	AGTTCTAACTTTGGCTCTTCAC	CTG	chr19	55115339	55115360	55115344	55115339	-
SEQ ID NO 3077	TAACTTTGGCTCTTCACCTTTC	TTC	chr19	55115334	55115355	55115339	55115334	-
SEQ ID NO 3078	ACTTTGGCTCTTCACCTTTCTA	CTA	chr19	55115332	55115353	55115337	55115332	-
SEQ ID NO 3079	TGGCTCTTCACCTTTCTAGTCC	CTT	chr19	55115328	55115349	55115333	55115328	-
SEQ ID NO 3080	GGCTCTTCACCTTTCTAGTCCC	TTT	chr19	55115327	55115348	55115332	55115327	-
SEQ ID NO 3081	GCTCTTCACCTTTCTAGTCCCC	TTG	chr19	55115326	55115347	55115331	55115326	-
SEQ ID NO 3082	TTCACCTTTCTAGTCCCCAATT	CTC	chr19	55115322	55115343	55115327	55115322	-
SEQ ID NO 3083	CACCTTTCTAGTCCCCAATTTA	CTT	chr19	55115320	55115341	55115325	55115320	-
SEQ ID NO 3084	ACCTTTCTAGTCCCCAATTTAT	TTC	chr19	55115319	55115340	55115324	55115319	-
SEQ ID NO 3085	TCTAGTCCCCAATTTATATTGT	CTT	chr19	55115314	55115335	55115319	55115314	-
SEQ ID NO 3086	CTAGTCCCCAATTTATATTGTT	TTT	chr19	55115313	55115334	55115318	55115313	-
SEQ ID NO 3087	TAGTCCCCAATTTATATTGTTC	TTC	chr19	55115312	55115333	55115317	55115312	-
SEQ ID NO 3088	GTCCCCAATTTATATTGTTCCT	CTA	chr19	55115310	55115331	55115315	55115310	-
SEQ ID NO 3089	ATATTGTTCCTCCGTGCGTCAG	TTT	chr19	55115299	55115320	55115304	55115299	-
SEQ ID NO 3090	TATTGTTCCTCCGTGCGTCAGT	TTA	chr19	55115298	55115319	55115303	55115298	-
SEQ ID NO 3091	TTCCTCCGTGCGTCAGTTTTAC	TTG	chr19	55115293	55115314	55115298	55115293	-
SEQ ID NO 3092	CTCCGTGCGTCAGTTTTACCTG	TTC	chr19	55115290	55115311	55115295	55115290	-
SEQ ID NO 3093	CGTGCGTCAGTTTTACCTGTGA	CTC	chr19	55115287	55115308	55115292	55115287	-
SEQ ID NO 3094	TACCTGTGAGATAAGGCCAGTA	TTT	chr19	55115274	55115295	55115279	55115274	-
SEQ ID NO 3095	ACCTGTGAGATAAGGCCAGTAG	TTT	chr19	55115273	55115294	55115278	55115273	-
SEQ ID NO 3096	CCTGTGAGATAAGGCCAGTAGC	TTA	chr19	55115272	55115293	55115277	55115272	-
SEQ ID NO 3097	TGAGATAAGGCCAGTAGCCAGC	CTG	chr19	55115268	55115289	55115273	55115268	-
SEQ ID NO 3098	GCAGGGCTGTGGTGAGGAGGGG	CTG	chr19	55115237	55115258	55115242	55115237	-
SEQ ID NO 3099	TGGTGAGGAGGGGGGTGTCCGT	CTG	chr19	55115228	55115249	55115233	55115228	-
SEQ ID NO 3100	CCTTTGTGAGAATGGTGCGTCC	CTC	chr19	55115195	55115216	55115200	55115195	-
SEQ ID NO 3101	TGTGAGAATGGTGCGTCCTAGG	CTT	chr19	55115191	55115212	55115196	55115191	-
SEQ ID NO 3102	GTGAGAATGGTGCGTCCTAGGT	TTT	chr19	55115190	55115211	55115195	55115190	-
SEQ ID NO 3103	TGAGAATGGTGCGTCCTAGGTG	TTG	chr19	55115189	55115210	55115194	55115189	-
SEQ ID NO 3104	GGTGTTCACCAGGTCGTGGCCG	CTA	chr19	55115171	55115192	55115176	55115171	-
SEQ ID NO 3105	ACCAGGTCGTGGCCGCCTCTAC	TTC	chr19	55115164	55115185	55115169	55115164	-
SEQ ID NO 3106	TACTCCCTTTCTCTTTCTCCAT	CTC	chr19	55115145	55115166	55115150	55115145	-
SEQ ID NO 3107	CTCCCTTTCTCTTTCTCCATCC	CTA	chr19	55115143	55115164	55115148	55115143	-
SEQ ID NO 3108	CCTTTCTCTTTCTCCATCCTTC	CTC	chr19	55115140	55115161	55115145	55115140	-
SEQ ID NO 3109	TCTCTTTCTCCATCCTTCTTTC	CTT	chr19	55115136	55115157	55115141	55115136	-
SEQ ID NO 3110	CTCTTTCTCCATCCTTCTTTCC	TTT	chr19	55115135	55115156	55115140	55115135	-
SEQ ID NO 3111	TCTTTCTCCATCCTTCTTTCCT	TTC	chr19	55115134	55115155	55115139	55115134	-
SEQ ID NO 3112	TTTCTCCATCCTTCTTTCCTTA	CTC	chr19	55115132	55115153	55115137	55115132	-
SEQ ID NO 3113	TCTCCATCCTTCTTTCCTTAAA	CTT	chr19	55115130	55115151	55115135	55115130	-
SEQ ID NO 3114	CTCCATCCTTCTTTCCTTAAAG	TTT	chr19	55115129	55115150	55115134	55115129	-
SEQ ID NO 3115	TCCATCCTTCTTTCCTTAAAGA	TTC	chr19	55115128	55115149	55115133	55115128	-
SEQ ID NO 3116	CATCCTTCTTTCCTTAAAGAGT	CTC	chr19	55115126	55115147	55115131	55115126	-
SEQ ID NO 3117	CTTTCCTTAAAGAGTCCCCAGT	CTT	chr19	55115119	55115140	55115124	55115119	-
SEQ ID NO 3118	TTTCCTTAAAGAGTCCCCAGTG	TTC	chr19	55115118	55115139	55115123	55115118	-
SEQ ID NO 3119	TCCTTAAAGAGTCCCCAGTGCT	CTT	chr19	55115116	55115137	55115121	55115116	-
SEQ ID NO 3120	CCTTAAAGAGTCCCCAGTGCTA	TTT	chr19	55115115	55115136	55115120	55115115	-
SEQ ID NO 3121	CTTAAAGAGTCCCCAGTGCTAT	TTC	chr19	55115114	55115135	55115119	55115114	-
SEQ ID NO 3122	AAAGAGTCCCCAGTGCTATCTG	CTT	chr19	55115111	55115132	55115116	55115111	-
SEQ ID NO 3123	AAGAGTCCCCAGTGCTATCTGG	TTA	chr19	55115110	55115131	55115115	55115110	-
SEQ ID NO 3124	TCTGGGACATATTCCTCCGCCC	CTA	chr19	55115093	55115114	55115098	55115093	-
SEQ ID NO 3125	GGACATATTCCTCCGCCCAGAG	CTG	chr19	55115089	55115110	55115094	55115089	-
SEQ ID NO 3126	CTCCGCCCAGAGCAGGGTCCCG	TTC	chr19	55115079	55115100	55115084	55115079	-
SEQ ID NO 3127	CGCCCAGAGCAGGGTCCCGCTT	CTC	chr19	55115076	55115097	55115081	55115076	-
SEQ ID NO 3128	CCCTAAGGCCCTGCTCTGGGCT	CTT	chr19	55115054	55115075	55115059	55115054	-
SEQ ID NO 3129	CCTAAGGCCCTGCTCTGGGCTT	TTC	chr19	55115053	55115074	55115058	55115053	-
SEQ ID NO 3130	AGGCCCTGCTCTGGGCTTCTGG	CTA	chr19	55115049	55115070	55115054	55115049	-

SEQ ID NO 3131	CTCTGGGCTTCTGGGTTTGAGT	CTG	chr19	55115041	55115062	55115046	55115041	-
SEQ ID NO 3132	TGGGCTTCTGGGTTTGAGTCCT	CTC	chr19	55115038	55115059	55115043	55115038	-
SEQ ID NO 3133	GGCTTCTGGGTTTGAGTCCTTG	CTG	chr19	55115036	55115057	55115041	55115036	-
SEQ ID NO 3134	CTGGGTTTGAGTCCTTGGCAAG	CTT	chr19	55115031	55115052	55115036	55115031	-
SEQ ID NO 3135	TGGGTTTGAGTCCTTGGCAAGC	TTC	chr19	55115030	55115051	55115035	55115030	-
SEQ ID NO 3136	GGTTTGAGTCCTTGGCAAGCCC	CTG	chr19	55115028	55115049	55115033	55115028	-
SEQ ID NO 3137	GAGTCCTTGGCAAGCCCAGGAG	TTT	chr19	55115023	55115044	55115028	55115023	-
SEQ ID NO 3138	AGTCCTTGGCAAGCCCAGGAGA	TTG	chr19	55115022	55115043	55115027	55115022	-
SEQ ID NO 3139	GGCAAGCCCAGGAGAGGCGCTC	CTT	chr19	55115015	55115036	55115020	55115015	-
SEQ ID NO 3140	GCAAGCCCAGGAGAGGCGCTCA	TTG	chr19	55115014	55115035	55115019	55115014	-
SEQ ID NO 3141	AGGCTTCCCTGTCCCCCTTCCT	CTC	chr19	55114993	55115014	55114998	55114993	-
SEQ ID NO 3142	CCCTGTCCCCCTTCCTCGTCCA	CTT	chr19	55114987	55115008	55114992	55114987	-
SEQ ID NO 3143	CCTGTCCCCCTTCCTCGTCCAC	TTC	chr19	55114986	55115007	55114991	55114986	-
SEQ ID NO 3144	TCCCCCTTCCTCGTCCACCATC	CTG	chr19	55114982	55115003	55114987	55114982	-
SEQ ID NO 3145	CCTCGTCCACCATCTCATGCCC	CTT	chr19	55114974	55114995	55114979	55114974	-
SEQ ID NO 3146	CTCGTCCACCATCTCATGCCCC	TTC	chr19	55114973	55114994	55114978	55114973	-
SEQ ID NO 3147	GTCCACCATCTCATGCCCCTGG	CTC	chr19	55114970	55114991	55114975	55114970	-
SEQ ID NO 3148	ATGCCCCTGGCTCTCCTGCCCC	CTC	chr19	55114958	55114979	55114963	55114958	-
SEQ ID NO 3149	GCTCTCCTGCCCCTTCCCTACA	CTG	chr19	55114949	55114970	55114954	55114949	-
SEQ ID NO 3150	TCCTGCCCCTTCCCTACAGGGG	CTC	chr19	55114945	55114966	55114950	55114945	-
SEQ ID NO 3151	CTGCCCCTTCCCTACAGGGGTT	CTC	chr19	55114943	55114964	55114948	55114943	-
SEQ ID NO 3152	CCCCTTCCCTACAGGGGTTCCT	CTG	chr19	55114940	55114961	55114945	55114940	-
SEQ ID NO 3153	CCCTACAGGGGTTCCTGGCTCT	CTT	chr19	55114934	55114955	55114939	55114934	-
SEQ ID NO 3154	CCTACAGGGGTTCCTGGCTCTG	TTC	chr19	55114933	55114954	55114938	55114933	-
SEQ ID NO 3155	CAGGGGTTCCTGGCTCTGCTCT	CTA	chr19	55114929	55114950	55114934	55114929	-
SEQ ID NO 3156	CTGGCTCTGCTCTTCAGACTGA	TTC	chr19	55114920	55114941	55114925	55114920	-
SEQ ID NO 3157	GCTCTGCTCTTCAGACTGAGCC	CTG	chr19	55114917	55114938	55114922	55114917	-
SEQ ID NO 3158	TGCTCTTCAGACTGAGCCCCGT	CTC	chr19	55114913	55114934	55114918	55114913	-
SEQ ID NO 3159	CTCTTCAGACTGAGCCCCGTTC	CTG	chr19	55114911	55114932	55114916	55114911	-
SEQ ID NO 3160	TTCAGACTGAGCCCCGTTCCCC	CTC	chr19	55114908	55114929	55114913	55114908	-
SEQ ID NO 3161	CAGACTGAGCCCCGTTCCCCTG	CTT	chr19	55114906	55114927	55114911	55114906	-
SEQ ID NO 3162	AGACTGAGCCCCGTTCCCCTGC	TTC	chr19	55114905	55114926	55114910	55114905	-
SEQ ID NO 3163	AGCCCCGTTCCCCTGCATCCCC	CTG	chr19	55114899	55114920	55114904	55114899	-
SEQ ID NO 3164	CCCTGCATCCCCGTTCCCCTGC	TTC	chr19	55114889	55114910	55114894	55114889	-
SEQ ID NO 3165	CATCCCCGTTCCCCTGCATCCC	CTG	chr19	55114884	55114905	55114889	55114884	-
SEQ ID NO 3166	CCCTGCATCCCCCTTCCCCTGC	TTC	chr19	55114873	55114894	55114878	55114873	-
SEQ ID NO 3167	CATCCCCCTTCCCCTGCATCCC	CTG	chr19	55114868	55114889	55114873	55114868	-
SEQ ID NO 3168	CCCCTGCATCCCCCAGAGGCCC	CTT	chr19	55114858	55114879	55114863	55114858	-
SEQ ID NO 3169	CCCTGCATCCCCCAGAGGCCCC	TTC	chr19	55114857	55114878	55114862	55114857	-
SEQ ID NO 3170	CATCCCCCAGAGGCCCCAGGCC	CTG	chr19	55114852	55114873	55114857	55114852	-
SEQ ID NO 3171	CTTGGCCTGGACCCCACGAGAG	CTA	chr19	55114825	55114846	55114830	55114825	-
SEQ ID NO 3172	GGCCTGGACCCCACGAGAGGCC	CTT	chr19	55114822	55114843	55114827	55114822	-
SEQ ID NO 3173	GCCTGGACCCCACGAGAGGCCA	TTG	chr19	55114821	55114842	55114826	55114821	-
SEQ ID NO 3174	GACCCCACGAGAGGCCACCCCA	CTG	chr19	55114816	55114837	55114821	55114816	-
SEQ ID NO 3175	TCTACCAGGCTGCCTTTTGGGT	CTG	chr19	55114788	55114809	55114793	55114788	-
SEQ ID NO 3176	CCAGGCTGCCTTTTGGGTGGAT	CTA	chr19	55114784	55114805	55114789	55114784	-
SEQ ID NO 3177	CCTTTTGGGTGGATTCTCCTCC	CTG	chr19	55114776	55114797	55114781	55114776	-
SEQ ID NO 3178	TTGGGTGGATTCTCCTCCAACT	CTT	chr19	55114772	55114793	55114777	55114772	-
SEQ ID NO 3179	TGGGTGGATTCTCCTCCAACTG	TTT	chr19	55114771	55114792	55114776	55114771	-
SEQ ID NO 3180	GGGTGGATTCTCCTCCAACTGT	TTT	chr19	55114770	55114791	55114775	55114770	-
SEQ ID NO 3181	GGTGGATTCTCCTCCAACTGTG	TTG	chr19	55114769	55114790	55114774	55114769	-
SEQ ID NO 3182	TCCTCCAACTGTGGGGTGACTG	TTC	chr19	55114760	55114781	55114765	55114760	-
SEQ ID NO 3183	CTCCAACTGTGGGGTGACTGCT	CTC	chr19	55114758	55114779	55114763	55114758	-
SEQ ID NO 3184	CAACTGTGGGGTGACTGCTTGG	CTC	chr19	55114755	55114776	55114760	55114755	-
SEQ ID NO 3185	TGGGGTGACTGCTTGGCAAACT	CTG	chr19	55114749	55114770	55114754	55114749	-
SEQ ID NO 3186	CTTGGCAAACTCACTCTTCGGG	CTG	chr19	55114738	55114759	55114743	55114738	-
SEQ ID NO 3187	GGCAAACTCACTCTTCGGGGTA	CTT	chr19	55114735	55114756	55114740	55114735	-
SEQ ID NO 3188	GCAAACTCACTCTTCGGGGTAT	TTG	chr19	55114734	55114755	55114739	55114734	-
SEQ ID NO 3189	ACTCTTCGGGGTATCCCAGGAG	CTC	chr19	55114726	55114747	55114731	55114726	-

SEQ ID NO 3190	TTCGGGGTATCCCAGGAGGCCT	CTC	chr19	55114722	55114743	55114727	55114722	-
SEQ ID NO 3191	CGGGGTATCCCAGGAGGCCTGG	CTT	chr19	55114720	55114741	55114725	55114720	-
SEQ ID NO 3192	GGGGTATCCCAGGAGGCCTGGA	TTC	chr19	55114719	55114740	55114724	55114719	-
SEQ ID NO 3193	GAGCATTGGGGTGGGCTGGGGT	CTG	chr19	55114699	55114720	55114704	55114699	-
SEQ ID NO 3194	GGGTGGGCTGGGGTTCAGAGAG	TTG	chr19	55114691	55114712	55114696	55114691	-
SEQ ID NO 3195	GGGTTCAGAGAGGAGGGATTCC	CTG	chr19	55114681	55114702	55114686	55114681	-
SEQ ID NO 3196	AGAGAGGAGGGATTCCCTTCTC	TTC	chr19	55114675	55114696	55114680	55114675	-
SEQ ID NO 3197	CCTTCTCAGGTTACGTGGCCAA	TTC	chr19	55114660	55114681	55114665	55114660	-
SEQ ID NO 3198	CTCAGGTTACGTGGCCAAGAAG	CTT	chr19	55114656	55114677	55114661	55114656	-
SEQ ID NO 3199	TCAGGTTACGTGGCCAAGAAGC	TTC	chr19	55114655	55114676	55114660	55114655	-
SEQ ID NO 3200	AGGTTACGTGGCCAAGAAGCAG	CTC	chr19	55114653	55114674	55114658	55114653	-
SEQ ID NO 3201	CGTGGCCAAGAAGCAGGGGAGC	TTA	chr19	55114647	55114668	55114652	55114647	-
SEQ ID NO 3202	GGTTTGGGTCAGGTCTGGGTGT	CTG	chr19	55114623	55114644	55114628	55114623	-
SEQ ID NO 3203	GGGTCAGGTCTGGGTGTGGGGT	TTT	chr19	55114618	55114639	55114623	55114618	-
SEQ ID NO 3204	GGTCAGGTCTGGGTGTGGGGTG	TTG	chr19	55114617	55114638	55114622	55114617	-
SEQ ID NO 3205	GGTGTGGGGTGACCAGCTTATG	CTG	chr19	55114606	55114627	55114611	55114606	-
SEQ ID NO 3206	ATGCTGTTTGCCCAGGACAGCC	CTT	chr19	55114587	55114608	55114592	55114587	-
SEQ ID NO 3207	TGCTGTTTGCCCAGGACAGCCT	TTA	chr19	55114586	55114607	55114591	55114586	-
SEQ ID NO 3208	TTTGCCCAGGACAGCCTAGTTT	CTG	chr19	55114581	55114602	55114586	55114581	-
SEQ ID NO 3209	GCCCAGGACAGCCTAGTTTTAG	TTT	chr19	55114578	55114599	55114583	55114578	-
SEQ ID NO 3210	CCCAGGACAGCCTAGTTTTAGC	TTG	chr19	55114577	55114598	55114582	55114577	-
SEQ ID NO 3211	GTTTTAGCACTGAAACCCTCAG	CTA	chr19	55114563	55114584	55114568	55114563	-
SEQ ID NO 3212	TAGCACTGAAACCCTCAGTCCT	TTT	chr19	55114559	55114580	55114564	55114559	-
SEQ ID NO 3213	AGCACTGAAACCCTCAGTCCTA	TTT	chr19	55114558	55114579	55114563	55114558	-
SEQ ID NO 3214	GCACTGAAACCCTCAGTCCTAG	TTA	chr19	55114557	55114578	55114562	55114557	-
SEQ ID NO 3215	AAACCCTCAGTCCTAGGAAAAC	CTG	chr19	55114551	55114572	55114556	55114551	-
SEQ ID NO 3216	AGTCCTAGGAAAACAGGGATGG	CTC	chr19	55114543	55114564	55114548	55114543	-
SEQ ID NO 3217	GGAAAACAGGGATGGTTGGTCA	CTA	chr19	55114536	55114557	55114541	55114536	-
SEQ ID NO 3218	GTCACTGTCTCTGGGTGACTCT	TTG	chr19	55114518	55114539	55114523	55114518	-
SEQ ID NO 3219	TCTCTGGGTGACTCTTGATTCC	CTG	chr19	55114511	55114532	55114516	55114511	-
SEQ ID NO 3220	TGGGTGACTCTTGATTCCCGGC	CTC	chr19	55114507	55114528	55114512	55114507	-
SEQ ID NO 3221	GGTGACTCTTGATTCCCGGCCA	CTG	chr19	55114505	55114526	55114510	55114505	-
SEQ ID NO 3222	TTGATTCCCGGCCAGTTTCTCC	CTC	chr19	55114497	55114518	55114502	55114497	-
SEQ ID NO 3223	GATTCCCGGCCAGTTTCTCCAC	CTT	chr19	55114495	55114516	55114500	55114495	-
SEQ ID NO 3224	ATTCCCGGCCAGTTTCTCCACC	TTG	chr19	55114494	55114515	55114499	55114494	-
SEQ ID NO 3225	CCGGCCAGTTTCTCCACCTGGG	TTC	chr19	55114490	55114511	55114495	55114490	-
SEQ ID NO 3226	CTCCACCTGGGGCTGTGTTTCT	TTT	chr19	55114479	55114500	55114484	55114479	-
SEQ ID NO 3227	TCCACCTGGGGCTGTGTTTCTC	TTC	chr19	55114478	55114499	55114483	55114478	-
SEQ ID NO 3228	CACCTGGGGCTGTGTTTCTCGT	CTC	chr19	55114476	55114497	55114481	55114476	-
SEQ ID NO 3229	GGGCTGTGTTTCTCGTCCTGCA	CTG	chr19	55114470	55114491	55114475	55114470	-
SEQ ID NO 3230	TGTTTCTCGTCCTGCATCCTTC	CTG	chr19	55114464	55114485	55114469	55114464	-
SEQ ID NO 3231	CTCGTCCTGCATCCTTCTCCAG	TTT	chr19	55114459	55114480	55114464	55114459	-
SEQ ID NO 3232	TCGTCCTGCATCCTTCTCCAGG	TTC	chr19	55114458	55114479	55114463	55114458	-
SEQ ID NO 3233	GTCCTGCATCCTTCTCCAGGCA	CTC	chr19	55114456	55114477	55114461	55114456	-
SEQ ID NO 3234	CATCCTTCTCCAGGCAGGTCCC	CTG	chr19	55114450	55114471	55114455	55114450	-
SEQ ID NO 3235	CTCCAGGCAGGTCCCCAAGCAT	CTT	chr19	55114443	55114464	55114448	55114443	-
SEQ ID NO 3236	TCCAGGCAGGTCCCCAAGCATC	TTC	chr19	55114442	55114463	55114447	55114442	-
SEQ ID NO 3237	CAGGCAGGTCCCCAAGCATCGC	CTC	chr19	55114440	55114461	55114445	55114440	-
SEQ ID NO 3238	CTGTGGCTGTTCCCAAGTTCTT	CTG	chr19	55114411	55114432	55114416	55114411	-
SEQ ID NO 3239	TGGCTGTTCCCAAGTTCTTAGG	CTG	chr19	55114408	55114429	55114413	55114408	-
SEQ ID NO 3240	TTCCCAAGTTCTTAGGGTACCC	CTG	chr19	55114402	55114423	55114407	55114402	-
SEQ ID NO 3241	CCAAGTTCTTAGGGTACCCCAC	TTC	chr19	55114399	55114420	55114404	55114399	-
SEQ ID NO 3242	TTAGGGTACCCCACGTGGGTTT	TTC	chr19	55114391	55114412	55114396	55114391	-
SEQ ID NO 3243	AGGGTACCCCACGTGGGTTTAT	CTT	chr19	55114389	55114410	55114394	55114389	-
SEQ ID NO 3244	GGGTACCCCACGTGGGTTTATC	TTA	chr19	55114388	55114409	55114393	55114388	-
SEQ ID NO 3245	ATCAACCACTTGGTGAGGCTGG	TTT	chr19	55114369	55114390	55114374	55114369	-
SEQ ID NO 3246	TCAACCACTTGGTGAGGCTGGT	TTA	chr19	55114368	55114389	55114373	55114368	-
SEQ ID NO 3247	GGTGAGGCTGGTACCCTGCCCC	CTT	chr19	55114358	55114379	55114363	55114358	-
SEQ ID NO 3248	GTGAGGCTGGTACCCTGCCCCC	TTG	chr19	55114357	55114378	55114362	55114357	-

SEQ ID NO 3249	GTACCCTGCCCCCATTCCTGCA	CTG	chr19	55114348	55114369	55114353	55114348	-
SEQ ID NO 3250	CCCCCATTCCTGCACCCCAATT	CTG	chr19	55114340	55114361	55114345	55114340	-
SEQ ID NO 3251	CTGCACCCCAATTGCCTTAGTG	TTC	chr19	55114331	55114352	55114336	55114331	-
SEQ ID NO 3252	CACCCCAATTGCCTTAGTGGCT	CTG	chr19	55114328	55114349	55114333	55114328	-
SEQ ID NO 3253	CCTTAGTGGCTAGGGGGTTGGG	TTG	chr19	55114317	55114338	55114322	55114317	-
SEQ ID NO 3254	AGTGGCTAGGGGGTTGGGGGCT	CTT	chr19	55114313	55114334	55114318	55114313	-
SEQ ID NO 3255	GTGGCTAGGGGGTTGGGGGCTA	TTA	chr19	55114312	55114333	55114317	55114312	-
SEQ ID NO 3256	GGGGGTTGGGGGCTAGAGTAGG	CTA	chr19	55114305	55114326	55114310	55114305	-
SEQ ID NO 3257	GGGGCTAGAGTAGGAGGGGCTG	TTG	chr19	55114297	55114318	55114302	55114297	-
SEQ ID NO 3258	GAGTAGGAGGGGCTGGAGCCAG	CTA	chr19	55114290	55114311	55114295	55114290	-
SEQ ID NO 3259	GAGCCAGGATTCTTAGGGCTGA	CTG	chr19	55114275	55114296	55114280	55114275	-
SEQ ID NO 3260	TTAGGGCTGAACAGAGAAGAGC	TTC	chr19	55114263	55114284	55114268	55114263	-
SEQ ID NO 3261	AGGGCTGAACAGAGAAGAGCTG	CTT	chr19	55114261	55114282	55114266	55114261	-
SEQ ID NO 3262	GGGCTGAACAGAGAAGAGCTGG	TTA	chr19	55114260	55114281	55114265	55114260	-
SEQ ID NO 3263	AACAGAGAAGAGCTGGGGGCCT	CTG	chr19	55114254	55114275	55114259	55114254	-
SEQ ID NO 3264	GGGGCCTGGGCTCCTGGGTTTG	CTG	chr19	55114239	55114260	55114244	55114239	-
SEQ ID NO 3265	GGCTCCTGGGTTTGAGAGAGGA	CTG	chr19	55114231	55114252	55114236	55114231	-
SEQ ID NO 3266	CTGGGTTTGAGAGAGGAGGGGC	CTC	chr19	55114226	55114247	55114231	55114226	-
SEQ ID NO 3267	GGTTTGAGAGAGGAGGGGCTGG	CTG	chr19	55114223	55114244	55114228	55114223	-
SEQ ID NO 3268	GAGAGAGGAGGGGCTGGGGCCT	TTT	chr19	55114218	55114239	55114223	55114218	-
SEQ ID NO 3269	AGAGAGGAGGGGCTGGGGCCTG	TTG	chr19	55114217	55114238	55114222	55114217	-
SEQ ID NO 3270	GGGCCTGGACTCCTGGGTCCGA	CTG	chr19	55114202	55114223	55114207	55114202	-
SEQ ID NO 3271	GACTCCTGGGTCCGAGGGAGGA	CTG	chr19	55114195	55114216	55114200	55114195	-
SEQ ID NO 3272	CTGGGTCCGAGGGAGGAGGGGC	CTC	chr19	55114190	55114211	55114195	55114190	-
SEQ ID NO 3273	GGTCCGAGGGAGGAGGGGCTGG	CTG	chr19	55114187	55114208	55114192	55114187	-
SEQ ID NO 3274	GGGCCTGGACTCCTGGGTCTGA	CTG	chr19	55114166	55114187	55114171	55114166	-
SEQ ID NO 3275	GACTCCTGGGTCTGAGGGTGGA	CTG	chr19	55114159	55114180	55114164	55114159	-
SEQ ID NO 3276	CTGGGTCTGAGGGTGGAGGGAC	CTC	chr19	55114154	55114175	55114159	55114154	-
SEQ ID NO 3277	GGTCTGAGGGTGGAGGGACTGG	CTG	chr19	55114151	55114172	55114156	55114151	-
SEQ ID NO 3278	AGGGTGGAGGGACTGGGGGCCT	CTG	chr19	55114145	55114166	55114150	55114145	-
SEQ ID NO 3279	GGGGCCTGGACTCCTGGGTCCG	CTG	chr19	55114130	55114151	55114135	55114130	-
SEQ ID NO 3280	GACTCCTGGGTCCGAGGGAGGA	CTG	chr19	55114122	55114143	55114127	55114122	-
SEQ ID NO 3281	CTGGGTCCGAGGGAGGAGGGGC	CTC	chr19	55114117	55114138	55114122	55114117	-
SEQ ID NO 3282	GGTCCGAGGGAGGAGGGGCTGG	CTG	chr19	55114114	55114135	55114119	55114114	-
SEQ ID NO 3283	GGGCCTGGACTCGTGGGTCTGA	CTG	chr19	55114093	55114114	55114098	55114093	-
SEQ ID NO 3284	GACTCGTGGGTCTGAGGGAGGA	CTG	chr19	55114086	55114107	55114091	55114086	-
SEQ ID NO 3285	GTGGGTCTGAGGGAGGAGGGGC	CTC	chr19	55114081	55114102	55114086	55114081	-
SEQ ID NO 3286	AGGGAGGAGGGGCTGGGGGCCT	CTG	chr19	55114072	55114093	55114077	55114072	-
SEQ ID NO 3287	GGGGCCTGGACTTCTGGGTCTT	CTG	chr19	55114057	55114078	55114062	55114057	-
SEQ ID NO 3288	GACTTCTGGGTCTTAGGGAGGC	CTG	chr19	55114049	55114070	55114054	55114049	-
SEQ ID NO 3289	CTGGGTCTTAGGGAGGCGGGGC	CTT	chr19	55114044	55114065	55114049	55114044	-
SEQ ID NO 3290	TGGGTCTTAGGGAGGCGGGGCT	TTC	chr19	55114043	55114064	55114048	55114043	-
SEQ ID NO 3291	GGTCTTAGGGAGGCGGGGCTGG	CTG	chr19	55114041	55114062	55114046	55114041	-
SEQ ID NO 3292	AGGGAGGCGGGGCTGGGCCTGG	CTT	chr19	55114035	55114056	55114040	55114035	-
SEQ ID NO 3293	GGGAGGCGGGGCTGGGCCTGGA	TTA	chr19	55114034	55114055	55114039	55114034	-
SEQ ID NO 3294	GGCCTGGACCCCTGGGTCTGAA	CTG	chr19	55114020	55114041	55114025	55114020	-
SEQ ID NO 3295	GACCCCTGGGTCTGAATGGGGA	CTG	chr19	55114014	55114035	55114019	55114014	-
SEQ ID NO 3296	GGTCTGAATGGGGAGAGGCTGG	CTG	chr19	55114006	55114027	55114011	55114006	-
SEQ ID NO 3297	AATGGGGAGAGGCTGGGGGCCT	CTG	chr19	55114000	55114021	55114005	55114000	-
SEQ ID NO 3298	GGGGCCTGGACTCCTTCATCTG	CTG	chr19	55113985	55114006	55113990	55113985	-
SEQ ID NO 3299	GACTCCTTCATCTGAGGGCGGA	CTG	chr19	55113977	55113998	55113982	55113977	-
SEQ ID NO 3300	CTTCATCTGAGGGCGGAAGGGC	CTC	chr19	55113972	55113993	55113977	55113972	-
SEQ ID NO 3301	CATCTGAGGGCGGAAGGGCTGG	CTT	chr19	55113969	55113990	55113974	55113969	-
SEQ ID NO 3302	ATCTGAGGGCGGAAGGGCTGGG	TTC	chr19	55113968	55113989	55113973	55113968	-
SEQ ID NO 3303	AGGGCGGAAGGGCTGGGGCCTG	CTG	chr19	55113963	55113984	55113968	55113963	-
SEQ ID NO 3304	GGGCCTGGCCTCCTGGGTTGAA	CTG	chr19	55113948	55113969	55113953	55113948	-
SEQ ID NO 3305	GCCTCCTGGGTTGAATGGGGAG	CTG	chr19	55113941	55113962	55113946	55113941	-
SEQ ID NO 3306	CTGGGTTGAATGGGGAGGGGTT	CTC	chr19	55113936	55113957	55113941	55113936	-
SEQ ID NO 3307	GGTTGAATGGGGAGGGGTTGGG	CTG	chr19	55113933	55113954	55113938	55113933	-

SEQ ID NO 3308	AATGGGGAGGGGTTGGGCCTGG	TTG	chr19	55113928	55113949	55113933	55113928	-
SEQ ID NO 3309	GGCCTGGACTCTGGAGTCCCTG	TTG	chr19	55113913	55113934	55113918	55113913	-
SEQ ID NO 3310	GACTCTGGAGTCCCTGGTGCCC	CTG	chr19	55113907	55113928	55113912	55113907	-
SEQ ID NO 3311	TGGAGTCCCTGGTGCCCAGGCC	CTC	chr19	55113902	55113923	55113907	55113902	-
SEQ ID NO 3312	GAGTCCCTGGTGCCCAGGCCTC	CTG	chr19	55113900	55113921	55113905	55113900	-
SEQ ID NO 3313	GTGCCCAGGCCTCAGGCATCTT	CTG	chr19	55113891	55113912	55113896	55113891	-
SEQ ID NO 3314	AGGCATCTTTCACAGGGATGCC	CTC	chr19	55113878	55113899	55113883	55113878	-
SEQ ID NO 3315	TCACAGGGATGCCTGTACTGGG	CTT	chr19	55113869	55113890	55113874	55113869	-
SEQ ID NO 3316	CACAGGGATGCCTGTACTGGGC	TTT	chr19	55113868	55113889	55113873	55113868	-
SEQ ID NO 3317	ACAGGGATGCCTGTACTGGGCA	TTC	chr19	55113867	55113888	55113872	55113867	-
SEQ ID NO 3318	TACTGGGCAGGTCCTTGAAAGG	CTG	chr19	55113854	55113875	55113859	55113854	-
SEQ ID NO 3319	GGCAGGTCCTTGAAAGGGAAAG	CTG	chr19	55113849	55113870	55113854	55113849	-
SEQ ID NO 3320	GAAAGGGAAAGGCCCATTGCTC	CTT	chr19	55113838	55113859	55113843	55113838	-
SEQ ID NO 3321	AAAGGGAAAGGCCCATTGCTCT	TTG	chr19	55113837	55113858	55113842	55113837	-
SEQ ID NO 3322	CTCTCCTTGCCCCCCTCCCCTA	TTG	chr19	55113819	55113840	55113824	55113819	-
SEQ ID NO 3323	TCCTTGCCCCCCTCCCCTATCG	CTC	chr19	55113816	55113837	55113821	55113816	-
SEQ ID NO 3324	CTTGCCCCCCTCCCCTATCGCC	CTC	chr19	55113814	55113835	55113819	55113814	-
SEQ ID NO 3325	GCCCCCCTCCCCTATCGCCATG	CTT	chr19	55113811	55113832	55113816	55113811	-
SEQ ID NO 3326	CCCCCCTCCCCTATCGCCATGA	TTG	chr19	55113810	55113831	55113815	55113810	-
SEQ ID NO 3327	CCCTATCGCCATGACAACTGGG	CTC	chr19	55113802	55113823	55113807	55113802	-
SEQ ID NO 3328	TCGCCATGACAACTGGGTGGAA	CTA	chr19	55113797	55113818	55113802	55113797	-
SEQ ID NO 3329	GGTGGAAATAAACGAGCCGAGT	CTG	chr19	55113782	55113803	55113787	55113782	-
SEQ ID NO 3330	ATCCCGTTCCCAGGGCACGTGC	TTC	chr19	55113758	55113779	55113763	55113758	-
SEQ ID NO 3331	CCAGGGCACGTGCGGCCCCTTC	TTC	chr19	55113749	55113770	55113754	55113749	-
SEQ ID NO 3332	CACAGCCCGAGTTTCCATGACC	CTT	chr19	55113728	55113749	55113733	55113728	-
SEQ ID NO 3333	ACAGCCCGAGTTTCCATGACCT	TTC	chr19	55113727	55113748	55113732	55113727	-
SEQ ID NO 3334	CCATGACCTCATGCTCTTGGCC	TTT	chr19	55113714	55113735	55113719	55113714	-
SEQ ID NO 3335	CATGACCTCATGCTCTTGGCCC	TTC	chr19	55113713	55113734	55113718	55113713	-
SEQ ID NO 3336	ATGCTCTTGGCCCTCGTAGCTC	CTC	chr19	55113704	55113725	55113709	55113704	-
SEQ ID NO 3337	TTGGCCCTCGTAGCTCCCTCCC	CTC	chr19	55113698	55113719	55113703	55113698	-
SEQ ID NO 3338	GGCCCTCGTAGCTCCCTCCCGC	CTT	chr19	55113696	55113717	55113701	55113696	-
SEQ ID NO 3339	GCCCTCGTAGCTCCCTCCCGCC	TTG	chr19	55113695	55113716	55113700	55113695	-
SEQ ID NO 3340	GTAGCTCCCTCCCGCCTCCTCC	CTC	chr19	55113689	55113710	55113694	55113689	-
SEQ ID NO 3341	CCTCCCGCCTCCTCCAGATGGG	CTC	chr19	55113682	55113703	55113687	55113682	-
SEQ ID NO 3342	CCGCCTCCTCCAGATGGGCAGC	CTC	chr19	55113678	55113699	55113683	55113678	-
SEQ ID NO 3343	CTCCAGATGGGCAGCTTTGGAG	CTC	chr19	55113671	55113692	55113676	55113671	-
SEQ ID NO 3344	CAGATGGGCAGCTTTGGAGAGG	CTC	chr19	55113668	55113689	55113673	55113668	-
SEQ ID NO 3345	TGGAGAGGTGAGGGACTTGGGG	CTT	chr19	55113654	55113675	55113659	55113654	-
SEQ ID NO 3346	GGAGAGGTGAGGGACTTGGGGG	TTT	chr19	55113653	55113674	55113658	55113653	-
SEQ ID NO 3347	GAGAGGTGAGGGACTTGGGGGG	TTG	chr19	55113652	55113673	55113657	55113652	-
SEQ ID NO 3348	GGGGGGTAATTTATCCCGTGGA	CTT	chr19	55113636	55113657	55113641	55113636	-
SEQ ID NO 3349	GGGGGTAATTTATCCCGTGGAT	TTG	chr19	55113635	55113656	55113640	55113635	-
SEQ ID NO 3350	ATCCCGTGGATCTAGGAGTTTA	TTT	chr19	55113624	55113645	55113629	55113624	-
SEQ ID NO 3351	TCCCGTGGATCTAGGAGTTTAG	TTA	chr19	55113623	55113644	55113628	55113623	-
SEQ ID NO 3352	GGAGTTTAGCTTCACTCCTTCC	CTA	chr19	55113610	55113631	55113615	55113610	-
SEQ ID NO 3353	AGCTTCACTCCTTCCTCAGCTC	TTT	chr19	55113603	55113624	55113608	55113603	-
SEQ ID NO 3354	GCTTCACTCCTTCCTCAGCTCC	TTA	chr19	55113602	55113623	55113607	55113602	-
SEQ ID NO 3355	CACTCCTTCCTCAGCTCCAGTT	CTT	chr19	55113598	55113619	55113603	55113598	-
SEQ ID NO 3356	ACTCCTTCCTCAGCTCCAGTTC	TTC	chr19	55113597	55113618	55113602	55113597	-
SEQ ID NO 3357	CTTCCTCAGCTCCAGTTCAGGT	CTC	chr19	55113593	55113614	55113598	55113593	-
SEQ ID NO 3358	CCTCAGCTCCAGTTCAGGTCCC	CTT	chr19	55113590	55113611	55113595	55113590	-
SEQ ID NO 3359	CTCAGCTCCAGTTCAGGTCCCG	TTC	chr19	55113589	55113610	55113594	55113589	-
SEQ ID NO 3360	AGCTCCAGTTCAGGTCCCGGAG	CTC	chr19	55113586	55113607	55113591	55113586	-
SEQ ID NO 3361	CAGTTCAGGTCCCGGAGCCCAC	CTC	chr19	55113581	55113602	55113586	55113581	-
SEQ ID NO 3362	AGGTCCCGGAGCCCACCCAGTG	TTC	chr19	55113575	55113596	55113580	55113575	-
SEQ ID NO 3363	GGGCAAGTCCCTCCTCCGACCC	CTG	chr19	55113540	55113561	55113545	55113540	-
SEQ ID NO 3364	CTCCGACCCCCTGGACTTCGGC	CTC	chr19	55113527	55113548	55113532	55113527	-
SEQ ID NO 3365	CGACCCCCTGGACTTCGGCTTT	CTC	chr19	55113524	55113545	55113529	55113524	-
SEQ ID NO 3366	GACTTCGGCTTTTGTCCCCCCA	CTG	chr19	55113514	55113535	55113519	55113514	-

SEQ ID NO 3367	CGGCTTTTGTCCCCCCAAGTTT	CTT	chr19	55113509	55113530	55113514	55113509	-
SEQ ID NO 3368	GGCTTTTGTCCCCCCAAGTTTT	TTC	chr19	55113508	55113529	55113513	55113508	-
SEQ ID NO 3369	TTGTCCCCCCAAGTTTTGGACC	CTT	chr19	55113503	55113524	55113508	55113503	-
SEQ ID NO 3370	TGTCCCCCCAAGTTTTGGACCC	TTT	chr19	55113502	55113523	55113507	55113502	-
SEQ ID NO 3371	GTCCCCCCAAGTTTTGGACCCC	TTT	chr19	55113501	55113522	55113506	55113501	-
SEQ ID NO 3372	TCCCCCCAAGTTTTGGACCCCT	TTG	chr19	55113500	55113521	55113505	55113500	-
SEQ ID NO 3373	TGGACCCCTAAGGGAAGAATGA	TTT	chr19	55113487	55113508	55113492	55113487	-
SEQ ID NO 3374	GGACCCCTAAGGGAAGAATGAG	TTT	chr19	55113486	55113507	55113491	55113486	-
SEQ ID NO 3375	GACCCCTAAGGGAAGAATGAGA	TTG	chr19	55113485	55113506	55113490	55113485	-
SEQ ID NO 3376	AGGGAAGAATGAGAAACGGTGG	CTA	chr19	55113477	55113498	55113482	55113477	-
SEQ ID NO 3377	GCTGCAGGGCCCCGTGCAGAGG	CTG	chr19	55113439	55113460	55113444	55113439	-
SEQ ID NO 3378	CAGGGCCCCGTGCAGAGGGGGC	CTG	chr19	55113435	55113456	55113440	55113435	-
SEQ ID NO 3379	AGTGAACTGGAGTGTGACAGCC	CTC	chr19	55113410	55113431	55113415	55113410	-
SEQ ID NO 3380	GAGTGTGACAGCCTGGGGCCCA	CTG	chr19	55113401	55113422	55113406	55113401	-
SEQ ID NO 3381	GGGCCCAGGCACACAGGTGTGC	CTG	chr19	55113386	55113407	55113391	55113386	-
SEQ ID NO 3382	TCTCACCCCTCTGGGAGTCCCG	CTG	chr19	55113359	55113380	55113364	55113359	-
SEQ ID NO 3383	ACCCCTCTGGGAGTCCCGCCCA	CTC	chr19	55113355	55113376	55113360	55113355	-
SEQ ID NO 3384	TGGGAGTCCCGCCCAGGCCCCT	CTC	chr19	55113348	55113369	55113353	55113348	-
SEQ ID NO 3385	GGAGTCCCGCCCAGGCCCCTGA	CTG	chr19	55113346	55113367	55113351	55113346	-
SEQ ID NO 3386	AGTCTGTCCCAGCACAGGGTGG	CTG	chr19	55113325	55113346	55113330	55113325	-
SEQ ID NO 3387	TCCCAGCACAGGGTGGCCTTCC	CTG	chr19	55113319	55113340	55113324	55113319	-
SEQ ID NO 3388	CCTCCACCCTGCATAGCCCTGG	CTT	chr19	55113299	55113320	55113304	55113299	-
SEQ ID NO 3389	CTCCACCCTGCATAGCCCTGGG	TTC	chr19	55113298	55113319	55113303	55113298	-
SEQ ID NO 3390	CACCCTGCATAGCCCTGGGCCC	CTC	chr19	55113295	55113316	55113300	55113295	-
SEQ ID NO 3391	CATAGCCCTGGGCCCACGGCTT	CTG	chr19	55113288	55113309	55113293	55113288	-
SEQ ID NO 3392	GGCCCACGGCTTCGTTCCTGCA	CTG	chr19	55113278	55113299	55113283	55113278	-
SEQ ID NO 3393	CGTTCCTGCAGAGTATCTGCTG	CTT	chr19	55113266	55113287	55113271	55113266	-
SEQ ID NO 3394	GTTCCTGCAGAGTATCTGCTGG	TTC	chr19	55113265	55113286	55113270	55113265	-
SEQ ID NO 3395	CTGCAGAGTATCTGCTGGGGTG	TTC	chr19	55113261	55113282	55113266	55113261	-
SEQ ID NO 3396	CAGAGTATCTGCTGGGGTGGTT	CTG	chr19	55113258	55113279	55113263	55113258	-
SEQ ID NO 3397	CTGGGGTGGTTTCCGAGCTTGA	CTG	chr19	55113247	55113268	55113252	55113247	-
SEQ ID NO 3398	GGGTGGTTTCCGAGCTTGACCC	CTG	chr19	55113244	55113265	55113249	55113244	-
SEQ ID NO 3399	CCGAGCTTGACCCTTGGAAGGA	TTT	chr19	55113235	55113256	55113240	55113235	-
SEQ ID NO 3400	CGAGCTTGACCCTTGGAAGGAC	TTC	chr19	55113234	55113255	55113239	55113234	-
SEQ ID NO 3401	GACCCTTGGAAGGACCTGGCTG	CTT	chr19	55113227	55113248	55113232	55113227	-
SEQ ID NO 3402	ACCCTTGGAAGGACCTGGCTGG	TTG	chr19	55113226	55113247	55113231	55113226	-
SEQ ID NO 3403	GGAAGGACCTGGCTGGGTTTAA	CTT	chr19	55113220	55113241	55113225	55113220	-
SEQ ID NO 3404	GAAGGACCTGGCTGGGTTTAAG	TTG	chr19	55113219	55113240	55113224	55113219	-
SEQ ID NO 3405	GCTGGGTTTAAGGCAGGAGGGG	CTG	chr19	55113209	55113230	55113214	55113209	-
SEQ ID NO 3406	GGTTTAAGGCAGGAGGGGCTGG	CTG	chr19	55113205	55113226	55113210	55113205	-
SEQ ID NO 3407	AAGGCAGGAGGGGCTGGGGGCC	TTT	chr19	55113200	55113221	55113205	55113200	-
SEQ ID NO 3408	AGGCAGGAGGGGCTGGGGGCCA	TTA	chr19	55113199	55113220	55113204	55113199	-
SEQ ID NO 3409	GGGGCCAGGACTCCTGGCTCTG	CTG	chr19	55113184	55113205	55113189	55113184	-
SEQ ID NO 3410	CTGGCTCTGAAGGAGGAGGGGC	CTC	chr19	55113171	55113192	55113176	55113171	-
SEQ ID NO 3411	GCTCTGAAGGAGGAGGGGCTGG	CTG	chr19	55113168	55113189	55113173	55113168	-
SEQ ID NO 3412	TGAAGGAGGAGGGGCTGGAACC	CTC	chr19	55113164	55113185	55113169	55113164	-
SEQ ID NO 3413	AAGGAGGAGGGGCTGGAACCTC	CTG	chr19	55113162	55113183	55113167	55113162	-
SEQ ID NO 3414	GAACCTCTTCCCTAGTCTGAGC	CTG	chr19	55113147	55113168	55113152	55113147	-
SEQ ID NO 3415	TTCCCTAGTCTGAGCACTGGAA	CTC	chr19	55113140	55113161	55113145	55113140	-
SEQ ID NO 3416	CCCTAGTCTGAGCACTGGAAGC	CTT	chr19	55113138	55113159	55113143	55113138	-
SEQ ID NO 3417	CCTAGTCTGAGCACTGGAAGCG	TTC	chr19	55113137	55113158	55113142	55113137	-
SEQ ID NO 3418	GTCTGAGCACTGGAAGCGCCAC	CTA	chr19	55113133	55113154	55113138	55113133	-
SEQ ID NO 3419	AGCACTGGAAGCGCCACCTGTG	CTG	chr19	55113128	55113149	55113133	55113128	-
SEQ ID NO 3420	GAAGCGCCACCTGTGGGTGGTG	CTG	chr19	55113121	55113142	55113126	55113121	-
SEQ ID NO 3421	TGGGTGGTGACGGGGGTTTTGC	CTG	chr19	55113108	55113129	55113113	55113108	-
SEQ ID NO 3422	TGCCGTGTCTAACAGGTACCAT	TTT	chr19	55113089	55113110	55113094	55113089	-
SEQ ID NO 3423	GCCGTGTCTAACAGGTACCATG	TTT	chr19	55113088	55113109	55113093	55113088	-
SEQ ID NO 3424	CCGTGTCTAACAGGTACCATGT	TTG	chr19	55113087	55113108	55113092	55113087	-
SEQ ID NO 3425	ACAGGTACCATGTGGGGTTCCC	CTA	chr19	55113078	55113099	55113083	55113078	-

SEQ ID NO 3426	CCGCACCCAGATGAGAAGCCCC	TTC	chr19	55113058	55113079	55113063	55113058	-
SEQ ID NO 3427	CCTTCCCCGTTCACTTCCTGTT	CTC	chr19	55113033	55113054	55113038	55113033	-
SEQ ID NO 3428	CCCCGTTCACTTCCTGTTTGCA	CTT	chr19	55113029	55113050	55113034	55113029	-
SEQ ID NO 3429	CCCGTTCACTTCCTGTTTGCAG	TTC	chr19	55113028	55113049	55113033	55113028	-
SEQ ID NO 3430	ACTTCCTGTTTGCAGATAGCCA	TTC	chr19	55113021	55113042	55113026	55113021	-
SEQ ID NO 3431	CCTGTTTGCAGATAGCCAGGAG	CTT	chr19	55113017	55113038	55113022	55113017	-
SEQ ID NO 3432	CTGTTTGCAGATAGCCAGGAGT	TTC	chr19	55113016	55113037	55113021	55113016	-
SEQ ID NO 3433	TTTGCAGATAGCCAGGAGTCCT	CTG	chr19	55113013	55113034	55113018	55113013	-
SEQ ID NO 3434	GCAGATAGCCAGGAGTCCTTTC	TTT	chr19	55113010	55113031	55113015	55113010	-
SEQ ID NO 3435	CAGATAGCCAGGAGTCCTTTCG	TTG	chr19	55113009	55113030	55113014	55113009	-
SEQ ID NO 3436	TCGTGGTTTCCACTGAGCACTG	CTT	chr19	55112990	55113011	55112995	55112990	-
SEQ ID NO 3437	CGTGGTTTCCACTGAGCACTGA	TTT	chr19	55112989	55113010	55112994	55112989	-
SEQ ID NO 3438	GTGGTTTCCACTGAGCACTGAA	TTC	chr19	55112988	55113009	55112993	55112988	-
SEQ ID NO 3439	CCACTGAGCACTGAAGGCCTGG	TTT	chr19	55112981	55113002	55112986	55112981	-
SEQ ID NO 3440	CACTGAGCACTGAAGGCCTGGC	TTC	chr19	55112980	55113001	55112985	55112980	-
SEQ ID NO 3441	AGCACTGAAGGCCTGGCCGGCC	CTG	chr19	55112975	55112996	55112980	55112975	-
SEQ ID NO 3442	AAGGCCTGGCCGGCCTGACCAC	CTG	chr19	55112968	55112989	55112973	55112968	-
SEQ ID NO 3443	GCCGGCCTGACCACTGGGCAAC	CTG	chr19	55112960	55112981	55112965	55112960	-
SEQ ID NO 3444	ACCACTGGGCAACCAGGCGTAT	CTG	chr19	55112951	55112972	55112956	55112951	-
SEQ ID NO 3445	GGCAACCAGGCGTATCTTAAAC	CTG	chr19	55112944	55112965	55112949	55112944	-
SEQ ID NO 3446	AAACAGCCAGTGGCCAGAGGCT	CTT	chr19	55112926	55112947	55112931	55112926	-
SEQ ID NO 3447	AACAGCCAGTGGCCAGAGGCTG	TTA	chr19	55112925	55112946	55112930	55112925	-
SEQ ID NO 3448	TTGGGTCATTTTCCCCACTGTC	CTG	chr19	55112903	55112924	55112908	55112903	-
SEQ ID NO 3449	GGTCATTTTCCCCACTGTCCTA	TTG	chr19	55112900	55112921	55112905	55112900	-
SEQ ID NO 3450	TCCCCACTGTCCTAGCACCGTG	TTT	chr19	55112892	55112913	55112897	55112892	-
SEQ ID NO 3451	CCCCACTGTCCTAGCACCGTGT	TTT	chr19	55112891	55112912	55112896	55112891	-
SEQ ID NO 3452	CCCACTGTCCTAGCACCGTGTC	TTC	chr19	55112890	55112911	55112895	55112890	-
SEQ ID NO 3453	TCCTAGCACCGTGTCCCTGGAT	CTG	chr19	55112883	55112904	55112888	55112883	-
SEQ ID NO 3454	GCACCGTGTCCCTGGATCTGTT	CTA	chr19	55112878	55112899	55112883	55112878	-
SEQ ID NO 3455	GATCTGTTTTCGTGGCTCCCTC	CTG	chr19	55112864	55112885	55112869	55112864	-
SEQ ID NO 3456	TTTTCGTGGCTCCCTCTGGAGT	CTG	chr19	55112858	55112879	55112863	55112858	-
SEQ ID NO 3457	TCGTGGCTCCCTCTGGAGTCCC	TTT	chr19	55112855	55112876	55112860	55112855	-
SEQ ID NO 3458	CGTGGCTCCCTCTGGAGTCCCG	TTT	chr19	55112854	55112875	55112859	55112854	-
SEQ ID NO 3459	GTGGCTCCCTCTGGAGTCCCGA	TTC	chr19	55112853	55112874	55112858	55112853	-
SEQ ID NO 3460	CCTCTGGAGTCCCGACTTGCTG	CTC	chr19	55112846	55112867	55112851	55112846	-
SEQ ID NO 3461	TGGAGTCCCGACTTGCTGGGAC	CTC	chr19	55112842	55112863	55112847	55112842	-
SEQ ID NO 3462	GAGTCCCGACTTGCTGGGACAC	CTG	chr19	55112840	55112861	55112845	55112840	-
SEQ ID NO 3463	GCTGGGACACCGTGGCTGGGGT	CTT	chr19	55112828	55112849	55112833	55112828	-
SEQ ID NO 3464	CTGGGACACCGTGGCTGGGGTA	TTG	chr19	55112827	55112848	55112832	55112827	-
SEQ ID NO 3465	GGACACCGTGGCTGGGGTAGGT	CTG	chr19	55112824	55112845	55112829	55112824	-
SEQ ID NO 3466	GGGTAGGTGCGGCTGACGGCTG	CTG	chr19	55112810	55112831	55112815	55112810	-
SEQ ID NO 3467	ACGGCTGTTTCCCACCCCCAGG	CTG	chr19	55112795	55112816	55112800	55112795	-
SEQ ID NO 3468	TTTCCCACCCCCAGGCCTGCAT	CTG	chr19	55112788	55112809	55112793	55112788	-
SEQ ID NO 3469	CCCACCCCCAGGCCTGCATTGA	TTT	chr19	55112785	55112806	55112790	55112785	-
SEQ ID NO 3470	CCACCCCCAGGCCTGCATTGAT	TTC	chr19	55112784	55112805	55112789	55112784	-
SEQ ID NO 3471	CATTGATGAGAACCTGGAGGTG	CTG	chr19	55112769	55112790	55112774	55112769	-
SEQ ID NO 3472	ATGAGAACCTGGAGGTGGTGCG	TTG	chr19	55112764	55112785	55112769	55112764	-
SEQ ID NO 3473	GAGGTGGTGCGCTTCTTGGTGG	CTG	chr19	55112753	55112774	55112758	55112753	-
SEQ ID NO 3474	CTTGGTGGAGCAGGGCGCCACT	CTT	chr19	55112739	55112760	55112744	55112739	-
SEQ ID NO 3475	TTGGTGGAGCAGGGCGCCACTG	TTC	chr19	55112738	55112759	55112743	55112738	-
SEQ ID NO 3476	GGTGGAGCAGGGCGCCACTGTG	CTT	chr19	55112736	55112757	55112741	55112736	-
SEQ ID NO 3477	GTGGAGCAGGGCGCCACTGTGA	TTG	chr19	55112735	55112756	55112740	55112735	-
SEQ ID NO 3478	TGAACCAGGCAGACAACGAGGG	CTG	chr19	55112716	55112737	55112721	55112716	-
SEQ ID NO 3479	GACGCCACTGCACGTGGCCGCC	CTG	chr19	55112691	55112712	55112696	55112691	-
SEQ ID NO 3480	CACGTGGCCGCCTCCTGTGGCT	CTG	chr19	55112681	55112702	55112686	55112681	-
SEQ ID NO 3481	CTGTGGCTACCTAGATATCGCC	CTC	chr19	55112667	55112688	55112672	55112667	-

Figure 7

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 3482	TAATTTCCCTCCGTTTGTCC	TAG	chr4	73404268	73404287	73404284	+
SEQ ID NO 3483	CTGTCAACCCCACACGCCTT	TGG	chr4	73404301	73404320	73404317	+
SEQ ID NO 3484	CACACGCCTTTGGCACAATG	AAG	chr4	73404311	73404330	73404327	+
SEQ ID NO 3485	ACGCCTTTGGCACAATGAAG	TGG	chr4	73404314	73404333	73404330	+
SEQ ID NO 3486	CGCCTTTGGCACAATGAAGT	GGG	chr4	73404315	73404334	73404331	+
SEQ ID NO 3487	ATTTCCCTTCTTTTTCTCTT	TAG	chr4	73404346	73404365	73404362	+
SEQ ID NO 3488	CCTTCTTTTTCTCTTTAGCT	CGG	chr4	73404351	73404370	73404367	+
SEQ ID NO 3489	CTCTTTAGCTCGGCTTATTC	CAG	chr4	73404361	73404380	73404377	+
SEQ ID NO 3490	TCTTTAGCTCGGCTTATTCC	AGG	chr4	73404362	73404381	73404378	+
SEQ ID NO 3491	CTTTAGCTCGGCTTATTCCA	GGG	chr4	73404363	73404382	73404379	+
SEQ ID NO 3492	TTTAGCTCGGCTTATTCCAG	GGG	chr4	73404364	73404383	73404380	+
SEQ ID NO 3493	TTCCAGGGGTGTGTTTCGTC	GAG	chr4	73404378	73404397	73404394	+
SEQ ID NO 3494	TGTTTCGTCGAGATGCACGT	AAG	chr4	73404389	73404408	73404405	+
SEQ ID NO 3495	CAACTTTTATTCTATTTTCC	CAG	chr4	73404432	73404451	73404448	+
SEQ ID NO 3496	TCTATTTTCCCAGTAAAATA	AAG	chr4	73404442	73404461	73404458	+
SEQ ID NO 3497	TTCCCAGTAAAATAAAGTTT	TAG	chr4	73404448	73404467	73404464	+
SEQ ID NO 3498	TAGTAAACTCTGCATCTTTA	AAG	chr4	73404468	73404487	73404484	+
SEQ ID NO 3499	GCATCTTTAAAGAATTATTT	TGG	chr4	73404479	73404498	73404495	+
SEQ ID NO 3500	TTTGGCATTTATTTCTAAAA	TGG	chr4	73404497	73404516	73404513	+
SEQ ID NO 3501	CATTTATTTCTAAAATGGCA	TAG	chr4	73404502	73404521	73404518	+
SEQ ID NO 3502	CATAGTATTTTGTATTTGTG	AAG	chr4	73404520	73404539	73404536	+
SEQ ID NO 3503	TTGTATTTGTGAAGTCTTAC	AAG	chr4	73404529	73404548	73404545	+
SEQ ID NO 3504	TGTATTTGTGAAGTCTTACA	AGG	chr4	73404530	73404549	73404546	+
SEQ ID NO 3505	TTAATAAAATTCAAACATCC	TAG	chr4	73404561	73404580	73404577	+
SEQ ID NO 3506	TAATAAAATTCAAACATCCT	AGG	chr4	73404562	73404581	73404578	+
SEQ ID NO 3507	ATCCTAGGTAAAAAAAAAAA	AAG	chr4	73404577	73404596	73404593	+
SEQ ID NO 3508	TCCTAGGTAAAAAAAAAAAA	AGG	chr4	73404578	73404597	73404594	+
SEQ ID NO 3509	AGGTAAAAAAAAAAAAAGGT	CAG	chr4	73404582	73404601	73404598	+
SEQ ID NO 3510	AAAAAAAGGTCAGAATTGTT	TAG	chr4	73404592	73404611	73404608	+
SEQ ID NO 3511	GTAATTTTCTTTTGCGCACT	AAG	chr4	73404620	73404639	73404636	+
SEQ ID NO 3512	TAATTTTCTTTTGCGCACTA	AGG	chr4	73404621	73404640	73404637	+
SEQ ID NO 3513	TTTCTTTTGCGCACTAAGGA	AAG	chr4	73404625	73404644	73404641	+
SEQ ID NO 3514	TGCGCACTAAGGAAAGTGCA	AAG	chr4	73404632	73404651	73404648	+
SEQ ID NO 3515	AAGGAAAGTGCAAAGTAACT	TAG	chr4	73404640	73404659	73404656	+
SEQ ID NO 3516	GGAAAGTGCAAAGTAACTTA	GAG	chr4	73404642	73404661	73404658	+
SEQ ID NO 3517	TTAGAGTGACTGAAACTTCA	CAG	chr4	73404659	73404678	73404675	+
SEQ ID NO 3518	GTGACTGAAACTTCACAGAA	TAG	chr4	73404664	73404683	73404680	+
SEQ ID NO 3519	TGACTGAAACTTCACAGAAT	AGG	chr4	73404665	73404684	73404681	+
SEQ ID NO 3520	GACTGAAACTTCACAGAATA	GGG	chr4	73404666	73404685	73404682	+
SEQ ID NO 3521	AACTTCACAGAATAGGGTTG	AAG	chr4	73404672	73404691	73404688	+
SEQ ID NO 3522	TTGAATTCATAACTATCCCA	AAG	chr4	73404696	73404715	73404712	+
SEQ ID NO 3523	TGTGCTGTTGATCTCATAAA	TAG	chr4	73404761	73404780	73404777	+
SEQ ID NO 3524	ATTTATATTTATTTTCATTT	TAG	chr4	73404791	73404810	73404807	+
SEQ ID NO 3525	TTCATTTTAGTCTGTCTTCT	TGG	chr4	73404804	73404823	73404820	+
SEQ ID NO 3526	GTCTTCTTGGTTGCTGTTGA	TAG	chr4	73404817	73404836	73404833	+
SEQ ID NO 3527	TTGCTGTTGATAGACACTAA	AAG	chr4	73404827	73404846	73404843	+

SEQ ID NO 3528	GCTGTTGATAGACACTAAAA	GAG	chr4	73404829	73404848	73404845	+
SEQ ID NO 3529	GATAGACACTAAAAGAGTAT	TAG	chr4	73404835	73404854	73404851	+
SEQ ID NO 3530	AAGAGTATTAGATATTATCT	AAG	chr4	73404847	73404866	73404863	+
SEQ ID NO 3531	TATTATCTAAGTTTGAATAT	AAG	chr4	73404859	73404878	73404875	+
SEQ ID NO 3532	ATTATCTAAGTTTGAATATA	AGG	chr4	73404860	73404879	73404876	+
SEQ ID NO 3533	ATATTTAATAATTTTTAAAA	TAG	chr4	73404889	73404908	73404905	+
SEQ ID NO 3534	AATTTTTAAAATAGTATTCT	TGG	chr4	73404898	73404917	73404914	+
SEQ ID NO 3535	TTGAATTATTCTTCTGTTTA	AAG	chr4	73404924	73404943	73404940	+
SEQ ID NO 3536	TGAATTATTCTTCTGTTTAA	AGG	chr4	73404925	73404944	73404941	+
SEQ ID NO 3537	ATTATTCTTCTGTTTAAAGG	CAG	chr4	73404928	73404947	73404944	+
SEQ ID NO 3538	ATTCTTCTGTTTAAAGGCAG	AAG	chr4	73404931	73404950	73404947	+
SEQ ID NO 3539	AAATAATTGAACATCATCCT	GAG	chr4	73404954	73404973	73404970	+
SEQ ID NO 3540	CATCATCCTGAGTTTTTCTG	TAG	chr4	73404965	73404984	73404981	+
SEQ ID NO 3541	ATCATCCTGAGTTTTTCTGT	AGG	chr4	73404966	73404985	73404982	+
SEQ ID NO 3542	CTGAGTTTTTCTGTAGGAAT	CAG	chr4	73404972	73404991	73404988	+
SEQ ID NO 3543	GAGTTTTTCTGTAGGAATCA	GAG	chr4	73404974	73404993	73404990	+
SEQ ID NO 3544	TTGAAACAAATGCATAATCT	AAG	chr4	73405006	73405025	73405022	+
SEQ ID NO 3545	AATGCATAATCTAAGTCAAA	TGG	chr4	73405014	73405033	73405030	+
SEQ ID NO 3546	CATAATCTAAGTCAAATGGA	AAG	chr4	73405018	73405037	73405034	+
SEQ ID NO 3547	CAAATGGAAAGAAATATAAA	AAG	chr4	73405030	73405049	73405046	+
SEQ ID NO 3548	TTATTACTTCTTGTTTTCTT	CAG	chr4	73405058	73405077	73405074	+
SEQ ID NO 3549	CTTTTTTTTCTTCCCTTGCC	CAG	chr4	73405093	73405112	73405109	+
SEQ ID NO 3550	TTTTCTTCCCTTGCCCAGAC	AAG	chr4	73405098	73405117	73405114	+
SEQ ID NO 3551	TTCTTCCCTTGCCCAGACAA	GAG	chr4	73405100	73405119	73405116	+
SEQ ID NO 3552	TCCCTTGCCCAGACAAGAGT	GAG	chr4	73405104	73405123	73405120	+
SEQ ID NO 3553	CCCTTGCCCAGACAAGAGTG	AGG	chr4	73405105	73405124	73405121	+
SEQ ID NO 3554	ACAAGAGTGAGGTTGCTCAT	CGG	chr4	73405116	73405135	73405132	+
SEQ ID NO 3555	TGAGGTTGCTCATCGGTTTA	AAG	chr4	73405123	73405142	73405139	+
SEQ ID NO 3556	TGCTCATCGGTTTAAAGATT	TGG	chr4	73405129	73405148	73405145	+
SEQ ID NO 3557	GCTCATCGGTTTAAAGATTT	GGG	chr4	73405130	73405149	73405146	+
SEQ ID NO 3558	TCATCGGTTTAAAGATTTGG	GAG	chr4	73405132	73405151	73405148	+
SEQ ID NO 3559	TCGGTTTAAAGATTTGGGAG	AAG	chr4	73405135	73405154	73405151	+
SEQ ID NO 3560	TTTGGGAGAAGAAAATTTCA	AAG	chr4	73405147	73405166	73405163	+
SEQ ID NO 3561	TCCCAAATCTTTAAACCGAT	GAG	chr4	73405134	73405153	73405137	-
SEQ ID NO 3562	TGAGCAACCTCACTCTTGTC	TGG	chr4	73405115	73405134	73405118	-
SEQ ID NO 3563	GAGCAACCTCACTCTTGTCT	GGG	chr4	73405114	73405133	73405117	-
SEQ ID NO 3564	AACCTCACTCTTGTCTGGGC	AAG	chr4	73405110	73405129	73405113	-
SEQ ID NO 3565	ACCTCACTCTTGTCTGGGCA	AGG	chr4	73405109	73405128	73405112	-
SEQ ID NO 3566	CCTCACTCTTGTCTGGGCAA	GGG	chr4	73405108	73405127	73405111	-
SEQ ID NO 3567	CACTCTTGTCTGGGCAAGGG	AAG	chr4	73405105	73405124	73405108	-
SEQ ID NO 3568	CTGGGCAAGGGAAGAAAAAA	AAG	chr4	73405096	73405115	73405099	-
SEQ ID NO 3569	TGGGCAAGGGAAGAAAAAAA	AGG	chr4	73405095	73405114	73405098	-
SEQ ID NO 3570	AAAAGGATTGTTAAATACTG	AAG	chr4	73405078	73405097	73405081	-
SEQ ID NO 3571	TGTTAAATACTGAAGAAAAC	AAG	chr4	73405070	73405089	73405073	-
SEQ ID NO 3572	TAAATACTGAAGAAAACAAG	AAG	chr4	73405067	73405086	73405070	-
SEQ ID NO 3573	ATATTTCTTTCCATTTGACT	TAG	chr4	73405027	73405046	73405030	-
SEQ ID NO 3574	ATGCATTTGTTTCAAAATAT	TGG	chr4	73405001	73405020	73405004	-

SEQ ID NO 3575	TGCATTTGTTTCAAAATATT	GGG	chr4	73405000	73405019	73405003	-
SEQ ID NO 3576	ATATTGGGCTCTGATTCCTA	CAG	chr4	73404985	73405004	73404988	-
SEQ ID NO 3577	CTGATTCCTACAGAAAAACT	CAG	chr4	73404975	73404994	73404978	-
SEQ ID NO 3578	TGATTCCTACAGAAAAACTC	AGG	chr4	73404974	73404993	73404977	-
SEQ ID NO 3579	TTATTTCTTCTGCCTTTAAA	CAG	chr4	73404940	73404959	73404943	-
SEQ ID NO 3580	TTTCTTCTGCCTTTAAACAG	AAG	chr4	73404937	73404956	73404940	-
SEQ ID NO 3581	AGAAGAATAATTCAATTACC	AAG	chr4	73404919	73404938	73404922	-
SEQ ID NO 3582	TAAAAATTATTAAATATTTA	TAG	chr4	73404886	73404905	73404889	-
SEQ ID NO 3583	TATAGCCTTATATTCAAACT	TAG	chr4	73404868	73404887	73404871	-
SEQ ID NO 3584	GATAATATCTAATACTCTTT	TAG	chr4	73404846	73404865	73404849	-
SEQ ID NO 3585	ACTCTTTTAGTGTCTATCAA	CAG	chr4	73404833	73404852	73404836	-
SEQ ID NO 3586	AGTGTCTATCAACAGCAACC	AAG	chr4	73404825	73404844	73404828	-
SEQ ID NO 3587	GTCTATCAACAGCAACCAAG	AAG	chr4	73404822	73404841	73404825	-
SEQ ID NO 3588	ATCAACAGCAACCAAGAAGA	CAG	chr4	73404818	73404837	73404821	-
SEQ ID NO 3589	ATGAAAATAAATATAAATAC	AAG	chr4	73404789	73404808	73404792	-
SEQ ID NO 3590	TAAATACAAGTTCTATTTAT	GAG	chr4	73404776	73404795	73404779	-
SEQ ID NO 3591	AGTTCTATTTATGAGATCAA	CAG	chr4	73404768	73404787	73404771	-
SEQ ID NO 3592	TATTTATGAGATCAACAGCA	CAG	chr4	73404763	73404782	73404766	-
SEQ ID NO 3593	ATTTATGAGATCAACAGCAC	AGG	chr4	73404762	73404781	73404765	-
SEQ ID NO 3594	GATCAACAGCACAGGTTTTG	TGG	chr4	73404754	73404773	73404757	-
SEQ ID NO 3595	GGTTTTGTGGTTTTTAAATA	AAG	chr4	73404741	73404760	73404744	-
SEQ ID NO 3596	TGTGGTTTTTAAATAAAGCA	TAG	chr4	73404736	73404755	73404739	-
SEQ ID NO 3597	TTAAATAAAGCATAGTGCAA	TGG	chr4	73404728	73404747	73404731	-
SEQ ID NO 3598	ATAAAGCATAGTGCAATGGA	TAG	chr4	73404724	73404743	73404727	-
SEQ ID NO 3599	TAAAGCATAGTGCAATGGAT	AGG	chr4	73404723	73404742	73404726	-
SEQ ID NO 3600	TAGTGCAATGGATAGGTCTT	TGG	chr4	73404716	73404735	73404719	-
SEQ ID NO 3601	AGTGCAATGGATAGGTCTTT	GGG	chr4	73404715	73404734	73404718	-
SEQ ID NO 3602	CAATGGATAGGTCTTTGGGA	TAG	chr4	73404711	73404730	73404714	-
SEQ ID NO 3603	ATCTTCAACCCTATTCTGTG	AAG	chr4	73404677	73404696	73404680	-
SEQ ID NO 3604	AACCCTATTCTGTGAAGTTT	CAG	chr4	73404671	73404690	73404674	-
SEQ ID NO 3605	TGTGAAGTTTCAGTCACTCT	AAG	chr4	73404661	73404680	73404664	-
SEQ ID NO 3606	AAGTTACTTTGCACTTTCCT	TAG	chr4	73404641	73404660	73404644	-
SEQ ID NO 3607	GCACTTTCCTTAGTGCGCAA	AAG	chr4	73404631	73404650	73404634	-
SEQ ID NO 3608	TAGTGCGCAAAAGAAAATTA	CAG	chr4	73404621	73404640	73404624	-
SEQ ID NO 3609	GACCTTTTTTTTTTTTTACC	TAG	chr4	73404583	73404602	73404586	-
SEQ ID NO 3610	ACCTTTTTTTTTTTTTACCT	AGG	chr4	73404582	73404601	73404585	-
SEQ ID NO 3611	GATGTTTGAATTTTATTAAT	AAG	chr4	73404560	73404579	73404563	-
SEQ ID NO 3612	TATTAATAAGATAACCTTGT	AAG	chr4	73404547	73404566	73404550	-
SEQ ID NO 3613	TACAAAATACTATGCCATTT	TAG	chr4	73404514	73404533	73404517	-
SEQ ID NO 3614	AATGCCAAAATAATTCTTTA	AAG	chr4	73404486	73404505	73404489	-
SEQ ID NO 3615	AAAATAATTCTTTAAAGATG	CAG	chr4	73404480	73404499	73404483	-
SEQ ID NO 3616	AATAATTCTTTAAAGATGCA	GAG	chr4	73404478	73404497	73404481	-
SEQ ID NO 3617	TTACTAAAACTTTATTTTAC	TGG	chr4	73404454	73404473	73404457	-
SEQ ID NO 3618	TACTAAAACTTTATTTTACT	GGG	chr4	73404453	73404472	73404456	-
SEQ ID NO 3619	ACTTTATTTTACTGGGAAAA	TAG	chr4	73404446	73404465	73404449	-
SEQ ID NO 3620	TTACTGGGAAAATAGAATAA	AAG	chr4	73404438	73404457	73404441	-
SEQ ID NO 3621	ATAGAATAAAAGTTGAACAA	TAG	chr4	73404427	73404446	73404430	-

SEQ ID NO 3622	AAAGTTGAACAATAGAAAAA	TGG	chr4	73404419	73404438	73404422	-
SEQ ID NO 3623	ATCTCGACGAAACACACCCC	TGG	chr4	73404383	73404402	73404386	-
SEQ ID NO 3624	ACGAAACACACCCCTGGAAT	AAG	chr4	73404377	73404396	73404380	-
SEQ ID NO 3625	ACACACCCCTGGAATAAGCC	GAG	chr4	73404372	73404391	73404375	-
SEQ ID NO 3626	CCCTGGAATAAGCCGAGCTA	AAG	chr4	73404366	73404385	73404369	-
SEQ ID NO 3627	CTGGAATAAGCCGAGCTAAA	GAG	chr4	73404364	73404383	73404367	-
SEQ ID NO 3628	TAAGCCGAGCTAAAGAGAAA	AAG	chr4	73404358	73404377	73404361	-
SEQ ID NO 3629	GCCGAGCTAAAGAGAAAAAG	AAG	chr4	73404355	73404374	73404358	-
SEQ ID NO 3630	CCGAGCTAAAGAGAAAAAGA	AGG	chr4	73404354	73404373	73404357	-
SEQ ID NO 3631	CGAGCTAAAGAGAAAAAGAA	GGG	chr4	73404353	73404372	73404356	-
SEQ ID NO 3632	AGAGAAAAAGAAGGGAAATA	AAG	chr4	73404345	73404364	73404348	-
SEQ ID NO 3633	GAGAAAAAGAAGGGAAATAA	AGG	chr4	73404344	73404363	73404347	-
SEQ ID NO 3634	TTACCCACTTCATTGTGCCA	AAG	chr4	73404321	73404340	73404324	-
SEQ ID NO 3635	TACCCACTTCATTGTGCCAA	AGG	chr4	73404320	73404339	73404323	-
SEQ ID NO 3636	TTCATTGTGCCAAAGGCGTG	TGG	chr4	73404313	73404332	73404316	-
SEQ ID NO 3637	TCATTGTGCCAAAGGCGTGT	GGG	chr4	73404312	73404331	73404315	-
SEQ ID NO 3638	CATTGTGCCAAAGGCGTGTG	GGG	chr4	73404311	73404330	73404314	-
SEQ ID NO 3639	CCAAAGGCGTGTGGGGTTGA	CAG	chr4	73404304	73404323	73404307	-
SEQ ID NO 3640	AAGGCGTGTGGGGTTGACAG	AAG	chr4	73404301	73404320	73404304	-
SEQ ID NO 3641	GGCGTGTGGGGTTGACAGAA	GAG	chr4	73404299	73404318	73404302	-
SEQ ID NO 3642	GTGGGGTTGACAGAAGAGAA	AAG	chr4	73404294	73404313	73404297	-
SEQ ID NO 3643	GGTTGACAGAAGAGAAAAGC	TAG	chr4	73404290	73404309	73404293	-
SEQ ID NO 3644	GTTGACAGAAGAGAAAAGCT	AGG	chr4	73404289	73404308	73404292	-
SEQ ID NO 3645	AAGAGAAAAGCTAGGACAAA	CGG	chr4	73404281	73404300	73404284	-
SEQ ID NO 3646	GAGAAAAGCTAGGACAAACG	GAG	chr4	73404279	73404298	73404282	-
SEQ ID NO 3647	AGAAAAGCTAGGACAAACGG	AGG	chr4	73404278	73404297	73404281	-
SEQ ID NO 3648	GAAAAGCTAGGACAAACGGA	GGG	chr4	73404277	73404296	73404280	-
SEQ ID NO 3649	TAGGACAAACGGAGGGAAAT	TAG	chr4	73404270	73404289	73404273	-

Figure 8

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 3650	CACGCCTTTGGCACAATGAA	GTGGGT	chr4	73404313	73404332	73404329	+
SEQ ID NO 3651	TCTTTAGCTCGGCTTATTCC	AGGGGT	chr4	73404362	73404381	73404378	+
SEQ ID NO 3652	TAGTAAACTCTGCATCTTTA	AAGAAT	chr4	73404468	73404487	73404484	+
SEQ ID NO 3653	AGGTAAAAAAAAAAAAAGGT	CAGAAT	chr4	73404582	73404601	73404598	+
SEQ ID NO 3654	AAGGAAAGTGCAAAGTAACT	TAGAGT	chr4	73404640	73404659	73404656	+
SEQ ID NO 3655	TTAGAGTGACTGAAACTTCA	CAGAAT	chr4	73404659	73404678	73404675	+
SEQ ID NO 3656	GTGACTGAAACTTCACAGAA	TAGGGT	chr4	73404664	73404683	73404680	+
SEQ ID NO 3657	TCACAGAATAGGGTTGAAGA	TTGAAT	chr4	73404676	73404695	73404692	+
SEQ ID NO 3658	TTGCTGTTGATAGACACTAA	AAGAGT	chr4	73404827	73404846	73404843	+
SEQ ID NO 3659	GTATTAGATATTATCTAAGT	TTGAAT	chr4	73404851	73404870	73404867	+
SEQ ID NO 3660	TAAAATAGTATTCTTGGTAA	TTGAAT	chr4	73404904	73404923	73404920	+
SEQ ID NO 3661	AGAAATAATTGAACATCATC	CTGAGT	chr4	73404952	73404971	73404968	+
SEQ ID NO 3662	ATCATCCTGAGTTTTTCTGT	AGGAAT	chr4	73404966	73404985	73404982	+
SEQ ID NO 3663	TTTTCTTCCCTTGCCCAGAC	AAGAGT	chr4	73405098	73405117	73405114	+
SEQ ID NO 3664	CTGGGCAAGGGAAGAAAAAA	AAGGAT	chr4	73405096	73405115	73405099	-
SEQ ID NO 3665	CTGATTCCTACAGAAAAACT	CAGGAT	chr4	73404975	73404994	73404978	-
SEQ ID NO 3666	TTTCTTCTGCCTTTAAACAG	AAGAAT	chr4	73404937	73404956	73404940	-
SEQ ID NO 3667	AGAAGAATAATTCAATTACC	AAGAAT	chr4	73404919	73404938	73404922	-
SEQ ID NO 3668	TTTAAATAAAGCATAGTGCA	ATGGAT	chr4	73404729	73404748	73404732	-
SEQ ID NO 3669	TAGTGCAATGGATAGGTCTT	TGGGAT	chr4	73404716	73404735	73404719	-
SEQ ID NO 3670	GATAGGTCTTTGGGATAGTT	ATGAAT	chr4	73404706	73404725	73404709	-
SEQ ID NO 3671	GACCTTTTTTTTTTTTTACC	TAGGAT	chr4	73404583	73404602	73404586	-
SEQ ID NO 3672	TTTTTTTTTACCTAGGATGT	TTGAAT	chr4	73404575	73404594	73404578	-
SEQ ID NO 3673	AAAATAATTCTTTAAAGATG	CAGAGT	chr4	73404480	73404499	73404483	-
SEQ ID NO 3674	ACTTTATTTTACTGGGAAAA	TAGAAT	chr4	73404446	73404465	73404449	-
SEQ ID NO 3675	AAAAGTTGAACAATAGAAAA	ATGGAT	chr4	73404420	73404439	73404423	-
SEQ ID NO 3676	ATCTCGACGAAACACACCCC	TGGAAT	chr4	73404383	73404402	73404386	-
SEQ ID NO 3677	TTCATTGTGCCAAAGGCGTG	TGGGGT	chr4	73404313	73404332	73404316	-

Figure 9

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 3678	GTGTTTCGTCGAGATGCACG	TAAGAAA	chr4	73404388	73404407	73404404	+
SEQ ID NO 3679	TTAGTAAACTCTGCATCTTT	AAAGAAT	chr4	73404467	73404486	73404483	+
SEQ ID NO 3680	TAGGTAAAAAAAAAAAAAGG	TCAGAAT	chr4	73404581	73404600	73404597	+
SEQ ID NO 3681	CTTAGAGTGACTGAAACTTC	ACAGAAT	chr4	73404658	73404677	73404674	+
SEQ ID NO 3682	TATTCTTCTGTTTAAAGGCA	GAAGAAA	chr4	73404930	73404949	73404946	+
SEQ ID NO 3683	GCATAATCTAAGTCAAATGG	AAAGAAA	chr4	73405017	73405036	73405033	+
SEQ ID NO 3684	ATCGGTTTAAAGATTTGGGA	GAAGAAA	chr4	73405134	73405153	73405150	+
SEQ ID NO 3685	TCACTCTTGTCTGGGCAAGG	GAAGAAA	chr4	73405106	73405125	73405109	-
SEQ ID NO 3686	AAAAAGGATTGTTAAATACT	GAAGAAA	chr4	73405079	73405098	73405082	-
SEQ ID NO 3687	AATATTGGGCTCTGATTCCT	ACAGAAA	chr4	73404986	73405005	73404989	-
SEQ ID NO 3688	ATTTCTTCTGCCTTTAAACA	GAAGAAT	chr4	73404938	73404957	73404941	-
SEQ ID NO 3689	CAGAAGAATAATTCAATTAC	CAAGAAT	chr4	73404920	73404939	73404923	-
SEQ ID NO 3690	TGCACTTTCCTTAGTGCGCA	AAAGAAA	chr4	73404632	73404651	73404635	-
SEQ ID NO 3691	ATACAAAATACTATGCCATT	TTAGAAA	chr4	73404515	73404534	73404518	-
SEQ ID NO 3692	AACTTTATTTTACTGGGAAA	ATAGAAT	chr4	73404447	73404466	73404450	-
SEQ ID NO 3693	AATAGAATAAAAGTTGAACA	ATAGAAA	chr4	73404428	73404447	73404431	-
SEQ ID NO 3694	CCTGGAATAAGCCGAGCTAA	AGAGAAA	chr4	73404365	73404384	73404368	-
SEQ ID NO 3695	AGGCGTGTGGGGTTGACAGA	AGAGAAA	chr4	73404300	73404319	73404303	-

Figure 10

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 3696	CATTGCACTATGCTTTATTT	AAAAAC	chr4	73404726	73404745	73404742	+
SEQ ID NO 3697	TATGCTTTATTTAAAAACCA	CAAAAC	chr4	73404734	73404753	73404750	+
SEQ ID NO 3698	AAGGATTGTTAAATACTGAA	GAAAAC	chr4	73405076	73405095	73405079	-
SEQ ID NO 3699	TTGGGCTCTGATTCCTACAG	AAAAAC	chr4	73404982	73405001	73404985	-
SEQ ID NO 3700	TTTAAAGATGCAGAGTTTAC	TAAAAC	chr4	73404470	73404489	73404473	-

Figure 11

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 3701	GTATATTAGTGCTAATTTCC	CTCCGTTT	chr4	73404256	73404275	73404272	+
SEQ ID NO 3702	GCTAATTTCCCTCCGTTTGT	CCTAGCTT	chr4	73404266	73404285	73404282	+
SEQ ID NO 3703	TCCCTTCTTTTTCTCTTTAG	CTCGGCTT	chr4	73404349	73404368	73404365	+
SEQ ID NO 3704	TAGCTCGGCTTATTCCAGGG	GTGTGTTT	chr4	73404366	73404385	73404382	+
SEQ ID NO 3705	ATTCTATTTTCCCAGTAAAA	TAAAGTTT	chr4	73404440	73404459	73404456	+
SEQ ID NO 3706	TAAAAAAAAAAAAAGGTCAG	AATTGTTT	chr4	73404585	73404604	73404601	+
SEQ ID NO 3707	GAAACTTCACAGAATAGGGT	TGAAGATT	chr4	73404670	73404689	73404686	+
SEQ ID NO 3708	CCAAAGACCTATCCATTGCA	CTATGCTT	chr4	73404713	73404732	73404729	+
SEQ ID NO 3709	AAAAGAGTATTAGATATTAT	CTAAGTTT	chr4	73404845	73404864	73404861	+
SEQ ID NO 3710	TCTTGGTAATTGAATTATTC	TTCTGTTT	chr4	73404915	73404934	73404931	+
SEQ ID NO 3711	AGAAATAATTGAACATCATC	CTGAGTTT	chr4	73404952	73404971	73404968	+
SEQ ID NO 3712	TAAAAAGTAACATTATTACT	TCTTGTTT	chr4	73405046	73405065	73405062	+
SEQ ID NO 3713	AGACAAGAGTGAGGTTGCTC	ATCGGTTT	chr4	73405114	73405133	73405130	+
SEQ ID NO 3714	AGTGAGGTTGCTCATCGGTT	TAAAGATT	chr4	73405121	73405140	73405137	+
SEQ ID NO 3715	TCTGGGCAAGGGAAGAAAAA	AAAGGATT	chr4	73405097	73405116	73405100	-
SEQ ID NO 3716	TTATATTTCTTTCCATTTGA	CTTAGATT	chr4	73405029	73405048	73405032	-
SEQ ID NO 3717	CCATTTGACTTAGATTATGC	ATTTGTTT	chr4	73405017	73405036	73405020	-
SEQ ID NO 3718	ATTTGTTTCAAAATATTGGG	CTCTGATT	chr4	73404997	73405016	73405000	-
SEQ ID NO 3719	CTATTTATGAGATCAACAGC	ACAGGTTT	chr4	73404764	73404783	73404767	-
SEQ ID NO 3720	GAGATCAACAGCACAGGTTT	TGTGGTTT	chr4	73404756	73404775	73404759	-
SEQ ID NO 3721	CAATCTTCAACCCTATTCTG	TGAAGTTT	chr4	73404679	73404698	73404682	-
SEQ ID NO 3722	CCTTTTTTTTTTTTTACCTA	GGATGTTT	chr4	73404581	73404600	73404584	-
SEQ ID NO 3723	AAAATAATTCTTTAAAGATG	CAGAGTTT	chr4	73404480	73404499	73404483	-
SEQ ID NO 3724	TAAAAGTTGAACAATAGAAA	AATGGATT	chr4	73404421	73404440	73404424	-

Figure 12

#	Sequence	PAM	Chr	Start	End	Cut site 1 (5' of)	Cut site 2 (5' of)	Str
SEQ ID N O 3725	GTGCTAATTTCCCTCCGTTTGT	TTA	chr4	73404264	73404285	73404281	73404286	+
SEQ ID N O 3726	ATTTCCCTCCGTTTGTCCTAGC	CTA	chr4	73404270	73404291	73404287	73404292	+
SEQ ID N O 3727	CCCTCCGTTTGTCCTAGCTTTT	TTT	chr4	73404274	73404295	73404291	73404296	+
SEQ ID N O 3728	CCTCCGTTTGTCCTAGCTTTTC	TTC	chr4	73404275	73404296	73404292	73404297	+
SEQ ID N O 3729	CGTTTGTCCTAGCTTTTCTCTT	CTC	chr4	73404279	73404300	73404296	73404301	+
SEQ ID N O 3730	GTCCTAGCTTTTCTCTTCTGTC	TTT	chr4	73404284	73404305	73404301	73404306	+
SEQ ID N O 3731	TCCTAGCTTTTCTCTTCTGTCA	TTG	chr4	73404285	73404306	73404302	73404307	+
SEQ ID N O 3732	GCTTTTCTCTTCTGTCAACCCC	CTA	chr4	73404290	73404311	73404307	73404312	+
SEQ ID N O 3733	TTCTCTTCTGTCAACCCCACAC	CTT	chr4	73404294	73404315	73404311	73404316	+
SEQ ID N O 3734	TCTCTTCTGTCAACCCCACACG	TTT	chr4	73404295	73404316	73404312	73404317	+
SEQ ID N O 3735	CTCTTCTGTCAACCCCACACGC	TTT	chr4	73404296	73404317	73404313	73404318	+
SEQ ID N O 3736	TCTTCTGTCAACCCCACACGCC	TTC	chr4	73404297	73404318	73404314	73404319	+
SEQ ID N O 3737	TTCTGTCAACCCCACACGCCTT	CTC	chr4	73404299	73404320	73404316	73404321	+
SEQ ID N O 3738	CTGTCAACCCCACACGCCTTTG	CTT	chr4	73404301	73404322	73404318	73404323	+
SEQ ID N O 3739	TGTCAACCCCACACGCCTTTGG	TTC	chr4	73404302	73404323	73404319	73404324	+
SEQ ID N O 3740	TCAACCCCACACGCCTTTGGCA	CTG	chr4	73404304	73404325	73404321	73404326	+
SEQ ID N O 3741	TGGCACAATGAAGTGGGTAACC	CTT	chr4	73404321	73404342	73404338	73404343	+
SEQ ID N O 3742	GGCACAATGAAGTGGGTAACCT	TTT	chr4	73404322	73404343	73404339	73404344	+
SEQ ID N O 3743	GCACAATGAAGTGGGTAACCTT	TTG	chr4	73404323	73404344	73404340	73404345	+
SEQ ID N O 3744	TATTTCCCTTCTTTTTCTCTTT	CTT	chr4	73404345	73404366	73404362	73404367	+
SEQ ID N O 3745	ATTTCCCTTCTTTTTCTCTTTA	TTT	chr4	73404346	73404367	73404363	73404368	+
SEQ ID N O 3746	TTTCCCTTCTTTTTCTCTTTAG	TTA	chr4	73404347	73404368	73404364	73404369	+
SEQ ID N O 3747	CCCTTCTTTTTCTCTTTAGCTC	TTT	chr4	73404350	73404371	73404367	73404372	+
SEQ ID N O 3748	CCTTCTTTTTCTCTTTAGCTCG	TTC	chr4	73404351	73404372	73404368	73404373	+
SEQ ID N O 3749	CTTTTTCTCTTTAGCTCGGCTT	CTT	chr4	73404355	73404376	73404372	73404377	+
SEQ ID N O 3750	TTTTTCTCTTTAGCTCGGCTTA	TTC	chr4	73404356	73404377	73404373	73404378	+
SEQ ID N O 3751	TTTCTCTTTAGCTCGGCTTATT	CTT	chr4	73404358	73404379	73404375	73404380	+
SEQ ID N O 3752	TTCTCTTTAGCTCGGCTTATTC	TTT	chr4	73404359	73404380	73404376	73404381	+
SEQ ID N O 3753	TCTCTTTAGCTCGGCTTATTCC	TTT	chr4	73404360	73404381	73404377	73404382	+
SEQ ID N O 3754	CTCTTTAGCTCGGCTTATTCCA	TTT	chr4	73404361	73404382	73404378	73404383	+
SEQ ID N O 3755	TCTTTAGCTCGGCTTATTCCAG	TTC	chr4	73404362	73404383	73404379	73404384	+
SEQ ID N O 3756	TTTAGCTCGGCTTATTCCAGGG	CTC	chr4	73404364	73404385	73404381	73404386	+
SEQ ID N O 3757	TAGCTCGGCTTATTCCAGGGGT	CTT	chr4	73404366	73404387	73404383	73404388	+
SEQ ID N O 3758	AGCTCGGCTTATTCCAGGGGTG	TTT	chr4	73404367	73404388	73404384	73404389	+
SEQ ID N O 3759	GCTCGGCTTATTCCAGGGGTGT	TTA	chr4	73404368	73404389	73404385	73404390	+
SEQ ID N O 3760	GGCTTATTCCAGGGGTGTGTTT	CTC	chr4	73404372	73404393	73404389	73404394	+
SEQ ID N O 3761	ATTCCAGGGGTGTGTTTCGTCG	CTT	chr4	73404377	73404398	73404394	73404399	+
SEQ ID N O 3762	TTCCAGGGGTGTGTTTCGTCGA	TTA	chr4	73404378	73404399	73404395	73404400	+
SEQ ID N O 3763	CAGGGGTGTGTTTCGTCGAGAT	TTC	chr4	73404381	73404402	73404398	73404403	+
SEQ ID N O 3764	CGTCGAGATGCACGTAAGAAAT	TTT	chr4	73404394	73404415	73404411	73404416	+
SEQ ID N O 3765	GTCGAGATGCACGTAAGAAATC	TTC	chr4	73404395	73404416	73404412	73404417	+
SEQ ID N O 3766	TTCTATTGTTCAACTTTTATTC	TTT	chr4	73404422	73404443	73404439	73404444	+
SEQ ID N O 3767	TCTATTGTTCAACTTTTATTCT	TTT	chr4	73404423	73404444	73404440	73404445	+
SEQ ID N O 3768	CTATTGTTCAACTTTTATTCTA	TTT	chr4	73404424	73404445	73404441	73404446	+
SEQ ID N O 3769	TATTGTTCAACTTTTATTCTAT	TTC	chr4	73404425	73404446	73404442	73404447	+
SEQ ID N O 3770	TTGTTCAACTTTTATTCTATTT	CTA	chr4	73404427	73404448	73404444	73404449	+
SEQ ID N O 3771	TTCAACTTTTATTCTATTTTCC	TTG	chr4	73404430	73404451	73404447	73404452	+
SEQ ID N O 3772	AACTTTTATTCTATTTTCCCAG	TTC	chr4	73404433	73404454	73404450	73404455	+
SEQ ID N O 3773	TTATTCTATTTTCCCAGTAAAA	CTT	chr4	73404438	73404459	73404455	73404460	+
SEQ ID N O 3774	TATTCTATTTTCCCAGTAAAAT	TTT	chr4	73404439	73404460	73404456	73404461	+
SEQ ID N O 3775	ATTCTATTTTCCCAGTAAAATA	TTT	chr4	73404440	73404461	73404457	73404462	+
SEQ ID N O 3776	TTCTATTTTCCCAGTAAAATAA	TTA	chr4	73404441	73404462	73404458	73404463	+
SEQ ID N O 3777	TATTTTCCCAGTAAAATAAAGT	TTC	chr4	73404444	73404465	73404461	73404466	+
SEQ ID N O 3778	TTTTCCCAGTAAAATAAAGTTT	CTA	chr4	73404446	73404467	73404463	73404468	+
SEQ ID N O 3779	TCCCAGTAAAATAAAGTTTTAG	TTT	chr4	73404449	73404470	73404466	73404471	+
SEQ ID N O 3780	CCCAGTAAAATAAAGTTTTAGT	TTT	chr4	73404450	73404471	73404467	73404472	+

SEQ ID N O 3781	CCAGTAAAATAAAGTTTTAGTA	TTC	chr4	73404451	73404472	73404468	73404473	+
SEQ ID N O 3782	TAGTAAACTCTGCATCTTTAAA	TTT	chr4	73404468	73404489	73404485	73404490	+
SEQ ID N O 3783	AGTAAACTCTGCATCTTTAAAG	TTT	chr4	73404469	73404490	73404486	73404491	+
SEQ ID N O 3784	GTAAACTCTGCATCTTTAAAGA	TTA	chr4	73404470	73404491	73404487	73404492	+
SEQ ID N O 3785	TGCATCTTTAAAGAATTATTTT	CTC	chr4	73404478	73404499	73404495	73404500	+
SEQ ID N O 3786	CATCTTTAAAGAATTATTTTGG	CTG	chr4	73404480	73404501	73404497	73404502	+
SEQ ID N O 3787	TAAAGAATTATTTTGGCATTTA	CTT	chr4	73404486	73404507	73404503	73404508	+
SEQ ID N O 3788	AAAGAATTATTTTGGCATTTAT	TTT	chr4	73404487	73404508	73404504	73404509	+
SEQ ID N O 3789	AAGAATTATTTTGGCATTTATT	TTA	chr4	73404488	73404509	73404505	73404510	+
SEQ ID N O 3790	TTTTGGCATTTATTTCTAAAAT	TTA	chr4	73404496	73404517	73404513	73404518	+
SEQ ID N O 3791	TGGCATTTATTTCTAAAATGGC	TTT	chr4	73404499	73404520	73404516	73404521	+
SEQ ID N O 3792	GGCATTTATTTCTAAAATGGCA	TTT	chr4	73404500	73404521	73404517	73404522	+
SEQ ID N O 3793	GCATTTATTTCTAAAATGGCAT	TTG	chr4	73404501	73404522	73404518	73404523	+
SEQ ID N O 3794	ATTTCTAAAATGGCATAGTATT	TTT	chr4	73404507	73404528	73404524	73404529	+
SEQ ID N O 3795	TTTCTAAAATGGCATAGTATTT	TTA	chr4	73404508	73404529	73404525	73404530	+
SEQ ID N O 3796	CTAAAATGGCATAGTATTTTGT	TTT	chr4	73404511	73404532	73404528	73404533	+
SEQ ID N O 3797	TAAAATGGCATAGTATTTTGTA	TTC	chr4	73404512	73404533	73404529	73404534	+
SEQ ID N O 3798	AAATGGCATAGTATTTTGTATT	CTA	chr4	73404514	73404535	73404531	73404536	+
SEQ ID N O 3799	TGTATTTGTGAAGTCTTACAAG	TTT	chr4	73404530	73404551	73404547	73404552	+
SEQ ID N O 3800	GTATTTGTGAAGTCTTACAAGG	TTT	chr4	73404531	73404552	73404548	73404553	+
SEQ ID N O 3801	TATTTGTGAAGTCTTACAAGGT	TTG	chr4	73404532	73404553	73404549	73404554	+
SEQ ID N O 3802	GTGAAGTCTTACAAGGTTATCT	TTT	chr4	73404537	73404558	73404554	73404559	+
SEQ ID N O 3803	TGAAGTCTTACAAGGTTATCTT	TTG	chr4	73404538	73404559	73404555	73404560	+
SEQ ID N O 3804	ACAAGGTTATCTTATTAATAAA	CTT	chr4	73404547	73404568	73404564	73404569	+
SEQ ID N O 3805	CAAGGTTATCTTATTAATAAAA	TTA	chr4	73404548	73404569	73404565	73404570	+
SEQ ID N O 3806	TCTTATTAATAAAATTCAAACA	TTA	chr4	73404556	73404577	73404573	73404578	+
SEQ ID N O 3807	ATTAATAAAATTCAAACATCCT	CTT	chr4	73404560	73404581	73404577	73404582	+
SEQ ID N O 3808	TTAATAAAATTCAAACATCCTA	TTA	chr4	73404561	73404582	73404578	73404583	+
SEQ ID N O 3809	ATAAAATTCAAACATCCTAGGT	TTA	chr4	73404564	73404585	73404581	73404586	+
SEQ ID N O 3810	AAACATCCTAGGTAAAAAAAAA	TTC	chr4	73404573	73404594	73404590	73404595	+
SEQ ID N O 3811	GGTAAAAAAAAAAAAAGGTCAG	CTA	chr4	73404583	73404604	73404600	73404605	+
SEQ ID N O 3812	TTTAGTGACTGTAATTTTCTTT	TTG	chr4	73404610	73404631	73404627	73404632	+
SEQ ID N O 3813	AGTGACTGTAATTTTCTTTTGC	TTT	chr4	73404613	73404634	73404630	73404635	+
SEQ ID N O 3814	GTGACTGTAATTTTCTTTTGCG	TTA	chr4	73404614	73404635	73404631	73404636	+
SEQ ID N O 3815	TAATTTTCTTTTGCGCACTAAG	CTG	chr4	73404621	73404642	73404638	73404643	+
SEQ ID N O 3816	TCTTTTGCGCACTAAGGAAAGT	TTT	chr4	73404627	73404648	73404644	73404649	+
SEQ ID N O 3817	CTTTTGCGCACTAAGGAAAGTG	TTT	chr4	73404628	73404649	73404645	73404650	+
SEQ ID N O 3818	TTTTGCGCACTAAGGAAAGTGC	TTC	chr4	73404629	73404650	73404646	73404651	+
SEQ ID N O 3819	TTGCGCACTAAGGAAAGTGCAA	CTT	chr4	73404631	73404652	73404648	73404653	+
SEQ ID N O 3820	TGCGCACTAAGGAAAGTGCAAA	TTT	chr4	73404632	73404653	73404649	73404654	+
SEQ ID N O 3821	GCGCACTAAGGAAAGTGCAAAG	TTT	chr4	73404633	73404654	73404650	73404655	+
SEQ ID N O 3822	CGCACTAAGGAAAGTGCAAAGT	TTG	chr4	73404634	73404655	73404651	73404656	+
SEQ ID N O 3823	AGGAAAGTGCAAAGTAACTTAG	CTA	chr4	73404641	73404662	73404658	73404663	+
SEQ ID N O 3824	AGAGTGACTGAAACTTCACAGA	CTT	chr4	73404661	73404682	73404678	73404683	+
SEQ ID N O 3825	GAGTGACTGAAACTTCACAGAA	TTA	chr4	73404662	73404683	73404679	73404684	+
SEQ ID N O 3826	AAACTTCACAGAATAGGGTTGA	CTG	chr4	73404671	73404692	73404688	73404693	+
SEQ ID N O 3827	CACAGAATAGGGTTGAAGATTG	CTT	chr4	73404677	73404698	73404694	73404699	+
SEQ ID N O 3828	ACAGAATAGGGTTGAAGATTGA	TTC	chr4	73404678	73404699	73404695	73404700	+
SEQ ID N O 3829	AAGATTGAATTCATAACTATCC	TTG	chr4	73404692	73404713	73404709	73404714	+
SEQ ID N O 3830	AATTCATAACTATCCCAAAGAC	TTG	chr4	73404699	73404720	73404716	73404721	+
SEQ ID N O 3831	ATAACTATCCCAAAGACCTATC	TTC	chr4	73404704	73404725	73404721	73404726	+
SEQ ID N O 3832	TCCCAAAGACCTATCCATTGCA	CTA	chr4	73404711	73404732	73404728	73404733	+
SEQ ID N O 3833	TCCATTGCACTATGCTTTATTT	CTA	chr4	73404724	73404745	73404741	73404746	+
SEQ ID N O 3834	CACTATGCTTTATTTAAAAACC	TTG	chr4	73404731	73404752	73404748	73404753	+
SEQ ID N O 3835	TGCTTTATTTAAAAACCACAAA	CTA	chr4	73404736	73404757	73404753	73404758	+
SEQ ID N O 3836	TATTTAAAAACCACAAAACCTG	CTT	chr4	73404741	73404762	73404758	73404763	+
SEQ ID N O 3837	ATTTAAAAACCACAAAACCTGT	TTT	chr4	73404742	73404763	73404759	73404764	+

SEQ ID N O 3838	TTTAAAAACCACAAAACCTGTG	TTA	chr4	73404743	73404764	73404760	73404765	+
SEQ ID N O 3839	AAAAACCACAAAACCTGTGCTG	TTT	chr4	73404746	73404767	73404763	73404768	+
SEQ ID N O 3840	AAAACCACAAAACCTGTGCTGT	TTA	chr4	73404747	73404768	73404764	73404769	+
SEQ ID N O 3841	TGCTGTTGATCTCATAAATAGA	CTG	chr4	73404763	73404784	73404780	73404785	+
SEQ ID N O 3842	TTGATCTCATAAATAGAACTTG	CTG	chr4	73404768	73404789	73404785	73404790	+
SEQ ID N O 3843	ATCTCATAAATAGAACTTGTAT	TTG	chr4	73404771	73404792	73404788	73404793	+
SEQ ID N O 3844	ATAAATAGAACTTGTATTTATA	CTC	chr4	73404776	73404797	73404793	73404798	+
SEQ ID N O 3845	GTATTTATATTTATTTTCATTT	CTT	chr4	73404789	73404810	73404806	73404811	+
SEQ ID N O 3846	TATTTATATTTATTTTCATTTT	TTG	chr4	73404790	73404811	73404807	73404812	+
SEQ ID N O 3847	ATATTTATTTTCATTTTAGTCT	TTT	chr4	73404795	73404816	73404812	73404817	+
SEQ ID N O 3848	TATTTATTTTCATTTTAGTCTG	TTA	chr4	73404796	73404817	73404813	73404818	+
SEQ ID N O 3849	ATTTTCATTTTAGTCTGTCTTC	TTT	chr4	73404801	73404822	73404818	73404823	+
SEQ ID N O 3850	TTTTCATTTTAGTCTGTCTTCT	TTA	chr4	73404802	73404823	73404819	73404824	+
SEQ ID N O 3851	TCATTTTAGTCTGTCTTCTTGG	TTT	chr4	73404805	73404826	73404822	73404827	+
SEQ ID N O 3852	CATTTTAGTCTGTCTTCTTGGT	TTT	chr4	73404806	73404827	73404823	73404828	+
SEQ ID N O 3853	ATTTTAGTCTGTCTTCTTGGTT	TTC	chr4	73404807	73404828	73404824	73404829	+
SEQ ID N O 3854	TAGTCTGTCTTCTTGGTTGCTG	TTT	chr4	73404811	73404832	73404828	73404833	+
SEQ ID N O 3855	AGTCTGTCTTCTTGGTTGCTGT	TTT	chr4	73404812	73404833	73404829	73404834	+
SEQ ID N O 3856	GTCTGTCTTCTTGGTTGCTGTT	TTA	chr4	73404813	73404834	73404830	73404835	+
SEQ ID N O 3857	TCTTCTTGGTTGCTGTTGATAG	CTG	chr4	73404818	73404839	73404835	73404840	+
SEQ ID N O 3858	CTTGGTTGCTGTTGATAGACAC	CTT	chr4	73404822	73404843	73404839	73404844	+
SEQ ID N O 3859	TTGGTTGCTGTTGATAGACACT	TTC	chr4	73404823	73404844	73404840	73404845	+
SEQ ID N O 3860	GGTTGCTGTTGATAGACACTAA	CTT	chr4	73404825	73404846	73404842	73404847	+
SEQ ID N O 3861	GTTGCTGTTGATAGACACTAAA	TTG	chr4	73404826	73404847	73404843	73404848	+
SEQ ID N O 3862	CTGTTGATAGACACTAAAAGAG	TTG	chr4	73404830	73404851	73404847	73404852	+
SEQ ID N O 3863	TTGATAGACACTAAAAGAGTAT	CTG	chr4	73404833	73404854	73404850	73404855	+
SEQ ID N O 3864	ATAGACACTAAAAGAGTATTAG	TTG	chr4	73404836	73404857	73404853	73404858	+
SEQ ID N O 3865	AAAGAGTATTAGATATTATCTA	CTA	chr4	73404846	73404867	73404863	73404868	+
SEQ ID N O 3866	GATATTATCTAAGTTTGAATAT	TTA	chr4	73404857	73404878	73404874	73404879	+
SEQ ID N O 3867	TCTAAGTTTGAATATAAGGCTA	TTA	chr4	73404864	73404885	73404881	73404886	+
SEQ ID N O 3868	AGTTTGAATATAAGGCTATAAA	CTA	chr4	73404868	73404889	73404885	73404890	+
SEQ ID N O 3869	GAATATAAGGCTATAAATATTT	TTT	chr4	73404873	73404894	73404890	73404895	+
SEQ ID N O 3870	AATATAAGGCTATAAATATTTA	TTG	chr4	73404874	73404895	73404891	73404896	+
SEQ ID N O 3871	TAAATATTTAATAATTTTTAAA	CTA	chr4	73404886	73404907	73404903	73404908	+
SEQ ID N O 3872	AATAATTTTTAAAATAGTATTC	TTT	chr4	73404895	73404916	73404912	73404917	+
SEQ ID N O 3873	ATAATTTTTAAAATAGTATTCT	TTA	chr4	73404896	73404917	73404913	73404918	+
SEQ ID N O 3874	TTAAAATAGTATTCTTGGTAAT	TTT	chr4	73404903	73404924	73404920	73404925	+
SEQ ID N O 3875	TAAAATAGTATTCTTGGTAATT	TTT	chr4	73404904	73404925	73404921	73404926	+
SEQ ID N O 3876	AAAATAGTATTCTTGGTAATTG	TTT	chr4	73404905	73404926	73404922	73404927	+
SEQ ID N O 3877	AAATAGTATTCTTGGTAATTGA	TTA	chr4	73404906	73404927	73404923	73404928	+
SEQ ID N O 3878	TTGGTAATTGAATTATTCTTCT	TTC	chr4	73404917	73404938	73404934	73404939	+
SEQ ID N O 3879	GGTAATTGAATTATTCTTCTGT	CTT	chr4	73404919	73404940	73404936	73404941	+
SEQ ID N O 3880	GTAATTGAATTATTCTTCTGTT	TTG	chr4	73404920	73404941	73404937	73404942	+
SEQ ID N O 3881	AATTATTCTTCTGTTTAAAGGC	TTG	chr4	73404927	73404948	73404944	73404949	+
SEQ ID N O 3882	TTCTTCTGTTTAAAGGCAGAAG	TTA	chr4	73404932	73404953	73404949	73404954	+
SEQ ID N O 3883	TTCTGTTTAAAGGCAGAAGAAA	TTC	chr4	73404935	73404956	73404952	73404957	+
SEQ ID N O 3884	CTGTTTAAAGGCAGAAGAAATA	CTT	chr4	73404937	73404958	73404954	73404959	+
SEQ ID N O 3885	TGTTTAAAGGCAGAAGAAATAA	TTC	chr4	73404938	73404959	73404955	73404960	+
SEQ ID N O 3886	TTTAAAGGCAGAAGAAATAATT	CTG	chr4	73404940	73404961	73404957	73404962	+
SEQ ID N O 3887	AAAGGCAGAAGAAATAATTGAA	TTT	chr4	73404943	73404964	73404960	73404965	+
SEQ ID N O 3888	AAGGCAGAAGAAATAATTGAAC	TTA	chr4	73404944	73404965	73404961	73404966	+
SEQ ID N O 3889	AACATCATCCTGAGTTTTTCTG	TTG	chr4	73404963	73404984	73404980	73404985	+
SEQ ID N O 3890	AGTTTTTCTGTAGGAATCAGAG	CTG	chr4	73404975	73404996	73404992	73404997	+
SEQ ID N O 3891	TTCTGTAGGAATCAGAGCCCAA	TTT	chr4	73404980	73405001	73404997	73405002	+
SEQ ID N O 3892	TCTGTAGGAATCAGAGCCCAAT	TTT	chr4	73404981	73405002	73404998	73405003	+
SEQ ID N O 3893	CTGTAGGAATCAGAGCCCAATA	TTT	chr4	73404982	73405003	73404999	73405004	+
SEQ ID N O 3894	TGTAGGAATCAGAGCCCAATAT	TTC	chr4	73404983	73405004	73405000	73405005	+

SEQ ID N O 3895	TAGGAATCAGAGCCCAATATTT	CTG	chr4	73404985	73405006	73405002	73405007	+
SEQ ID N O 3896	TGAAACAAATGCATAATCTAAG	TTT	chr4	73405007	73405028	73405024	73405029	+
SEQ ID N O 3897	GAAACAAATGCATAATCTAAGT	TTT	chr4	73405008	73405029	73405025	73405030	+
SEQ ID N O 3898	AAACAAATGCATAATCTAAGTC	TTG	chr4	73405009	73405030	73405026	73405031	+
SEQ ID N O 3899	AGTCAAATGGAAAGAAATATAA	CTA	chr4	73405027	73405048	73405044	73405049	+
SEQ ID N O 3900	TTACTTCTTGTTTTCTTCAGTA	TTA	chr4	73405061	73405082	73405078	73405083	+
SEQ ID N O 3901	CTTCTTGTTTTCTTCAGTATTT	TTA	chr4	73405064	73405085	73405081	73405086	+
SEQ ID N O 3902	CTTGTTTTCTTCAGTATTTAAC	CTT	chr4	73405067	73405088	73405084	73405089	+
SEQ ID N O 3903	TTGTTTTCTTCAGTATTTAACA	TTC	chr4	73405068	73405089	73405085	73405090	+
SEQ ID N O 3904	GTTTTCTTCAGTATTTAACAAT	CTT	chr4	73405070	73405091	73405087	73405092	+
SEQ ID N O 3905	TTTTCTTCAGTATTTAACAATC	TTG	chr4	73405071	73405092	73405088	73405093	+
SEQ ID N O 3906	TCTTCAGTATTTAACAATCCTT	TTT	chr4	73405074	73405095	73405091	73405096	+
SEQ ID N O 3907	CTTCAGTATTTAACAATCCTTT	TTT	chr4	73405075	73405096	73405092	73405097	+
SEQ ID N O 3908	TTCAGTATTTAACAATCCTTTT	TTC	chr4	73405076	73405097	73405093	73405098	+
SEQ ID N O 3909	CAGTATTTAACAATCCTTTTTT	CTT	chr4	73405078	73405099	73405095	73405100	+
SEQ ID N O 3910	AGTATTTAACAATCCTTTTTTT	TTC	chr4	73405079	73405100	73405096	73405101	+
SEQ ID N O 3911	AACAATCCTTTTTTTTCTTCCC	TTT	chr4	73405086	73405107	73405103	73405108	+
SEQ ID N O 3912	ACAATCCTTTTTTTTCTTCCCT	TTA	chr4	73405087	73405108	73405104	73405109	+
SEQ ID N O 3913	TTTTTTCTTCCCTTGCCCAGAC	CTT	chr4	73405096	73405117	73405113	73405118	+
SEQ ID N O 3914	TTTTTCTTCCCTTGCCCAGACA	TTT	chr4	73405097	73405118	73405114	73405119	+
SEQ ID N O 3915	TTTTCTTCCCTTGCCCAGACAA	TTT	chr4	73405098	73405119	73405115	73405120	+
SEQ ID N O 3916	TTTCTTCCCTTGCCCAGACAAG	TTT	chr4	73405099	73405120	73405116	73405121	+
SEQ ID N O 3917	TTCTTCCCTTGCCCAGACAAGA	TTT	chr4	73405100	73405121	73405117	73405122	+
SEQ ID N O 3918	TCTTCCCTTGCCCAGACAAGAG	TTT	chr4	73405101	73405122	73405118	73405123	+
SEQ ID N O 3919	CTTCCCTTGCCCAGACAAGAGT	TTT	chr4	73405102	73405123	73405119	73405124	+
SEQ ID N O 3920	TTCCCTTGCCCAGACAAGAGTG	TTC	chr4	73405103	73405124	73405120	73405125	+
SEQ ID N O 3921	CCCTTGCCCAGACAAGAGTGAG	CTT	chr4	73405105	73405126	73405122	73405127	+
SEQ ID N O 3922	CCTTGCCCAGACAAGAGTGAGG	TTC	chr4	73405106	73405127	73405123	73405128	+
SEQ ID N O 3923	GCCCAGACAAGAGTGAGGTTGC	CTT	chr4	73405110	73405131	73405127	73405132	+
SEQ ID N O 3924	CCCAGACAAGAGTGAGGTTGCT	TTG	chr4	73405111	73405132	73405128	73405133	+
SEQ ID N O 3925	CTCATCGGTTTAAAGATTTGGG	TTG	chr4	73405131	73405152	73405148	73405153	+
SEQ ID N O 3926	ATCGGTTTAAAGATTTGGGAGA	CTC	chr4	73405134	73405155	73405151	73405156	+
SEQ ID N O 3927	AAAGATTTGGGAGAAGAAAATT	TTT	chr4	73405142	73405163	73405159	73405164	+
SEQ ID N O 3928	AAGATTTGGGAGAAGAAAATTT	TTA	chr4	73405143	73405164	73405160	73405165	+
SEQ ID N O 3929	GGGAGAAGAAAATTTCAAAGCC	TTT	chr4	73405150	73405171	73405167	73405172	+
SEQ ID N O 3930	GGAGAAGAAAATTTCAAAGCCT	TTG	chr4	73405151	73405172	73405168	73405173	+
SEQ ID N O 3931	TGAAATTTTCTTCTCCCAAATC	CTT	chr4	73405145	73405166	73405150	73405145	-
SEQ ID N O 3932	GAAATTTTCTTCTCCCAAATCT	TTT	chr4	73405144	73405165	73405149	73405144	-
SEQ ID N O 3933	AAATTTTCTTCTCCCAAATCTT	TTG	chr4	73405143	73405164	73405148	73405143	-
SEQ ID N O 3934	TCTTCTCCCAAATCTTTAAACC	TTT	chr4	73405137	73405158	73405142	73405137	-
SEQ ID N O 3935	CTTCTCCCAAATCTTTAAACCG	TTT	chr4	73405136	73405157	73405141	73405136	-
SEQ ID N O 3936	TTCTCCCAAATCTTTAAACCGA	TTC	chr4	73405135	73405156	73405140	73405135	-
SEQ ID N O 3937	CTCCCAAATCTTTAAACCGATG	CTT	chr4	73405133	73405154	73405138	73405133	-
SEQ ID N O 3938	TCCCAAATCTTTAAACCGATGA	TTC	chr4	73405132	73405153	73405137	73405132	-
SEQ ID N O 3939	CCAAATCTTTAAACCGATGAGC	CTC	chr4	73405130	73405151	73405135	73405130	-
SEQ ID N O 3940	TAAACCGATGAGCAACCTCACT	CTT	chr4	73405121	73405142	73405126	73405121	-
SEQ ID N O 3941	AAACCGATGAGCAACCTCACTC	TTT	chr4	73405120	73405141	73405125	73405120	-
SEQ ID N O 3942	AACCGATGAGCAACCTCACTCT	TTA	chr4	73405119	73405140	73405124	73405119	-
SEQ ID N O 3943	ACTCTTGTCTGGGCAAGGGAAG	CTC	chr4	73405102	73405123	73405107	73405102	-
SEQ ID N O 3944	TTGTCTGGGCAAGGGAAGAAAA	CTC	chr4	73405098	73405119	73405103	73405098	-
SEQ ID N O 3945	GTCTGGGCAAGGGAAGAAAAAA	CTT	chr4	73405096	73405117	73405101	73405096	-
SEQ ID N O 3946	TCTGGGCAAGGGAAGAAAAAAA	TTG	chr4	73405095	73405116	73405100	73405095	-
SEQ ID N O 3947	GGCAAGGGAAGAAAAAAAAGGA	CTG	chr4	73405091	73405112	73405096	73405091	-
SEQ ID N O 3948	TTAAATACTGAAGAAAACAAGA	TTG	chr4	73405066	73405087	73405071	73405066	-
SEQ ID N O 3949	AATACTGAAGAAAACAAGAAGT	TTA	chr4	73405063	73405084	73405068	73405063	-
SEQ ID N O 3950	AAGAAAACAAGAAGTAATAATG	CTG	chr4	73405056	73405077	73405061	73405056	-
SEQ ID N O 3951	CTTTTTATATTTCTTTCCATTT	TTA	chr4	73405031	73405052	73405036	73405031	-

SEQ ID N O 3952	TTTATATTTCTTTCCATTTGAC	CTT	chr4	73405028	73405049	73405033	73405028	-
SEQ ID N O 3953	TTATATTTCTTTCCATTTGACT	TTT	chr4	73405027	73405048	73405032	73405027	-
SEQ ID N O 3954	TATATTTCTTTCCATTTGACTT	TTT	chr4	73405026	73405047	73405031	73405026	-
SEQ ID N O 3955	ATATTTCTTTCCATTTGACTTA	TTT	chr4	73405025	73405046	73405030	73405025	-
SEQ ID N O 3956	TATTTCTTTCCATTTGACTTAG	TTA	chr4	73405024	73405045	73405029	73405024	-
SEQ ID N O 3957	CTTTCCATTTGACTTAGATTAT	TTT	chr4	73405019	73405040	73405024	73405019	-
SEQ ID N O 3958	TTTCCATTTGACTTAGATTATG	TTC	chr4	73405018	73405039	73405023	73405018	-
SEQ ID N O 3959	TCCATTTGACTTAGATTATGCA	CTT	chr4	73405016	73405037	73405021	73405016	-
SEQ ID N O 3960	CCATTTGACTTAGATTATGCAT	TTT	chr4	73405015	73405036	73405020	73405015	-
SEQ ID N O 3961	CATTTGACTTAGATTATGCATT	TTC	chr4	73405014	73405035	73405019	73405014	-
SEQ ID N O 3962	GACTTAGATTATGCATTTGTTT	TTT	chr4	73405009	73405030	73405014	73405009	-
SEQ ID N O 3963	ACTTAGATTATGCATTTGTTTC	TTG	chr4	73405008	73405029	73405013	73405008	-
SEQ ID N O 3964	AGATTATGCATTTGTTTCAAAA	CTT	chr4	73405004	73405025	73405009	73405004	-
SEQ ID N O 3965	GATTATGCATTTGTTTCAAAAT	TTA	chr4	73405003	73405024	73405008	73405003	-
SEQ ID N O 3966	TGCATTTGTTTCAAAATATTGG	TTA	chr4	73404998	73405019	73405003	73404998	-
SEQ ID N O 3967	GTTTCAAAATATTGGGCTCTGA	TTT	chr4	73404991	73405012	73404996	73404991	-
SEQ ID N O 3968	TTTCAAAATATTGGGCTCTGAT	TTG	chr4	73404990	73405011	73404995	73404990	-
SEQ ID N O 3969	CAAAATATTGGGCTCTGATTCC	TTT	chr4	73404987	73405008	73404992	73404987	-
SEQ ID N O 3970	AAAATATTGGGCTCTGATTCCT	TTC	chr4	73404986	73405007	73404991	73404986	-
SEQ ID N O 3971	GGCTCTGATTCCTACAGAAAAA	TTG	chr4	73404977	73404998	73404982	73404977	-
SEQ ID N O 3972	TGATTCCTACAGAAAAACTCAG	CTC	chr4	73404972	73404993	73404977	73404972	-
SEQ ID N O 3973	ATTCCTACAGAAAAACTCAGGA	CTG	chr4	73404970	73404991	73404975	73404970	-
SEQ ID N O 3974	CTACAGAAAAACTCAGGATGAT	TTC	chr4	73404966	73404987	73404971	73404966	-
SEQ ID N O 3975	CAGAAAAACTCAGGATGATGTT	CTA	chr4	73404963	73404984	73404968	73404963	-
SEQ ID N O 3976	AGGATGATGTTCAATTATTTCT	CTC	chr4	73404952	73404973	73404957	73404952	-
SEQ ID N O 3977	AATTATTTCTTCTGCCTTTAAA	TTC	chr4	73404940	73404961	73404945	73404940	-
SEQ ID N O 3978	TTTCTTCTGCCTTTAAACAGAA	TTA	chr4	73404935	73404956	73404940	73404935	-
SEQ ID N O 3979	CTTCTGCCTTTAAACAGAAGAA	TTT	chr4	73404932	73404953	73404937	73404932	-
SEQ ID N O 3980	TTCTGCCTTTAAACAGAAGAAT	TTC	chr4	73404931	73404952	73404936	73404931	-
SEQ ID N O 3981	CTGCCTTTAAACAGAAGAATAA	CTT	chr4	73404929	73404950	73404934	73404929	-
SEQ ID N O 3982	TGCCTTTAAACAGAAGAATAAT	TTC	chr4	73404928	73404949	73404933	73404928	-
SEQ ID N O 3983	CCTTTAAACAGAAGAATAATTC	CTG	chr4	73404926	73404947	73404931	73404926	-
SEQ ID N O 3984	TAAACAGAAGAATAATTCAATT	CTT	chr4	73404922	73404943	73404927	73404922	-
SEQ ID N O 3985	AAACAGAAGAATAATTCAATTA	TTT	chr4	73404921	73404942	73404926	73404921	-
SEQ ID N O 3986	AACAGAAGAATAATTCAATTAC	TTA	chr4	73404920	73404941	73404925	73404920	-
SEQ ID N O 3987	AATTACCAAGAATACTATTTTA	TTC	chr4	73404904	73404925	73404909	73404904	-
SEQ ID N O 3988	CCAAGAATACTATTTTAAAAAT	TTA	chr4	73404899	73404920	73404904	73404899	-
SEQ ID N O 3989	TTTTAAAAATTATTAAATATTT	CTA	chr4	73404887	73404908	73404892	73404887	-
SEQ ID N O 3990	TAAAAATTATTAAATATTTATA	TTT	chr4	73404884	73404905	73404889	73404884	-
SEQ ID N O 3991	AAAAATTATTAAATATTTATAG	TTT	chr4	73404883	73404904	73404888	73404883	-
SEQ ID N O 3992	AAAATTATTAAATATTTATAGC	TTA	chr4	73404882	73404903	73404887	73404882	-
SEQ ID N O 3993	TTAAATATTTATAGCCTTATAT	TTA	chr4	73404875	73404896	73404880	73404875	-
SEQ ID N O 3994	AATATTTATAGCCTTATATTCA	TTA	chr4	73404872	73404893	73404877	73404872	-
SEQ ID N O 3995	ATAGCCTTATATTCAAACTTAG	TTT	chr4	73404865	73404886	73404870	73404865	-
SEQ ID N O 3996	TAGCCTTATATTCAAACTTAGA	TTA	chr4	73404864	73404885	73404869	73404864	-
SEQ ID N O 3997	ATATTCAAACTTAGATAATATC	CTT	chr4	73404857	73404878	73404862	73404857	-
SEQ ID N O 3998	TATTCAAACTTAGATAATATCT	TTA	chr4	73404856	73404877	73404861	73404856	-
SEQ ID N O 3999	AAACTTAGATAATATCTAATAC	TTC	chr4	73404851	73404872	73404856	73404851	-
SEQ ID N O 4000	AGATAATATCTAATACTCTTTT	CTT	chr4	73404845	73404866	73404850	73404845	-
SEQ ID N O 4001	GATAATATCTAATACTCTTTTA	TTA	chr4	73404844	73404865	73404849	73404844	-
SEQ ID N O 4002	ATACTCTTTTAGTGTCTATCAA	CTA	chr4	73404833	73404854	73404838	73404833	-
SEQ ID N O 4003	TTTTAGTGTCTATCAACAGCAA	CTC	chr4	73404827	73404848	73404832	73404827	-
SEQ ID N O 4004	TTAGTGTCTATCAACAGCAACC	CTT	chr4	73404825	73404846	73404830	73404825	-
SEQ ID N O 4005	TAGTGTCTATCAACAGCAACCA	TTT	chr4	73404824	73404845	73404829	73404824	-
SEQ ID N O 4006	AGTGTCTATCAACAGCAACCAA	TTT	chr4	73404823	73404844	73404828	73404823	-
SEQ ID N O 4007	GTGTCTATCAACAGCAACCAAG	TTA	chr4	73404822	73404843	73404827	73404822	-
SEQ ID N O 4008	TCAACAGCAACCAAGAAGACAG	CTA	chr4	73404815	73404836	73404820	73404815	-

SEQ ID N O 4009	AAATGAAAATAAATATAAATAC	CTA	chr4	73404789	73404810	73404794	73404789	-
SEQ ID N O 4010	TATTTATGAGATCAACAGCACA	TTC	chr4	73404761	73404782	73404766	73404761	-
SEQ ID N O 4011	TTTATGAGATCAACAGCACAGG	CTA	chr4	73404759	73404780	73404764	73404759	-
SEQ ID N O 4012	ATGAGATCAACAGCACAGGTTT	TTT	chr4	73404756	73404777	73404761	73404756	-
SEQ ID N O 4013	TGAGATCAACAGCACAGGTTTT	TTA	chr4	73404755	73404776	73404760	73404755	-
SEQ ID N O 4014	TGTGGTTTTTAAATAAAGCATA	TTT	chr4	73404734	73404755	73404739	73404734	-
SEQ ID N O 4015	GTGGTTTTTAAATAAAGCATAG	TTT	chr4	73404733	73404754	73404738	73404733	-
SEQ ID N O 4016	TGGTTTTTAAATAAAGCATAGT	TTG	chr4	73404732	73404753	73404737	73404732	-
SEQ ID N O 4017	TTAAATAAAGCATAGTGCAATG	TTT	chr4	73404726	73404747	73404731	73404726	-
SEQ ID N O 4018	TAAATAAAGCATAGTGCAATGG	TTT	chr4	73404725	73404746	73404730	73404725	-
SEQ ID N O 4019	AAATAAAGCATAGTGCAATGGA	TTT	chr4	73404724	73404745	73404729	73404724	-
SEQ ID N O 4020	AATAAAGCATAGTGCAATGGAT	TTA	chr4	73404723	73404744	73404728	73404723	-
SEQ ID N O 4021	TGGGATAGTTATGAATTCAATC	CTT	chr4	73404694	73404715	73404699	73404694	-
SEQ ID N O 4022	GGGATAGTTATGAATTCAATCT	TTT	chr4	73404693	73404714	73404698	73404693	-
SEQ ID N O 4023	GGATAGTTATGAATTCAATCTT	TTG	chr4	73404692	73404713	73404697	73404692	-
SEQ ID N O 4024	TGAATTCAATCTTCAACCCTAT	TTA	chr4	73404683	73404704	73404688	73404683	-
SEQ ID N O 4025	AATCTTCAACCCTATTCTGTGA	TTC	chr4	73404676	73404697	73404681	73404676	-
SEQ ID N O 4026	CAACCCTATTCTGTGAAGTTTC	CTT	chr4	73404670	73404691	73404675	73404670	-
SEQ ID N O 4027	AACCCTATTCTGTGAAGTTTCA	TTC	chr4	73404669	73404690	73404674	73404669	-
SEQ ID N O 4028	TTCTGTGAAGTTTCAGTCACTC	CTA	chr4	73404662	73404683	73404667	73404662	-
SEQ ID N O 4029	TGTGAAGTTTCAGTCACTCTAA	TTC	chr4	73404659	73404680	73404664	73404659	-
SEQ ID N O 4030	TGAAGTTTCAGTCACTCTAAGT	CTG	chr4	73404657	73404678	73404662	73404657	-
SEQ ID N O 4031	CAGTCACTCTAAGTTACTTTGC	TTT	chr4	73404649	73404670	73404654	73404649	-
SEQ ID N O 4032	AGTCACTCTAAGTTACTTTGCA	TTC	chr4	73404648	73404669	73404653	73404648	-
SEQ ID N O 4033	TAAGTTACTTTGCACTTTCCTT	CTC	chr4	73404640	73404661	73404645	73404640	-
SEQ ID N O 4034	AGTTACTTTGCACTTTCCTTAG	CTA	chr4	73404638	73404659	73404643	73404638	-
SEQ ID N O 4035	CTTTGCACTTTCCTTAGTGCGC	TTA	chr4	73404633	73404654	73404638	73404633	-
SEQ ID N O 4036	TGCACTTTCCTTAGTGCGCAAA	CTT	chr4	73404630	73404651	73404635	73404630	-
SEQ ID N O 4037	GCACTTTCCTTAGTGCGCAAAA	TTT	chr4	73404629	73404650	73404634	73404629	-
SEQ ID N O 4038	CACTTTCCTTAGTGCGCAAAAG	TTG	chr4	73404628	73404649	73404633	73404628	-
SEQ ID N O 4039	TCCTTAGTGCGCAAAAGAAAAT	CTT	chr4	73404623	73404644	73404628	73404623	-
SEQ ID N O 4040	CCTTAGTGCGCAAAAGAAAATT	TTT	chr4	73404622	73404643	73404627	73404622	-
SEQ ID N O 4041	CTTAGTGCGCAAAAGAAAATTA	TTC	chr4	73404621	73404642	73404626	73404621	-
SEQ ID N O 4042	AGTGCGCAAAAGAAAATTACAG	CTT	chr4	73404618	73404639	73404623	73404618	-
SEQ ID N O 4043	GTGCGCAAAAGAAAATTACAGT	TTA	chr4	73404617	73404638	73404622	73404617	-
SEQ ID N O 4044	CAGTCACTAAACAATTCTGACC	TTA	chr4	73404599	73404620	73404604	73404599	-
SEQ ID N O 4045	AACAATTCTGACCTTTTTTTTT	CTA	chr4	73404590	73404611	73404595	73404590	-
SEQ ID N O 4046	TGACCTTTTTTTTTTTTTACCT	TTC	chr4	73404582	73404603	73404587	73404582	-
SEQ ID N O 4047	ACCTTTTTTTTTTTTTACCTAG	CTG	chr4	73404580	73404601	73404585	73404580	-
SEQ ID N O 4048	TTTTTTTTTTTACCTAGGATGT	CTT	chr4	73404575	73404596	73404580	73404575	-
SEQ ID N O 4049	TTTTTTTTTTACCTAGGATGTT	TTT	chr4	73404574	73404595	73404579	73404574	-
SEQ ID N O 4050	TTTTTTTTTACCTAGGATGTTT	TTT	chr4	73404573	73404594	73404578	73404573	-
SEQ ID N O 4051	TTTTTTTTACCTAGGATGTTTG	TTT	chr4	73404572	73404593	73404577	73404572	-
SEQ ID N O 4052	TTTTTTTACCTAGGATGTTTGA	TTT	chr4	73404571	73404592	73404576	73404571	-
SEQ ID N O 4053	TTTTTTACCTAGGATGTTTGAA	TTT	chr4	73404570	73404591	73404575	73404570	-
SEQ ID N O 4054	TTTTTACCTAGGATGTTTGAAT	TTT	chr4	73404569	73404590	73404574	73404569	-
SEQ ID N O 4055	TTTTACCTAGGATGTTTGAATT	TTT	chr4	73404568	73404589	73404573	73404568	-
SEQ ID N O 4056	TTTACCTAGGATGTTTGAATTT	TTT	chr4	73404567	73404588	73404572	73404567	-
SEQ ID N O 4057	TTACCTAGGATGTTTGAATTTT	TTT	chr4	73404566	73404587	73404571	73404566	-
SEQ ID N O 4058	TACCTAGGATGTTTGAATTTTA	TTT	chr4	73404565	73404586	73404570	73404565	-
SEQ ID N O 4059	ACCTAGGATGTTTGAATTTTAT	TTT	chr4	73404564	73404585	73404569	73404564	-
SEQ ID N O 4060	CCTAGGATGTTTGAATTTTATT	TTA	chr4	73404563	73404584	73404568	73404563	-
SEQ ID N O 4061	GGATGTTTGAATTTTATTAATA	CTA	chr4	73404559	73404580	73404564	73404559	-
SEQ ID N O 4062	GAATTTTATTAATAAGATAACC	TTT	chr4	73404551	73404572	73404556	73404551	-
SEQ ID N O 4063	AATTTTATTAATAAGATAACCT	TTG	chr4	73404550	73404571	73404555	73404550	-
SEQ ID N O 4064	TATTAATAAGATAACCTTGTAA	TTT	chr4	73404545	73404566	73404550	73404545	-
SEQ ID N O 4065	ATTAATAAGATAACCTTGTAAG	TTT	chr4	73404544	73404565	73404549	73404544	-

SEQ ID N O 4066	TTAATAAGATAACCTTGTAAGA	TTA	chr4	73404543	73404564	73404548	73404543	-
SEQ ID N O 4067	ATAAGATAACCTTGTAAGACTT	TTA	chr4	73404540	73404561	73404545	73404540	-
SEQ ID N O 4068	GTAAGACTTCACAAATACAAAA	CTT	chr4	73404527	73404548	73404532	73404527	-
SEQ ID N O 4069	TAAGACTTCACAAATACAAAAT	TTG	chr4	73404526	73404547	73404531	73404526	-
SEQ ID N O 4070	CACAAATACAAAATACTATGCC	CTT	chr4	73404518	73404539	73404523	73404518	-
SEQ ID N O 4071	ACAAATACAAAATACTATGCCA	TTC	chr4	73404517	73404538	73404522	73404517	-
SEQ ID N O 4072	TGCCATTTTAGAAATAAATGCC	CTA	chr4	73404500	73404521	73404505	73404500	-
SEQ ID N O 4073	TAGAAATAAATGCCAAAATAAT	TTT	chr4	73404492	73404513	73404497	73404492	-
SEQ ID N O 4074	AGAAATAAATGCCAAAATAATT	TTT	chr4	73404491	73404512	73404496	73404491	-
SEQ ID N O 4075	GAAATAAATGCCAAAATAATTC	TTA	chr4	73404490	73404511	73404495	73404490	-
SEQ ID N O 4076	TTTAAAGATGCAGAGTTTACTA	TTC	chr4	73404468	73404489	73404473	73404468	-
SEQ ID N O 4077	TAAAGATGCAGAGTTTACTAAA	CTT	chr4	73404466	73404487	73404471	73404466	-
SEQ ID N O 4078	AAAGATGCAGAGTTTACTAAAA	TTT	chr4	73404465	73404486	73404470	73404465	-
SEQ ID N O 4079	AAGATGCAGAGTTTACTAAAAC	TTA	chr4	73404464	73404485	73404469	73404464	-
SEQ ID N O 4080	ACTAAAACTTTATTTTACTGGG	TTT	chr4	73404450	73404471	73404455	73404450	-
SEQ ID N O 4081	CTAAAACTTTATTTTACTGGGA	TTA	chr4	73404449	73404470	73404454	73404449	-
SEQ ID N O 4082	AAACTTTATTTTACTGGGAAAA	CTA	chr4	73404446	73404467	73404451	73404446	-
SEQ ID N O 4083	TATTTTACTGGGAAAATAGAAT	CTT	chr4	73404440	73404461	73404445	73404440	-
SEQ ID N O 4084	ATTTTACTGGGAAAATAGAATA	TTT	chr4	73404439	73404460	73404444	73404439	-
SEQ ID N O 4085	TTTTACTGGGAAAATAGAATAA	TTA	chr4	73404438	73404459	73404443	73404438	-
SEQ ID N O 4086	TACTGGGAAAATAGAATAAAAG	TTT	chr4	73404435	73404456	73404440	73404435	-
SEQ ID N O 4087	ACTGGGAAAATAGAATAAAAGT	TTT	chr4	73404434	73404455	73404439	73404434	-
SEQ ID N O 4088	CTGGGAAAATAGAATAAAAGTT	TTA	chr4	73404433	73404454	73404438	73404433	-
SEQ ID N O 4089	GGAAAATAGAATAAAAGTTGAA	CTG	chr4	73404430	73404451	73404435	73404430	-
SEQ ID N O 4090	AACAATAGAAAAATGGATTTCT	TTG	chr4	73404410	73404431	73404415	73404410	-
SEQ ID N O 4091	CTTACGTGCATCTCGACGAAAC	TTT	chr4	73404390	73404411	73404395	73404390	-
SEQ ID N O 4092	TTACGTGCATCTCGACGAAACA	TTC	chr4	73404389	73404410	73404394	73404389	-
SEQ ID N O 4093	ACGTGCATCTCGACGAAACACA	CTT	chr4	73404387	73404408	73404392	73404387	-
SEQ ID N O 4094	CGTGCATCTCGACGAAACACAC	TTA	chr4	73404386	73404407	73404391	73404386	-
SEQ ID N O 4095	GACGAAACACACCCCTGGAATA	CTC	chr4	73404376	73404397	73404381	73404376	-
SEQ ID N O 4096	GAATAAGCCGAGCTAAAGAGAA	CTG	chr4	73404359	73404380	73404364	73404359	-
SEQ ID N O 4097	AAGAGAAAAAGAAGGGAAATAA	CTA	chr4	73404344	73404365	73404349	73404344	-
SEQ ID N O 4098	CCCACTTCATTGTGCCAAAGGC	TTA	chr4	73404316	73404337	73404321	73404316	-
SEQ ID N O 4099	CATTGTGCCAAAGGCGTGTGGG	CTT	chr4	73404309	73404330	73404314	73404309	-
SEQ ID N O 4100	ATTGTGCCAAAGGCGTGTGGGG	TTC	chr4	73404308	73404329	73404313	73404308	-
SEQ ID N O 4101	TGCCAAAGGCGTGTGGGGTTGA	TTG	chr4	73404304	73404325	73404309	73404304	-
SEQ ID N O 4102	ACAGAAGAGAAAAGCTAGGACA	TTG	chr4	73404283	73404304	73404288	73404283	-
SEQ ID N O 4103	GGACAAACGGAGGGAAATTAGC	CTA	chr4	73404266	73404287	73404271	73404266	-

Figure 13

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 4104	AATAAATTTACCCAACAAAA	AAG	chr1	62597191	62597210	62597207	+
SEQ ID NO 4105	AATCTCTTAAAATCATAAAA	AAG	chr1	62597231	62597250	62597247	+
SEQ ID NO 4106	AAATCATAAAAAAGTAAAAT	TAG	chr1	62597240	62597259	62597256	+
SEQ ID NO 4107	GTAAAATTAGCTTTTAAAAA	CAG	chr1	62597253	62597272	62597269	+
SEQ ID NO 4108	TAAAATTAGCTTTTAAAAAC	AGG	chr1	62597254	62597273	62597270	+
SEQ ID NO 4109	AATTAGCTTTTAAAAACAGG	TAG	chr1	62597257	62597276	62597273	+
SEQ ID NO 4110	TTAAAAACAGGTAGTCACCA	TAG	chr1	62597266	62597285	62597282	+
SEQ ID NO 4111	TCACCATAGCATTGAATGTG	TAG	chr1	62597280	62597299	62597296	+
SEQ ID NO 4112	TGAATGTGTAGTTTATAATA	CAG	chr1	62597292	62597311	62597308	+
SEQ ID NO 4113	GTGTAGTTTATAATACAGCA	AAG	chr1	62597297	62597316	62597313	+
SEQ ID NO 4114	ACAATTTCAAATTACCTATT	AAG	chr1	62597326	62597345	62597342	+
SEQ ID NO 4115	TTTCAAATTACCTATTAAGT	TAG	chr1	62597330	62597349	62597346	+
SEQ ID NO 4116	CTCATTTCTTTGATTTCATT	TAG	chr1	62597356	62597375	62597372	+
SEQ ID NO 4117	AGCATTGATCTAACTCAATG	TGG	chr1	62597377	62597396	62597393	+
SEQ ID NO 4118	ATTGATCTAACTCAATGTGG	AAG	chr1	62597380	62597399	62597396	+
SEQ ID NO 4119	GATCTAACTCAATGTGGAAG	AAG	chr1	62597383	62597402	62597399	+
SEQ ID NO 4120	ATCTAACTCAATGTGGAAGA	AGG	chr1	62597384	62597403	62597400	+
SEQ ID NO 4121	GAAGAAGGTTACATTCGTGC	AAG	chr1	62597399	62597418	62597415	+
SEQ ID NO 4122	TACATTCGTGCAAGTTAACA	CGG	chr1	62597408	62597427	62597424	+
SEQ ID NO 4123	CCTACCAACCTTACCTTTTC	TGG	chr1	62597452	62597471	62597468	+
SEQ ID NO 4124	CTACCAACCTTACCTTTTCT	GGG	chr1	62597453	62597472	62597469	+
SEQ ID NO 4125	TACCTTTTCTGGGCAAATAT	TGG	chr1	62597463	62597482	62597479	+
SEQ ID NO 4126	TGGGCAAATATTGGTATATA	TAG	chr1	62597472	62597491	62597488	+
SEQ ID NO 4127	GGCAAATATTGGTATATATA	GAG	chr1	62597474	62597493	62597490	+
SEQ ID NO 4128	ATATTGGTATATATAGAGTT	AAG	chr1	62597479	62597498	62597495	+
SEQ ID NO 4129	TTGGTATATATAGAGTTAAG	AAG	chr1	62597482	62597501	62597498	+
SEQ ID NO 4130	ATATATAGAGTTAAGAAGTC	TAG	chr1	62597487	62597506	62597503	+
SEQ ID NO 4131	TATATAGAGTTAAGAAGTCT	AGG	chr1	62597488	62597507	62597504	+
SEQ ID NO 4132	AAGAAGTCTAGGTCTGCTTC	CAG	chr1	62597499	62597518	62597515	+
SEQ ID NO 4133	AAGTCTAGGTCTGCTTCCAG	AAG	chr1	62597502	62597521	62597518	+
SEQ ID NO 4134	GGTCTGCTTCCAGAAGAAAA	CAG	chr1	62597509	62597528	62597525	+
SEQ ID NO 4135	GTTGCTTGAAATTGAAAATC	AAG	chr1	62597538	62597557	62597554	+
SEQ ID NO 4136	AGATAAAAATGTTCACAATT	AAG	chr1	62597559	62597578	62597575	+
SEQ ID NO 4137	CCTTCTTTTTATTGTTCCTC	TAG	chr1	62597584	62597603	62597600	+
SEQ ID NO 4138	GTTCCTCTAGTTATTTCCTC	CAG	chr1	62597597	62597616	62597613	+
SEQ ID NO 4139	TATTTCCTCCAGAATTGATC	AAG	chr1	62597608	62597627	62597624	+
SEQ ID NO 4140	ATCATTTGATTCTCTATCTC	CAG	chr1	62597638	62597657	62597654	+
SEQ ID NO 4141	CATTTGATTCTCTATCTCCA	GAG	chr1	62597640	62597659	62597656	+
SEQ ID NO 4142	CTATCTCCAGAGCCAAAATC	AAG	chr1	62597651	62597670	62597667	+
SEQ ID NO 4143	AAAATCAAGATTTGCTATGT	TAG	chr1	62597665	62597684	62597681	+
SEQ ID NO 4144	GTTAGACGATGTAAAAATTT	TAG	chr1	62597683	62597702	62597699	+
SEQ ID NO 4145	GATGTAAAAATTTTAGCCAA	TGG	chr1	62597690	62597709	62597706	+
SEQ ID NO 4146	TTTTAGCCAATGGCCTCCTT	CAG	chr1	62597700	62597719	62597716	+
SEQ ID NO 4147	AGCCAATGGCCTCCTTCAGT	TGG	chr1	62597704	62597723	62597720	+
SEQ ID NO 4148	GCCAATGGCCTCCTTCAGTT	GGG	chr1	62597705	62597724	62597721	+
SEQ ID NO 4149	GGCCTCCTTCAGTTGGGACA	TGG	chr1	62597711	62597730	62597727	+

SEQ ID NO 4150	TCAGTTGGGACATGGTCTTA	AAG	chr1	62597719	62597738	62597735	+
SEQ ID NO 4151	GTCTTAAAGACTTTGTCCAT	AAG	chr1	62597733	62597752	62597749	+
SEQ ID NO 4152	AAGACTTTGTCCATAAGACG	AAG	chr1	62597739	62597758	62597755	+
SEQ ID NO 4153	AGACTTTGTCCATAAGACGA	AGG	chr1	62597740	62597759	62597756	+
SEQ ID NO 4154	GACTTTGTCCATAAGACGAA	GGG	chr1	62597741	62597760	62597757	+
SEQ ID NO 4155	AAAAACTCAACATATTTGAT	CAG	chr1	62597784	62597803	62597800	+
SEQ ID NO 4156	TATGATCTATCGCTGCAAAC	CAG	chr1	62597813	62597832	62597829	+
SEQ ID NO 4157	GCTGCAAACCAGTGAAATCA	AAG	chr1	62597824	62597843	62597840	+
SEQ ID NO 4158	GCAAACCAGTGAAATCAAAG	AAG	chr1	62597827	62597846	62597843	+
SEQ ID NO 4159	AACCAGTGAAATCAAAGAAG	AAG	chr1	62597830	62597849	62597846	+
SEQ ID NO 4160	GTGAAATCAAAGAAGAAGAA	AAG	chr1	62597835	62597854	62597851	+
SEQ ID NO 4161	TGAAATCAAAGAAGAAGAAA	AGG	chr1	62597836	62597855	62597852	+
SEQ ID NO 4162	AAAGAAGAAGAAAAGGAACT	GAG	chr1	62597843	62597862	62597859	+
SEQ ID NO 4163	GAAGAAGAAAAGGAACTGAG	AAG	chr1	62597846	62597865	62597862	+
SEQ ID NO 4164	AAGAACTACATATAAACTAC	AAG	chr1	62597866	62597885	62597882	+
SEQ ID NO 4165	TAAACTACAAGTCAAAAATG	AAG	chr1	62597878	62597897	62597894	+
SEQ ID NO 4166	AACTACAAGTCAAAAATGAA	GAG	chr1	62597880	62597899	62597896	+
SEQ ID NO 4167	ACTACAAGTCAAAAATGAAG	AGG	chr1	62597881	62597900	62597897	+
SEQ ID NO 4168	AAGTCAAAAATGAAGAGGTA	AAG	chr1	62597886	62597905	62597902	+
SEQ ID NO 4169	GAACTCAACTCAAAACTTGA	AAG	chr1	62597921	62597940	62597937	+
SEQ ID NO 4170	CTCAAAACTTGAAAGCCTCC	TAG	chr1	62597929	62597948	62597945	+
SEQ ID NO 4171	AAAACTTGAAAGCCTCCTAG	AAG	chr1	62597932	62597951	62597948	+
SEQ ID NO 4172	AAAAATTCTACTTCAACAAA	AAG	chr1	62597956	62597975	62597972	+
SEQ ID NO 4173	TCAACAAAAAGTGAAATATT	TAG	chr1	62597968	62597987	62597984	+
SEQ ID NO 4174	ACAAAAAGTGAAATATTTAG	AAG	chr1	62597971	62597990	62597987	+
SEQ ID NO 4175	AAAAAGTGAAATATTTAGAA	GAG	chr1	62597973	62597992	62597989	+
SEQ ID NO 4176	TCAAAATCAACCTGAAACTC	CAG	chr1	62598013	62598032	62598029	+
SEQ ID NO 4177	ACCTGAAACTCCAGAACACC	CAG	chr1	62598022	62598041	62598038	+
SEQ ID NO 4178	TGAAACTCCAGAACACCCAG	AAG	chr1	62598025	62598044	62598041	+
SEQ ID NO 4179	CCCAGAAGTAACTTCACTTA	AAG	chr1	62598040	62598059	62598056	+
SEQ ID NO 4180	GAAGTAACTTCACTTAAAGT	AAG	chr1	62598044	62598063	62598060	+
SEQ ID NO 4181	GTAACTTCACTTAAAGTAAG	TAG	chr1	62598047	62598066	62598063	+
SEQ ID NO 4182	CTTAAAGTAAGTAGAAAATA	AAG	chr1	62598056	62598075	62598072	+
SEQ ID NO 4183	TAAAGTAAGTAGAAAATAAA	GAG	chr1	62598058	62598077	62598074	+
SEQ ID NO 4184	AAAGTAAGTAGAAAATAAAG	AGG	chr1	62598059	62598078	62598075	+
SEQ ID NO 4185	AAGTAAGTAGAAAATAAAGA	GGG	chr1	62598060	62598079	62598076	+
SEQ ID NO 4186	TCATGTTTATGTTTTCAATG	TGG	chr1	62598084	62598103	62598100	+
SEQ ID NO 4187	CTTTTAAAAAAAATATTTCT	AAG	chr1	62598109	62598128	62598125	+
SEQ ID NO 4188	TTTTAAAAAAAATATTTCTA	AGG	chr1	62598110	62598129	62598126	+
SEQ ID NO 4189	GTTGAAATACTTTTTTTTCC	AAG	chr1	62598161	62598180	62598177	+
SEQ ID NO 4190	TTTCCAAGAAAAATAATCTC	CAG	chr1	62598176	62598195	62598192	+
SEQ ID NO 4191	AAATTTCCTATTATAATTTC	AAG	chr1	62598205	62598224	62598221	+
SEQ ID NO 4192	TTCCTATTATAATTTCAAGT	TAG	chr1	62598209	62598228	62598225	+
SEQ ID NO 4193	TTTATATGAAAATTACAAAT	CGG	chr1	62598279	62598298	62598295	+
SEQ ID NO 4194	ATCGGTTAAATTATACAATC	TAG	chr1	62598297	62598316	62598313	+
SEQ ID NO 4195	TACACTATTGTAAATTACTG	AAG	chr1	62598333	62598352	62598349	+
SEQ ID NO 4196	ACACTATTGTAAATTACTGA	AGG	chr1	62598334	62598353	62598350	+

SEQ ID NO 4197	TATTGTAAATTACTGAAGGT	AAG	chr1	62598338	62598357	62598354 +
SEQ ID NO 4198	AATTACTGAAGGTAAGTAAA	AAG	chr1	62598345	62598364	62598361 +
SEQ ID NO 4199	AAAAATTTAAAACTATTCTC	CAG	chr1	62598373	62598392	62598389 +
SEQ ID NO 4200	CTATTCTCCAGTGTTTAAAA	CAG	chr1	62598385	62598404	62598401 +
SEQ ID NO 4201	TTAAAACAGATTAAATAATA	CAG	chr1	62598399	62598418	62598415 +
SEQ ID NO 4202	AGATTAAATAATACAGTAAA	TGG	chr1	62598406	62598425	62598422 +
SEQ ID NO 4203	AAATAATACAGTAAATGGAA	AAG	chr1	62598411	62598430	62598427 +
SEQ ID NO 4204	TTATTCATATGAAAATATGC	TGG	chr1	62598436	62598455	62598452 +
SEQ ID NO 4205	TATTCATATGAAAATATGCT	GGG	chr1	62598437	62598456	62598453 +
SEQ ID NO 4206	TGGGCTTTTTCTTTTAATTG	AAG	chr1	62598456	62598475	62598472 +
SEQ ID NO 4207	TTTTTCTTTTAATTGAAGTT	CAG	chr1	62598461	62598480	62598477 +
SEQ ID NO 4208	AAGTTCAGAAAATCAAATTT	TAG	chr1	62598476	62598495	62598492 +
SEQ ID NO 4209	GTTCAGAAAATCAAATTTTA	GAG	chr1	62598478	62598497	62598494 +
SEQ ID NO 4210	AGAAAATCAAATTTTAGAGA	TAG	chr1	62598482	62598501	62598498 +
SEQ ID NO 4211	TACAATTTAAATAAAATGTT	AAG	chr1	62598505	62598524	62598521 +
SEQ ID NO 4212	ACAATTTAAATAAAATGTTA	AGG	chr1	62598506	62598525	62598522 +
SEQ ID NO 4213	CAAAAATATGTGCTATTTGA	AAG	chr1	62598530	62598549	62598546 +
SEQ ID NO 4214	AAATATGTGCTATTTGAAAG	AAG	chr1	62598533	62598552	62598549 +
SEQ ID NO 4215	GCTATTTGAAAGAAGCATAC	AAG	chr1	62598541	62598560	62598557 +
SEQ ID NO 4216	CTATTTGAAAGAAGCATACA	AGG	chr1	62598542	62598561	62598558 +
SEQ ID NO 4217	TATTTGAAAGAAGCATACAA	GGG	chr1	62598543	62598562	62598559 +
SEQ ID NO 4218	ATTTGAAAGAAGCATACAAG	GGG	chr1	62598544	62598563	62598560 +
SEQ ID NO 4219	TGAAAGAAGCATACAAGGGG	AAG	chr1	62598547	62598566	62598563 +
SEQ ID NO 4220	GAAAGAAGCATACAAGGGGA	AGG	chr1	62598548	62598567	62598564 +
SEQ ID NO 4221	TCATTTTTCAAATCCATTAT	TAG	chr1	62598583	62598602	62598599 +
SEQ ID NO 4222	CCATTATTAGTTTAAAAATT	TAG	chr1	62598596	62598615	62598612 +
SEQ ID NO 4223	TTTAAAAATTTAGATTATGA	TAG	chr1	62598606	62598625	62598622 +
SEQ ID NO 4224	TTTAGATTATGATAGTGTTA	CAG	chr1	62598614	62598633	62598630 +
SEQ ID NO 4225	TTAGATTATGATAGTGTTAC	AGG	chr1	62598615	62598634	62598631 +
SEQ ID NO 4226	ATAGTGTTACAGGAAATTAA	TAG	chr1	62598625	62598644	62598641 +
SEQ ID NO 4227	GTTACAGGAAATTAATAGAA	AAG	chr1	62598630	62598649	62598646 +
SEQ ID NO 4228	CAGGAAATTAATAGAAAAGA	AAG	chr1	62598634	62598653	62598650 +
SEQ ID NO 4229	GGAAATTAATAGAAAAGAAA	GAG	chr1	62598636	62598655	62598652 +
SEQ ID NO 4230	GAAATTAATAGAAAAGAAAG	AGG	chr1	62598637	62598656	62598653 +
SEQ ID NO 4231	TTAATAGAAAAGAAAGAGGA	AAG	chr1	62598641	62598660	62598657 +
SEQ ID NO 4232	ACCAACCTACTCTCTATATC	CAG	chr1	62598673	62598692	62598689 +
SEQ ID NO 4233	TCTCTATATCCAGACTTTTG	TAG	chr1	62598683	62598702	62598699 +
SEQ ID NO 4234	CCAGACTTTTGTAGAAAAAC	AAG	chr1	62598692	62598711	62598708 +
SEQ ID NO 4235	TTTGTAGAAAAACAAGATAA	TAG	chr1	62598699	62598718	62598715 +
SEQ ID NO 4236	AAAACAAGATAATAGCATCA	AAG	chr1	62598707	62598726	62598723 +
SEQ ID NO 4237	ATAGCATCAAAGACCTTCTC	CAG	chr1	62598718	62598737	62598734 +
SEQ ID NO 4238	CAAAGACCTTCTCCAGACCG	TGG	chr1	62598725	62598744	62598741 +
SEQ ID NO 4239	AGACCTTCTCCAGACCGTGG	AAG	chr1	62598728	62598747	62598744 +
SEQ ID NO 4240	AATATAAACAATTAAACCAA	CAG	chr1	62598754	62598773	62598770 +
SEQ ID NO 4241	AAACAATTAAACCAACAGCA	TAG	chr1	62598759	62598778	62598775 +
SEQ ID NO 4242	CCAACAGCATAGTCAAATAA	AAG	chr1	62598770	62598789	62598786 +
SEQ ID NO 4243	GCATAGTCAAATAAAAGAAA	TAG	chr1	62598776	62598795	62598792 +

SEQ ID NO 4244	AAATAAAAGAAATAGAAAAT	CAG	chr1	62598784	62598803	62598800	+
SEQ ID NO 4245	AATAAAAGAAATAGAAAATC	AGG	chr1	62598785	62598804	62598801	+
SEQ ID NO 4246	AAAGAAATAGAAAATCAGGT	AAG	chr1	62598789	62598808	62598805	+
SEQ ID NO 4247	AAATAGAAAATCAGGTAAGT	CAG	chr1	62598793	62598812	62598809	+
SEQ ID NO 4248	CAGGTAAGTCAGTATTTTAA	TGG	chr1	62598804	62598823	62598820	+
SEQ ID NO 4249	GGTATGTCCCATCTTTCACA	CAG	chr1	62598825	62598844	62598841	+
SEQ ID NO 4250	GTATGTCCCATCTTTCACAC	AGG	chr1	62598826	62598845	62598842	+
SEQ ID NO 4251	TGAATCCTAAAATTATTTAC	AAG	chr1	62598862	62598881	62598878	+
SEQ ID NO 4252	AATTATTTACAAGCTTTAAC	TGG	chr1	62598872	62598891	62598888	+
SEQ ID NO 4253	ACAAGCTTTAACTGGATCAT	GAG	chr1	62598880	62598899	62598896	+
SEQ ID NO 4254	CATGAGTAAAATTATCACAT	CAG	chr1	62598897	62598916	62598913	+
SEQ ID NO 4255	CAGCATAACTGTTAAAATTG	CAG	chr1	62598917	62598936	62598933	+
SEQ ID NO 4256	AGCATAACTGTTAAAATTGC	AGG	chr1	62598918	62598937	62598934	+
SEQ ID NO 4257	TGTTAAAATTGCAGGCTCTG	AAG	chr1	62598926	62598945	62598942	+
SEQ ID NO 4258	AACTACCTGCATTTAAACCA	TGG	chr1	62598955	62598974	62598971	+
SEQ ID NO 4259	TACTTCACCCCTTTATCTCT	CAG	chr1	62599008	62599027	62599024	+
SEQ ID NO 4260	GTTTCCTCACATATACTACA	AAG	chr1	62599030	62599049	62599046	+
SEQ ID NO 4261	ATATACTACAAAGATAATAA	CAG	chr1	62599040	62599059	62599056	+
SEQ ID NO 4262	AAAGATAATAACAGAACTTA	TAG	chr1	62599049	62599068	62599065	+
SEQ ID NO 4263	AAGATAATAACAGAACTTAT	AGG	chr1	62599050	62599069	62599066	+
SEQ ID NO 4264	AGAACTTATAGGATTATTGT	AAG	chr1	62599061	62599080	62599077	+
SEQ ID NO 4265	TAAGAAAAAAAATTAATTCA	TAG	chr1	62599080	62599099	62599096	+
SEQ ID NO 4266	GAAAAAAAATTAATTCATAG	CAG	chr1	62599083	62599102	62599099	+
SEQ ID NO 4267	CATCTTACTAAAATTCAAAT	TAG	chr1	62599113	62599132	62599129	+
SEQ ID NO 4268	CTTTGCTCAAAACCACACAA	TAG	chr1	62599147	62599166	62599163	+
SEQ ID NO 4269	GCTTTCCATTTCACTCATAT	TGG	chr1	62599169	62599188	62599185	+
SEQ ID NO 4270	TTTCACTCATATTGGCTCTT	TAG	chr1	62599177	62599196	62599193	+
SEQ ID NO 4271	TCATATTGGCTCTTTAGACC	AAG	chr1	62599183	62599202	62599199	+
SEQ ID NO 4272	TTGGGTAATCTTGGTCTAAA	GAG	chr1	62599195	62599214	62599198	-
SEQ ID NO 4273	TTGGTCTAAAGAGCCAATAT	GAG	chr1	62599185	62599204	62599188	-
SEQ ID NO 4274	AAGAGCCAATATGAGTGAAA	TGG	chr1	62599177	62599196	62599180	-
SEQ ID NO 4275	GCCAATATGAGTGAAATGGA	AAG	chr1	62599173	62599192	62599176	-
SEQ ID NO 4276	TGAAATGGAAAGCTATTGTG	TGG	chr1	62599162	62599181	62599165	-
SEQ ID NO 4277	GAAAGCTATTGTGTGGTTTT	GAG	chr1	62599155	62599174	62599158	-
SEQ ID NO 4278	CTATTGTGTGGTTTTGAGCA	AAG	chr1	62599150	62599169	62599153	-
SEQ ID NO 4279	ATTGTGTGGTTTTGAGCAAA	GAG	chr1	62599148	62599167	62599151	-
SEQ ID NO 4280	ACATGATCTAATTTGAATTT	TAG	chr1	62599123	62599142	62599126	-
SEQ ID NO 4281	GATCTAATTTGAATTTTAGT	AAG	chr1	62599119	62599138	62599122	-
SEQ ID NO 4282	GAATTTTAGTAAGATGACAT	TGG	chr1	62599109	62599128	62599112	-
SEQ ID NO 4283	TTTTCTTACAATAATCCTAT	AAG	chr1	62599068	62599087	62599071	-
SEQ ID NO 4284	AAGTTCTGTTATTATCTTTG	TAG	chr1	62599048	62599067	62599051	-
SEQ ID NO 4285	ATTATCTTTGTAGTATATGT	GAG	chr1	62599038	62599057	62599041	-
SEQ ID NO 4286	TTATCTTTGTAGTATATGTG	AGG	chr1	62599037	62599056	62599040	-
SEQ ID NO 4287	GTAGTATATGTGAGGAAACT	GAG	chr1	62599029	62599048	62599032	-
SEQ ID NO 4288	AGTATATGTGAGGAAACTGA	GAG	chr1	62599027	62599046	62599030	-
SEQ ID NO 4289	TGTGAGGAAACTGAGAGATA	AAG	chr1	62599021	62599040	62599024	-
SEQ ID NO 4290	GTGAGGAAACTGAGAGATAA	AGG	chr1	62599020	62599039	62599023	-

SEQ ID NO 4291	TGAGGAAACTGAGAGATAAA	GGG	chr1	62599019	62599038	62599022	-
SEQ ID NO 4292	GAGGAAACTGAGAGATAAAG	GGG	chr1	62599018	62599037	62599021	-
SEQ ID NO 4293	AACTGAGAGATAAAGGGGTG	AAG	chr1	62599013	62599032	62599016	-
SEQ ID NO 4294	AGGGGTGAAGTAATTTATTC	AAG	chr1	62599000	62599019	62599003	-
SEQ ID NO 4295	GGGGTGAAGTAATTTATTCA	AGG	chr1	62598999	62599018	62599002	-
SEQ ID NO 4296	AATTTATTCAAGGTCACACA	AAG	chr1	62598989	62599008	62598992	-
SEQ ID NO 4297	TTCAAGGTCACACAAAGTTT	TAG	chr1	62598983	62599002	62598986	-
SEQ ID NO 4298	CAAGGTCACACAAAGTTTTA	GAG	chr1	62598981	62599000	62598984	-
SEQ ID NO 4299	CACACAAAGTTTTAGAGCCA	TGG	chr1	62598975	62598994	62598978	-
SEQ ID NO 4300	TTAGAGCCATGGTTTAAATG	CAG	chr1	62598964	62598983	62598967	-
SEQ ID NO 4301	TAGAGCCATGGTTTAAATGC	AGG	chr1	62598963	62598982	62598966	-
SEQ ID NO 4302	AGCCATGGTTTAAATGCAGG	TAG	chr1	62598960	62598979	62598963	-
SEQ ID NO 4303	TTTAAATGCAGGTAGTTTAT	TAG	chr1	62598952	62598971	62598955	-
SEQ ID NO 4304	TGCAGGTAGTTTATTAGCTT	CAG	chr1	62598946	62598965	62598949	-
SEQ ID NO 4305	CAGGTAGTTTATTAGCTTCA	GAG	chr1	62598944	62598963	62598947	-
SEQ ID NO 4306	TTCAGAGCCTGCAATTTTAA	CAG	chr1	62598928	62598947	62598931	-
SEQ ID NO 4307	TGATAATTTTACTCATGATC	CAG	chr1	62598894	62598913	62598897	-
SEQ ID NO 4308	TTTTACTCATGATCCAGTTA	AAG	chr1	62598888	62598907	62598891	-
SEQ ID NO 4309	TTAAAGCTTGTAAATAATTT	TAG	chr1	62598871	62598890	62598874	-
SEQ ID NO 4310	TAAAGCTTGTAAATAATTTT	AGG	chr1	62598870	62598889	62598873	-
SEQ ID NO 4311	TTGTAAATAATTTTAGGATT	CAG	chr1	62598864	62598883	62598867	-
SEQ ID NO 4312	TTTAGGATTCAGTGTTTTTA	CAG	chr1	62598853	62598872	62598856	-
SEQ ID NO 4313	GTTTTTACAGACCTGTGTGA	AAG	chr1	62598840	62598859	62598843	-
SEQ ID NO 4314	TTACAGACCTGTGTGAAAGA	TGG	chr1	62598836	62598855	62598839	-
SEQ ID NO 4315	TACAGACCTGTGTGAAAGAT	GGG	chr1	62598835	62598854	62598838	-
SEQ ID NO 4316	CTTTTATTTGACTATGCTGT	TGG	chr1	62598773	62598792	62598776	-
SEQ ID NO 4317	GTTGGTTTAATTGTTTATAT	TGG	chr1	62598755	62598774	62598758	-
SEQ ID NO 4318	TTGTTTATATTGGTCTTCCA	CGG	chr1	62598745	62598764	62598748	-
SEQ ID NO 4319	TATATTGGTCTTCCACGGTC	TGG	chr1	62598740	62598759	62598743	-
SEQ ID NO 4320	TATTGGTCTTCCACGGTCTG	GAG	chr1	62598738	62598757	62598741	-
SEQ ID NO 4321	TGGTCTTCCACGGTCTGGAG	AAG	chr1	62598735	62598754	62598738	-
SEQ ID NO 4322	GGTCTTCCACGGTCTGGAGA	AGG	chr1	62598734	62598753	62598737	-
SEQ ID NO 4323	ATTATCTTGTTTTTCTACAA	AAG	chr1	62598700	62598719	62598703	-
SEQ ID NO 4324	CTTGTTTTTCTACAAAAGTC	TGG	chr1	62598695	62598714	62598698	-
SEQ ID NO 4325	TTTCTACAAAAGTCTGGATA	TAG	chr1	62598689	62598708	62598692	-
SEQ ID NO 4326	TCTACAAAAGTCTGGATATA	GAG	chr1	62598687	62598706	62598690	-
SEQ ID NO 4327	TACAAAAGTCTGGATATAGA	GAG	chr1	62598685	62598704	62598688	-
SEQ ID NO 4328	AAAAGTCTGGATATAGAGAG	TAG	chr1	62598682	62598701	62598685	-
SEQ ID NO 4329	AAAGTCTGGATATAGAGAGT	AGG	chr1	62598681	62598700	62598684	-
SEQ ID NO 4330	TCTGGATATAGAGAGTAGGT	TGG	chr1	62598677	62598696	62598680	-
SEQ ID NO 4331	ATAGAGAGTAGGTTGGTTAT	AAG	chr1	62598670	62598689	62598673	-
SEQ ID NO 4332	CTAAATTTTTAAACTAATAA	TGG	chr1	62598599	62598618	62598602	-
SEQ ID NO 4333	TGGATTTGAAAAATGAATAT	TGG	chr1	62598579	62598598	62598582	-
SEQ ID NO 4334	CCTTGTATGCTTCTTTCAAA	TAG	chr1	62598545	62598564	62598548	-
SEQ ID NO 4335	ATTTTCTGAACTTCAATTAA	AAG	chr1	62598469	62598488	62598472	-
SEQ ID NO 4336	TGAACTTCAATTAAAAGAAA	AAG	chr1	62598463	62598482	62598466	-
SEQ ID NO 4337	TTCAATTAAAAGAAAAAGCC	CAG	chr1	62598458	62598477	62598461	-

SEQ ID NO 4338	ATTTAATCTGTTTTAAACAC	TGG	chr1	62598395	62598414	62598398	-
SEQ ID NO 4339	TTAATCTGTTTTAAACACTG	GAG	chr1	62598393	62598412	62598396	-
SEQ ID NO 4340	CTGTTTTAAACACTGGAGAA	TAG	chr1	62598388	62598407	62598391	-
SEQ ID NO 4341	TTTAACTTTTTACTTACCTT	CAG	chr1	62598353	62598372	62598356	-
SEQ ID NO 4342	TTACCTTCAGTAATTTACAA	TAG	chr1	62598340	62598359	62598343	-
SEQ ID NO 4343	TTTACAATAGTGTAATGACA	TAG	chr1	62598327	62598346	62598330	-
SEQ ID NO 4344	AGTGTAATGACATAGTGTTC	TAG	chr1	62598319	62598338	62598322	-
SEQ ID NO 4345	TCATATAAAATGCAAATTTT	CAG	chr1	62598268	62598287	62598271	-
SEQ ID NO 4346	AGTGTTTTCATATATAACAT	TAG	chr1	62598247	62598266	62598250	-
SEQ ID NO 4347	GTGTTTTCATATATAACATT	AGG	chr1	62598246	62598265	62598249	-
SEQ ID NO 4348	TGTTTTCATATATAACATTA	GGG	chr1	62598245	62598264	62598248	-
SEQ ID NO 4349	AAACTAACTTGAAATTATAA	TAG	chr1	62598215	62598234	62598218	-
SEQ ID NO 4350	AACTAACTTGAAATTATAAT	AGG	chr1	62598214	62598233	62598217	-
SEQ ID NO 4351	TAATAGGAAATTTTATTTTC	TGG	chr1	62598198	62598217	62598201	-
SEQ ID NO 4352	ATAGGAAATTTTATTTTCTG	GAG	chr1	62598196	62598215	62598199	-
SEQ ID NO 4353	TTTCTGGAGATTATTTTTCT	TGG	chr1	62598182	62598201	62598185	-
SEQ ID NO 4354	ATTATTTTTCTTGGAAAAAA	AAG	chr1	62598173	62598192	62598176	-
SEQ ID NO 4355	AGTATTTCAACAATGCAACA	AAG	chr1	62598152	62598171	62598155	-
SEQ ID NO 4356	ATGCAACAAAGTATTTCAAA	TGG	chr1	62598140	62598159	62598143	-
SEQ ID NO 4357	GTATTTCAAATGGCATGCCT	TAG	chr1	62598130	62598149	62598133	-
SEQ ID NO 4358	CTTAGAAATATTTTTTTTAA	AAG	chr1	62598112	62598131	62598115	-
SEQ ID NO 4359	CTTTATTTTCTACTTACTTT	AAG	chr1	62598059	62598078	62598062	-
SEQ ID NO 4360	TTTTCTACTTACTTTAAGTG	AAG	chr1	62598054	62598073	62598057	-
SEQ ID NO 4361	ACTTTAAGTGAAGTTACTTC	TGG	chr1	62598044	62598063	62598047	-
SEQ ID NO 4362	CTTTAAGTGAAGTTACTTCT	GGG	chr1	62598043	62598062	62598046	-
SEQ ID NO 4363	GAAGTTACTTCTGGGTGTTC	TGG	chr1	62598035	62598054	62598038	-
SEQ ID NO 4364	AGTTACTTCTGGGTGTTCTG	GAG	chr1	62598033	62598052	62598036	-
SEQ ID NO 4365	TTCTGGGTGTTCTGGAGTTT	CAG	chr1	62598027	62598046	62598030	-
SEQ ID NO 4366	TCTGGGTGTTCTGGAGTTTC	AGG	chr1	62598026	62598045	62598029	-
SEQ ID NO 4367	TTTCAGGTTGATTTTGAATT	AAG	chr1	62598010	62598029	62598013	-
SEQ ID NO 4368	AGGTTGATTTTGAATTAAGT	TAG	chr1	62598006	62598025	62598009	-
SEQ ID NO 4369	TGATTTTGAATTAAGTTAGT	TAG	chr1	62598002	62598021	62598005	-
SEQ ID NO 4370	AAATATTTCACTTTTTGTTG	AAG	chr1	62597969	62597988	62597972	-
SEQ ID NO 4371	TATTTCACTTTTTGTTGAAG	TAG	chr1	62597966	62597985	62597969	-
SEQ ID NO 4372	TGAAGTAGAATTTTTTCTTC	TAG	chr1	62597951	62597970	62597954	-
SEQ ID NO 4373	GAAGTAGAATTTTTTCTTCT	AGG	chr1	62597950	62597969	62597953	-
SEQ ID NO 4374	AGTAGAATTTTTTCTTCTAG	GAG	chr1	62597948	62597967	62597951	-
SEQ ID NO 4375	GTAGAATTTTTTCTTCTAGG	AGG	chr1	62597947	62597966	62597950	-
SEQ ID NO 4376	TTTTCTTCTAGGAGGCTTTC	AAG	chr1	62597939	62597958	62597942	-
SEQ ID NO 4377	CTAGGAGGCTTTCAAGTTTT	GAG	chr1	62597932	62597951	62597935	-
SEQ ID NO 4378	AGGCTTTCAAGTTTTGAGTT	GAG	chr1	62597927	62597946	62597930	-
SEQ ID NO 4379	TCAAGTTTTGAGTTGAGTTC	AAG	chr1	62597921	62597940	62597924	-
SEQ ID NO 4380	ACCTCTTCATTTTTGACTTG	TAG	chr1	62597885	62597904	62597888	-
SEQ ID NO 4381	TTTGACTTGTAGTTTATATG	TAG	chr1	62597874	62597893	62597877	-
SEQ ID NO 4382	AGTTTATATGTAGTTCTTCT	CAG	chr1	62597864	62597883	62597867	-
SEQ ID NO 4383	TTCTTCTTCTTTGATTTCAC	TGG	chr1	62597835	62597854	62597838	-
SEQ ID NO 4384	TCTTTGATTTCACTGGTTTG	CAG	chr1	62597828	62597847	62597831	-

SEQ ID NO 4385	ATTTCACTGGTTTGCAGCGA	TAG	chr1	62597822	62597841	62597825	-
SEQ ID NO 4386	TTGCAGCGATAGATCATAAA	AAG	chr1	62597811	62597830	62597814	-
SEQ ID NO 4387	AAAGACTGATCAAATATGTT	GAG	chr1	62597792	62597811	62597795	-
SEQ ID NO 4388	TTTGAAATATGTCATTAATT	TGG	chr1	62597767	62597786	62597770	-
SEQ ID NO 4389	TAATTTGGCCCTTCGTCTTA	TGG	chr1	62597752	62597771	62597755	-
SEQ ID NO 4390	GGCCCTTCGTCTTATGGACA	AAG	chr1	62597746	62597765	62597749	-
SEQ ID NO 4391	GTCTTATGGACAAAGTCTTT	AAG	chr1	62597738	62597757	62597741	-
SEQ ID NO 4392	TTAAGACCATGTCCCAACTG	AAG	chr1	62597720	62597739	62597723	-
SEQ ID NO 4393	TAAGACCATGTCCCAACTGA	AGG	chr1	62597719	62597738	62597722	-
SEQ ID NO 4394	AGACCATGTCCCAACTGAAG	GAG	chr1	62597717	62597736	62597720	-
SEQ ID NO 4395	GACCATGTCCCAACTGAAGG	AGG	chr1	62597716	62597735	62597719	-
SEQ ID NO 4396	TCCCAACTGAAGGAGGCCAT	TGG	chr1	62597709	62597728	62597712	-
SEQ ID NO 4397	AATTTTTACATCGTCTAACA	TAG	chr1	62597682	62597701	62597685	-
SEQ ID NO 4398	AACATAGCAAATCTTGATTT	TGG	chr1	62597666	62597685	62597669	-
SEQ ID NO 4399	GCAAATCTTGATTTTGGCTC	TGG	chr1	62597660	62597679	62597663	-
SEQ ID NO 4400	AAATCTTGATTTTGGCTCTG	GAG	chr1	62597658	62597677	62597661	-
SEQ ID NO 4401	CTTGATTTTGGCTCTGGAGA	TAG	chr1	62597654	62597673	62597657	-
SEQ ID NO 4402	TGATTTTGGCTCTGGAGATA	GAG	chr1	62597652	62597671	62597655	-
SEQ ID NO 4403	TGAATTGTCTTGATCAATTC	TGG	chr1	62597619	62597638	62597622	-
SEQ ID NO 4404	AATTGTCTTGATCAATTCTG	GAG	chr1	62597617	62597636	62597620	-
SEQ ID NO 4405	ATTGTCTTGATCAATTCTGG	AGG	chr1	62597616	62597635	62597619	-
SEQ ID NO 4406	TCAATTCTGGAGGAAATAAC	TAG	chr1	62597606	62597625	62597609	-
SEQ ID NO 4407	AATTCTGGAGGAAATAACTA	GAG	chr1	62597604	62597623	62597607	-
SEQ ID NO 4408	ATTCTGGAGGAAATAACTAG	AGG	chr1	62597603	62597622	62597606	-
SEQ ID NO 4409	ATAACTAGAGGAACAATAAA	AAG	chr1	62597591	62597610	62597594	-
SEQ ID NO 4410	ACTAGAGGAACAATAAAAAG	AAG	chr1	62597588	62597607	62597591	-
SEQ ID NO 4411	CTAGAGGAACAATAAAAAGA	AGG	chr1	62597587	62597606	62597590	-
SEQ ID NO 4412	AGAGGAACAATAAAAAGAAG	GAG	chr1	62597585	62597604	62597588	-
SEQ ID NO 4413	TTATCTTGATTTTCAATTTC	AAG	chr1	62597545	62597564	62597548	-
SEQ ID NO 4414	ATTTTCAATTTCAAGCAACG	TGG	chr1	62597537	62597556	62597540	-
SEQ ID NO 4415	AACGTGGAACTGTTTTCTTC	TGG	chr1	62597521	62597540	62597524	-
SEQ ID NO 4416	GTGGAACTGTTTTCTTCTGG	AAG	chr1	62597518	62597537	62597521	-
SEQ ID NO 4417	GAACTGTTTTCTTCTGGAAG	CAG	chr1	62597515	62597534	62597518	-
SEQ ID NO 4418	TTTTCTTCTGGAAGCAGACC	TAG	chr1	62597509	62597528	62597512	-
SEQ ID NO 4419	TATATATACCAATATTTGCC	CAG	chr1	62597474	62597493	62597477	-
SEQ ID NO 4420	ATACCAATATTTGCCCAGAA	AAG	chr1	62597469	62597488	62597472	-
SEQ ID NO 4421	TACCAATATTTGCCCAGAAA	AGG	chr1	62597468	62597487	62597471	-
SEQ ID NO 4422	AATATTTGCCCAGAAAAGGT	AAG	chr1	62597464	62597483	62597467	-
SEQ ID NO 4423	ATATTTGCCCAGAAAAGGTA	AGG	chr1	62597463	62597482	62597466	-
SEQ ID NO 4424	TTGCCCAGAAAAGGTAAGGT	TGG	chr1	62597459	62597478	62597462	-
SEQ ID NO 4425	CCCAGAAAAGGTAAGGTTGG	TAG	chr1	62597456	62597475	62597459	-
SEQ ID NO 4426	CCAGAAAAGGTAAGGTTGGT	AGG	chr1	62597455	62597474	62597458	-
SEQ ID NO 4427	GTAAGGTTGGTAGGTGAACA	TAG	chr1	62597446	62597465	62597449	-
SEQ ID NO 4428	GGTGAACATAGTTAATCATT	AAG	chr1	62597434	62597453	62597437	-
SEQ ID NO 4429	ATGTAACCTTCTTCCACATT	GAG	chr1	62597393	62597412	62597396	-
SEQ ID NO 4430	AACCTTCTTCCACATTGAGT	TAG	chr1	62597389	62597408	62597392	-
SEQ ID NO 4431	ATCAATGCTAAATGAAATCA	AAG	chr1	62597366	62597385	62597369	-

SEQ ID NO 4432	CTAAATGAAATCAAAGAAAT	GAG	chr1	62597359	62597378	62597362 -
SEQ ID NO 4433	GAAATGAGCAACTAACTTAA	TAG	chr1	62597344	62597363	62597347 -
SEQ ID NO 4434	AAATGAGCAACTAACTTAAT	AGG	chr1	62597343	62597362	62597346 -
SEQ ID NO 4435	AAACTACACATTCAATGCTA	TGG	chr1	62597286	62597305	62597289 -
SEQ ID NO 4436	TGGTGACTACCTGTTTTTAA	AAG	chr1	62597266	62597285	62597269 -
SEQ ID NO 4437	TTTTACTTTTTTATGATTTT	AAG	chr1	62597239	62597258	62597242 -
SEQ ID NO 4438	TTACTTTTTTATGATTTTAA	GAG	chr1	62597237	62597256	62597240 -
SEQ ID NO 4439	TATGATTTTAAGAGATTTAC	AAG	chr1	62597228	62597247	62597231 -
SEQ ID NO 4440	TCAAAAATAAACTTTTTTGT	TGG	chr1	62597205	62597224	62597208 -
SEQ ID NO 4441	CAAAAATAAACTTTTTTGTT	GGG	chr1	62597204	62597223	62597207 -
SEQ ID NO 4442	GTTGGGTAAATTTATTATTA	AAG	chr1	62597187	62597206	62597190 -
SEQ ID NO 4443	GTAAATTTATTATTAAAGTT	GAG	chr1	62597182	62597201	62597185 -
SEQ ID NO 4444	TAAATTTATTATTAAAGTTG	AGG	chr1	62597181	62597200	62597184 -
SEQ ID NO 4445	AAATTTATTATTAAAGTTGA	GGG	chr1	62597180	62597199	62597183 -
SEQ ID NO 4446	AATTTATTATTAAAGTTGAG	GGG	chr1	62597179	62597198	62597182 -
SEQ ID NO 4447	TATTAAAGTTGAGGGGAAAA	AAG	chr1	62597172	62597191	62597175 -
SEQ ID NO 4448	GGGGAAAAAAGTAATGAATT	AAG	chr1	62597160	62597179	62597163 -

Figure 14

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 4449	AACAGGTAGTCACCATAGCA	TTGAAT	chr1	62597271	62597290	62597287	+
SEQ ID NO 4450	TGGGCAAATATTGGTATATA	TAGAGT	chr1	62597472	62597491	62597488	+
SEQ ID NO 4451	GTTCCTCTAGTTATTTCCTC	CAGAAT	chr1	62597597	62597616	62597613	+
SEQ ID NO 4452	AAGTCAAAAATGAAGAGGTA	AAGAAT	chr1	62597886	62597905	62597902	+
SEQ ID NO 4453	TAAAGTAAGTAGAAAATAAA	GAGGGT	chr1	62598058	62598077	62598074	+
SEQ ID NO 4454	TTCATGTTTATGTTTTCAAT	GTGGAT	chr1	62598083	62598102	62598099	+
SEQ ID NO 4455	GAAAGAAGCATACAAGGGGA	AGGAAT	chr1	62598548	62598567	62598564	+
SEQ ID NO 4456	CACACAGGTCTGTAAAAACA	CTGAAT	chr1	62598841	62598860	62598857	+
SEQ ID NO 4457	AAATTATTTACAAGCTTTAA	CTGGAT	chr1	62598871	62598890	62598887	+
SEQ ID NO 4458	TTACAAGCTTTAACTGGATC	ATGAGT	chr1	62598878	62598897	62598894	+
SEQ ID NO 4459	CTCTAAAACTTTGTGTGACC	TTGAAT	chr1	62598978	62598997	62598994	+
SEQ ID NO 4460	AAAGATAATAACAGAACTTA	TAGGAT	chr1	62599049	62599068	62599065	+
SEQ ID NO 4461	TCTTGGTCTAAAGAGCCAAT	ATGAGT	chr1	62599187	62599206	62599190	-
SEQ ID NO 4462	AAAGAGAAACATGATCTAAT	TTGAAT	chr1	62599131	62599150	62599134	-
SEQ ID NO 4463	GTAAGATGACATTGGCTGCT	ATGAAT	chr1	62599101	62599120	62599104	-
SEQ ID NO 4464	GTGAGGAAACTGAGAGATAA	AGGGGT	chr1	62599020	62599039	62599023	-
SEQ ID NO 4465	TTAAAGCTTGTAAATAATTT	TAGGAT	chr1	62598871	62598890	62598874	-
SEQ ID NO 4466	TCTTGTTTTTCTACAAAAGT	CTGGAT	chr1	62598696	62598715	62598699	-
SEQ ID NO 4467	TCTACAAAAGTCTGGATATA	GAGAGT	chr1	62598687	62598706	62598690	-
SEQ ID NO 4468	TCTAAATTTTTAAACTAATA	ATGGAT	chr1	62598600	62598619	62598603	-
SEQ ID NO 4469	ACTAATAATGGATTTGAAAA	ATGAAT	chr1	62598587	62598606	62598590	-
SEQ ID NO 4470	AAAGCCCAGCATATTTTCAT	ATGAAT	chr1	62598444	62598463	62598447	-
SEQ ID NO 4471	TTAATCTGTTTTAAACACTG	GAGAAT	chr1	62598393	62598412	62598396	-
SEQ ID NO 4472	TACTTTAAGTGAAGTTACTT	CTGGGT	chr1	62598045	62598064	62598048	-
SEQ ID NO 4473	GAAGTTACTTCTGGGTGTTC	TGGAGT	chr1	62598035	62598054	62598038	-
SEQ ID NO 4474	TCTGGAGTTTCAGGTTGATT	TTGAAT	chr1	62598017	62598036	62598020	-
SEQ ID NO 4475	TATTTCACTTTTTGTTGAAG	TAGAAT	chr1	62597966	62597985	62597969	-
SEQ ID NO 4476	TTCTAGGAGGCTTTCAAGTT	TTGAGT	chr1	62597934	62597953	62597937	-
SEQ ID NO 4477	GGAGGCTTTCAAGTTTTGAG	TTGAGT	chr1	62597929	62597948	62597932	-
SEQ ID NO 4478	AAAAAGACTGATCAAATATG	TTGAGT	chr1	62597794	62597813	62597797	-
SEQ ID NO 4479	TGATTTTGGCTCTGGAGATA	GAGAAT	chr1	62597652	62597671	62597655	-
SEQ ID NO 4480	TGGAGATAGAGAATCAAATG	ATGAAT	chr1	62597640	62597659	62597643	-
SEQ ID NO 4481	ATTAAGCCGTGTTAACTTGC	ACGAAT	chr1	62597417	62597436	62597420	-
SEQ ID NO 4482	GAATGTAACCTTCTTCCACA	TTGAGT	chr1	62597395	62597414	62597398	-
SEQ ID NO 4483	GTCAAAAATAAACTTTTTTG	TTGGGT	chr1	62597206	62597225	62597209	-
SEQ ID NO 4484	AAGTTGAGGGGAAAAAAGTA	ATGAAT	chr1	62597167	62597186	62597170	-

Figure 15

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 4485	GAAGTCTAGGTCTGCTTCCA	GAAGAAA	chr1	62597501	62597520	62597517	+
SEQ ID NO 4486	TGTTCCTCTAGTTATTTCCT	CCAGAAT	chr1	62597596	62597615	62597612	+
SEQ ID NO 4487	AAACCAGTGAAATCAAAGAA	GAAGAAA	chr1	62597829	62597848	62597845	+
SEQ ID NO 4488	CAAGTCAAAAATGAAGAGGT	AAAGAAT	chr1	62597885	62597904	62597901	+
SEQ ID NO 4489	CAAAACTTGAAAGCCTCCTA	GAAGAAA	chr1	62597931	62597950	62597947	+
SEQ ID NO 4490	AGTAACTTCACTTAAAGTAA	GTAGAAA	chr1	62598046	62598065	62598062	+
SEQ ID NO 4491	TGTTGAAATACTTTTTTTTC	CAAGAAA	chr1	62598160	62598179	62598176	+
SEQ ID NO 4492	TTTTCCAAGAAAAATAATCT	CCAGAAA	chr1	62598175	62598194	62598191	+
SEQ ID NO 4493	CTTTTTCTTTTAATTGAAGT	TCAGAAA	chr1	62598460	62598479	62598476	+
SEQ ID NO 4494	GATAGTGTTACAGGAAATTA	ATAGAAA	chr1	62598624	62598643	62598640	+
SEQ ID NO 4495	TGTTACAGGAAATTAATAGA	AAAGAAA	chr1	62598629	62598648	62598645	+
SEQ ID NO 4496	CTCTCTATATCCAGACTTTT	GTAGAAA	chr1	62598682	62598701	62598698	+
SEQ ID NO 4497	ACCAACAGCATAGTCAAATA	AAAGAAA	chr1	62598769	62598788	62598785	+
SEQ ID NO 4498	AGCATAGTCAAATAAAAGAA	ATAGAAA	chr1	62598775	62598794	62598791	+
SEQ ID NO 4499	CAGAACTTATAGGATTATTG	TAAGAAA	chr1	62599060	62599079	62599076	+
SEQ ID NO 4500	TATTGTGTGGTTTTGAGCAA	AGAGAAA	chr1	62599149	62599168	62599152	-
SEQ ID NO 4501	GATTTTCTGAACTTCAATTA	AAAGAAA	chr1	62598470	62598489	62598473	-
SEQ ID NO 4502	TTTAATCTGTTTTAAACACT	GGAGAAT	chr1	62598394	62598413	62598397	-
SEQ ID NO 4503	AGTATTTCAAATGGCATGCC	TTAGAAA	chr1	62598131	62598150	62598134	-
SEQ ID NO 4504	ATATTTCACTTTTTGTTGAA	GTAGAAT	chr1	62597967	62597986	62597970	-
SEQ ID NO 4505	TTGATTTTGGCTCTGGAGAT	AGAGAAT	chr1	62597653	62597672	62597656	-
SEQ ID NO 4506	CTATATATACCAATATTTGC	CCAGAAA	chr1	62597475	62597494	62597478	-
SEQ ID NO 4507	GATCAATGCTAAATGAAATC	AAAGAAA	chr1	62597367	62597386	62597370	-

Figure 16

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 4508	AAAAAGTAAAATTAGCTTTT	AAAAAC	chr1	62597248	62597267	62597264	+
SEQ ID NO 4509	GTCTAGGTCTGCTTCCAGAA	GAAAAC	chr1	62597504	62597523	62597520	+
SEQ ID NO 4510	CCAAATTAATGACATATTTC	AAAAAC	chr1	62597764	62597783	62597780	+
SEQ ID NO 4511	TATGTCACTTGAACTCAACT	CAAAAC	chr1	62597911	62597930	62597927	+
SEQ ID NO 4512	GTTTCCCTAATGTTATATAT	GAAAAC	chr1	62598238	62598257	62598254	+
SEQ ID NO 4513	GTAAAAAGTTAAAAAAAATT	TAAAAC	chr1	62598360	62598379	62598376	+
SEQ ID NO 4514	TAAAACTATTCTCCAGTGTT	TAAAAC	chr1	62598380	62598399	62598396	+
SEQ ID NO 4515	CTATATCCAGACTTTTGTAG	AAAAAC	chr1	62598686	62598705	62598702	+
SEQ ID NO 4516	CATCTTTCACACAGGTCTGT	AAAAAC	chr1	62598834	62598853	62598850	+
SEQ ID NO 4517	CTGCATTTAAACCATGGCTC	TAAAAC	chr1	62598961	62598980	62598977	+
SEQ ID NO 4518	AGATCATGTTTCTCTTTGCT	CAAAAC	chr1	62599134	62599153	62599150	+
SEQ ID NO 4519	TATATAACATTAGGGAAACA	AAAAAC	chr1	62598237	62598256	62598240	-
SEQ ID NO 4520	TTTTTTAAAAGATCCACATT	GAAAAC	chr1	62598100	62598119	62598103	-

Figure 17

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 4521	ATAATAAATTTACCCAACAA	AAAAGTTT	chr1	62597189	62597208	62597205	+
SEQ ID NO 4522	TAAAATCATAAAAAAGTAAA	ATTAGCTT	chr1	62597238	62597257	62597254	+
SEQ ID NO 4523	AGTCACCATAGCATTGAATG	TGTAGTTT	chr1	62597278	62597297	62597294	+
SEQ ID NO 4524	ATTAAGTTAGTTGCTCATTT	CTTTGATT	chr1	62597343	62597362	62597359	+
SEQ ID NO 4525	GTTACATTCGTGCAAGTTAA	CACGGCTT	chr1	62597406	62597425	62597422	+
SEQ ID NO 4526	TCGTGCAAGTTAACACGGCT	TAATGATT	chr1	62597413	62597432	62597429	+
SEQ ID NO 4527	TATAGAGTTAAGAAGTCTAG	GTCTGCTT	chr1	62597490	62597509	62597506	+
SEQ ID NO 4528	TCCAGAAGAAAACAGTTCCA	CGTTGCTT	chr1	62597517	62597536	62597533	+
SEQ ID NO 4529	ATTGATCAAGACAATTCATC	ATTTGATT	chr1	62597621	62597640	62597637	+
SEQ ID NO 4530	CTCTATCTCCAGAGCCAAAA	TCAAGATT	chr1	62597649	62597668	62597665	+
SEQ ID NO 4531	AAGTAGAAAATAAAGAGGGT	TCATGTTT	chr1	62598064	62598083	62598080	+
SEQ ID NO 4532	AAAATAAAGAGGGTTCATGT	TTATGTTT	chr1	62598070	62598089	62598086	+
SEQ ID NO 4533	ATTTCCTATTATAATTTCAA	GTTAGTTT	chr1	62598207	62598226	62598223	+
SEQ ID NO 4534	ATTATAATTTCAAGTTAGTT	TTTTGTTT	chr1	62598214	62598233	62598230	+
SEQ ID NO 4535	AAAAATTTAAAACTATTCTC	CAGTGTTT	chr1	62598373	62598392	62598389	+
SEQ ID NO 4536	AACTATTCTCCAGTGTTTAA	AACAGATT	chr1	62598383	62598402	62598399	+
SEQ ID NO 4537	TTAAATAATACAGTAAATGG	AAAAGATT	chr1	62598409	62598428	62598425	+
SEQ ID NO 4538	TTTATTCATATGAAAATATG	CTGGGCTT	chr1	62598435	62598454	62598451	+
SEQ ID NO 4539	ATTCATTTTTCAAATCCATT	ATTAGTTT	chr1	62598581	62598600	62598597	+
SEQ ID NO 4540	ATCCATTATTAGTTTAAAAA	TTTAGATT	chr1	62598594	62598613	62598610	+
SEQ ID NO 4541	ACTGAATCCTAAAATTATTT	ACAAGCTT	chr1	62598860	62598879	62598876	+
SEQ ID NO 4542	ATTACTTCACCCCTTTATCT	CTCAGTTT	chr1	62599006	62599025	62599022	+
SEQ ID NO 4543	CAAAGATAATAACAGAACTT	ATAGGATT	chr1	62599048	62599067	62599064	+
SEQ ID NO 4544	TTACTAAAATTCAAATTAGA	TCATGTTT	chr1	62599117	62599136	62599133	+
SEQ ID NO 4545	CTCTTTGCTCAAAACCACAC	AATAGCTT	chr1	62599145	62599164	62599161	+
SEQ ID NO 4546	ACTCATATTGGCTCTTTAGA	CCAAGATT	chr1	62599181	62599200	62599197	+
SEQ ID NO 4547	AGTGAAATGGAAAGCTATTG	TGTGGTTT	chr1	62599164	62599183	62599167	-
SEQ ID NO 4548	GTAATTTATTCAAGGTCACA	CAAAGTTT	chr1	62598991	62599010	62598994	-
SEQ ID NO 4549	GTCACACAAAGTTTTAGAGC	CATGGTTT	chr1	62598977	62598996	62598980	-
SEQ ID NO 4550	AGAGCCATGGTTTAAATGCA	GGTAGTTT	chr1	62598962	62598981	62598965	-
SEQ ID NO 4551	GGTTTAAATGCAGGTAGTTT	ATTAGCTT	chr1	62598954	62598973	62598957	-
SEQ ID NO 4552	AATTTTACTCATGATCCAGT	TAAAGCTT	chr1	62598890	62598909	62598893	-
SEQ ID NO 4553	GTTAAAGCTTGTAAATAATT	TTAGGATT	chr1	62598872	62598891	62598875	-
SEQ ID NO 4554	TTGTAAATAATTTTAGGATT	CAGTGTTT	chr1	62598864	62598883	62598867	-
SEQ ID NO 4555	TACCATTAAAATACTGACTT	ACCTGATT	chr1	62598809	62598828	62598812	-
SEQ ID NO 4556	TTCTTTTATTTGACTATGCT	GTTGGTTT	chr1	62598775	62598794	62598778	-
SEQ ID NO 4557	TTTGACTATGCTGTTGGTTT	AATTGTTT	chr1	62598767	62598786	62598770	-
SEQ ID NO 4558	GAAGGTCTTTGATGCTATTA	TCTTGTTT	chr1	62598716	62598735	62598719	-
SEQ ID NO 4559	TAGAGAGTAGGTTGGTTATA	AGTTGCTT	chr1	62598669	62598688	62598672	-
SEQ ID NO 4560	ATCTAAATTTTTAAACTAAT	AATGGATT	chr1	62598601	62598620	62598604	-
SEQ ID NO 4561	ATTGGCAATTCCTTCCCCTT	GTATGCTT	chr1	62598561	62598580	62598564	-
SEQ ID NO 4562	TAAATTGTACTATCTCTAAA	ATTTGATT	chr1	62598494	62598513	62598497	-
SEQ ID NO 4563	TCCATTTACTGTATTATTTA	ATCTGTTT	chr1	62598410	62598429	62598413	-
SEQ ID NO 4564	ATCTGTTTTAAACACTGGAG	AATAGTTT	chr1	62598390	62598409	62598393	-
SEQ ID NO 4565	ATAGTGTAATGACATAGTGT	TCTAGATT	chr1	62598321	62598340	62598324	-
SEQ ID NO 4566	TGTTCTAGATTGTATAATTT	AACCGATT	chr1	62598304	62598323	62598307	-
SEQ ID NO 4567	TCATATAAAATGCAAATTTT	CAGTGTTT	chr1	62598268	62598287	62598271	-
SEQ ID NO 4568	TAATAGGAAATTTTATTTTC	TGGAGATT	chr1	62598198	62598217	62598201	-
SEQ ID NO 4569	GAAGTTACTTCTGGGTGTTC	TGGAGTTT	chr1	62598035	62598054	62598038	-
SEQ ID NO 4570	CTGGGTGTTCTGGAGTTTCA	GGTTGATT	chr1	62598025	62598044	62598028	-

SEQ ID NO 4571	AAGTAGAATTTTTTCTTCTA	GGAGGCTT	chr1	62597949	62597968	62597952	-
SEQ ID NO 4572	TTTTTTCTTCTAGGAGGCTT	TCAAGTTT	chr1	62597941	62597960	62597944	-
SEQ ID NO 4573	TTACCTCTTCATTTTTGACT	TGTAGTTT	chr1	62597887	62597906	62597890	-
SEQ ID NO 4574	TCTCAGTTCCTTTTCTTCTT	CTTTGATT	chr1	62597847	62597866	62597850	-
SEQ ID NO 4575	TTTTCTTCTTCTTTGATTTC	ACTGGTTT	chr1	62597837	62597856	62597840	-
SEQ ID NO 4576	AAAAAGACTGATCAAATATG	TTGAGTTT	chr1	62597794	62597813	62597797	-
SEQ ID NO 4577	ACATCGTCTAACATAGCAAA	TCTTGATT	chr1	62597675	62597694	62597678	-
SEQ ID NO 4578	CTAGAGGAACAATAAAAAGA	AGGAGCTT	chr1	62597587	62597606	62597590	-
SEQ ID NO 4579	CTTAATTGTGAACATTTTTA	TCTTGATT	chr1	62597562	62597581	62597565	-
SEQ ID NO 4580	TTCAATTTCAAGCAACGTGG	AACTGTTT	chr1	62597534	62597553	62597537	-
SEQ ID NO 4581	CATTCAATGCTATGGTGACT	ACCTGTTT	chr1	62597278	62597297	62597281	-
SEQ ID NO 4582	TAAAAGCTAATTTTACTTTT	TTATGATT	chr1	62597249	62597268	62597252	-
SEQ ID NO 4583	TTTTACTTTTTTATGATTTT	AAGAGATT	chr1	62597239	62597258	62597242	-

Figure 18

#	Sequence	PAM	Chr	Start	End	Cut site 1 (5' of)	Cut site 2 (5' of)	Str
SEQ ID NO 4584	AATTCATTACTTTTTTCCCCTC	CTT	chr1	62597160	62597181	62597177	62597182	+
SEQ ID NO 4585	ATTCATTACTTTTTTCCCCTCA	TTA	chr1	62597161	62597182	62597178	62597183	+
SEQ ID NO 4586	ATTACTTTTTTCCCCTCAACTT	TTC	chr1	62597165	62597186	62597182	62597187	+
SEQ ID NO 4587	CTTTTTTCCCCTCAACTTTAAT	TTA	chr1	62597169	62597190	62597186	62597191	+
SEQ ID NO 4588	TTTTCCCCTCAACTTTAATAAT	CTT	chr1	62597172	62597193	62597189	62597194	+
SEQ ID NO 4589	TTTCCCCTCAACTTTAATAATA	TTT	chr1	62597173	62597194	62597190	62597195	+
SEQ ID NO 4590	TTCCCCTCAACTTTAATAATAA	TTT	chr1	62597174	62597195	62597191	62597196	+
SEQ ID NO 4591	TCCCCTCAACTTTAATAATAAA	TTT	chr1	62597175	62597196	62597192	62597197	+
SEQ ID NO 4592	CCCCTCAACTTTAATAATAAAT	TTT	chr1	62597176	62597197	62597193	62597198	+
SEQ ID NO 4593	CCCTCAACTTTAATAATAAATT	TTC	chr1	62597177	62597198	62597194	62597199	+
SEQ ID NO 4594	AACTTTAATAATAAATTTACCC	CTC	chr1	62597182	62597203	62597199	62597204	+
SEQ ID NO 4595	TAATAATAAATTTACCCAACAA	CTT	chr1	62597187	62597208	62597204	62597209	+
SEQ ID NO 4596	AATAATAAATTTACCCAACAAA	TTT	chr1	62597188	62597209	62597205	62597210	+
SEQ ID NO 4597	ATAATAAATTTACCCAACAAAA	TTA	chr1	62597189	62597210	62597206	62597211	+
SEQ ID NO 4598	ACCCAACAAAAAAGTTTATTTT	TTT	chr1	62597200	62597221	62597217	62597222	+
SEQ ID NO 4599	CCCAACAAAAAAGTTTATTTTT	TTA	chr1	62597201	62597222	62597218	62597223	+
SEQ ID NO 4600	ATTTTTGACTTGTAAATCTCTT	TTT	chr1	62597217	62597238	62597234	62597239	+
SEQ ID NO 4601	TTTTTGACTTGTAAATCTCTTA	TTA	chr1	62597218	62597239	62597235	62597240	+
SEQ ID NO 4602	TTGACTTGTAAATCTCTTAAAA	TTT	chr1	62597221	62597242	62597238	62597243	+
SEQ ID NO 4603	TGACTTGTAAATCTCTTAAAAT	TTT	chr1	62597222	62597243	62597239	62597244	+
SEQ ID NO 4604	GACTTGTAAATCTCTTAAAATC	TTT	chr1	62597223	62597244	62597240	62597245	+
SEQ ID NO 4605	ACTTGTAAATCTCTTAAAATCA	TTG	chr1	62597224	62597245	62597241	62597246	+
SEQ ID NO 4606	GTAAATCTCTTAAAATCATAAA	CTT	chr1	62597228	62597249	62597245	62597250	+
SEQ ID NO 4607	TAAATCTCTTAAAATCATAAAA	TTG	chr1	62597229	62597250	62597246	62597251	+
SEQ ID NO 4608	TTAAAATCATAAAAAAGTAAAA	CTC	chr1	62597237	62597258	62597254	62597259	+
SEQ ID NO 4609	AAAATCATAAAAAAGTAAAATT	CTT	chr1	62597239	62597260	62597256	62597261	+
SEQ ID NO 4610	AAATCATAAAAAAGTAAAATTA	TTA	chr1	62597240	62597261	62597257	62597262	+
SEQ ID NO 4611	GCTTTTAAAAACAGGTAGTCAC	TTA	chr1	62597262	62597283	62597279	62597284	+
SEQ ID NO 4612	TTAAAAACAGGTAGTCACCATA	CTT	chr1	62597266	62597287	62597283	62597288	+
SEQ ID NO 4613	TAAAAACAGGTAGTCACCATAG	TTT	chr1	62597267	62597288	62597284	62597289	+
SEQ ID NO 4614	AAAAACAGGTAGTCACCATAGC	TTT	chr1	62597268	62597289	62597285	62597290	+
SEQ ID NO 4615	AAAACAGGTAGTCACCATAGCA	TTA	chr1	62597269	62597290	62597286	62597291	+
SEQ ID NO 4616	AATGTGTAGTTTATAATACAGC	TTG	chr1	62597294	62597315	62597311	62597316	+
SEQ ID NO 4617	ATAATACAGCAAAGTTAAATAC	TTT	chr1	62597306	62597327	62597323	62597328	+
SEQ ID NO 4618	TAATACAGCAAAGTTAAATACA	TTA	chr1	62597307	62597328	62597324	62597329	+
SEQ ID NO 4619	AATACAATTTCAAATTACCTAT	TTA	chr1	62597323	62597344	62597340	62597345	+
SEQ ID NO 4620	CAAATTACCTATTAAGTTAGTT	TTT	chr1	62597333	62597354	62597350	62597355	+
SEQ ID NO 4621	AAATTACCTATTAAGTTAGTTG	TTC	chr1	62597334	62597355	62597351	62597356	+
SEQ ID NO 4622	CCTATTAAGTTAGTTGCTCATT	TTA	chr1	62597340	62597361	62597357	62597362	+
SEQ ID NO 4623	TTAAGTTAGTTGCTCATTTCTT	CTA	chr1	62597344	62597365	62597361	62597366	+
SEQ ID NO 4624	AGTTAGTTGCTCATTTCTTTGA	TTA	chr1	62597347	62597368	62597364	62597369	+
SEQ ID NO 4625	GTTGCTCATTTCTTTGATTTCA	TTA	chr1	62597352	62597373	62597369	62597374	+
SEQ ID NO 4626	CTCATTTCTTTGATTTCATTTA	TTG	chr1	62597356	62597377	62597373	62597378	+
SEQ ID NO 4627	ATTTCTTTGATTTCATTTAGCA	CTC	chr1	62597359	62597380	62597376	62597381	+
SEQ ID NO 4628	CTTTGATTTCATTTAGCATTGA	TTT	chr1	62597363	62597384	62597380	62597385	+
SEQ ID NO 4629	TTTGATTTCATTTAGCATTGAT	TTC	chr1	62597364	62597385	62597381	62597386	+
SEQ ID NO 4630	TGATTTCATTTAGCATTGATCT	CTT	chr1	62597366	62597387	62597383	62597388	+
SEQ ID NO 4631	GATTTCATTTAGCATTGATCTA	TTT	chr1	62597367	62597388	62597384	62597389	+
SEQ ID NO 4632	ATTTCATTTAGCATTGATCTAA	TTG	chr1	62597368	62597389	62597385	62597390	+
SEQ ID NO 4633	CATTTAGCATTGATCTAACTCA	TTT	chr1	62597372	62597393	62597389	62597394	+
SEQ ID NO 4634	ATTTAGCATTGATCTAACTCAA	TTC	chr1	62597373	62597394	62597390	62597395	+
SEQ ID NO 4635	AGCATTGATCTAACTCAATGTG	TTT	chr1	62597377	62597398	62597394	62597399	+
SEQ ID NO 4636	GCATTGATCTAACTCAATGTGG	TTA	chr1	62597378	62597399	62597395	62597400	+
SEQ ID NO 4637	ATCTAACTCAATGTGGAAGAAG	TTG	chr1	62597384	62597405	62597401	62597406	+
SEQ ID NO 4638	ACTCAATGTGGAAGAAGGTTAC	CTA	chr1	62597389	62597410	62597406	62597411	+
SEQ ID NO 4639	AATGTGGAAGAAGGTTACATTC	CTC	chr1	62597393	62597414	62597410	62597415	+
SEQ ID NO 4640	CATTCGTGCAAGTTAACACGGC	TTA	chr1	62597410	62597431	62597427	62597432	+

SEQ ID NO 4641	GTGCAAGTTAACACGGCTTAAT	TTC	chr1	62597415	62597436	62597432	62597437	+
SEQ ID NO 4642	ACACGGCTTAATGATTAACTAT	TTA	chr1	62597425	62597446	62597442	62597447	+
SEQ ID NO 4643	AATGATTAACTATGTTCACCTA	CTT	chr1	62597434	62597455	62597451	62597456	+
SEQ ID NO 4644	ATGATTAACTATGTTCACCTAC	TTA	chr1	62597435	62597456	62597452	62597457	+
SEQ ID NO 4645	ACTATGTTCACCTACCAACCTT	TTA	chr1	62597442	62597463	62597459	62597464	+
SEQ ID NO 4646	TGTTCACCTACCAACCTTACCT	CTA	chr1	62597446	62597467	62597463	62597468	+
SEQ ID NO 4647	ACCTACCAACCTTACCTTTTCT	TTC	chr1	62597451	62597472	62597468	62597473	+
SEQ ID NO 4648	CCAACCTTACCTTTTCTGGGCA	CTA	chr1	62597456	62597477	62597473	62597478	+
SEQ ID NO 4649	ACCTTTTCTGGGCAAATATTGG	CTT	chr1	62597464	62597485	62597481	62597486	+
SEQ ID NO 4650	CCTTTTCTGGGCAAATATTGGT	TTA	chr1	62597465	62597486	62597482	62597487	+
SEQ ID NO 4651	TTCTGGGCAAATATTGGTATAT	CTT	chr1	62597469	62597490	62597486	62597491	+
SEQ ID NO 4652	TCTGGGCAAATATTGGTATATA	TTT	chr1	62597470	62597491	62597487	62597492	+
SEQ ID NO 4653	CTGGGCAAATATTGGTATATAT	TTT	chr1	62597471	62597492	62597488	62597493	+
SEQ ID NO 4654	TGGGCAAATATTGGTATATATA	TTC	chr1	62597472	62597493	62597489	62597494	+
SEQ ID NO 4655	GGCAAATATTGGTATATATAGA	CTG	chr1	62597474	62597495	62597491	62597496	+
SEQ ID NO 4656	GTATATATAGAGTTAAGAAGTC	TTG	chr1	62597485	62597506	62597502	62597507	+
SEQ ID NO 4657	AGAAGTCTAGGTCTGCTTCCAG	TTA	chr1	62597500	62597521	62597517	62597522	+
SEQ ID NO 4658	GGTCTGCTTCCAGAAGAAAACA	CTA	chr1	62597509	62597530	62597526	62597531	+
SEQ ID NO 4659	CTTCCAGAAGAAAACAGTTCCA	CTG	chr1	62597515	62597536	62597532	62597537	+
SEQ ID NO 4660	CCAGAAGAAAACAGTTCCACGT	CTT	chr1	62597518	62597539	62597535	62597540	+
SEQ ID NO 4661	CAGAAGAAAACAGTTCCACGTT	TTC	chr1	62597519	62597540	62597536	62597541	+
SEQ ID NO 4662	CACGTTGCTTGAAATTGAAAAT	TTC	chr1	62597535	62597556	62597552	62597557	+
SEQ ID NO 4663	CTTGAAATTGAAAATCAAGATA	TTG	chr1	62597542	62597563	62597559	62597564	+
SEQ ID NO 4664	GAAATTGAAAATCAAGATAAAA	CTT	chr1	62597545	62597566	62597562	62597567	+
SEQ ID NO 4665	AAATTGAAAATCAAGATAAAAA	TTG	chr1	62597546	62597567	62597563	62597568	+
SEQ ID NO 4666	AAAATCAAGATAAAAATGTTCA	TTG	chr1	62597552	62597573	62597569	62597574	+
SEQ ID NO 4667	ACAATTAAGCTCCTTCTTTTTA	TTC	chr1	62597573	62597594	62597590	62597595	+
SEQ ID NO 4668	AGCTCCTTCTTTTTATTGTTCC	TTA	chr1	62597580	62597601	62597597	62597602	+
SEQ ID NO 4669	CTTCTTTTTATTGTTCCTCTAG	CTC	chr1	62597585	62597606	62597602	62597607	+
SEQ ID NO 4670	CTTTTTATTGTTCCTCTAGTTA	CTT	chr1	62597588	62597609	62597605	62597610	+
SEQ ID NO 4671	TTTTTATTGTTCCTCTAGTTAT	TTC	chr1	62597589	62597610	62597606	62597611	+
SEQ ID NO 4672	TTTATTGTTCCTCTAGTTATTT	CTT	chr1	62597591	62597612	62597608	62597613	+
SEQ ID NO 4673	TTATTGTTCCTCTAGTTATTTC	TTT	chr1	62597592	62597613	62597609	62597614	+
SEQ ID NO 4674	TATTGTTCCTCTAGTTATTTCC	TTT	chr1	62597593	62597614	62597610	62597615	+
SEQ ID NO 4675	ATTGTTCCTCTAGTTATTTCCT	TTT	chr1	62597594	62597615	62597611	62597616	+
SEQ ID NO 4676	TTGTTCCTCTAGTTATTTCCTC	TTA	chr1	62597595	62597616	62597612	62597617	+
SEQ ID NO 4677	TTCCTCTAGTTATTTCCTCCAG	TTG	chr1	62597598	62597619	62597615	62597620	+
SEQ ID NO 4678	CTCTAGTTATTTCCTCCAGAAT	TTC	chr1	62597601	62597622	62597618	62597623	+
SEQ ID NO 4679	TAGTTATTTCCTCCAGAATTGA	CTC	chr1	62597604	62597625	62597621	62597626	+
SEQ ID NO 4680	GTTATTTCCTCCAGAATTGATC	CTA	chr1	62597606	62597627	62597623	62597628	+
SEQ ID NO 4681	TTTCCTCCAGAATTGATCAAGA	TTA	chr1	62597610	62597631	62597627	62597632	+
SEQ ID NO 4682	CCTCCAGAATTGATCAAGACAA	TTT	chr1	62597613	62597634	62597630	62597635	+
SEQ ID NO 4683	CTCCAGAATTGATCAAGACAAT	TTC	chr1	62597614	62597635	62597631	62597636	+
SEQ ID NO 4684	CAGAATTGATCAAGACAATTCA	CTC	chr1	62597617	62597638	62597634	62597639	+
SEQ ID NO 4685	ATCAAGACAATTCATCATTTGA	TTG	chr1	62597625	62597646	62597642	62597647	+
SEQ ID NO 4686	ATCATTTGATTCTCTATCTCCA	TTC	chr1	62597638	62597659	62597655	62597660	+
SEQ ID NO 4687	GATTCTCTATCTCCAGAGCCAA	TTT	chr1	62597645	62597666	62597662	62597667	+
SEQ ID NO 4688	ATTCTCTATCTCCAGAGCCAAA	TTG	chr1	62597646	62597667	62597663	62597668	+
SEQ ID NO 4689	TCTATCTCCAGAGCCAAAATCA	TTC	chr1	62597650	62597671	62597667	62597672	+
SEQ ID NO 4690	TATCTCCAGAGCCAAAATCAAG	CTC	chr1	62597652	62597673	62597669	62597674	+
SEQ ID NO 4691	TCTCCAGAGCCAAAATCAAGAT	CTA	chr1	62597654	62597675	62597671	62597676	+
SEQ ID NO 4692	CAGAGCCAAAATCAAGATTTGC	CTC	chr1	62597658	62597679	62597675	62597680	+
SEQ ID NO 4693	GCTATGTTAGACGATGTAAAAA	TTT	chr1	62597678	62597699	62597695	62597700	+
SEQ ID NO 4694	CTATGTTAGACGATGTAAAAAT	TTG	chr1	62597679	62597700	62597696	62597701	+
SEQ ID NO 4695	TGTTAGACGATGTAAAAATTTT	CTA	chr1	62597682	62597703	62597699	62597704	+
SEQ ID NO 4696	GACGATGTAAAAATTTTAGCCA	TTA	chr1	62597687	62597708	62597704	62597709	+
SEQ ID NO 4697	TAGCCAATGGCCTCCTTCAGTT	TTT	chr1	62597703	62597724	62597720	62597725	+
SEQ ID NO 4698	AGCCAATGGCCTCCTTCAGTTG	TTT	chr1	62597704	62597725	62597721	62597726	+

SEQ ID NO 4699	GCCAATGGCCTCCTTCAGTTGG	TTA	chr1	62597705	62597726	62597722	62597727	+
SEQ ID NO 4700	CTTCAGTTGGGACATGGTCTTA	CTC	chr1	62597717	62597738	62597734	62597739	+
SEQ ID NO 4701	CAGTTGGGACATGGTCTTAAAG	CTT	chr1	62597720	62597741	62597737	62597742	+
SEQ ID NO 4702	AGTTGGGACATGGTCTTAAAGA	TTC	chr1	62597721	62597742	62597738	62597743	+
SEQ ID NO 4703	GGACATGGTCTTAAAGACTTTG	TTG	chr1	62597726	62597747	62597743	62597748	+
SEQ ID NO 4704	AAAGACTTTGTCCATAAGACGA	CTT	chr1	62597738	62597759	62597755	62597760	+
SEQ ID NO 4705	AAGACTTTGTCCATAAGACGAA	TTA	chr1	62597739	62597760	62597756	62597761	+
SEQ ID NO 4706	TGTCCATAAGACGAAGGGCCAA	CTT	chr1	62597746	62597767	62597763	62597768	+
SEQ ID NO 4707	GTCCATAAGACGAAGGGCCAAA	TTT	chr1	62597747	62597768	62597764	62597769	+
SEQ ID NO 4708	TCCATAAGACGAAGGGCCAAAT	TTG	chr1	62597748	62597769	62597765	62597770	+
SEQ ID NO 4709	ATGACATATTTCAAAAACTCAA	TTA	chr1	62597772	62597793	62597789	62597794	+
SEQ ID NO 4710	CAAAAACTCAACATATTTGATC	TTT	chr1	62597783	62597804	62597800	62597805	+
SEQ ID NO 4711	AAAAACTCAACATATTTGATCA	TTC	chr1	62597784	62597805	62597801	62597806	+
SEQ ID NO 4712	AACATATTTGATCAGTCTTTTT	CTC	chr1	62597792	62597813	62597809	62597814	+
SEQ ID NO 4713	GATCAGTCTTTTTATGATCTAT	TTT	chr1	62597801	62597822	62597818	62597823	+
SEQ ID NO 4714	ATCAGTCTTTTTATGATCTATC	TTG	chr1	62597802	62597823	62597819	62597824	+
SEQ ID NO 4715	TTTATGATCTATCGCTGCAAAC	CTT	chr1	62597811	62597832	62597828	62597833	+
SEQ ID NO 4716	TTATGATCTATCGCTGCAAACC	TTT	chr1	62597812	62597833	62597829	62597834	+
SEQ ID NO 4717	TATGATCTATCGCTGCAAACCA	TTT	chr1	62597813	62597834	62597830	62597835	+
SEQ ID NO 4718	ATGATCTATCGCTGCAAACCAG	TTT	chr1	62597814	62597835	62597831	62597836	+
SEQ ID NO 4719	TGATCTATCGCTGCAAACCAGT	TTA	chr1	62597815	62597836	62597832	62597837	+
SEQ ID NO 4720	TCGCTGCAAACCAGTGAAATCA	CTA	chr1	62597822	62597843	62597839	62597844	+
SEQ ID NO 4721	CAAACCAGTGAAATCAAAGAAG	CTG	chr1	62597828	62597849	62597845	62597850	+
SEQ ID NO 4722	AGAAGAACTACATATAAACTAC	CTG	chr1	62597864	62597885	62597881	62597886	+
SEQ ID NO 4723	CATATAAACTACAAGTCAAAAA	CTA	chr1	62597874	62597895	62597891	62597896	+
SEQ ID NO 4724	CAAGTCAAAAATGAAGAGGTAA	CTA	chr1	62597885	62597906	62597902	62597907	+
SEQ ID NO 4725	GAACTCAACTCAAAACTTGAAA	CTT	chr1	62597921	62597942	62597938	62597943	+
SEQ ID NO 4726	AACTCAACTCAAAACTTGAAAG	TTG	chr1	62597922	62597943	62597939	62597944	+
SEQ ID NO 4727	AACTCAAAACTTGAAAGCCTCC	CTC	chr1	62597927	62597948	62597944	62597949	+
SEQ ID NO 4728	AAAACTTGAAAGCCTCCTAGAA	CTC	chr1	62597932	62597953	62597949	62597954	+
SEQ ID NO 4729	GAAAGCCTCCTAGAAGAAAAAA	CTT	chr1	62597939	62597960	62597956	62597961	+
SEQ ID NO 4730	AAAGCCTCCTAGAAGAAAAAAT	TTG	chr1	62597940	62597961	62597957	62597962	+
SEQ ID NO 4731	CTAGAAGAAAAAATTCTACTTC	CTC	chr1	62597948	62597969	62597965	62597970	+
SEQ ID NO 4732	GAAGAAAAAATTCTACTTCAAC	CTA	chr1	62597951	62597972	62597968	62597973	+
SEQ ID NO 4733	TACTTCAACAAAAAGTGAAATA	TTC	chr1	62597964	62597985	62597981	62597986	+
SEQ ID NO 4734	CTTCAACAAAAAGTGAAATATT	CTA	chr1	62597966	62597987	62597983	62597988	+
SEQ ID NO 4735	CAACAAAAAGTGAAATATTTAG	CTT	chr1	62597969	62597990	62597986	62597991	+
SEQ ID NO 4736	AACAAAAAGTGAAATATTTAGA	TTC	chr1	62597970	62597991	62597987	62597992	+
SEQ ID NO 4737	AGAAGAGCAACTAACTAACTTA	TTT	chr1	62597989	62598010	62598006	62598011	+
SEQ ID NO 4738	GAAGAGCAACTAACTAACTTAA	TTA	chr1	62597990	62598011	62598007	62598012	+
SEQ ID NO 4739	ACTAACTTAATTCAAAATCAAC	CTA	chr1	62598002	62598023	62598019	62598024	+
SEQ ID NO 4740	ACTTAATTCAAAATCAACCTGA	CTA	chr1	62598006	62598027	62598023	62598028	+
SEQ ID NO 4741	AATTCAAAATCAACCTGAAACT	CTT	chr1	62598010	62598031	62598027	62598032	+
SEQ ID NO 4742	ATTCAAAATCAACCTGAAACTC	TTA	chr1	62598011	62598032	62598028	62598033	+
SEQ ID NO 4743	AAAATCAACCTGAAACTCCAGA	TTC	chr1	62598015	62598036	62598032	62598037	+
SEQ ID NO 4744	AAACTCCAGAACACCCAGAAGT	CTG	chr1	62598027	62598048	62598044	62598049	+
SEQ ID NO 4745	CAGAACACCCAGAAGTAACTTC	CTC	chr1	62598033	62598054	62598050	62598055	+
SEQ ID NO 4746	CACTTAAAGTAAGTAGAAAATA	CTT	chr1	62598054	62598075	62598071	62598076	+
SEQ ID NO 4747	ACTTAAAGTAAGTAGAAAATAA	TTC	chr1	62598055	62598076	62598072	62598077	+
SEQ ID NO 4748	AAAGTAAGTAGAAAATAAAGAG	CTT	chr1	62598059	62598080	62598076	62598081	+
SEQ ID NO 4749	AAGTAAGTAGAAAATAAAGAGG	TTA	chr1	62598060	62598081	62598077	62598082	+
SEQ ID NO 4750	ATGTTTATGTTTTCAATGTGGA	TTC	chr1	62598086	62598107	62598103	62598108	+
SEQ ID NO 4751	ATGTTTTCAATGTGGATCTTTT	TTT	chr1	62598092	62598113	62598109	62598114	+
SEQ ID NO 4752	TGTTTTCAATGTGGATCTTTTA	TTA	chr1	62598093	62598114	62598110	62598115	+
SEQ ID NO 4753	TCAATGTGGATCTTTTAAAAAA	TTT	chr1	62598098	62598119	62598115	62598120	+
SEQ ID NO 4754	CAATGTGGATCTTTTAAAAAAA	TTT	chr1	62598099	62598120	62598116	62598121	+
SEQ ID NO 4755	AATGTGGATCTTTTAAAAAAAA	TTC	chr1	62598100	62598121	62598117	62598122	+
SEQ ID NO 4756	TTAAAAAAAATATTTCTAAGGC	CTT	chr1	62598112	62598133	62598129	62598134	+

SEQ ID NO 4757	TAAAAAAAATATTTCTAAGGCA	TTT	chr1	62598113	62598134	62598130	62598135	+
SEQ ID NO 4758	AAAAAAAATATTTCTAAGGCAT	TTT	chr1	62598114	62598135	62598131	62598136	+
SEQ ID NO 4759	AAAAAAATATTTCTAAGGCATG	TTA	chr1	62598115	62598136	62598132	62598137	+
SEQ ID NO 4760	CTAAGGCATGCCATTTGAAATA	TTT	chr1	62598127	62598148	62598144	62598149	+
SEQ ID NO 4761	TAAGGCATGCCATTTGAAATAC	TTC	chr1	62598128	62598149	62598145	62598150	+
SEQ ID NO 4762	AGGCATGCCATTTGAAATACTT	CTA	chr1	62598130	62598151	62598147	62598152	+
SEQ ID NO 4763	GAAATACTTTGTTGCATTGTTG	TTT	chr1	62598143	62598164	62598160	62598165	+
SEQ ID NO 4764	AAATACTTTGTTGCATTGTTGA	TTG	chr1	62598144	62598165	62598161	62598166	+
SEQ ID NO 4765	TGTTGCATTGTTGAAATACTTT	CTT	chr1	62598152	62598173	62598169	62598174	+
SEQ ID NO 4766	GTTGCATTGTTGAAATACTTTT	TTT	chr1	62598153	62598174	62598170	62598175	+
SEQ ID NO 4767	TTGCATTGTTGAAATACTTTTT	TTG	chr1	62598154	62598175	62598171	62598176	+
SEQ ID NO 4768	CATTGTTGAAATACTTTTTTTT	TTG	chr1	62598157	62598178	62598174	62598179	+
SEQ ID NO 4769	TTGAAATACTTTTTTTTCCAAG	TTG	chr1	62598162	62598183	62598179	62598184	+
SEQ ID NO 4770	AAATACTTTTTTTTCCAAGAAA	TTG	chr1	62598165	62598186	62598182	62598187	+
SEQ ID NO 4771	TTTTTTCCAAGAAAAATAATCT	CTT	chr1	62598173	62598194	62598190	62598195	+
SEQ ID NO 4772	TTTTTCCAAGAAAAATAATCTC	TTT	chr1	62598174	62598195	62598191	62598196	+
SEQ ID NO 4773	TTTTCCAAGAAAAATAATCTCC	TTT	chr1	62598175	62598196	62598192	62598197	+
SEQ ID NO 4774	TTTCCAAGAAAAATAATCTCCA	TTT	chr1	62598176	62598197	62598193	62598198	+
SEQ ID NO 4775	TTCCAAGAAAAATAATCTCCAG	TTT	chr1	62598177	62598198	62598194	62598199	+
SEQ ID NO 4776	TCCAAGAAAAATAATCTCCAGA	TTT	chr1	62598178	62598199	62598195	62598200	+
SEQ ID NO 4777	CCAAGAAAAATAATCTCCAGAA	TTT	chr1	62598179	62598200	62598196	62598201	+
SEQ ID NO 4778	CAAGAAAAATAATCTCCAGAAA	TTC	chr1	62598180	62598201	62598197	62598202	+
SEQ ID NO 4779	CAGAAAATAAAATTTCCTATTA	CTC	chr1	62598196	62598217	62598213	62598218	+
SEQ ID NO 4780	CCTATTATAATTTCAAGTTAGT	TTT	chr1	62598211	62598232	62598228	62598233	+
SEQ ID NO 4781	CTATTATAATTTCAAGTTAGTT	TTC	chr1	62598212	62598233	62598229	62598234	+
SEQ ID NO 4782	TTATAATTTCAAGTTAGTTTTT	CTA	chr1	62598215	62598236	62598232	62598237	+
SEQ ID NO 4783	TAATTTCAAGTTAGTTTTTTGT	TTA	chr1	62598218	62598239	62598235	62598240	+
SEQ ID NO 4784	CAAGTTAGTTTTTTGTTTCCCT	TTT	chr1	62598224	62598245	62598241	62598246	+
SEQ ID NO 4785	AAGTTAGTTTTTTGTTTCCCTA	TTC	chr1	62598225	62598246	62598242	62598247	+
SEQ ID NO 4786	GTTTTTTGTTTCCCTAATGTTA	TTA	chr1	62598231	62598252	62598248	62598253	+
SEQ ID NO 4787	TTTGTTTCCCTAATGTTATATA	TTT	chr1	62598235	62598256	62598252	62598257	+
SEQ ID NO 4788	TTGTTTCCCTAATGTTATATAT	TTT	chr1	62598236	62598257	62598253	62598258	+
SEQ ID NO 4789	TGTTTCCCTAATGTTATATATG	TTT	chr1	62598237	62598258	62598254	62598259	+
SEQ ID NO 4790	GTTTCCCTAATGTTATATATGA	TTT	chr1	62598238	62598259	62598255	62598260	+
SEQ ID NO 4791	TTTCCCTAATGTTATATATGAA	TTG	chr1	62598239	62598260	62598256	62598261	+
SEQ ID NO 4792	CCCTAATGTTATATATGAAAAC	TTT	chr1	62598242	62598263	62598259	62598264	+
SEQ ID NO 4793	CCTAATGTTATATATGAAAACA	TTC	chr1	62598243	62598264	62598260	62598265	+
SEQ ID NO 4794	ATGTTATATATGAAAACACTGA	CTA	chr1	62598247	62598268	62598264	62598269	+
SEQ ID NO 4795	TATATGAAAACACTGAAAATTT	TTA	chr1	62598253	62598274	62598270	62598275	+
SEQ ID NO 4796	AAAATTTGCATTTTATATGAAA	CTG	chr1	62598268	62598289	62598285	62598290	+
SEQ ID NO 4797	GCATTTTATATGAAAATTACAA	TTT	chr1	62598275	62598296	62598292	62598297	+
SEQ ID NO 4798	CATTTTATATGAAAATTACAAA	TTG	chr1	62598276	62598297	62598293	62598298	+
SEQ ID NO 4799	TATATGAAAATTACAAATCGGT	TTT	chr1	62598281	62598302	62598298	62598303	+
SEQ ID NO 4800	ATATGAAAATTACAAATCGGTT	TTT	chr1	62598282	62598303	62598299	62598304	+
SEQ ID NO 4801	TATGAAAATTACAAATCGGTTA	TTA	chr1	62598283	62598304	62598300	62598305	+
SEQ ID NO 4802	CAAATCGGTTAAATTATACAAT	TTA	chr1	62598294	62598315	62598311	62598316	+
SEQ ID NO 4803	AATTATACAATCTAGAACACTA	TTA	chr1	62598305	62598326	62598322	62598327	+
SEQ ID NO 4804	TACAATCTAGAACACTATGTCA	TTA	chr1	62598310	62598331	62598327	62598332	+
SEQ ID NO 4805	GAACACTATGTCATTACACTAT	CTA	chr1	62598319	62598340	62598336	62598341	+
SEQ ID NO 4806	TGTCATTACACTATTGTAAATT	CTA	chr1	62598327	62598348	62598344	62598349	+
SEQ ID NO 4807	CACTATTGTAAATTACTGAAGG	TTA	chr1	62598335	62598356	62598352	62598357	+
SEQ ID NO 4808	TTGTAAATTACTGAAGGTAAGT	CTA	chr1	62598340	62598361	62598357	62598362	+
SEQ ID NO 4809	TAAATTACTGAAGGTAAGTAAA	TTG	chr1	62598343	62598364	62598360	62598365	+
SEQ ID NO 4810	CTGAAGGTAAGTAAAAAGTTAA	TTA	chr1	62598350	62598371	62598367	62598372	+
SEQ ID NO 4811	AAGGTAAGTAAAAAGTTAAAAA	CTG	chr1	62598353	62598374	62598370	62598375	+
SEQ ID NO 4812	AAAAAAATTTAAAACTATTCTC	TTA	chr1	62598371	62598392	62598388	62598393	+
SEQ ID NO 4813	AAAACTATTCTCCAGTGTTTAA	TTT	chr1	62598381	62598402	62598398	62598403	+
SEQ ID NO 4814	AAACTATTCTCCAGTGTTTAAA	TTA	chr1	62598382	62598403	62598399	62598404	+

SEQ ID NO 4815	TTCTCCAGTGTTTAAAACAGAT	CTA	chr1	62598388	62598409	62598405	62598410	+
SEQ ID NO 4816	TCCAGTGTTTAAAACAGATTAA	TTC	chr1	62598391	62598412	62598408	62598413	+
SEQ ID NO 4817	CAGTGTTTAAAACAGATTAAAT	CTC	chr1	62598393	62598414	62598410	62598415	+
SEQ ID NO 4818	AAAACAGATTAAATAATACAGT	TTT	chr1	62598401	62598422	62598418	62598423	+
SEQ ID NO 4819	AAACAGATTAAATAATACAGTA	TTA	chr1	62598402	62598423	62598419	62598424	+
SEQ ID NO 4820	AATAATACAGTAAATGGAAAAG	TTA	chr1	62598412	62598433	62598429	62598434	+
SEQ ID NO 4821	ATTCATATGAAAATATGCTGGG	TTT	chr1	62598438	62598459	62598455	62598460	+
SEQ ID NO 4822	TTCATATGAAAATATGCTGGGC	TTA	chr1	62598439	62598460	62598456	62598461	+
SEQ ID NO 4823	ATATGAAAATATGCTGGGCTTT	TTC	chr1	62598442	62598463	62598459	62598464	+
SEQ ID NO 4824	GGCTTTTTCTTTTAATTGAAGT	CTG	chr1	62598458	62598479	62598475	62598480	+
SEQ ID NO 4825	TTTCTTTTAATTGAAGTTCAGA	CTT	chr1	62598463	62598484	62598480	62598485	+
SEQ ID NO 4826	TTCTTTTAATTGAAGTTCAGAA	TTT	chr1	62598464	62598485	62598481	62598486	+
SEQ ID NO 4827	TCTTTTAATTGAAGTTCAGAAA	TTT	chr1	62598465	62598486	62598482	62598487	+
SEQ ID NO 4828	CTTTTAATTGAAGTTCAGAAAA	TTT	chr1	62598466	62598487	62598483	62598488	+
SEQ ID NO 4829	TTTTAATTGAAGTTCAGAAAAT	TTC	chr1	62598467	62598488	62598484	62598489	+
SEQ ID NO 4830	TTAATTGAAGTTCAGAAAATCA	CTT	chr1	62598469	62598490	62598486	62598491	+
SEQ ID NO 4831	TAATTGAAGTTCAGAAAATCAA	TTT	chr1	62598470	62598491	62598487	62598492	+
SEQ ID NO 4832	AATTGAAGTTCAGAAAATCAAA	TTT	chr1	62598471	62598492	62598488	62598493	+
SEQ ID NO 4833	ATTGAAGTTCAGAAAATCAAAT	TTA	chr1	62598472	62598493	62598489	62598494	+
SEQ ID NO 4834	AAGTTCAGAAAATCAAATTTTA	TTG	chr1	62598476	62598497	62598493	62598498	+
SEQ ID NO 4835	AGAAAATCAAATTTTAGAGATA	TTC	chr1	62598482	62598503	62598499	62598504	+
SEQ ID NO 4836	TAGAGATAGTACAATTTAAATA	TTT	chr1	62598496	62598517	62598513	62598518	+
SEQ ID NO 4837	AGAGATAGTACAATTTAAATAA	TTT	chr1	62598497	62598518	62598514	62598519	+
SEQ ID NO 4838	GAGATAGTACAATTTAAATAAA	TTA	chr1	62598498	62598519	62598515	62598520	+
SEQ ID NO 4839	AAATAAAATGTTAAGGACAAAA	TTT	chr1	62598513	62598534	62598530	62598535	+
SEQ ID NO 4840	AATAAAATGTTAAGGACAAAAA	TTA	chr1	62598514	62598535	62598531	62598536	+
SEQ ID NO 4841	AGGACAAAAATATGTGCTATTT	TTA	chr1	62598526	62598547	62598543	62598548	+
SEQ ID NO 4842	TTTGAAAGAAGCATACAAGGGG	CTA	chr1	62598545	62598566	62598562	62598567	+
SEQ ID NO 4843	GAAAGAAGCATACAAGGGGAAG	TTT	chr1	62598548	62598569	62598565	62598570	+
SEQ ID NO 4844	AAAGAAGCATACAAGGGGAAGG	TTG	chr1	62598549	62598570	62598566	62598571	+
SEQ ID NO 4845	CCAATATTCATTTTTCAAATCC	TTG	chr1	62598576	62598597	62598593	62598598	+
SEQ ID NO 4846	ATTTTTCAAATCCATTATTAGT	TTC	chr1	62598585	62598606	62598602	62598607	+
SEQ ID NO 4847	TTCAAATCCATTATTAGTTTAA	TTT	chr1	62598589	62598610	62598606	62598611	+
SEQ ID NO 4848	TCAAATCCATTATTAGTTTAAA	TTT	chr1	62598590	62598611	62598607	62598612	+
SEQ ID NO 4849	CAAATCCATTATTAGTTTAAAA	TTT	chr1	62598591	62598612	62598608	62598613	+
SEQ ID NO 4850	AAATCCATTATTAGTTTAAAAA	TTC	chr1	62598592	62598613	62598609	62598614	+
SEQ ID NO 4851	TTAGTTTAAAAATTTAGATTAT	TTA	chr1	62598602	62598623	62598619	62598624	+
SEQ ID NO 4852	GTTTAAAAATTTAGATTATGAT	TTA	chr1	62598605	62598626	62598622	62598627	+
SEQ ID NO 4853	AAAAATTTAGATTATGATAGTG	TTT	chr1	62598609	62598630	62598626	62598631	+
SEQ ID NO 4854	AAAATTTAGATTATGATAGTGT	TTA	chr1	62598610	62598631	62598627	62598632	+
SEQ ID NO 4855	AGATTATGATAGTGTTACAGGA	TTT	chr1	62598617	62598638	62598634	62598639	+
SEQ ID NO 4856	GATTATGATAGTGTTACAGGAA	TTA	chr1	62598618	62598639	62598635	62598640	+
SEQ ID NO 4857	TGATAGTGTTACAGGAAATTAA	TTA	chr1	62598623	62598644	62598640	62598645	+
SEQ ID NO 4858	CAGGAAATTAATAGAAAAGAAA	TTA	chr1	62598634	62598655	62598651	62598656	+
SEQ ID NO 4859	ATAGAAAAGAAAGAGGAAAGCA	TTA	chr1	62598644	62598665	62598661	62598666	+
SEQ ID NO 4860	ATAACCAACCTACTCTCTATAT	CTT	chr1	62598670	62598691	62598687	62598692	+
SEQ ID NO 4861	TAACCAACCTACTCTCTATATC	TTA	chr1	62598671	62598692	62598688	62598693	+
SEQ ID NO 4862	CTCTCTATATCCAGACTTTTGT	CTA	chr1	62598682	62598703	62598699	62598704	+
SEQ ID NO 4863	TCTATATCCAGACTTTTGTAGA	CTC	chr1	62598685	62598706	62598702	62598707	+
SEQ ID NO 4864	TATATCCAGACTTTTGTAGAAA	CTC	chr1	62598687	62598708	62598704	62598709	+
SEQ ID NO 4865	TATCCAGACTTTTGTAGAAAAA	CTA	chr1	62598689	62598710	62598706	62598711	+
SEQ ID NO 4866	TTGTAGAAAAACAAGATAATAG	CTT	chr1	62598700	62598721	62598717	62598722	+
SEQ ID NO 4867	TGTAGAAAAACAAGATAATAGC	TTT	chr1	62598701	62598722	62598718	62598723	+
SEQ ID NO 4868	GTAGAAAAACAAGATAATAGCA	TTT	chr1	62598702	62598723	62598719	62598724	+
SEQ ID NO 4869	TAGAAAAACAAGATAATAGCAT	TTG	chr1	62598703	62598724	62598720	62598725	+
SEQ ID NO 4870	CTCCAGACCGTGGAAGACCAAT	CTT	chr1	62598735	62598756	62598752	62598757	+
SEQ ID NO 4871	TCCAGACCGTGGAAGACCAATA	TTC	chr1	62598736	62598757	62598753	62598758	+
SEQ ID NO 4872	CAGACCGTGGAAGACCAATATA	CTC	chr1	62598738	62598759	62598755	62598760	+

SEQ ID NO 4873	AACCAACAGCATAGTCAAATAA	TTA	chr1	62598768	62598789	62598785	62598790	+
SEQ ID NO 4874	TAATGGTATGTCCCATCTTTCA	TTT	chr1	62598821	62598842	62598838	62598843	+
SEQ ID NO 4875	AATGGTATGTCCCATCTTTCAC	TTT	chr1	62598822	62598843	62598839	62598844	+
SEQ ID NO 4876	ATGGTATGTCCCATCTTTCACA	TTA	chr1	62598823	62598844	62598840	62598845	+
SEQ ID NO 4877	TCACACAGGTCTGTAAAAACAC	CTT	chr1	62598840	62598861	62598857	62598862	+
SEQ ID NO 4878	CACACAGGTCTGTAAAAACACT	TTT	chr1	62598841	62598862	62598858	62598863	+
SEQ ID NO 4879	ACACAGGTCTGTAAAAACACTG	TTC	chr1	62598842	62598863	62598859	62598864	+
SEQ ID NO 4880	TAAAAACACTGAATCCTAAAAT	CTG	chr1	62598853	62598874	62598870	62598875	+
SEQ ID NO 4881	AATCCTAAAATTATTTACAAGC	CTG	chr1	62598864	62598885	62598881	62598886	+
SEQ ID NO 4882	AAATTATTTACAAGCTTTAACT	CTA	chr1	62598871	62598892	62598888	62598893	+
SEQ ID NO 4883	TTTACAAGCTTTAACTGGATCA	TTA	chr1	62598877	62598898	62598894	62598899	+
SEQ ID NO 4884	ACAAGCTTTAACTGGATCATGA	TTT	chr1	62598880	62598901	62598897	62598902	+
SEQ ID NO 4885	CAAGCTTTAACTGGATCATGAG	TTA	chr1	62598881	62598902	62598898	62598903	+
SEQ ID NO 4886	TAACTGGATCATGAGTAAAATT	CTT	chr1	62598888	62598909	62598905	62598910	+
SEQ ID NO 4887	AACTGGATCATGAGTAAAATTA	TTT	chr1	62598889	62598910	62598906	62598911	+
SEQ ID NO 4888	ACTGGATCATGAGTAAAATTAT	TTA	chr1	62598890	62598911	62598907	62598912	+
SEQ ID NO 4889	GATCATGAGTAAAATTATCACA	CTG	chr1	62598894	62598915	62598911	62598916	+
SEQ ID NO 4890	TCACATCAGCATAACTGTTAAA	TTA	chr1	62598911	62598932	62598928	62598933	+
SEQ ID NO 4891	TTAAAATTGCAGGCTCTGAAGC	CTG	chr1	62598928	62598949	62598945	62598950	+
SEQ ID NO 4892	AAATTGCAGGCTCTGAAGCTAA	TTA	chr1	62598931	62598952	62598948	62598953	+
SEQ ID NO 4893	CAGGCTCTGAAGCTAATAAACT	TTG	chr1	62598937	62598958	62598954	62598959	+
SEQ ID NO 4894	TGAAGCTAATAAACTACCTGCA	CTC	chr1	62598944	62598965	62598961	62598966	+
SEQ ID NO 4895	AAGCTAATAAACTACCTGCATT	CTG	chr1	62598946	62598967	62598963	62598968	+
SEQ ID NO 4896	ATAAACTACCTGCATTTAAACC	CTA	chr1	62598952	62598973	62598969	62598974	+
SEQ ID NO 4897	CCTGCATTTAAACCATGGCTCT	CTA	chr1	62598960	62598981	62598977	62598982	+
SEQ ID NO 4898	CATTTAAACCATGGCTCTAAAA	CTG	chr1	62598964	62598985	62598981	62598986	+
SEQ ID NO 4899	AAACCATGGCTCTAAAACTTTG	TTT	chr1	62598969	62598990	62598986	62598991	+
SEQ ID NO 4900	AACCATGGCTCTAAAACTTTGT	TTA	chr1	62598970	62598991	62598987	62598992	+
SEQ ID NO 4901	TAAAACTTTGTGTGACCTTGAA	CTC	chr1	62598981	62599002	62598998	62599003	+
SEQ ID NO 4902	AAACTTTGTGTGACCTTGAATA	CTA	chr1	62598983	62599004	62599000	62599005	+
SEQ ID NO 4903	TGTGTGACCTTGAATAAATTAC	CTT	chr1	62598989	62599010	62599006	62599011	+
SEQ ID NO 4904	GTGTGACCTTGAATAAATTACT	TTT	chr1	62598990	62599011	62599007	62599012	+
SEQ ID NO 4905	TGTGACCTTGAATAAATTACTT	TTG	chr1	62598991	62599012	62599008	62599013	+
SEQ ID NO 4906	GAATAAATTACTTCACCCCTTT	CTT	chr1	62599000	62599021	62599017	62599022	+
SEQ ID NO 4907	AATAAATTACTTCACCCCTTTA	TTG	chr1	62599001	62599022	62599018	62599023	+
SEQ ID NO 4908	CTTCACCCCTTTATCTCTCAGT	TTA	chr1	62599010	62599031	62599027	62599032	+
SEQ ID NO 4909	CACCCCTTTATCTCTCAGTTTC	CTT	chr1	62599013	62599034	62599030	62599035	+
SEQ ID NO 4910	ACCCCTTTATCTCTCAGTTTCC	TTC	chr1	62599014	62599035	62599031	62599036	+
SEQ ID NO 4911	TATCTCTCAGTTTCCTCACATA	CTT	chr1	62599021	62599042	62599038	62599043	+
SEQ ID NO 4912	ATCTCTCAGTTTCCTCACATAT	TTT	chr1	62599022	62599043	62599039	62599044	+
SEQ ID NO 4913	TCTCTCAGTTTCCTCACATATA	TTA	chr1	62599023	62599044	62599040	62599045	+
SEQ ID NO 4914	TCAGTTTCCTCACATATACTAC	CTC	chr1	62599027	62599048	62599044	62599049	+
SEQ ID NO 4915	AGTTTCCTCACATATACTACAA	CTC	chr1	62599029	62599050	62599046	62599051	+
SEQ ID NO 4916	CCTCACATATACTACAAAGATA	TTT	chr1	62599034	62599055	62599051	62599056	+
SEQ ID NO 4917	CTCACATATACTACAAAGATAA	TTC	chr1	62599035	62599056	62599052	62599057	+
SEQ ID NO 4918	ACATATACTACAAAGATAATAA	CTC	chr1	62599038	62599059	62599055	62599060	+
SEQ ID NO 4919	CAAAGATAATAACAGAACTTAT	CTA	chr1	62599048	62599069	62599065	62599070	+
SEQ ID NO 4920	ATAGGATTATTGTAAGAAAAAA	CTT	chr1	62599068	62599089	62599085	62599090	+
SEQ ID NO 4921	TAGGATTATTGTAAGAAAAAAA	TTA	chr1	62599069	62599090	62599086	62599091	+
SEQ ID NO 4922	TTGTAAGAAAAAAAATTAATTC	TTA	chr1	62599077	62599098	62599094	62599099	+
SEQ ID NO 4923	TAAGAAAAAAAATTAATTCATA	TTG	chr1	62599080	62599101	62599097	62599102	+
SEQ ID NO 4924	ATTCATAGCAGCCAATGTCATC	TTA	chr1	62599095	62599116	62599112	62599117	+
SEQ ID NO 4925	ATAGCAGCCAATGTCATCTTAC	TTC	chr1	62599099	62599120	62599116	62599121	+
SEQ ID NO 4926	ACTAAAATTCAAATTAGATCAT	CTT	chr1	62599119	62599140	62599136	62599141	+
SEQ ID NO 4927	CTAAAATTCAAATTAGATCATG	TTA	chr1	62599120	62599141	62599137	62599142	+
SEQ ID NO 4928	AAATTCAAATTAGATCATGTTT	CTA	chr1	62599123	62599144	62599140	62599145	+
SEQ ID NO 4929	AAATTAGATCATGTTTCTCTTT	TTC	chr1	62599129	62599150	62599146	62599151	+
SEQ ID NO 4930	GATCATGTTTCTCTTTGCTCAA	TTA	chr1	62599135	62599156	62599152	62599157	+

SEQ ID NO 4931	CTCTTTGCTCAAAACCACACAA	TTT	chr1	62599145	62599166	62599162	62599167	+
SEQ ID NO 4932	TCTTTGCTCAAAACCACACAAT	TTC	chr1	62599146	62599167	62599163	62599168	+
SEQ ID NO 4933	TTTGCTCAAAACCACACAATAG	CTC	chr1	62599148	62599169	62599165	62599170	+
SEQ ID NO 4934	TGCTCAAAACCACACAATAGCT	CTT	chr1	62599150	62599171	62599167	62599172	+
SEQ ID NO 4935	GCTCAAAACCACACAATAGCTT	TTT	chr1	62599151	62599172	62599168	62599173	+
SEQ ID NO 4936	CTCAAAACCACACAATAGCTTT	TTG	chr1	62599152	62599173	62599169	62599174	+
SEQ ID NO 4937	AAAACCACACAATAGCTTTCCA	CTC	chr1	62599155	62599176	62599172	62599177	+
SEQ ID NO 4938	TCCATTTCACTCATATTGGCTC	CTT	chr1	62599173	62599194	62599190	62599195	+
SEQ ID NO 4939	CCATTTCACTCATATTGGCTCT	TTT	chr1	62599174	62599195	62599191	62599196	+
SEQ ID NO 4940	CATTTCACTCATATTGGCTCTT	TTC	chr1	62599175	62599196	62599192	62599197	+
SEQ ID NO 4941	CACTCATATTGGCTCTTTAGAC	TTT	chr1	62599180	62599201	62599197	62599202	+
SEQ ID NO 4942	ACTCATATTGGCTCTTTAGACC	TTC	chr1	62599181	62599202	62599198	62599203	+
SEQ ID NO 4943	ATATTGGCTCTTTAGACCAAGA	CTC	chr1	62599185	62599206	62599202	62599207	+
SEQ ID NO 4944	GCTCTTTAGACCAAGATTACCC	TTG	chr1	62599191	62599212	62599208	62599213	+
SEQ ID NO 4945	GGTAATCTTGGTCTAAAGAGCC	TTG	chr1	62599190	62599211	62599195	62599190	-
SEQ ID NO 4946	GGTCTAAAGAGCCAATATGAGT	CTT	chr1	62599181	62599202	62599186	62599181	-
SEQ ID NO 4947	GTCTAAAGAGCCAATATGAGTG	TTG	chr1	62599180	62599201	62599185	62599180	-
SEQ ID NO 4948	AAGAGCCAATATGAGTGAAATG	CTA	chr1	62599175	62599196	62599180	62599175	-
SEQ ID NO 4949	TTGTGTGGTTTTGAGCAAAGAG	CTA	chr1	62599145	62599166	62599150	62599145	-
SEQ ID NO 4950	TGTGGTTTTGAGCAAAGAGAAA	TTG	chr1	62599142	62599163	62599147	62599142	-
SEQ ID NO 4951	TGAGCAAAGAGAAACATGATCT	TTT	chr1	62599134	62599155	62599139	62599134	-
SEQ ID NO 4952	GAGCAAAGAGAAACATGATCTA	TTT	chr1	62599133	62599154	62599138	62599133	-
SEQ ID NO 4953	AGCAAAGAGAAACATGATCTAA	TTG	chr1	62599132	62599153	62599137	62599132	-
SEQ ID NO 4954	ATTTGAATTTTAGTAAGATGAC	CTA	chr1	62599111	62599132	62599116	62599111	-
SEQ ID NO 4955	GAATTTTAGTAAGATGACATTG	TTT	chr1	62599107	62599128	62599112	62599107	-
SEQ ID NO 4956	AATTTTAGTAAGATGACATTGG	TTG	chr1	62599106	62599127	62599111	62599106	-
SEQ ID NO 4957	TAGTAAGATGACATTGGCTGCT	TTT	chr1	62599101	62599122	62599106	62599101	-
SEQ ID NO 4958	AGTAAGATGACATTGGCTGCTA	TTT	chr1	62599100	62599121	62599105	62599100	-
SEQ ID NO 4959	GTAAGATGACATTGGCTGCTAT	TTA	chr1	62599099	62599120	62599104	62599099	-
SEQ ID NO 4960	GCTGCTATGAATTAATTTTTTT	TTG	chr1	62599085	62599106	62599090	62599085	-
SEQ ID NO 4961	CTATGAATTAATTTTTTTTCTT	CTG	chr1	62599081	62599102	62599086	62599081	-
SEQ ID NO 4962	TGAATTAATTTTTTTTCTTACA	CTA	chr1	62599078	62599099	62599083	62599078	-
SEQ ID NO 4963	ATTTTTTTTCTTACAATAATCC	TTA	chr1	62599071	62599092	62599076	62599071	-
SEQ ID NO 4964	TTTTTCTTACAATAATCCTATA	TTT	chr1	62599067	62599088	62599072	62599067	-
SEQ ID NO 4965	TTTTCTTACAATAATCCTATAA	TTT	chr1	62599066	62599087	62599071	62599066	-
SEQ ID NO 4966	TTTCTTACAATAATCCTATAAG	TTT	chr1	62599065	62599086	62599070	62599065	-
SEQ ID NO 4967	TTCTTACAATAATCCTATAAGT	TTT	chr1	62599064	62599085	62599069	62599064	-
SEQ ID NO 4968	TCTTACAATAATCCTATAAGTT	TTT	chr1	62599063	62599084	62599068	62599063	-
SEQ ID NO 4969	CTTACAATAATCCTATAAGTTC	TTT	chr1	62599062	62599083	62599067	62599062	-
SEQ ID NO 4970	TTACAATAATCCTATAAGTTCT	TTC	chr1	62599061	62599082	62599066	62599061	-
SEQ ID NO 4971	ACAATAATCCTATAAGTTCTGT	CTT	chr1	62599059	62599080	62599064	62599059	-
SEQ ID NO 4972	CAATAATCCTATAAGTTCTGTT	TTA	chr1	62599058	62599079	62599063	62599058	-
SEQ ID NO 4973	TAAGTTCTGTTATTATCTTTGT	CTA	chr1	62599047	62599068	62599052	62599047	-
SEQ ID NO 4974	TGTTATTATCTTTGTAGTATAT	TTC	chr1	62599040	62599061	62599045	62599040	-
SEQ ID NO 4975	TTATTATCTTTGTAGTATATGT	CTG	chr1	62599038	62599059	62599043	62599038	-
SEQ ID NO 4976	TTATCTTTGTAGTATATGTGAG	TTA	chr1	62599035	62599056	62599040	62599035	-
SEQ ID NO 4977	TCTTTGTAGTATATGTGAGGAA	TTA	chr1	62599032	62599053	62599037	62599032	-
SEQ ID NO 4978	TGTAGTATATGTGAGGAAACTG	CTT	chr1	62599028	62599049	62599033	62599028	-
SEQ ID NO 4979	GTAGTATATGTGAGGAAACTGA	TTT	chr1	62599027	62599048	62599032	62599027	-
SEQ ID NO 4980	TAGTATATGTGAGGAAACTGAG	TTG	chr1	62599026	62599047	62599031	62599026	-
SEQ ID NO 4981	AGAGATAAAGGGGTGAAGTAAT	CTG	chr1	62599006	62599027	62599011	62599006	-
SEQ ID NO 4982	ATTCAAGGTCACACAAAGTTTT	TTT	chr1	62598982	62599003	62598987	62598982	-
SEQ ID NO 4983	TTCAAGGTCACACAAAGTTTTA	TTA	chr1	62598981	62599002	62598986	62598981	-
SEQ ID NO 4984	AAGGTCACACAAAGTTTTAGAG	TTC	chr1	62598978	62598999	62598983	62598978	-
SEQ ID NO 4985	TAGAGCCATGGTTTAAATGCAG	TTT	chr1	62598961	62598982	62598966	62598961	-
SEQ ID NO 4986	AGAGCCATGGTTTAAATGCAGG	TTT	chr1	62598960	62598981	62598965	62598960	-
SEQ ID NO 4987	GAGCCATGGTTTAAATGCAGGT	TTA	chr1	62598959	62598980	62598964	62598959	-
SEQ ID NO 4988	AAATGCAGGTAGTTTATTAGCT	TTT	chr1	62598947	62598968	62598952	62598947	-

SEQ ID NO 4989	AATGCAGGTAGTTTATTAGCTT	TTA	chr1	62598946	62598967	62598951	62598946	-
SEQ ID NO 4990	ATTAGCTTCAGAGCCTGCAATT	TTT	chr1	62598932	62598953	62598937	62598932	-
SEQ ID NO 4991	TTAGCTTCAGAGCCTGCAATTT	TTA	chr1	62598931	62598952	62598936	62598931	-
SEQ ID NO 4992	GCTTCAGAGCCTGCAATTTTAA	TTA	chr1	62598928	62598949	62598933	62598928	-
SEQ ID NO 4993	CAGAGCCTGCAATTTTAACAGT	CTT	chr1	62598924	62598945	62598929	62598924	-
SEQ ID NO 4994	AGAGCCTGCAATTTTAACAGTT	TTC	chr1	62598923	62598944	62598928	62598923	-
SEQ ID NO 4995	CAATTTTAACAGTTATGCTGAT	CTG	chr1	62598915	62598936	62598920	62598915	-
SEQ ID NO 4996	TAACAGTTATGCTGATGTGATA	TTT	chr1	62598909	62598930	62598914	62598909	-
SEQ ID NO 4997	AACAGTTATGCTGATGTGATAA	TTT	chr1	62598908	62598929	62598913	62598908	-
SEQ ID NO 4998	ACAGTTATGCTGATGTGATAAT	TTA	chr1	62598907	62598928	62598912	62598907	-
SEQ ID NO 4999	TGCTGATGTGATAATTTTACTC	TTA	chr1	62598900	62598921	62598905	62598900	-
SEQ ID NO 5000	ATGTGATAATTTTACTCATGAT	CTG	chr1	62598895	62598916	62598900	62598895	-
SEQ ID NO 5001	TACTCATGATCCAGTTAAAGCT	TTT	chr1	62598883	62598904	62598888	62598883	-
SEQ ID NO 5002	ACTCATGATCCAGTTAAAGCTT	TTT	chr1	62598882	62598903	62598887	62598882	-
SEQ ID NO 5003	CTCATGATCCAGTTAAAGCTTG	TTA	chr1	62598881	62598902	62598886	62598881	-
SEQ ID NO 5004	ATGATCCAGTTAAAGCTTGTAA	CTC	chr1	62598878	62598899	62598883	62598878	-
SEQ ID NO 5005	AAGCTTGTAAATAATTTTAGGA	TTA	chr1	62598866	62598887	62598871	62598866	-
SEQ ID NO 5006	GTAAATAATTTTAGGATTCAGT	CTT	chr1	62598860	62598881	62598865	62598860	-
SEQ ID NO 5007	TAAATAATTTTAGGATTCAGTG	TTG	chr1	62598859	62598880	62598864	62598859	-
SEQ ID NO 5008	TAGGATTCAGTGTTTTTACAGA	TTT	chr1	62598849	62598870	62598854	62598849	-
SEQ ID NO 5009	AGGATTCAGTGTTTTTACAGAC	TTT	chr1	62598848	62598869	62598853	62598848	-
SEQ ID NO 5010	GGATTCAGTGTTTTTACAGACC	TTA	chr1	62598847	62598868	62598852	62598847	-
SEQ ID NO 5011	AGTGTTTTTACAGACCTGTGTG	TTC	chr1	62598841	62598862	62598846	62598841	-
SEQ ID NO 5012	TTACAGACCTGTGTGAAAGATG	TTT	chr1	62598834	62598855	62598839	62598834	-
SEQ ID NO 5013	TACAGACCTGTGTGAAAGATGG	TTT	chr1	62598833	62598854	62598838	62598833	-
SEQ ID NO 5014	ACAGACCTGTGTGAAAGATGGG	TTT	chr1	62598832	62598853	62598837	62598832	-
SEQ ID NO 5015	CAGACCTGTGTGAAAGATGGGA	TTA	chr1	62598831	62598852	62598836	62598831	-
SEQ ID NO 5016	TGTGAAAGATGGGACATACCAT	CTG	chr1	62598823	62598844	62598828	62598823	-
SEQ ID NO 5017	AAATACTGACTTACCTGATTTT	TTA	chr1	62598799	62598820	62598804	62598799	-
SEQ ID NO 5018	ACTTACCTGATTTTCTATTTCT	CTG	chr1	62598791	62598812	62598796	62598791	-
SEQ ID NO 5019	ACCTGATTTTCTATTTCTTTTA	CTT	chr1	62598787	62598808	62598792	62598787	-
SEQ ID NO 5020	CCTGATTTTCTATTTCTTTTAT	TTA	chr1	62598786	62598807	62598791	62598786	-
SEQ ID NO 5021	ATTTTCTATTTCTTTTATTTGA	CTG	chr1	62598782	62598803	62598787	62598782	-
SEQ ID NO 5022	TCTATTTCTTTTATTTGACTAT	TTT	chr1	62598778	62598799	62598783	62598778	-
SEQ ID NO 5023	CTATTTCTTTTATTTGACTATG	TTT	chr1	62598777	62598798	62598782	62598777	-
SEQ ID NO 5024	TATTTCTTTTATTTGACTATGC	TTC	chr1	62598776	62598797	62598781	62598776	-
SEQ ID NO 5025	TTTCTTTTATTTGACTATGCTG	CTA	chr1	62598774	62598795	62598779	62598774	-
SEQ ID NO 5026	CTTTTATTTGACTATGCTGTTG	TTT	chr1	62598771	62598792	62598776	62598771	-
SEQ ID NO 5027	TTTTATTTGACTATGCTGTTGG	TTC	chr1	62598770	62598791	62598775	62598770	-
SEQ ID NO 5028	TTATTTGACTATGCTGTTGGTT	CTT	chr1	62598768	62598789	62598773	62598768	-
SEQ ID NO 5029	TATTTGACTATGCTGTTGGTTT	TTT	chr1	62598767	62598788	62598772	62598767	-
SEQ ID NO 5030	ATTTGACTATGCTGTTGGTTTA	TTT	chr1	62598766	62598787	62598771	62598766	-
SEQ ID NO 5031	TTTGACTATGCTGTTGGTTTAA	TTA	chr1	62598765	62598786	62598770	62598765	-
SEQ ID NO 5032	GACTATGCTGTTGGTTTAATTG	TTT	chr1	62598762	62598783	62598767	62598762	-
SEQ ID NO 5033	ACTATGCTGTTGGTTTAATTGT	TTG	chr1	62598761	62598782	62598766	62598761	-
SEQ ID NO 5034	TGCTGTTGGTTTAATTGTTTAT	CTA	chr1	62598757	62598778	62598762	62598757	-
SEQ ID NO 5035	TTGGTTTAATTGTTTATATTGG	CTG	chr1	62598752	62598773	62598757	62598752	-
SEQ ID NO 5036	GTTTAATTGTTTATATTGGTCT	TTG	chr1	62598749	62598770	62598754	62598749	-
SEQ ID NO 5037	AATTGTTTATATTGGTCTTCCA	TTT	chr1	62598745	62598766	62598750	62598745	-
SEQ ID NO 5038	ATTGTTTATATTGGTCTTCCAC	TTA	chr1	62598744	62598765	62598749	62598744	-
SEQ ID NO 5039	TTTATATTGGTCTTCCACGGTC	TTG	chr1	62598740	62598761	62598745	62598740	-
SEQ ID NO 5040	ATATTGGTCTTCCACGGTCTGG	TTT	chr1	62598737	62598758	62598742	62598737	-
SEQ ID NO 5041	TATTGGTCTTCCACGGTCTGGA	TTA	chr1	62598736	62598757	62598741	62598736	-
SEQ ID NO 5042	GTCTTCCACGGTCTGGAGAAGG	TTG	chr1	62598731	62598752	62598736	62598731	-
SEQ ID NO 5043	CCACGGTCTGGAGAAGGTCTTT	CTT	chr1	62598726	62598747	62598731	62598726	-
SEQ ID NO 5044	CACGGTCTGGAGAAGGTCTTTG	TTC	chr1	62598725	62598746	62598730	62598725	-
SEQ ID NO 5045	GAGAAGGTCTTTGATGCTATTA	CTG	chr1	62598716	62598737	62598721	62598716	-
SEQ ID NO 5046	TGATGCTATTATCTTGTTTTTC	CTT	chr1	62598705	62598726	62598710	62598705	-

SEQ ID NO 5047	GATGCTATTATCTTGTTTTTCT	TTT	chr1	62598704	62598725	62598709	62598704	-
SEQ ID NO 5048	ATGCTATTATCTTGTTTTTCTA	TTG	chr1	62598703	62598724	62598708	62598703	-
SEQ ID NO 5049	TTATCTTGTTTTTCTACAAAAG	CTA	chr1	62598697	62598718	62598702	62598697	-
SEQ ID NO 5050	TCTTGTTTTTCTACAAAAGTCT	TTA	chr1	62598694	62598715	62598699	62598694	-
SEQ ID NO 5051	GTTTTTCTACAAAAGTCTGGAT	CTT	chr1	62598690	62598711	62598695	62598690	-
SEQ ID NO 5052	TTTTTCTACAAAAGTCTGGATA	TTG	chr1	62598689	62598710	62598694	62598689	-
SEQ ID NO 5053	TTCTACAAAAGTCTGGATATAG	TTT	chr1	62598686	62598707	62598691	62598686	-
SEQ ID NO 5054	TCTACAAAAGTCTGGATATAGA	TTT	chr1	62598685	62598706	62598690	62598685	-
SEQ ID NO 5055	CTACAAAAGTCTGGATATAGAG	TTT	chr1	62598684	62598705	62598689	62598684	-
SEQ ID NO 5056	TACAAAAGTCTGGATATAGAGA	TTC	chr1	62598683	62598704	62598688	62598683	-
SEQ ID NO 5057	CAAAAGTCTGGATATAGAGAGT	CTA	chr1	62598681	62598702	62598686	62598681	-
SEQ ID NO 5058	GATATAGAGAGTAGGTTGGTTA	CTG	chr1	62598671	62598692	62598676	62598671	-
SEQ ID NO 5059	GTTATAAGTTGCTTTCCTCTTT	TTG	chr1	62598653	62598674	62598658	62598653	-
SEQ ID NO 5060	TAAGTTGCTTTCCTCTTTCTTT	TTA	chr1	62598649	62598670	62598654	62598649	-
SEQ ID NO 5061	CTTTCCTCTTTCTTTTCTATTA	TTG	chr1	62598642	62598663	62598647	62598642	-
SEQ ID NO 5062	TCCTCTTTCTTTTCTATTAATT	CTT	chr1	62598639	62598660	62598644	62598639	-
SEQ ID NO 5063	CCTCTTTCTTTTCTATTAATTT	TTT	chr1	62598638	62598659	62598643	62598638	-
SEQ ID NO 5064	CTCTTTCTTTTCTATTAATTTC	TTC	chr1	62598637	62598658	62598642	62598637	-
SEQ ID NO 5065	TTTCTTTTCTATTAATTTCCTG	CTC	chr1	62598634	62598655	62598639	62598634	-
SEQ ID NO 5066	TCTTTTCTATTAATTTCCTGTA	CTT	chr1	62598632	62598653	62598637	62598632	-
SEQ ID NO 5067	CTTTTCTATTAATTTCCTGTAA	TTT	chr1	62598631	62598652	62598636	62598631	-
SEQ ID NO 5068	TTTTCTATTAATTTCCTGTAAC	TTC	chr1	62598630	62598651	62598635	62598630	-
SEQ ID NO 5069	TTCTATTAATTTCCTGTAACAC	CTT	chr1	62598628	62598649	62598633	62598628	-
SEQ ID NO 5070	TCTATTAATTTCCTGTAACACT	TTT	chr1	62598627	62598648	62598632	62598627	-
SEQ ID NO 5071	CTATTAATTTCCTGTAACACTA	TTT	chr1	62598626	62598647	62598631	62598626	-
SEQ ID NO 5072	TATTAATTTCCTGTAACACTAT	TTC	chr1	62598625	62598646	62598630	62598625	-
SEQ ID NO 5073	TTAATTTCCTGTAACACTATCA	CTA	chr1	62598623	62598644	62598628	62598623	-
SEQ ID NO 5074	ATTTCCTGTAACACTATCATAA	TTA	chr1	62598620	62598641	62598625	62598620	-
SEQ ID NO 5075	CCTGTAACACTATCATAATCTA	TTT	chr1	62598616	62598637	62598621	62598616	-
SEQ ID NO 5076	CTGTAACACTATCATAATCTAA	TTC	chr1	62598615	62598636	62598620	62598615	-
SEQ ID NO 5077	TAACACTATCATAATCTAAATT	CTG	chr1	62598612	62598633	62598617	62598612	-
SEQ ID NO 5078	TCATAATCTAAATTTTTAAACT	CTA	chr1	62598604	62598625	62598609	62598604	-
SEQ ID NO 5079	AATTTTTAAACTAATAATGGAT	CTA	chr1	62598594	62598615	62598599	62598594	-
SEQ ID NO 5080	TTAAACTAATAATGGATTTGAA	TTT	chr1	62598589	62598610	62598594	62598589	-
SEQ ID NO 5081	TAAACTAATAATGGATTTGAAA	TTT	chr1	62598588	62598609	62598593	62598588	-
SEQ ID NO 5082	AAACTAATAATGGATTTGAAAA	TTT	chr1	62598587	62598608	62598592	62598587	-
SEQ ID NO 5083	AACTAATAATGGATTTGAAAAA	TTA	chr1	62598586	62598607	62598591	62598586	-
SEQ ID NO 5084	ATAATGGATTTGAAAAATGAAT	CTA	chr1	62598581	62598602	62598586	62598581	-
SEQ ID NO 5085	GAAAAATGAATATTGGCAATTC	TTT	chr1	62598570	62598591	62598575	62598570	-
SEQ ID NO 5086	AAAAATGAATATTGGCAATTCC	TTG	chr1	62598569	62598590	62598574	62598569	-
SEQ ID NO 5087	GCAATTCCTTCCCCTTGTATGC	TTG	chr1	62598555	62598576	62598560	62598555	-
SEQ ID NO 5088	CTTCCCCTTGTATGCTTCTTTC	TTC	chr1	62598548	62598569	62598553	62598548	-
SEQ ID NO 5089	CCCCTTGTATGCTTCTTTCAAA	CTT	chr1	62598545	62598566	62598550	62598545	-
SEQ ID NO 5090	CCCTTGTATGCTTCTTTCAAAT	TTC	chr1	62598544	62598565	62598549	62598544	-
SEQ ID NO 5091	GTATGCTTCTTTCAAATAGCAC	CTT	chr1	62598539	62598560	62598544	62598539	-
SEQ ID NO 5092	TATGCTTCTTTCAAATAGCACA	TTG	chr1	62598538	62598559	62598543	62598538	-
SEQ ID NO 5093	CTTTCAAATAGCACATATTTTT	CTT	chr1	62598531	62598552	62598536	62598531	-
SEQ ID NO 5094	TTTCAAATAGCACATATTTTTG	TTC	chr1	62598530	62598551	62598535	62598530	-
SEQ ID NO 5095	TCAAATAGCACATATTTTTGTC	CTT	chr1	62598528	62598549	62598533	62598528	-
SEQ ID NO 5096	CAAATAGCACATATTTTTGTCC	TTT	chr1	62598527	62598548	62598532	62598527	-
SEQ ID NO 5097	AAATAGCACATATTTTTGTCCT	TTC	chr1	62598526	62598547	62598531	62598526	-
SEQ ID NO 5098	TTGTCCTTAACATTTTATTTAA	TTT	chr1	62598511	62598532	62598516	62598511	-
SEQ ID NO 5099	TGTCCTTAACATTTTATTTAAA	TTT	chr1	62598510	62598531	62598515	62598510	-
SEQ ID NO 5100	GTCCTTAACATTTTATTTAAAT	TTT	chr1	62598509	62598530	62598514	62598509	-
SEQ ID NO 5101	TCCTTAACATTTTATTTAAATT	TTG	chr1	62598508	62598529	62598513	62598508	-
SEQ ID NO 5102	AACATTTTATTTAAATTGTACT	CTT	chr1	62598503	62598524	62598508	62598503	-
SEQ ID NO 5103	ACATTTTATTTAAATTGTACTA	TTA	chr1	62598502	62598523	62598507	62598502	-
SEQ ID NO 5104	TATTTAAATTGTACTATCTCTA	TTT	chr1	62598496	62598517	62598501	62598496	-

SEQ ID NO 5105	ATTTAAATTGTACTATCTCTAA	TTT	chr1	62598495	62598516	62598500	62598495	-
SEQ ID NO 5106	TTTAAATTGTACTATCTCTAAA	TTA	chr1	62598494	62598515	62598499	62598494	-
SEQ ID NO 5107	AAATTGTACTATCTCTAAAATT	TTT	chr1	62598491	62598512	62598496	62598491	-
SEQ ID NO 5108	AATTGTACTATCTCTAAAATTT	TTA	chr1	62598490	62598511	62598495	62598490	-
SEQ ID NO 5109	TACTATCTCTAAAATTTGATTT	TTG	chr1	62598485	62598506	62598490	62598485	-
SEQ ID NO 5110	TCTCTAAAATTTGATTTTCTGA	CTA	chr1	62598480	62598501	62598485	62598480	-
SEQ ID NO 5111	TAAAATTTGATTTTCTGAACTT	CTC	chr1	62598476	62598497	62598481	62598476	-
SEQ ID NO 5112	AAATTTGATTTTCTGAACTTCA	CTA	chr1	62598474	62598495	62598479	62598474	-
SEQ ID NO 5113	GATTTTCTGAACTTCAATTAAA	TTT	chr1	62598468	62598489	62598473	62598468	-
SEQ ID NO 5114	ATTTTCTGAACTTCAATTAAAA	TTG	chr1	62598467	62598488	62598472	62598467	-
SEQ ID NO 5115	TCTGAACTTCAATTAAAAGAAA	TTT	chr1	62598463	62598484	62598468	62598463	-
SEQ ID NO 5116	CTGAACTTCAATTAAAAGAAAA	TTT	chr1	62598462	62598483	62598467	62598462	-
SEQ ID NO 5117	TGAACTTCAATTAAAAGAAAAA	TTC	chr1	62598461	62598482	62598466	62598461	-
SEQ ID NO 5118	AACTTCAATTAAAAGAAAAAGC	CTG	chr1	62598459	62598480	62598464	62598459	-
SEQ ID NO 5119	CAATTAAAAGAAAAAGCCCAGC	CTT	chr1	62598454	62598475	62598459	62598454	-
SEQ ID NO 5120	AATTAAAAGAAAAAGCCCAGCA	TTC	chr1	62598453	62598474	62598458	62598453	-
SEQ ID NO 5121	AAAGAAAAAGCCCAGCATATTT	TTA	chr1	62598448	62598469	62598453	62598448	-
SEQ ID NO 5122	TCATATGAATAAATCTTTTCCA	TTT	chr1	62598426	62598447	62598431	62598426	-
SEQ ID NO 5123	CATATGAATAAATCTTTTCCAT	TTT	chr1	62598425	62598446	62598430	62598425	-
SEQ ID NO 5124	ATATGAATAAATCTTTTCCATT	TTC	chr1	62598424	62598445	62598429	62598424	-
SEQ ID NO 5125	TTCCATTTACTGTATTATTTAA	CTT	chr1	62598409	62598430	62598414	62598409	-
SEQ ID NO 5126	TCCATTTACTGTATTATTTAAT	TTT	chr1	62598408	62598429	62598413	62598408	-
SEQ ID NO 5127	CCATTTACTGTATTATTTAATC	TTT	chr1	62598407	62598428	62598412	62598407	-
SEQ ID NO 5128	CATTTACTGTATTATTTAATCT	TTC	chr1	62598406	62598427	62598411	62598406	-
SEQ ID NO 5129	ACTGTATTATTTAATCTGTTTT	TTT	chr1	62598401	62598422	62598406	62598401	-
SEQ ID NO 5130	CTGTATTATTTAATCTGTTTTA	TTA	chr1	62598400	62598421	62598405	62598400	-
SEQ ID NO 5131	TATTATTTAATCTGTTTTAAAC	CTG	chr1	62598397	62598418	62598402	62598397	-
SEQ ID NO 5132	TTTAATCTGTTTTAAACACTGG	TTA	chr1	62598392	62598413	62598397	62598392	-
SEQ ID NO 5133	AATCTGTTTTAAACACTGGAGA	TTT	chr1	62598389	62598410	62598394	62598389	-
SEQ ID NO 5134	ATCTGTTTTAAACACTGGAGAA	TTA	chr1	62598388	62598409	62598393	62598388	-
SEQ ID NO 5135	TTTTAAACACTGGAGAATAGTT	CTG	chr1	62598383	62598404	62598388	62598383	-
SEQ ID NO 5136	TAAACACTGGAGAATAGTTTTA	TTT	chr1	62598380	62598401	62598385	62598380	-
SEQ ID NO 5137	AAACACTGGAGAATAGTTTTAA	TTT	chr1	62598379	62598400	62598384	62598379	-
SEQ ID NO 5138	AACACTGGAGAATAGTTTTAAA	TTA	chr1	62598378	62598399	62598383	62598378	-
SEQ ID NO 5139	GAGAATAGTTTTAAATTTTTTT	CTG	chr1	62598371	62598392	62598376	62598371	-
SEQ ID NO 5140	TAAATTTTTTTTAACTTTTTAC	TTT	chr1	62598360	62598381	62598365	62598360	-
SEQ ID NO 5141	AAATTTTTTTTAACTTTTTACT	TTT	chr1	62598359	62598380	62598364	62598359	-
SEQ ID NO 5142	AATTTTTTTTTAACTTTTTACTT	TTA	chr1	62598358	62598379	62598363	62598358	-
SEQ ID NO 5143	TTTTTAACTTTTTACTTACCTT	TTT	chr1	62598353	62598374	62598358	62598353	-
SEQ ID NO 5144	TTTTAACTTTTTACTTACCTTC	TTT	chr1	62598352	62598373	62598357	62598352	-
SEQ ID NO 5145	TTTAACTTTTTACTTACCTTCA	TTT	chr1	62598351	62598372	62598356	62598351	-
SEQ ID NO 5146	TTAACTTTTTACTTACCTTCAG	TTT	chr1	62598350	62598371	62598355	62598350	-
SEQ ID NO 5147	TAACTTTTTACTTACCTTCAGT	TTT	chr1	62598349	62598370	62598354	62598349	-
SEQ ID NO 5148	AACTTTTTACTTACCTTCAGTA	TTT	chr1	62598348	62598369	62598353	62598348	-
SEQ ID NO 5149	ACTTTTTACTTACCTTCAGTAA	TTA	chr1	62598347	62598368	62598352	62598347	-
SEQ ID NO 5150	TTTACTTACCTTCAGTAATTTA	CTT	chr1	62598343	62598364	62598348	62598343	-
SEQ ID NO 5151	TTACTTACCTTCAGTAATTTAC	TTT	chr1	62598342	62598363	62598347	62598342	-
SEQ ID NO 5152	TACTTACCTTCAGTAATTTACA	TTT	chr1	62598341	62598362	62598346	62598341	-
SEQ ID NO 5153	ACTTACCTTCAGTAATTTACAA	TTT	chr1	62598340	62598361	62598345	62598340	-
SEQ ID NO 5154	CTTACCTTCAGTAATTTACAAT	TTA	chr1	62598339	62598360	62598344	62598339	-
SEQ ID NO 5155	ACCTTCAGTAATTTACAATAGT	CTT	chr1	62598336	62598357	62598341	62598336	-
SEQ ID NO 5156	CCTTCAGTAATTTACAATAGTG	TTA	chr1	62598335	62598356	62598340	62598335	-
SEQ ID NO 5157	CAGTAATTTACAATAGTGTAAT	CTT	chr1	62598331	62598352	62598336	62598331	-
SEQ ID NO 5158	AGTAATTTACAATAGTGTAATG	TTC	chr1	62598330	62598351	62598335	62598330	-
SEQ ID NO 5159	ACAATAGTGTAATGACATAGTG	TTT	chr1	62598322	62598343	62598327	62598322	-
SEQ ID NO 5160	CAATAGTGTAATGACATAGTGT	TTA	chr1	62598321	62598342	62598326	62598321	-
SEQ ID NO 5161	TAGATTGTATAATTTAACCGAT	TTC	chr1	62598297	62598318	62598302	62598297	-
SEQ ID NO 5162	GATTGTATAATTTAACCGATTT	CTA	chr1	62598295	62598316	62598300	62598295	-

SEQ ID NO 5163	TATAATTTAACCGATTTGTAAT	TTG	chr1	62598290	62598311	62598295	62598290	-
SEQ ID NO 5164	AACCGATTTGTAATTTTCATAT	TTT	chr1	62598282	62598303	62598287	62598282	-
SEQ ID NO 5165	ACCGATTTGTAATTTTCATATA	TTA	chr1	62598281	62598302	62598286	62598281	-
SEQ ID NO 5166	GTAATTTTCATATAAAATGCAA	TTT	chr1	62598273	62598294	62598278	62598273	-
SEQ ID NO 5167	TAATTTTCATATAAAATGCAAA	TTG	chr1	62598272	62598293	62598277	62598272	-
SEQ ID NO 5168	TCATATAAAATGCAAATTTTCA	TTT	chr1	62598266	62598287	62598271	62598266	-
SEQ ID NO 5169	CATATAAAATGCAAATTTTCAG	TTT	chr1	62598265	62598286	62598270	62598265	-
SEQ ID NO 5170	ATATAAAATGCAAATTTTCAGT	TTC	chr1	62598264	62598285	62598269	62598264	-
SEQ ID NO 5171	TCAGTGTTTTCATATATAACAT	TTT	chr1	62598247	62598268	62598252	62598247	-
SEQ ID NO 5172	CAGTGTTTTCATATATAACATT	TTT	chr1	62598246	62598267	62598251	62598246	-
SEQ ID NO 5173	AGTGTTTTCATATATAACATTA	TTC	chr1	62598245	62598266	62598250	62598245	-
SEQ ID NO 5174	TCATATATAACATTAGGGAAAC	TTT	chr1	62598238	62598259	62598243	62598238	-
SEQ ID NO 5175	CATATATAACATTAGGGAAACA	TTT	chr1	62598237	62598258	62598242	62598237	-
SEQ ID NO 5176	ATATATAACATTAGGGAAACAA	TTC	chr1	62598236	62598257	62598241	62598236	-
SEQ ID NO 5177	GGGAAACAAAAAACTAACTTGA	TTA	chr1	62598223	62598244	62598228	62598223	-
SEQ ID NO 5178	ACTTGAAATTATAATAGGAAAT	CTA	chr1	62598207	62598228	62598212	62598207	-
SEQ ID NO 5179	GAAATTATAATAGGAAATTTTA	CTT	chr1	62598203	62598224	62598208	62598203	-
SEQ ID NO 5180	AAATTATAATAGGAAATTTTAT	TTG	chr1	62598202	62598223	62598207	62598202	-
SEQ ID NO 5181	TAATAGGAAATTTTATTTTCTG	TTA	chr1	62598196	62598217	62598201	62598196	-
SEQ ID NO 5182	TATTTTCTGGAGATTATTTTTC	TTT	chr1	62598183	62598204	62598188	62598183	-
SEQ ID NO 5183	ATTTTCTGGAGATTATTTTTCT	TTT	chr1	62598182	62598203	62598187	62598182	-
SEQ ID NO 5184	TTTTCTGGAGATTATTTTTCTT	TTA	chr1	62598181	62598202	62598186	62598181	-
SEQ ID NO 5185	TCTGGAGATTATTTTTCTTGGA	TTT	chr1	62598178	62598199	62598183	62598178	-
SEQ ID NO 5186	CTGGAGATTATTTTTCTTGGAA	TTT	chr1	62598177	62598198	62598182	62598177	-
SEQ ID NO 5187	TGGAGATTATTTTTCTTGGAAA	TTC	chr1	62598176	62598197	62598181	62598176	-
SEQ ID NO 5188	GAGATTATTTTTCTTGGAAAAA	CTG	chr1	62598174	62598195	62598179	62598174	-
SEQ ID NO 5189	TTTTTCTTGGAAAAAAAAGTAT	TTA	chr1	62598167	62598188	62598172	62598167	-
SEQ ID NO 5190	TTCTTGGAAAAAAAAGTATTTC	TTT	chr1	62598164	62598185	62598169	62598164	-
SEQ ID NO 5191	TCTTGGAAAAAAAAGTATTTCA	TTT	chr1	62598163	62598184	62598168	62598163	-
SEQ ID NO 5192	CTTGGAAAAAAAAGTATTTCAA	TTT	chr1	62598162	62598183	62598167	62598162	-
SEQ ID NO 5193	TTGGAAAAAAAAGTATTTCAAC	TTC	chr1	62598161	62598182	62598166	62598161	-
SEQ ID NO 5194	GGAAAAAAAAGTATTTCAACAA	CTT	chr1	62598159	62598180	62598164	62598159	-
SEQ ID NO 5195	GAAAAAAAAGTATTTCAACAAT	TTG	chr1	62598158	62598179	62598163	62598158	-
SEQ ID NO 5196	CAACAATGCAACAAAGTATTTC	TTT	chr1	62598143	62598164	62598148	62598143	-
SEQ ID NO 5197	AACAATGCAACAAAGTATTTCA	TTC	chr1	62598142	62598163	62598147	62598142	-
SEQ ID NO 5198	CAAATGGCATGCCTTAGAAATA	TTT	chr1	62598122	62598143	62598127	62598122	-
SEQ ID NO 5199	AAATGGCATGCCTTAGAAATAT	TTC	chr1	62598121	62598142	62598126	62598121	-
SEQ ID NO 5200	AGAAATATTTTTTTTTAAAAGAT	CTT	chr1	62598107	62598128	62598112	62598107	-
SEQ ID NO 5201	GAAATATTTTTTTTAAAAGATC	TTA	chr1	62598106	62598127	62598111	62598106	-
SEQ ID NO 5202	TTTTTAAAAGATCCACATTGAA	TTT	chr1	62598097	62598118	62598102	62598097	-
SEQ ID NO 5203	TTTTAAAAGATCCACATTGAAA	TTT	chr1	62598096	62598117	62598101	62598096	-
SEQ ID NO 5204	TTTAAAAGATCCACATTGAAAA	TTT	chr1	62598095	62598116	62598100	62598095	-
SEQ ID NO 5205	TTAAAAGATCCACATTGAAAAC	TTT	chr1	62598094	62598115	62598099	62598094	-
SEQ ID NO 5206	TAAAAGATCCACATTGAAAACA	TTT	chr1	62598093	62598114	62598098	62598093	-
SEQ ID NO 5207	AAAAGATCCACATTGAAAACAT	TTT	chr1	62598092	62598113	62598097	62598092	-
SEQ ID NO 5208	AAAGATCCACATTGAAAACATA	TTA	chr1	62598091	62598112	62598096	62598091	-
SEQ ID NO 5209	AAAACATAAACATGAACCCTCT	TTG	chr1	62598077	62598098	62598082	62598077	-
SEQ ID NO 5210	TTTATTTTCTACTTACTTTAAG	CTC	chr1	62598056	62598077	62598061	62598056	-
SEQ ID NO 5211	TATTTTCTACTTACTTTAAGTG	CTT	chr1	62598054	62598075	62598059	62598054	-
SEQ ID NO 5212	ATTTTCTACTTACTTTAAGTGA	TTT	chr1	62598053	62598074	62598058	62598053	-
SEQ ID NO 5213	TTTTCTACTTACTTTAAGTGAA	TTA	chr1	62598052	62598073	62598057	62598052	-
SEQ ID NO 5214	TCTACTTACTTTAAGTGAAGTT	TTT	chr1	62598049	62598070	62598054	62598049	-
SEQ ID NO 5215	CTACTTACTTTAAGTGAAGTTA	TTT	chr1	62598048	62598069	62598053	62598048	-
SEQ ID NO 5216	TACTTACTTTAAGTGAAGTTAC	TTC	chr1	62598047	62598068	62598052	62598047	-
SEQ ID NO 5217	CTTACTTTAAGTGAAGTTACTT	CTA	chr1	62598045	62598066	62598050	62598045	-
SEQ ID NO 5218	ACTTTAAGTGAAGTTACTTCTG	CTT	chr1	62598042	62598063	62598047	62598042	-
SEQ ID NO 5219	CTTTAAGTGAAGTTACTTCTGG	TTA	chr1	62598041	62598062	62598046	62598041	-
SEQ ID NO 5220	TAAGTGAAGTTACTTCTGGGTG	CTT	chr1	62598038	62598059	62598043	62598038	-

SEQ ID NO 5221	AAGTGAAGTTACTTCTGGGTGT	TTT	chr1	62598037	62598058	62598042	62598037	-
SEQ ID NO 5222	AGTGAAGTTACTTCTGGGTGTT	TTA	chr1	62598036	62598057	62598041	62598036	-
SEQ ID NO 5223	CTTCTGGGTGTTCTGGAGTTTC	TTA	chr1	62598026	62598047	62598031	62598026	-
SEQ ID NO 5224	CTGGGTGTTCTGGAGTTTCAGG	CTT	chr1	62598023	62598044	62598028	62598023	-
SEQ ID NO 5225	TGGGTGTTCTGGAGTTTCAGGT	TTC	chr1	62598022	62598043	62598027	62598022	-
SEQ ID NO 5226	GGTGTTCTGGAGTTTCAGGTTG	CTG	chr1	62598020	62598041	62598025	62598020	-
SEQ ID NO 5227	TGGAGTTTCAGGTTGATTTTGA	TTC	chr1	62598013	62598034	62598018	62598013	-
SEQ ID NO 5228	GAGTTTCAGGTTGATTTTGAAT	CTG	chr1	62598011	62598032	62598016	62598011	-
SEQ ID NO 5229	CAGGTTGATTTTGAATTAAGTT	TTT	chr1	62598005	62598026	62598010	62598005	-
SEQ ID NO 5230	AGGTTGATTTTGAATTAAGTTA	TTC	chr1	62598004	62598025	62598009	62598004	-
SEQ ID NO 5231	ATTTTGAATTAAGTTAGTTAGT	TTG	chr1	62597998	62598019	62598003	62597998	-
SEQ ID NO 5232	TGAATTAAGTTAGTTAGTTGCT	TTT	chr1	62597994	62598015	62597999	62597994	-
SEQ ID NO 5233	GAATTAAGTTAGTTAGTTGCTC	TTT	chr1	62597993	62598014	62597998	62597993	-
SEQ ID NO 5234	AATTAAGTTAGTTAGTTGCTCT	TTG	chr1	62597992	62598013	62597997	62597992	-
SEQ ID NO 5235	AGTTAGTTAGTTGCTCTTCTAA	TTA	chr1	62597987	62598008	62597992	62597987	-
SEQ ID NO 5236	GTTAGTTGCTCTTCTAAATATT	TTA	chr1	62597982	62598003	62597987	62597982	-
SEQ ID NO 5237	GTTGCTCTTCTAAATATTTCAC	TTA	chr1	62597978	62597999	62597983	62597978	-
SEQ ID NO 5238	CTCTTCTAAATATTTCACTTTT	TTG	chr1	62597974	62597995	62597979	62597974	-
SEQ ID NO 5239	TTCTAAATATTTCACTTTTTGT	CTC	chr1	62597971	62597992	62597976	62597971	-
SEQ ID NO 5240	CTAAATATTTCACTTTTTGTTG	CTT	chr1	62597969	62597990	62597974	62597969	-
SEQ ID NO 5241	TAAATATTTCACTTTTTGTTGA	TTC	chr1	62597968	62597989	62597973	62597968	-
SEQ ID NO 5242	AATATTTCACTTTTTGTTGAAG	CTA	chr1	62597966	62597987	62597971	62597966	-
SEQ ID NO 5243	CACTTTTTGTTGAAGTAGAATT	TTT	chr1	62597959	62597980	62597964	62597959	-
SEQ ID NO 5244	ACTTTTTGTTGAAGTAGAATTT	TTC	chr1	62597958	62597979	62597963	62597958	-
SEQ ID NO 5245	TTTGTTGAAGTAGAATTTTTTC	CTT	chr1	62597954	62597975	62597959	62597954	-
SEQ ID NO 5246	TTGTTGAAGTAGAATTTTTTCT	TTT	chr1	62597953	62597974	62597958	62597953	-
SEQ ID NO 5247	TGTTGAAGTAGAATTTTTTCTT	TTT	chr1	62597952	62597973	62597957	62597952	-
SEQ ID NO 5248	GTTGAAGTAGAATTTTTTCTTC	TTT	chr1	62597951	62597972	62597956	62597951	-
SEQ ID NO 5249	TTGAAGTAGAATTTTTTCTTCT	TTG	chr1	62597950	62597971	62597955	62597950	-
SEQ ID NO 5250	AAGTAGAATTTTTTCTTCTAGG	TTG	chr1	62597947	62597968	62597952	62597947	-
SEQ ID NO 5251	TTTCTTCTAGGAGGCTTTCAAG	TTT	chr1	62597936	62597957	62597941	62597936	-
SEQ ID NO 5252	TTCTTCTAGGAGGCTTTCAAGT	TTT	chr1	62597935	62597956	62597940	62597935	-
SEQ ID NO 5253	TCTTCTAGGAGGCTTTCAAGTT	TTT	chr1	62597934	62597955	62597939	62597934	-
SEQ ID NO 5254	CTTCTAGGAGGCTTTCAAGTTT	TTT	chr1	62597933	62597954	62597938	62597933	-
SEQ ID NO 5255	TTCTAGGAGGCTTTCAAGTTTT	TTC	chr1	62597932	62597953	62597937	62597932	-
SEQ ID NO 5256	CTAGGAGGCTTTCAAGTTTTGA	CTT	chr1	62597930	62597951	62597935	62597930	-
SEQ ID NO 5257	TAGGAGGCTTTCAAGTTTTGAG	TTC	chr1	62597929	62597950	62597934	62597929	-
SEQ ID NO 5258	GGAGGCTTTCAAGTTTTGAGTT	CTA	chr1	62597927	62597948	62597932	62597927	-
SEQ ID NO 5259	TCAAGTTTTGAGTTGAGTTCAA	CTT	chr1	62597919	62597940	62597924	62597919	-
SEQ ID NO 5260	CAAGTTTTGAGTTGAGTTCAAG	TTT	chr1	62597918	62597939	62597923	62597918	-
SEQ ID NO 5261	AAGTTTTGAGTTGAGTTCAAGT	TTC	chr1	62597917	62597938	62597922	62597917	-
SEQ ID NO 5262	TGAGTTGAGTTCAAGTGACATA	TTT	chr1	62597911	62597932	62597916	62597911	-
SEQ ID NO 5263	GAGTTGAGTTCAAGTGACATAT	TTT	chr1	62597910	62597931	62597915	62597910	-
SEQ ID NO 5264	AGTTGAGTTCAAGTGACATATT	TTG	chr1	62597909	62597930	62597914	62597909	-
SEQ ID NO 5265	AGTTCAAGTGACATATTCTTTA	TTG	chr1	62597904	62597925	62597909	62597904	-
SEQ ID NO 5266	AAGTGACATATTCTTTACCTCT	TTC	chr1	62597899	62597920	62597904	62597899	-
SEQ ID NO 5267	TTTACCTCTTCATTTTTGACTT	TTC	chr1	62597886	62597907	62597891	62597886	-
SEQ ID NO 5268	TACCTCTTCATTTTTGACTTGT	CTT	chr1	62597884	62597905	62597889	62597884	-
SEQ ID NO 5269	ACCTCTTCATTTTTGACTTGTA	TTT	chr1	62597883	62597904	62597888	62597883	-
SEQ ID NO 5270	CCTCTTCATTTTTGACTTGTAG	TTA	chr1	62597882	62597903	62597887	62597882	-
SEQ ID NO 5271	TTCATTTTTGACTTGTAGTTTA	CTC	chr1	62597878	62597899	62597883	62597878	-
SEQ ID NO 5272	CATTTTTGACTTGTAGTTTATA	CTT	chr1	62597876	62597897	62597881	62597876	-
SEQ ID NO 5273	ATTTTTGACTTGTAGTTTATAT	TTC	chr1	62597875	62597896	62597880	62597875	-
SEQ ID NO 5274	TTGACTTGTAGTTTATATGTAG	TTT	chr1	62597871	62597892	62597876	62597871	-
SEQ ID NO 5275	TGACTTGTAGTTTATATGTAGT	TTT	chr1	62597870	62597891	62597875	62597870	-
SEQ ID NO 5276	GACTTGTAGTTTATATGTAGTT	TTT	chr1	62597869	62597890	62597874	62597869	-
SEQ ID NO 5277	ACTTGTAGTTTATATGTAGTTC	TTG	chr1	62597868	62597889	62597873	62597868	-
SEQ ID NO 5278	GTAGTTTATATGTAGTTCTTCT	CTT	chr1	62597864	62597885	62597869	62597864	-

SEQ ID NO 5279	TAGTTTATATGTAGTTCTTCTC	TTG	chr1	62597863	62597884	62597868	62597863	-
SEQ ID NO 5280	ATATGTAGTTCTTCTCAGTTCC	TTT	chr1	62597857	62597878	62597862	62597857	-
SEQ ID NO 5281	TATGTAGTTCTTCTCAGTTCCT	TTA	chr1	62597856	62597877	62597861	62597856	-
SEQ ID NO 5282	TTCTCAGTTCCTTTTCTTCTTC	TTC	chr1	62597846	62597867	62597851	62597846	-
SEQ ID NO 5283	CTCAGTTCCTTTTCTTCTTCTT	CTT	chr1	62597844	62597865	62597849	62597844	-
SEQ ID NO 5284	TCAGTTCCTTTTCTTCTTCTTT	TTC	chr1	62597843	62597864	62597848	62597843	-
SEQ ID NO 5285	AGTTCCTTTTCTTCTTCTTTGA	CTC	chr1	62597841	62597862	62597846	62597841	-
SEQ ID NO 5286	CTTTTCTTCTTCTTTGATTTCA	TTC	chr1	62597836	62597857	62597841	62597836	-
SEQ ID NO 5287	TTCTTCTTCTTTGATTTCACTG	CTT	chr1	62597833	62597854	62597838	62597833	-
SEQ ID NO 5288	TCTTCTTCTTTGATTTCACTGG	TTT	chr1	62597832	62597853	62597837	62597832	-
SEQ ID NO 5289	CTTCTTCTTTGATTTCACTGGT	TTT	chr1	62597831	62597852	62597836	62597831	-
SEQ ID NO 5290	TTCTTCTTTGATTTCACTGGTT	TTC	chr1	62597830	62597851	62597835	62597830	-
SEQ ID NO 5291	CTTCTTTGATTTCACTGGTTTG	CTT	chr1	62597828	62597849	62597833	62597828	-
SEQ ID NO 5292	TTCTTTGATTTCACTGGTTTGC	TTC	chr1	62597827	62597848	62597832	62597827	-
SEQ ID NO 5293	CTTTGATTTCACTGGTTTGCAG	CTT	chr1	62597825	62597846	62597830	62597825	-
SEQ ID NO 5294	TTTGATTTCACTGGTTTGCAGC	TTC	chr1	62597824	62597845	62597829	62597824	-
SEQ ID NO 5295	TGATTTCACTGGTTTGCAGCGA	CTT	chr1	62597822	62597843	62597827	62597822	-
SEQ ID NO 5296	GATTTCACTGGTTTGCAGCGAT	TTT	chr1	62597821	62597842	62597826	62597821	-
SEQ ID NO 5297	ATTTCACTGGTTTGCAGCGATA	TTG	chr1	62597820	62597841	62597825	62597820	-
SEQ ID NO 5298	CACTGGTTTGCAGCGATAGATC	TTT	chr1	62597816	62597837	62597821	62597816	-
SEQ ID NO 5299	ACTGGTTTGCAGCGATAGATCA	TTC	chr1	62597815	62597836	62597820	62597815	-
SEQ ID NO 5300	GTTTGCAGCGATAGATCATAAA	CTG	chr1	62597811	62597832	62597816	62597811	-
SEQ ID NO 5301	GCAGCGATAGATCATAAAAAGA	TTT	chr1	62597807	62597828	62597812	62597807	-
SEQ ID NO 5302	CAGCGATAGATCATAAAAAGAC	TTG	chr1	62597806	62597827	62597811	62597806	-
SEQ ID NO 5303	ATCAAATATGTTGAGTTTTTGA	CTG	chr1	62597782	62597803	62597787	62597782	-
SEQ ID NO 5304	AGTTTTTGAAATATGTCATTAA	TTG	chr1	62597769	62597790	62597774	62597769	-
SEQ ID NO 5305	TTGAAATATGTCATTAATTTGG	TTT	chr1	62597764	62597785	62597769	62597764	-
SEQ ID NO 5306	TGAAATATGTCATTAATTTGGC	TTT	chr1	62597763	62597784	62597768	62597763	-
SEQ ID NO 5307	GAAATATGTCATTAATTTGGCC	TTT	chr1	62597762	62597783	62597767	62597762	-
SEQ ID NO 5308	AAATATGTCATTAATTTGGCCC	TTG	chr1	62597761	62597782	62597766	62597761	-
SEQ ID NO 5309	ATTTGGCCCTTCGTCTTATGGA	TTA	chr1	62597748	62597769	62597753	62597748	-
SEQ ID NO 5310	GGCCCTTCGTCTTATGGACAAA	TTT	chr1	62597744	62597765	62597749	62597744	-
SEQ ID NO 5311	GCCCTTCGTCTTATGGACAAAG	TTG	chr1	62597743	62597764	62597748	62597743	-
SEQ ID NO 5312	CGTCTTATGGACAAAGTCTTTA	CTT	chr1	62597737	62597758	62597742	62597737	-
SEQ ID NO 5313	GTCTTATGGACAAAGTCTTTAA	TTC	chr1	62597736	62597757	62597741	62597736	-
SEQ ID NO 5314	ATGGACAAAGTCTTTAAGACCA	CTT	chr1	62597731	62597752	62597736	62597731	-
SEQ ID NO 5315	TGGACAAAGTCTTTAAGACCAT	TTA	chr1	62597730	62597751	62597735	62597730	-
SEQ ID NO 5316	TAAGACCATGTCCCAACTGAAG	CTT	chr1	62597717	62597738	62597722	62597717	-
SEQ ID NO 5317	AAGACCATGTCCCAACTGAAGG	TTT	chr1	62597716	62597737	62597721	62597716	-
SEQ ID NO 5318	AGACCATGTCCCAACTGAAGGA	TTA	chr1	62597715	62597736	62597720	62597715	-
SEQ ID NO 5319	AAGGAGGCCATTGGCTAAAATT	CTG	chr1	62597698	62597719	62597703	62597698	-
SEQ ID NO 5320	GCTAAAATTTTTACATCGTCTA	TTG	chr1	62597685	62597706	62597690	62597685	-
SEQ ID NO 5321	AAATTTTTACATCGTCTAACAT	CTA	chr1	62597681	62597702	62597686	62597681	-
SEQ ID NO 5322	TTACATCGTCTAACATAGCAAA	TTT	chr1	62597675	62597696	62597680	62597675	-
SEQ ID NO 5323	TACATCGTCTAACATAGCAAAT	TTT	chr1	62597674	62597695	62597679	62597674	-
SEQ ID NO 5324	ACATCGTCTAACATAGCAAATC	TTT	chr1	62597673	62597694	62597678	62597673	-
SEQ ID NO 5325	CATCGTCTAACATAGCAAATCT	TTA	chr1	62597672	62597693	62597677	62597672	-
SEQ ID NO 5326	ACATAGCAAATCTTGATTTTGG	CTA	chr1	62597663	62597684	62597668	62597663	-
SEQ ID NO 5327	GATTTTGGCTCTGGAGATAGAG	CTT	chr1	62597649	62597670	62597654	62597649	-
SEQ ID NO 5328	ATTTTGGCTCTGGAGATAGAGA	TTG	chr1	62597648	62597669	62597653	62597648	-
SEQ ID NO 5329	TGGCTCTGGAGATAGAGAATCA	TTT	chr1	62597644	62597665	62597649	62597644	-
SEQ ID NO 5330	GGCTCTGGAGATAGAGAATCAA	TTT	chr1	62597643	62597664	62597648	62597643	-
SEQ ID NO 5331	GCTCTGGAGATAGAGAATCAAA	TTG	chr1	62597642	62597663	62597647	62597642	-
SEQ ID NO 5332	TGGAGATAGAGAATCAAATGAT	CTC	chr1	62597638	62597659	62597643	62597638	-
SEQ ID NO 5333	GAGATAGAGAATCAAATGATGA	CTG	chr1	62597636	62597657	62597641	62597636	-
SEQ ID NO 5334	TCTTGATCAATTCTGGAGGAAA	TTG	chr1	62597610	62597631	62597615	62597610	-
SEQ ID NO 5335	GATCAATTCTGGAGGAAATAAC	CTT	chr1	62597606	62597627	62597611	62597606	-
SEQ ID NO 5336	ATCAATTCTGGAGGAAATAACT	TTG	chr1	62597605	62597626	62597610	62597605	-

SEQ ID NO 5337	TGGAGGAAATAACTAGAGGAAC	TTC	chr1	62597597	62597618	62597602	62597597	-
SEQ ID NO 5338	GAGGAAATAACTAGAGGAACAA	CTG	chr1	62597595	62597616	62597600	62597595	-
SEQ ID NO 5339	GAGGAACAATAAAAAGAAGGAG	CTA	chr1	62597582	62597603	62597587	62597582	-
SEQ ID NO 5340	AATTGTGAACATTTTTATCTTG	CTT	chr1	62597557	62597578	62597562	62597557	-
SEQ ID NO 5341	ATTGTGAACATTTTTATCTTGA	TTA	chr1	62597556	62597577	62597561	62597556	-
SEQ ID NO 5342	TGAACATTTTTATCTTGATTTT	TTG	chr1	62597552	62597573	62597557	62597552	-
SEQ ID NO 5343	TTATCTTGATTTTCAATTTCAA	TTT	chr1	62597543	62597564	62597548	62597543	-
SEQ ID NO 5344	TATCTTGATTTTCAATTTCAAG	TTT	chr1	62597542	62597563	62597547	62597542	-
SEQ ID NO 5345	ATCTTGATTTTCAATTTCAAGC	TTT	chr1	62597541	62597562	62597546	62597541	-
SEQ ID NO 5346	TCTTGATTTTCAATTTCAAGCA	TTA	chr1	62597540	62597561	62597545	62597540	-
SEQ ID NO 5347	GATTTTCAATTTCAAGCAACGT	CTT	chr1	62597536	62597557	62597541	62597536	-
SEQ ID NO 5348	ATTTTCAATTTCAAGCAACGTG	TTG	chr1	62597535	62597556	62597540	62597535	-
SEQ ID NO 5349	TCAATTTCAAGCAACGTGGAAC	TTT	chr1	62597531	62597552	62597536	62597531	-
SEQ ID NO 5350	CAATTTCAAGCAACGTGGAACT	TTT	chr1	62597530	62597551	62597535	62597530	-
SEQ ID NO 5351	AATTTCAAGCAACGTGGAACTG	TTC	chr1	62597529	62597550	62597534	62597529	-
SEQ ID NO 5352	CAAGCAACGTGGAACTGTTTTC	TTT	chr1	62597524	62597545	62597529	62597524	-
SEQ ID NO 5353	AAGCAACGTGGAACTGTTTTCT	TTC	chr1	62597523	62597544	62597528	62597523	-
SEQ ID NO 5354	TTTTCTTCTGGAAGCAGACCTA	CTG	chr1	62597507	62597528	62597512	62597507	-
SEQ ID NO 5355	TCTTCTGGAAGCAGACCTAGAC	TTT	chr1	62597504	62597525	62597509	62597504	-
SEQ ID NO 5356	CTTCTGGAAGCAGACCTAGACT	TTT	chr1	62597503	62597524	62597508	62597503	-
SEQ ID NO 5357	TTCTGGAAGCAGACCTAGACTT	TTC	chr1	62597502	62597523	62597507	62597502	-
SEQ ID NO 5358	CTGGAAGCAGACCTAGACTTCT	CTT	chr1	62597500	62597521	62597505	62597500	-
SEQ ID NO 5359	TGGAAGCAGACCTAGACTTCTT	TTC	chr1	62597499	62597520	62597504	62597499	-
SEQ ID NO 5360	GAAGCAGACCTAGACTTCTTAA	CTG	chr1	62597497	62597518	62597502	62597497	-
SEQ ID NO 5361	GACTTCTTAACTCTATATATAC	CTA	chr1	62597485	62597506	62597490	62597485	-
SEQ ID NO 5362	CTTAACTCTATATATACCAATA	CTT	chr1	62597480	62597501	62597485	62597480	-
SEQ ID NO 5363	TTAACTCTATATATACCAATAT	TTC	chr1	62597479	62597500	62597484	62597479	-
SEQ ID NO 5364	AACTCTATATATACCAATATTT	CTT	chr1	62597477	62597498	62597482	62597477	-
SEQ ID NO 5365	ACTCTATATATACCAATATTTG	TTA	chr1	62597476	62597497	62597481	62597476	-
SEQ ID NO 5366	TATATATACCAATATTTGCCCA	CTC	chr1	62597472	62597493	62597477	62597472	-
SEQ ID NO 5367	TATATACCAATATTTGCCCAGA	CTA	chr1	62597470	62597491	62597475	62597470	-
SEQ ID NO 5368	GCCCAGAAAAGGTAAGGTTGGT	TTT	chr1	62597455	62597476	62597460	62597455	-
SEQ ID NO 5369	CCCAGAAAAGGTAAGGTTGGTA	TTG	chr1	62597454	62597475	62597459	62597454	-
SEQ ID NO 5370	GTAGGTGAACATAGTTAATCAT	TTG	chr1	62597435	62597456	62597440	62597435	-
SEQ ID NO 5371	ATCATTAAGCCGTGTTAACTTG	TTA	chr1	62597418	62597439	62597423	62597418	-
SEQ ID NO 5372	AGCCGTGTTAACTTGCACGAAT	TTA	chr1	62597411	62597432	62597416	62597411	-
SEQ ID NO 5373	ACTTGCACGAATGTAACCTTCT	TTA	chr1	62597401	62597422	62597406	62597401	-
SEQ ID NO 5374	GCACGAATGTAACCTTCTTCCA	CTT	chr1	62597397	62597418	62597402	62597397	-
SEQ ID NO 5375	CACGAATGTAACCTTCTTCCAC	TTG	chr1	62597396	62597417	62597401	62597396	-
SEQ ID NO 5376	CTTCCACATTGAGTTAGATCAA	CTT	chr1	62597381	62597402	62597386	62597381	-
SEQ ID NO 5377	TTCCACATTGAGTTAGATCAAT	TTC	chr1	62597380	62597401	62597385	62597380	-
SEQ ID NO 5378	CCACATTGAGTTAGATCAATGC	CTT	chr1	62597378	62597399	62597383	62597378	-
SEQ ID NO 5379	CACATTGAGTTAGATCAATGCT	TTC	chr1	62597377	62597398	62597382	62597377	-
SEQ ID NO 5380	AGTTAGATCAATGCTAAATGAA	TTG	chr1	62597370	62597391	62597375	62597370	-
SEQ ID NO 5381	GATCAATGCTAAATGAAATCAA	TTA	chr1	62597365	62597386	62597370	62597365	-
SEQ ID NO 5382	AATGAAATCAAAGAAATGAGCA	CTA	chr1	62597354	62597375	62597359	62597354	-
SEQ ID NO 5383	ACTTAATAGGTAATTTGAAATT	CTA	chr1	62597328	62597349	62597333	62597328	-
SEQ ID NO 5384	AATAGGTAATTTGAAATTGTAT	CTT	chr1	62597324	62597345	62597329	62597324	-
SEQ ID NO 5385	ATAGGTAATTTGAAATTGTATT	TTA	chr1	62597323	62597344	62597328	62597323	-
SEQ ID NO 5386	GAAATTGTATTTAACTTTGCTG	TTT	chr1	62597312	62597333	62597317	62597312	-
SEQ ID NO 5387	AAATTGTATTTAACTTTGCTGT	TTG	chr1	62597311	62597332	62597316	62597311	-
SEQ ID NO 5388	TATTTAACTTTGCTGTATTATA	TTG	chr1	62597305	62597326	62597310	62597305	-
SEQ ID NO 5389	AACTTTGCTGTATTATAAACTA	TTT	chr1	62597300	62597321	62597305	62597300	-
SEQ ID NO 5390	ACTTTGCTGTATTATAAACTAC	TTA	chr1	62597299	62597320	62597304	62597299	-
SEQ ID NO 5391	TGCTGTATTATAAACTACACAT	CTT	chr1	62597295	62597316	62597300	62597295	-
SEQ ID NO 5392	GCTGTATTATAAACTACACATT	TTT	chr1	62597294	62597315	62597299	62597294	-
SEQ ID NO 5393	CTGTATTATAAACTACACATTC	TTG	chr1	62597293	62597314	62597298	62597293	-
SEQ ID NO 5394	TATTATAAACTACACATTCAAT	CTG	chr1	62597290	62597311	62597295	62597290	-

SEQ ID NO 5395	TAAACTACACATTCAATGCTAT	TTA	chr1	62597285	62597306	62597290	62597285	-
SEQ ID NO 5396	CACATTCAATGCTATGGTGACT	CTA	chr1	62597278	62597299	62597283	62597278	-
SEQ ID NO 5397	AATGCTATGGTGACTACCTGTT	TTC	chr1	62597271	62597292	62597276	62597271	-
SEQ ID NO 5398	TGGTGACTACCTGTTTTTAAAA	CTA	chr1	62597264	62597285	62597269	62597264	-
SEQ ID NO 5399	CCTGTTTTTAAAAGCTAATTTT	CTA	chr1	62597255	62597276	62597260	62597255	-
SEQ ID NO 5400	TTTTTAAAAGCTAATTTTACTT	CTG	chr1	62597251	62597272	62597256	62597251	-
SEQ ID NO 5401	TTAAAAGCTAATTTTACTTTTT	TTT	chr1	62597248	62597269	62597253	62597248	-
SEQ ID NO 5402	TAAAAGCTAATTTTACTTTTTT	TTT	chr1	62597247	62597268	62597252	62597247	-
SEQ ID NO 5403	AAAAGCTAATTTTACTTTTTTA	TTT	chr1	62597246	62597267	62597251	62597246	-
SEQ ID NO 5404	AAAGCTAATTTTACTTTTTTAT	TTA	chr1	62597245	62597266	62597250	62597245	-
SEQ ID NO 5405	ATTTTACTTTTTTATGATTTTA	CTA	chr1	62597238	62597259	62597243	62597238	-
SEQ ID NO 5406	TACTTTTTTATGATTTTAAGAG	TTT	chr1	62597234	62597255	62597239	62597234	-
SEQ ID NO 5407	ACTTTTTTATGATTTTAAGAGA	TTT	chr1	62597233	62597254	62597238	62597233	-
SEQ ID NO 5408	CTTTTTTATGATTTTAAGAGAT	TTA	chr1	62597232	62597253	62597237	62597232	-
SEQ ID NO 5409	TTTTATGATTTTAAGAGATTTA	CTT	chr1	62597229	62597250	62597234	62597229	-
SEQ ID NO 5410	TTTATGATTTTAAGAGATTTAC	TTT	chr1	62597228	62597249	62597233	62597228	-
SEQ ID NO 5411	TTATGATTTTAAGAGATTTACA	TTT	chr1	62597227	62597248	62597232	62597227	-
SEQ ID NO 5412	TATGATTTTAAGAGATTTACAA	TTT	chr1	62597226	62597247	62597231	62597226	-
SEQ ID NO 5413	ATGATTTTAAGAGATTTACAAG	TTT	chr1	62597225	62597246	62597230	62597225	-
SEQ ID NO 5414	TGATTTTAAGAGATTTACAAGT	TTA	chr1	62597224	62597245	62597229	62597224	-
SEQ ID NO 5415	TAAGAGATTTACAAGTCAAAAA	TTT	chr1	62597218	62597239	62597223	62597218	-
SEQ ID NO 5416	AAGAGATTTACAAGTCAAAAAT	TTT	chr1	62597217	62597238	62597222	62597217	-
SEQ ID NO 5417	AGAGATTTACAAGTCAAAAATA	TTA	chr1	62597216	62597237	62597221	62597216	-
SEQ ID NO 5418	ACAAGTCAAAAATAAACTTTTT	TTT	chr1	62597208	62597229	62597213	62597208	-
SEQ ID NO 5419	CAAGTCAAAAATAAACTTTTTT	TTA	chr1	62597207	62597228	62597212	62597207	-
SEQ ID NO 5420	TTTTGTTGGGTAAATTTATTAT	CTT	chr1	62597189	62597210	62597194	62597189	-
SEQ ID NO 5421	TTTGTTGGGTAAATTTATTATT	TTT	chr1	62597188	62597209	62597193	62597188	-
SEQ ID NO 5422	TTGTTGGGTAAATTTATTATTA	TTT	chr1	62597187	62597208	62597192	62597187	-
SEQ ID NO 5423	TGTTGGGTAAATTTATTATTAA	TTT	chr1	62597186	62597207	62597191	62597186	-
SEQ ID NO 5424	GTTGGGTAAATTTATTATTAAA	TTT	chr1	62597185	62597206	62597190	62597185	-
SEQ ID NO 5425	TTGGGTAAATTTATTATTAAAG	TTG	chr1	62597184	62597205	62597189	62597184	-
SEQ ID NO 5426	GGTAAATTTATTATTAAAGTTG	TTG	chr1	62597181	62597202	62597186	62597181	-
SEQ ID NO 5427	ATTATTAAAGTTGAGGGGAAAA	TTT	chr1	62597172	62597193	62597177	62597172	-
SEQ ID NO 5428	TTATTAAAGTTGAGGGGAAAAA	TTA	chr1	62597171	62597192	62597176	62597171	-
SEQ ID NO 5429	TTAAAGTTGAGGGGAAAAAAGT	TTA	chr1	62597168	62597189	62597173	62597168	-
SEQ ID NO 5430	AAGTTGAGGGGAAAAAAGTAAT	TTA	chr1	62597165	62597186	62597170	62597165	-
SEQ ID NO 5431	AGGGGAAAAAAGTAATGAATTA	TTG	chr1	62597159	62597180	62597164	62597159	-

Figure 19

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 5432	TCCCGCCCGCTTGCTGCATC	TGG	chr11	116829764	116829783	116829780	+
SEQ ID NO 5433	TGCATCTGGACACCCTGCCT	CAG	chr11	116829778	116829797	116829794	+
SEQ ID NO 5434	GCATCTGGACACCCTGCCTC	AGG	chr11	116829779	116829798	116829795	+
SEQ ID NO 5435	CCTCAGGCCCTCATCTCCAC	TGG	chr11	116829795	116829814	116829811	+
SEQ ID NO 5436	AGGCCCTCATCTCCACTGGT	CAG	chr11	116829799	116829818	116829815	+
SEQ ID NO 5437	CCCTCATCTCCACTGGTCAG	CAG	chr11	116829802	116829821	116829818	+
SEQ ID NO 5438	CCTCATCTCCACTGGTCAGC	AGG	chr11	116829803	116829822	116829819	+
SEQ ID NO 5439	GTCAGCAGGTGACCTTTGCC	CAG	chr11	116829817	116829836	116829833	+
SEQ ID NO 5440	GTGACCTTTGCCCAGCGCCC	TGG	chr11	116829825	116829844	116829841	+
SEQ ID NO 5441	TGACCTTTGCCCAGCGCCCT	GGG	chr11	116829826	116829845	116829842	+
SEQ ID NO 5442	TGCCCAGCGCCCTGGGTCCT	CAG	chr11	116829833	116829852	116829849	+
SEQ ID NO 5443	GTCCTCAGTGCCTGCTGCCC	TGG	chr11	116829848	116829867	116829864	+
SEQ ID NO 5444	CCTCAGTGCCTGCTGCCCTG	GAG	chr11	116829850	116829869	116829866	+
SEQ ID NO 5445	GCCCTGGAGATGATATAAAA	CAG	chr11	116829864	116829883	116829880	+
SEQ ID NO 5446	CCCTGGAGATGATATAAAAC	AGG	chr11	116829865	116829884	116829881	+
SEQ ID NO 5447	GGAGATGATATAAAACAGGT	CAG	chr11	116829869	116829888	116829885	+
SEQ ID NO 5448	AACCCTCCTGCCTGTCTGCT	CAG	chr11	116829892	116829911	116829908	+
SEQ ID NO 5449	CTGTCTGCTCAGTTCATCCC	TAG	chr11	116829903	116829922	116829919	+
SEQ ID NO 5450	GTCTGCTCAGTTCATCCCTA	GAG	chr11	116829905	116829924	116829921	+
SEQ ID NO 5451	TCTGCTCAGTTCATCCCTAG	AGG	chr11	116829906	116829925	116829922	+
SEQ ID NO 5452	GCTCAGTTCATCCCTAGAGG	CAG	chr11	116829909	116829928	116829925	+
SEQ ID NO 5453	ATCCCTAGAGGCAGCTGCTC	CAG	chr11	116829918	116829937	116829934	+
SEQ ID NO 5454	TCCCTAGAGGCAGCTGCTCC	AGG	chr11	116829919	116829938	116829935	+
SEQ ID NO 5455	CTGCTCCAGGTAATGCCCTC	TGG	chr11	116829932	116829951	116829948	+
SEQ ID NO 5456	TGCTCCAGGTAATGCCCTCT	GGG	chr11	116829933	116829952	116829949	+
SEQ ID NO 5457	GCTCCAGGTAATGCCCTCTG	GGG	chr11	116829934	116829953	116829950	+
SEQ ID NO 5458	TCCAGGTAATGCCCTCTGGG	GAG	chr11	116829936	116829955	116829952	+
SEQ ID NO 5459	CCAGGTAATGCCCTCTGGGG	AGG	chr11	116829937	116829956	116829953	+
SEQ ID NO 5460	CAGGTAATGCCCTCTGGGGA	GGG	chr11	116829938	116829957	116829954	+
SEQ ID NO 5461	AGGTAATGCCCTCTGGGGAG	GGG	chr11	116829939	116829958	116829955	+
SEQ ID NO 5462	AATGCCCTCTGGGGAGGGGA	AAG	chr11	116829943	116829962	116829959	+
SEQ ID NO 5463	TGCCCTCTGGGGAGGGGAAA	GAG	chr11	116829945	116829964	116829961	+
SEQ ID NO 5464	GCCCTCTGGGGAGGGGAAAG	AGG	chr11	116829946	116829965	116829962	+
SEQ ID NO 5465	CCTCTGGGGAGGGGAAAGAG	GAG	chr11	116829948	116829967	116829964	+
SEQ ID NO 5466	CTCTGGGGAGGGGAAAGAGG	AGG	chr11	116829949	116829968	116829965	+
SEQ ID NO 5467	TCTGGGGAGGGGAAAGAGGA	GGG	chr11	116829950	116829969	116829966	+
SEQ ID NO 5468	CTGGGGAGGGGAAAGAGGAG	GGG	chr11	116829951	116829970	116829967	+
SEQ ID NO 5469	GGGGAGGGGAAAGAGGAGGG	GAG	chr11	116829953	116829972	116829969	+
SEQ ID NO 5470	GGGAGGGGAAAGAGGAGGGG	AGG	chr11	116829954	116829973	116829970	+
SEQ ID NO 5471	GAGGGGAAAGAGGAGGGGAG	GAG	chr11	116829956	116829975	116829972	+
SEQ ID NO 5472	AGGGGAAAGAGGAGGGGAGG	AGG	chr11	116829957	116829976	116829973	+
SEQ ID NO 5473	AAGAGGAGGGGAGGAGGATG	AAG	chr11	116829963	116829982	116829979	+
SEQ ID NO 5474	GAGGAGGGGAGGAGGATGAA	GAG	chr11	116829965	116829984	116829981	+
SEQ ID NO 5475	AGGAGGGGAGGAGGATGAAG	AGG	chr11	116829966	116829985	116829982	+
SEQ ID NO 5476	GGAGGGGAGGAGGATGAAGA	GGG	chr11	116829967	116829986	116829983	+
SEQ ID NO 5477	GAGGGGAGGAGGATGAAGAG	GGG	chr11	116829968	116829987	116829984	+
SEQ ID NO 5478	GGAGGAGGATGAAGAGGGGC	AAG	chr11	116829972	116829991	116829988	+
SEQ ID NO 5479	AGGAGGATGAAGAGGGGCAA	GAG	chr11	116829974	116829993	116829990	+

SEQ ID NO 5480	GGAGGATGAAGAGGGGCAAG	AGG	chr11	116829975	116829994	116829991 +
SEQ ID NO 5481	AGGATGAAGAGGGGCAAGAG	GAG	chr11	116829977	116829996	116829993 +
SEQ ID NO 5482	GGCAAGAGGAGCTCCCTGCC	CAG	chr11	116829989	116830008	116830005 +
SEQ ID NO 5483	GAGGAGCTCCCTGCCCAGCC	CAG	chr11	116829994	116830013	116830010 +
SEQ ID NO 5484	AGCTCCCTGCCCAGCCCAGC	CAG	chr11	116829998	116830017	116830014 +
SEQ ID NO 5485	CCCTGCCCAGCCCAGCCAGC	AAG	chr11	116830002	116830021	116830018 +
SEQ ID NO 5486	CCCAGCCCAGCCAGCAAGCC	TGG	chr11	116830007	116830026	116830023 +
SEQ ID NO 5487	CAGCCCAGCCAGCAAGCCTG	GAG	chr11	116830009	116830028	116830025 +
SEQ ID NO 5488	CCCAGCCAGCAAGCCTGGAG	AAG	chr11	116830012	116830031	116830028 +
SEQ ID NO 5489	AAGCCTGGAGAAGCACTTGC	TAG	chr11	116830022	116830041	116830038 +
SEQ ID NO 5490	GCCTGGAGAAGCACTTGCTA	GAG	chr11	116830024	116830043	116830040 +
SEQ ID NO 5491	GAGAAGCACTTGCTAGAGCT	AAG	chr11	116830029	116830048	116830045 +
SEQ ID NO 5492	AGAAGCACTTGCTAGAGCTA	AGG	chr11	116830030	116830049	116830046 +
SEQ ID NO 5493	AGCACTTGCTAGAGCTAAGG	AAG	chr11	116830033	116830052	116830049 +
SEQ ID NO 5494	TGCTAGAGCTAAGGAAGCCT	CGG	chr11	116830039	116830058	116830055 +
SEQ ID NO 5495	CTAGAGCTAAGGAAGCCTCG	GAG	chr11	116830041	116830060	116830057 +
SEQ ID NO 5496	AGCTAAGGAAGCCTCGGAGC	TGG	chr11	116830045	116830064	116830061 +
SEQ ID NO 5497	AAGGAAGCCTCGGAGCTGGA	CGG	chr11	116830049	116830068	116830065 +
SEQ ID NO 5498	AGGAAGCCTCGGAGCTGGAC	GGG	chr11	116830050	116830069	116830066 +
SEQ ID NO 5499	CCACCCCTCATCATAACCTG	AAG	chr11	116830079	116830098	116830095 +
SEQ ID NO 5500	TCATCATAACCTGAAGAACA	TGG	chr11	116830086	116830105	116830102 +
SEQ ID NO 5501	ATCATAACCTGAAGAACATG	GAG	chr11	116830088	116830107	116830104 +
SEQ ID NO 5502	TCATAACCTGAAGAACATGG	AGG	chr11	116830089	116830108	116830105 +
SEQ ID NO 5503	ACCTGAAGAACATGGAGGCC	CGG	chr11	116830094	116830113	116830110 +
SEQ ID NO 5504	CCTGAAGAACATGGAGGCCC	GGG	chr11	116830095	116830114	116830111 +
SEQ ID NO 5505	TGAAGAACATGGAGGCCCGG	GAG	chr11	116830097	116830116	116830113 +
SEQ ID NO 5506	GAAGAACATGGAGGCCCGGG	AGG	chr11	116830098	116830117	116830114 +
SEQ ID NO 5507	AAGAACATGGAGGCCCGGGA	GGG	chr11	116830099	116830118	116830115 +
SEQ ID NO 5508	AGAACATGGAGGCCCGGGAG	GGG	chr11	116830100	116830119	116830116 +
SEQ ID NO 5509	GGAGGGGTGTCACTTGCCCA	AAG	chr11	116830116	116830135	116830132 +
SEQ ID NO 5510	GTCACTTGCCCAAAGCTACA	CAG	chr11	116830124	116830143	116830140 +
SEQ ID NO 5511	TCACTTGCCCAAAGCTACAC	AGG	chr11	116830125	116830144	116830141 +
SEQ ID NO 5512	CACTTGCCCAAAGCTACACA	GGG	chr11	116830126	116830145	116830142 +
SEQ ID NO 5513	ACTTGCCCAAAGCTACACAG	GGG	chr11	116830127	116830146	116830143 +
SEQ ID NO 5514	CTTGCCCAAAGCTACACAGG	GGG	chr11	116830128	116830147	116830144 +
SEQ ID NO 5515	GCCCAAAGCTACACAGGGGG	TGG	chr11	116830131	116830150	116830147 +
SEQ ID NO 5516	CCCAAAGCTACACAGGGGGT	GGG	chr11	116830132	116830151	116830148 +
SEQ ID NO 5517	CCAAAGCTACACAGGGGGTG	GGG	chr11	116830133	116830152	116830149 +
SEQ ID NO 5518	AGCTACACAGGGGGTGGGGC	TGG	chr11	116830137	116830156	116830153 +
SEQ ID NO 5519	TACACAGGGGGTGGGGCTGG	AAG	chr11	116830140	116830159	116830156 +
SEQ ID NO 5520	ACAGGGGGTGGGGCTGGAAG	TGG	chr11	116830143	116830162	116830159 +
SEQ ID NO 5521	GTGGGGCTGGAAGTGGCTCC	AAG	chr11	116830150	116830169	116830166 +
SEQ ID NO 5522	GCTGGAAGTGGCTCCAAGTG	CAG	chr11	116830155	116830174	116830171 +
SEQ ID NO 5523	CTGGAAGTGGCTCCAAGTGC	AGG	chr11	116830156	116830175	116830172 +
SEQ ID NO 5524	CAGGTTCCCCCCTCATTCTT	CAG	chr11	116830175	116830194	116830191 +
SEQ ID NO 5525	AGGTTCCCCCCTCATTCTTC	AGG	chr11	116830176	116830195	116830192 +
SEQ ID NO 5526	CCCCCCTCATTCTTCAGGCT	TAG	chr11	116830181	116830200	116830197 +
SEQ ID NO 5527	CCCCCTCATTCTTCAGGCTT	AGG	chr11	116830182	116830201	116830198 +
SEQ ID NO 5528	CCCCTCATTCTTCAGGCTTA	GGG	chr11	116830183	116830202	116830199 +

SEQ ID NO 5529	TCATTCTTCAGGCTTAGGGC	TGG	chr11	116830187	116830206	116830203 +
SEQ ID NO 5530	ATTCTTCAGGCTTAGGGCTG	GAG	chr11	116830189	116830208	116830205 +
SEQ ID NO 5531	TTCTTCAGGCTTAGGGCTGG	AGG	chr11	116830190	116830209	116830206 +
SEQ ID NO 5532	TTCAGGCTTAGGGCTGGAGG	AAG	chr11	116830193	116830212	116830209 +
SEQ ID NO 5533	CTTAGGGCTGGAGGAAGCCT	TAG	chr11	116830199	116830218	116830215 +
SEQ ID NO 5534	GGGCTGGAGGAAGCCTTAGA	CAG	chr11	116830203	116830222	116830219 +
SEQ ID NO 5535	GGAGGAAGCCTTAGACAGCC	CAG	chr11	116830208	116830227	116830224 +
SEQ ID NO 5536	TAGACAGCCCAGTCCTACCC	CAG	chr11	116830219	116830238	116830235 +
SEQ ID NO 5537	CAGCCCAGTCCTACCCCAGA	CAG	chr11	116830223	116830242	116830239 +
SEQ ID NO 5538	AGCCCAGTCCTACCCCAGAC	AGG	chr11	116830224	116830243	116830240 +
SEQ ID NO 5539	GCCCAGTCCTACCCCAGACA	GGG	chr11	116830225	116830244	116830241 +
SEQ ID NO 5540	CTACCCCAGACAGGGAAACT	GAG	chr11	116830233	116830252	116830249 +
SEQ ID NO 5541	TACCCCAGACAGGGAAACTG	AGG	chr11	116830234	116830253	116830250 +
SEQ ID NO 5542	CAGACAGGGAAACTGAGGCC	TGG	chr11	116830239	116830258	116830255 +
SEQ ID NO 5543	GACAGGGAAACTGAGGCCTG	GAG	chr11	116830241	116830260	116830257 +
SEQ ID NO 5544	CAGGGAAACTGAGGCCTGGA	GAG	chr11	116830243	116830262	116830259 +
SEQ ID NO 5545	AGGGAAACTGAGGCCTGGAG	AGG	chr11	116830244	116830263	116830260 +
SEQ ID NO 5546	GGGAAACTGAGGCCTGGAGA	GGG	chr11	116830245	116830264	116830261 +
SEQ ID NO 5547	AACTGAGGCCTGGAGAGGGC	CAG	chr11	116830249	116830268	116830265 +
SEQ ID NO 5548	AGAGGGCCAGAAATCACCCA	AAG	chr11	116830262	116830281	116830278 +
SEQ ID NO 5549	AGAAATCACCCAAAGACACA	CAG	chr11	116830270	116830289	116830286 +
SEQ ID NO 5550	CCCAAAGACACACAGCATGT	TGG	chr11	116830278	116830297	116830294 +
SEQ ID NO 5551	AAGACACACAGCATGTTGGC	TGG	chr11	116830282	116830301	116830298 +
SEQ ID NO 5552	ACACAGCATGTTGGCTGGAC	TGG	chr11	116830287	116830306	116830303 +
SEQ ID NO 5553	AGCATGTTGGCTGGACTGGA	CGG	chr11	116830291	116830310	116830307 +
SEQ ID NO 5554	CATGTTGGCTGGACTGGACG	GAG	chr11	116830293	116830312	116830309 +
SEQ ID NO 5555	TGGCTGGACTGGACGGAGAT	CAG	chr11	116830298	116830317	116830314 +
SEQ ID NO 5556	GGACTGGACGGAGATCAGTC	CAG	chr11	116830303	116830322	116830319 +
SEQ ID NO 5557	ACGGAGATCAGTCCAGACCG	CAG	chr11	116830310	116830329	116830326 +
SEQ ID NO 5558	CGGAGATCAGTCCAGACCGC	AGG	chr11	116830311	116830330	116830327 +
SEQ ID NO 5559	ACCGCAGGTGCCTTGATGTT	CAG	chr11	116830326	116830345	116830342 +
SEQ ID NO 5560	AGGTGCCTTGATGTTCAGTC	TGG	chr11	116830331	116830350	116830347 +
SEQ ID NO 5561	TGCCTTGATGTTCAGTCTGG	TGG	chr11	116830334	116830353	116830350 +
SEQ ID NO 5562	GCCTTGATGTTCAGTCTGGT	GGG	chr11	116830335	116830354	116830351 +
SEQ ID NO 5563	CCATCCCACCCACCTCCCTT	TGG	chr11	116830367	116830386	116830383 +
SEQ ID NO 5564	CATCCCACCCACCTCCCTTT	GGG	chr11	116830368	116830387	116830384 +
SEQ ID NO 5565	CTCGATCCCTCGCCCCTCAC	CAG	chr11	116830392	116830411	116830408 +
SEQ ID NO 5566	CCCTCACCAGTCCCCCTTCT	GAG	chr11	116830405	116830424	116830421 +
SEQ ID NO 5567	CTCACCAGTCCCCCTTCTGA	GAG	chr11	116830407	116830426	116830423 +
SEQ ID NO 5568	CCCCTTCTGAGAGCCCGTAT	TAG	chr11	116830417	116830436	116830433 +
SEQ ID NO 5569	CTTCTGAGAGCCCGTATTAG	CAG	chr11	116830420	116830439	116830436 +
SEQ ID NO 5570	TTCTGAGAGCCCGTATTAGC	AGG	chr11	116830421	116830440	116830437 +
SEQ ID NO 5571	TCTGAGAGCCCGTATTAGCA	GGG	chr11	116830422	116830441	116830438 +
SEQ ID NO 5572	TGAGAGCCCGTATTAGCAGG	GAG	chr11	116830424	116830443	116830440 +
SEQ ID NO 5573	AGCCCGTATTAGCAGGGAGC	CGG	chr11	116830428	116830447	116830444 +
SEQ ID NO 5574	GAGCCGGCCCCTACTCCTTC	TGG	chr11	116830444	116830463	116830460 +
SEQ ID NO 5575	CCGGCCCCTACTCCTTCTGG	CAG	chr11	116830447	116830466	116830463 +
SEQ ID NO 5576	CCTACTCCTTCTGGCAGACC	CAG	chr11	116830453	116830472	116830469 +
SEQ ID NO 5577	TCCTTCTGGCAGACCCAGCT	AAG	chr11	116830458	116830477	116830474 +

SEQ ID NO 5578	CCTTCTGGCAGACCCAGCTA	AGG	chr11	116830459	116830478	116830475 +
SEQ ID NO 5579	ACCCAGCTAAGGTTCTACCT	TAG	chr11	116830470	116830489	116830486 +
SEQ ID NO 5580	CCCAGCTAAGGTTCTACCTT	AGG	chr11	116830471	116830490	116830487 +
SEQ ID NO 5581	CCAGCTAAGGTTCTACCTTA	GGG	chr11	116830472	116830491	116830488 +
SEQ ID NO 5582	CAGCTAAGGTTCTACCTTAG	GGG	chr11	116830473	116830492	116830489 +
SEQ ID NO 5583	TAGGGGCCACGCCACCTCCC	CAG	chr11	116830490	116830509	116830506 +
SEQ ID NO 5584	AGGGGCCACGCCACCTCCCC	AGG	chr11	116830491	116830510	116830507 +
SEQ ID NO 5585	GGGGCCACGCCACCTCCCCA	GGG	chr11	116830492	116830511	116830508 +
SEQ ID NO 5586	GGCCACGCCACCTCCCCAGG	GAG	chr11	116830494	116830513	116830510 +
SEQ ID NO 5587	GCCACGCCACCTCCCCAGGG	AGG	chr11	116830495	116830514	116830511 +
SEQ ID NO 5588	CCACGCCACCTCCCCAGGGA	GGG	chr11	116830496	116830515	116830512 +
SEQ ID NO 5589	CACGCCACCTCCCCAGGGAG	GGG	chr11	116830497	116830516	116830513 +
SEQ ID NO 5590	CACCTCCCCAGGGAGGGGTC	CAG	chr11	116830502	116830521	116830518 +
SEQ ID NO 5591	CCTCCCCAGGGAGGGGTCCA	GAG	chr11	116830504	116830523	116830520 +
SEQ ID NO 5592	CTCCCCAGGGAGGGGTCCAG	AGG	chr11	116830505	116830524	116830521 +
SEQ ID NO 5593	CAGGGAGGGGTCCAGAGGCA	TGG	chr11	116830510	116830529	116830526 +
SEQ ID NO 5594	AGGGAGGGGTCCAGAGGCAT	GGG	chr11	116830511	116830530	116830527 +
SEQ ID NO 5595	GGGAGGGGTCCAGAGGCATG	GGG	chr11	116830512	116830531	116830528 +
SEQ ID NO 5596	GGTCCAGAGGCATGGGGACC	TGG	chr11	116830518	116830537	116830534 +
SEQ ID NO 5597	GTCCAGAGGCATGGGGACCT	GGG	chr11	116830519	116830538	116830535 +
SEQ ID NO 5598	TCCAGAGGCATGGGGACCTG	GGG	chr11	116830520	116830539	116830536 +
SEQ ID NO 5599	GGGACCTGGGGTGCCCCTCA	CAG	chr11	116830532	116830551	116830548 +
SEQ ID NO 5600	GGACCTGGGGTGCCCCTCAC	AGG	chr11	116830533	116830552	116830549 +
SEQ ID NO 5601	CCTCACAGGACACTTCCTTG	CAG	chr11	116830547	116830566	116830563 +
SEQ ID NO 5602	CTCACAGGACACTTCCTTGC	AGG	chr11	116830548	116830567	116830564 +
SEQ ID NO 5603	AGGACACTTCCTTGCAGGAA	CAG	chr11	116830553	116830572	116830569 +
SEQ ID NO 5604	GACACTTCCTTGCAGGAACA	GAG	chr11	116830555	116830574	116830571 +
SEQ ID NO 5605	ACACTTCCTTGCAGGAACAG	AGG	chr11	116830556	116830575	116830572 +
SEQ ID NO 5606	GCAGGAACAGAGGTGCCATG	CAG	chr11	116830566	116830585	116830582 +
SEQ ID NO 5607	ACAGAGGTGCCATGCAGCCC	CGG	chr11	116830572	116830591	116830588 +
SEQ ID NO 5608	CAGAGGTGCCATGCAGCCCC	GGG	chr11	116830573	116830592	116830589 +
SEQ ID NO 5609	ACTCCTTGTTGTTGCCCTCC	TGG	chr11	116830597	116830616	116830613 +
SEQ ID NO 5610	TGTTGCCCTCCTGGCGCTCC	TGG	chr11	116830606	116830625	116830622 +
SEQ ID NO 5611	CGCTCCTGGCCTCTGCCCGT	AAG	chr11	116830620	116830639	116830636 +
SEQ ID NO 5612	GGCCTCTGCCCGTAAGCACT	TGG	chr11	116830627	116830646	116830643 +
SEQ ID NO 5613	CTCTGCCCGTAAGCACTTGG	TGG	chr11	116830630	116830649	116830646 +
SEQ ID NO 5614	TCTGCCCGTAAGCACTTGGT	GGG	chr11	116830631	116830650	116830647 +
SEQ ID NO 5615	CCGTAAGCACTTGGTGGGAC	TGG	chr11	116830636	116830655	116830652 +
SEQ ID NO 5616	CGTAAGCACTTGGTGGGACT	GGG	chr11	116830637	116830656	116830653 +
SEQ ID NO 5617	AGCACTTGGTGGGACTGGGC	TGG	chr11	116830641	116830660	116830657 +
SEQ ID NO 5618	GCACTTGGTGGGACTGGGCT	GGG	chr11	116830642	116830661	116830658 +
SEQ ID NO 5619	CACTTGGTGGGACTGGGCTG	GGG	chr11	116830643	116830662	116830659 +
SEQ ID NO 5620	ACTTGGTGGGACTGGGCTGG	GGG	chr11	116830644	116830663	116830660 +
SEQ ID NO 5621	TGGTGGGACTGGGCTGGGGG	CAG	chr11	116830647	116830666	116830663 +
SEQ ID NO 5622	GGTGGGACTGGGCTGGGGGC	AGG	chr11	116830648	116830667	116830664 +
SEQ ID NO 5623	GTGGGACTGGGCTGGGGGCA	GGG	chr11	116830649	116830668	116830665 +
SEQ ID NO 5624	GCCCCCAGCCCAGTCCCACC	AAG	chr11	116830648	116830667	116830651 -
SEQ ID NO 5625	CCAGTCCCACCAAGTGCTTA	CGG	chr11	116830639	116830658	116830642 -
SEQ ID NO 5626	CAGTCCCACCAAGTGCTTAC	GGG	chr11	116830638	116830657	116830641 -

SEQ ID NO 5627	TCCCACCAAGTGCTTACGGG	CAG	chr11	116830635	116830654	116830638 -
SEQ ID NO 5628	CCACCAAGTGCTTACGGGCA	GAG	chr11	116830633	116830652	116830636 -
SEQ ID NO 5629	CACCAAGTGCTTACGGGCAG	AGG	chr11	116830632	116830651	116830635 -
SEQ ID NO 5630	AAGTGCTTACGGGCAGAGGC	CAG	chr11	116830628	116830647	116830631 -
SEQ ID NO 5631	AGTGCTTACGGGCAGAGGCC	AGG	chr11	116830627	116830646	116830630 -
SEQ ID NO 5632	TGCTTACGGGCAGAGGCCAG	GAG	chr11	116830625	116830644	116830628 -
SEQ ID NO 5633	CGGGCAGAGGCCAGGAGCGC	CAG	chr11	116830619	116830638	116830622 -
SEQ ID NO 5634	GGGCAGAGGCCAGGAGCGCC	AGG	chr11	116830618	116830637	116830621 -
SEQ ID NO 5635	GCAGAGGCCAGGAGCGCCAG	GAG	chr11	116830616	116830635	116830619 -
SEQ ID NO 5636	CAGAGGCCAGGAGCGCCAGG	AGG	chr11	116830615	116830634	116830618 -
SEQ ID NO 5637	AGAGGCCAGGAGCGCCAGGA	GGG	chr11	116830614	116830633	116830617 -
SEQ ID NO 5638	AGCGCCAGGAGGGCAACAAC	AAG	chr11	116830604	116830623	116830607 -
SEQ ID NO 5639	GCGCCAGGAGGGCAACAACA	AGG	chr11	116830603	116830622	116830606 -
SEQ ID NO 5640	GCCAGGAGGGCAACAACAAG	GAG	chr11	116830601	116830620	116830604 -
SEQ ID NO 5641	GGGCAACAACAAGGAGTACC	CGG	chr11	116830594	116830613	116830597 -
SEQ ID NO 5642	GGCAACAACAAGGAGTACCC	GGG	chr11	116830593	116830612	116830596 -
SEQ ID NO 5643	GCAACAACAAGGAGTACCCG	GGG	chr11	116830592	116830611	116830595 -
SEQ ID NO 5644	AAGGAGTACCCGGGGCTGCA	TGG	chr11	116830584	116830603	116830587 -
SEQ ID NO 5645	CATGGCACCTCTGTTCCTGC	AAG	chr11	116830566	116830585	116830569 -
SEQ ID NO 5646	ATGGCACCTCTGTTCCTGCA	AGG	chr11	116830565	116830584	116830568 -
SEQ ID NO 5647	GCACCTCTGTTCCTGCAAGG	AAG	chr11	116830562	116830581	116830565 -
SEQ ID NO 5648	CCTGCAAGGAAGTGTCCTGT	GAG	chr11	116830551	116830570	116830554 -
SEQ ID NO 5649	CTGCAAGGAAGTGTCCTGTG	AGG	chr11	116830550	116830569	116830553 -
SEQ ID NO 5650	TGCAAGGAAGTGTCCTGTGA	GGG	chr11	116830549	116830568	116830552 -
SEQ ID NO 5651	GCAAGGAAGTGTCCTGTGAG	GGG	chr11	116830548	116830567	116830551 -
SEQ ID NO 5652	GTGTCCTGTGAGGGGCACCC	CAG	chr11	116830540	116830559	116830543 -
SEQ ID NO 5653	TGTCCTGTGAGGGGCACCCC	AGG	chr11	116830539	116830558	116830542 -
SEQ ID NO 5654	ACCCCAGGTCCCCATGCCTC	TGG	chr11	116830524	116830543	116830527 -
SEQ ID NO 5655	CATGCCTCTGGACCCCTCCC	TGG	chr11	116830512	116830531	116830515 -
SEQ ID NO 5656	ATGCCTCTGGACCCCTCCCT	GGG	chr11	116830511	116830530	116830514 -
SEQ ID NO 5657	TGCCTCTGGACCCCTCCCTG	GGG	chr11	116830510	116830529	116830513 -
SEQ ID NO 5658	CCTCTGGACCCCTCCCTGGG	GAG	chr11	116830508	116830527	116830511 -
SEQ ID NO 5659	CTCTGGACCCCTCCCTGGGG	AGG	chr11	116830507	116830526	116830510 -
SEQ ID NO 5660	TGGACCCCTCCCTGGGGAGG	TGG	chr11	116830504	116830523	116830507 -
SEQ ID NO 5661	CCCTCCCTGGGGAGGTGGCG	TGG	chr11	116830499	116830518	116830502 -
SEQ ID NO 5662	GGGGAGGTGGCGTGGCCCCT	AAG	chr11	116830491	116830510	116830494 -
SEQ ID NO 5663	GGGAGGTGGCGTGGCCCCTA	AGG	chr11	116830490	116830509	116830493 -
SEQ ID NO 5664	AGGTGGCGTGGCCCCTAAGG	TAG	chr11	116830487	116830506	116830490 -
SEQ ID NO 5665	TGGCCCCTAAGGTAGAACCT	TAG	chr11	116830479	116830498	116830482 -
SEQ ID NO 5666	CCCTAAGGTAGAACCTTAGC	TGG	chr11	116830475	116830494	116830478 -
SEQ ID NO 5667	CCTAAGGTAGAACCTTAGCT	GGG	chr11	116830474	116830493	116830477 -
SEQ ID NO 5668	AGAACCTTAGCTGGGTCTGC	CAG	chr11	116830466	116830485	116830469 -
SEQ ID NO 5669	ACCTTAGCTGGGTCTGCCAG	AAG	chr11	116830463	116830482	116830466 -
SEQ ID NO 5670	CCTTAGCTGGGTCTGCCAGA	AGG	chr11	116830462	116830481	116830465 -
SEQ ID NO 5671	TTAGCTGGGTCTGCCAGAAG	GAG	chr11	116830460	116830479	116830463 -
SEQ ID NO 5672	GCTGGGTCTGCCAGAAGGAG	TAG	chr11	116830457	116830476	116830460 -
SEQ ID NO 5673	CTGGGTCTGCCAGAAGGAGT	AGG	chr11	116830456	116830475	116830459 -
SEQ ID NO 5674	TGGGTCTGCCAGAAGGAGTA	GGG	chr11	116830455	116830474	116830458 -
SEQ ID NO 5675	GGGTCTGCCAGAAGGAGTAG	GGG	chr11	116830454	116830473	116830457 -

SEQ ID NO 5676	CTGCCAGAAGGAGTAGGGGC	CGG	chr11	116830450	116830469	116830453	-
SEQ ID NO 5677	GGGCCGGCTCCCTGCTAATA	CGG	chr11	116830434	116830453	116830437	-
SEQ ID NO 5678	GGCCGGCTCCCTGCTAATAC	GGG	chr11	116830433	116830452	116830436	-
SEQ ID NO 5679	TCCCTGCTAATACGGGCTCT	CAG	chr11	116830426	116830445	116830429	-
SEQ ID NO 5680	CTGCTAATACGGGCTCTCAG	AAG	chr11	116830423	116830442	116830426	-
SEQ ID NO 5681	TGCTAATACGGGCTCTCAGA	AGG	chr11	116830422	116830441	116830425	-
SEQ ID NO 5682	GCTAATACGGGCTCTCAGAA	GGG	chr11	116830421	116830440	116830424	-
SEQ ID NO 5683	CTAATACGGGCTCTCAGAAG	GGG	chr11	116830420	116830439	116830423	-
SEQ ID NO 5684	TAATACGGGCTCTCAGAAGG	GGG	chr11	116830419	116830438	116830422	-
SEQ ID NO 5685	CGGGCTCTCAGAAGGGGGAC	TGG	chr11	116830414	116830433	116830417	-
SEQ ID NO 5686	CTCTCAGAAGGGGGACTGGT	GAG	chr11	116830410	116830429	116830413	-
SEQ ID NO 5687	TCTCAGAAGGGGGACTGGTG	AGG	chr11	116830409	116830428	116830412	-
SEQ ID NO 5688	CTCAGAAGGGGGACTGGTGA	GGG	chr11	116830408	116830427	116830411	-
SEQ ID NO 5689	TCAGAAGGGGGACTGGTGAG	GGG	chr11	116830407	116830426	116830410	-
SEQ ID NO 5690	AAGGGGGACTGGTGAGGGGC	GAG	chr11	116830403	116830422	116830406	-
SEQ ID NO 5691	AGGGGGACTGGTGAGGGGCG	AGG	chr11	116830402	116830421	116830405	-
SEQ ID NO 5692	GGGGGACTGGTGAGGGGCGA	GGG	chr11	116830401	116830420	116830404	-
SEQ ID NO 5693	CTGGTGAGGGGCGAGGGATC	GAG	chr11	116830395	116830414	116830398	-
SEQ ID NO 5694	TGGTGAGGGGCGAGGGATCG	AGG	chr11	116830394	116830413	116830397	-
SEQ ID NO 5695	GGGCGAGGGATCGAGGCCCA	AAG	chr11	116830387	116830406	116830390	-
SEQ ID NO 5696	GGCGAGGGATCGAGGCCCAA	AGG	chr11	116830386	116830405	116830389	-
SEQ ID NO 5697	GCGAGGGATCGAGGCCCAAA	GGG	chr11	116830385	116830404	116830388	-
SEQ ID NO 5698	GAGGGATCGAGGCCCAAAGG	GAG	chr11	116830383	116830402	116830386	-
SEQ ID NO 5699	AGGGATCGAGGCCCAAAGGG	AGG	chr11	116830382	116830401	116830385	-
SEQ ID NO 5700	GATCGAGGCCCAAAGGGAGG	TGG	chr11	116830379	116830398	116830382	-
SEQ ID NO 5701	ATCGAGGCCCAAAGGGAGGT	GGG	chr11	116830378	116830397	116830381	-
SEQ ID NO 5702	GAGGCCCAAAGGGAGGTGGG	TGG	chr11	116830375	116830394	116830378	-
SEQ ID NO 5703	AGGCCCAAAGGGAGGTGGGT	GGG	chr11	116830374	116830393	116830377	-
SEQ ID NO 5704	CCAAAGGGAGGTGGGTGGGA	TGG	chr11	116830370	116830389	116830373	-
SEQ ID NO 5705	AAAGGGAGGTGGGTGGGATG	GAG	chr11	116830368	116830387	116830371	-
SEQ ID NO 5706	GGGAGGTGGGTGGGATGGAG	CAG	chr11	116830365	116830384	116830368	-
SEQ ID NO 5707	GGATGGAGCAGAAAACCCAC	CAG	chr11	116830353	116830372	116830356	-
SEQ ID NO 5708	AACCCACCAGACTGAACATC	AAG	chr11	116830340	116830359	116830343	-
SEQ ID NO 5709	ACCCACCAGACTGAACATCA	AGG	chr11	116830339	116830358	116830342	-
SEQ ID NO 5710	ACTGAACATCAAGGCACCTG	CGG	chr11	116830330	116830349	116830333	-
SEQ ID NO 5711	ACATCAAGGCACCTGCGGTC	TGG	chr11	116830325	116830344	116830328	-
SEQ ID NO 5712	GGTCTGGACTGATCTCCGTC	CAG	chr11	116830309	116830328	116830312	-
SEQ ID NO 5713	GGACTGATCTCCGTCCAGTC	CAG	chr11	116830304	116830323	116830307	-
SEQ ID NO 5714	GCCAACATGCTGTGTGTCTT	TGG	chr11	116830282	116830301	116830285	-
SEQ ID NO 5715	CCAACATGCTGTGTGTCTTT	GGG	chr11	116830281	116830300	116830284	-
SEQ ID NO 5716	GTGTGTCTTTGGGTGATTTC	TGG	chr11	116830271	116830290	116830274	-
SEQ ID NO 5717	GGGTGATTTCTGGCCCTCTC	CAG	chr11	116830261	116830280	116830264	-
SEQ ID NO 5718	GGTGATTTCTGGCCCTCTCC	AGG	chr11	116830260	116830279	116830263	-
SEQ ID NO 5719	TTCTGGCCCTCTCCAGGCCT	CAG	chr11	116830254	116830273	116830257	-
SEQ ID NO 5720	CAGGCCTCAGTTTCCCTGTC	TGG	chr11	116830241	116830260	116830244	-
SEQ ID NO 5721	AGGCCTCAGTTTCCCTGTCT	GGG	chr11	116830240	116830259	116830243	-
SEQ ID NO 5722	GGCCTCAGTTTCCCTGTCTG	GGG	chr11	116830239	116830258	116830242	-
SEQ ID NO 5723	CTCAGTTTCCCTGTCTGGGG	TAG	chr11	116830236	116830255	116830239	-
SEQ ID NO 5724	TCAGTTTCCCTGTCTGGGGT	AGG	chr11	116830235	116830254	116830238	-

SEQ ID NO 5725	TTCCCTGTCTGGGGTAGGAC	TGG	chr11	116830230	116830249	116830233	-
SEQ ID NO 5726	TCCCTGTCTGGGGTAGGACT	GGG	chr11	116830229	116830248	116830232	-
SEQ ID NO 5727	GGGGTAGGACTGGGCTGTCT	AAG	chr11	116830220	116830239	116830223	-
SEQ ID NO 5728	GGGTAGGACTGGGCTGTCTA	AGG	chr11	116830219	116830238	116830222	-
SEQ ID NO 5729	GGGCTGTCTAAGGCTTCCTC	CAG	chr11	116830209	116830228	116830212	-
SEQ ID NO 5730	CTAAGGCTTCCTCCAGCCCT	AAG	chr11	116830202	116830221	116830205	-
SEQ ID NO 5731	TTCCTCCAGCCCTAAGCCTG	AAG	chr11	116830195	116830214	116830198	-
SEQ ID NO 5732	CAGCCCTAAGCCTGAAGAAT	GAG	chr11	116830189	116830208	116830192	-
SEQ ID NO 5733	AGCCCTAAGCCTGAAGAATG	AGG	chr11	116830188	116830207	116830191	-
SEQ ID NO 5734	GCCCTAAGCCTGAAGAATGA	GGG	chr11	116830187	116830206	116830190	-
SEQ ID NO 5735	CCCTAAGCCTGAAGAATGAG	GGG	chr11	116830186	116830205	116830189	-
SEQ ID NO 5736	CCTAAGCCTGAAGAATGAGG	GGG	chr11	116830185	116830204	116830188	-
SEQ ID NO 5737	CTAAGCCTGAAGAATGAGGG	GGG	chr11	116830184	116830203	116830187	-
SEQ ID NO 5738	ATGAGGGGGGAACCTGCACT	TGG	chr11	116830171	116830190	116830174	-
SEQ ID NO 5739	GAGGGGGGAACCTGCACTTG	GAG	chr11	116830169	116830188	116830172	-
SEQ ID NO 5740	CCTGCACTTGGAGCCACTTC	CAG	chr11	116830159	116830178	116830162	-
SEQ ID NO 5741	TTCCAGCCCCACCCCCTGTG	TAG	chr11	116830142	116830161	116830145	-
SEQ ID NO 5742	CCCCACCCCCTGTGTAGCTT	TGG	chr11	116830136	116830155	116830139	-
SEQ ID NO 5743	CCCACCCCCTGTGTAGCTTT	GGG	chr11	116830135	116830154	116830138	-
SEQ ID NO 5744	CCCCCTGTGTAGCTTTGGGC	AAG	chr11	116830131	116830150	116830134	-
SEQ ID NO 5745	TGGGCAAGTGACACCCCTCC	CGG	chr11	116830116	116830135	116830119	-
SEQ ID NO 5746	GGGCAAGTGACACCCCTCCC	GGG	chr11	116830115	116830134	116830118	-
SEQ ID NO 5747	TCCCGGGCCTCCATGTTCTT	CAG	chr11	116830099	116830118	116830102	-
SEQ ID NO 5748	CCCGGGCCTCCATGTTCTTC	AGG	chr11	116830098	116830117	116830101	-
SEQ ID NO 5749	CATGTTCTTCAGGTTATGAT	GAG	chr11	116830088	116830107	116830091	-
SEQ ID NO 5750	ATGTTCTTCAGGTTATGATG	AGG	chr11	116830087	116830106	116830090	-
SEQ ID NO 5751	TGTTCTTCAGGTTATGATGA	GGG	chr11	116830086	116830105	116830089	-
SEQ ID NO 5752	GTTCTTCAGGTTATGATGAG	GGG	chr11	116830085	116830104	116830088	-
SEQ ID NO 5753	CTTCAGGTTATGATGAGGGG	TGG	chr11	116830082	116830101	116830085	-
SEQ ID NO 5754	TTCAGGTTATGATGAGGGGT	GGG	chr11	116830081	116830100	116830084	-
SEQ ID NO 5755	TCAGGTTATGATGAGGGGTG	GGG	chr11	116830080	116830099	116830083	-
SEQ ID NO 5756	CAGGTTATGATGAGGGGTGG	GGG	chr11	116830079	116830098	116830082	-
SEQ ID NO 5757	AGGTTATGATGAGGGGTGGG	GGG	chr11	116830078	116830097	116830081	-
SEQ ID NO 5758	AGGGGTGGGGGGCACCCGTC	CAG	chr11	116830067	116830086	116830070	-
SEQ ID NO 5759	GGGGGCACCCGTCCAGCTCC	GAG	chr11	116830060	116830079	116830063	-
SEQ ID NO 5760	GGGGCACCCGTCCAGCTCCG	AGG	chr11	116830059	116830078	116830062	-
SEQ ID NO 5761	GTCCAGCTCCGAGGCTTCCT	TAG	chr11	116830050	116830069	116830053	-
SEQ ID NO 5762	CTCCGAGGCTTCCTTAGCTC	TAG	chr11	116830044	116830063	116830047	-
SEQ ID NO 5763	GAGGCTTCCTTAGCTCTAGC	AAG	chr11	116830040	116830059	116830043	-
SEQ ID NO 5764	AGCTCTAGCAAGTGCTTCTC	CAG	chr11	116830029	116830048	116830032	-
SEQ ID NO 5765	GCTCTAGCAAGTGCTTCTCC	AGG	chr11	116830028	116830047	116830031	-
SEQ ID NO 5766	AAGTGCTTCTCCAGGCTTGC	TGG	chr11	116830020	116830039	116830023	-
SEQ ID NO 5767	GCTTCTCCAGGCTTGCTGGC	TGG	chr11	116830016	116830035	116830019	-
SEQ ID NO 5768	CTTCTCCAGGCTTGCTGGCT	GGG	chr11	116830015	116830034	116830018	-
SEQ ID NO 5769	TCCAGGCTTGCTGGCTGGGC	TGG	chr11	116830011	116830030	116830014	-
SEQ ID NO 5770	CCAGGCTTGCTGGCTGGGCT	GGG	chr11	116830010	116830029	116830013	-
SEQ ID NO 5771	GGCTTGCTGGCTGGGCTGGG	CAG	chr11	116830007	116830026	116830010	-
SEQ ID NO 5772	GCTTGCTGGCTGGGCTGGGC	AGG	chr11	116830006	116830025	116830009	-
SEQ ID NO 5773	CTTGCTGGCTGGGCTGGGCA	GGG	chr11	116830005	116830024	116830008	-

SEQ ID NO 5774	TGCTGGCTGGGCTGGGCAGG	GAG	chr11	116830003	116830022	116830006	-
SEQ ID NO 5775	CCCCTCCTCTTTCCCCTCCC	CAG	chr11	116829954	116829973	116829957	-
SEQ ID NO 5776	CCTCCTCTTTCCCCTCCCCA	GAG	chr11	116829952	116829971	116829955	-
SEQ ID NO 5777	CTCCTCTTTCCCCTCCCCAG	AGG	chr11	116829951	116829970	116829954	-
SEQ ID NO 5778	TCCTCTTTCCCCTCCCCAGA	GGG	chr11	116829950	116829969	116829953	-
SEQ ID NO 5779	CCTCCCCAGAGGGCATTACC	TGG	chr11	116829940	116829959	116829943	-
SEQ ID NO 5780	TCCCCAGAGGGCATTACCTG	GAG	chr11	116829938	116829957	116829941	-
SEQ ID NO 5781	CCAGAGGGCATTACCTGGAG	CAG	chr11	116829935	116829954	116829938	-
SEQ ID NO 5782	TTACCTGGAGCAGCTGCCTC	TAG	chr11	116829925	116829944	116829928	-
SEQ ID NO 5783	TACCTGGAGCAGCTGCCTCT	AGG	chr11	116829924	116829943	116829927	-
SEQ ID NO 5784	ACCTGGAGCAGCTGCCTCTA	GGG	chr11	116829923	116829942	116829926	-
SEQ ID NO 5785	GCTGCCTCTAGGGATGAACT	GAG	chr11	116829913	116829932	116829916	-
SEQ ID NO 5786	GCCTCTAGGGATGAACTGAG	CAG	chr11	116829910	116829929	116829913	-
SEQ ID NO 5787	CTAGGGATGAACTGAGCAGA	CAG	chr11	116829906	116829925	116829909	-
SEQ ID NO 5788	TAGGGATGAACTGAGCAGAC	AGG	chr11	116829905	116829924	116829908	-
SEQ ID NO 5789	GGATGAACTGAGCAGACAGG	CAG	chr11	116829902	116829921	116829905	-
SEQ ID NO 5790	GATGAACTGAGCAGACAGGC	AGG	chr11	116829901	116829920	116829904	-
SEQ ID NO 5791	TGAACTGAGCAGACAGGCAG	GAG	chr11	116829899	116829918	116829902	-
SEQ ID NO 5792	GAACTGAGCAGACAGGCAGG	AGG	chr11	116829898	116829917	116829901	-
SEQ ID NO 5793	AACTGAGCAGACAGGCAGGA	GGG	chr11	116829897	116829916	116829900	-
SEQ ID NO 5794	GACCTGTTTTATATCATCTC	CAG	chr11	116829870	116829889	116829873	-
SEQ ID NO 5795	ACCTGTTTTATATCATCTCC	AGG	chr11	116829869	116829888	116829872	-
SEQ ID NO 5796	CCTGTTTTATATCATCTCCA	GGG	chr11	116829868	116829887	116829871	-
SEQ ID NO 5797	GTTTTATATCATCTCCAGGG	CAG	chr11	116829865	116829884	116829868	-
SEQ ID NO 5798	TTATATCATCTCCAGGGCAG	CAG	chr11	116829862	116829881	116829865	-
SEQ ID NO 5799	TATATCATCTCCAGGGCAGC	AGG	chr11	116829861	116829880	116829864	-
SEQ ID NO 5800	TCTCCAGGGCAGCAGGCACT	GAG	chr11	116829854	116829873	116829857	-
SEQ ID NO 5801	CTCCAGGGCAGCAGGCACTG	AGG	chr11	116829853	116829872	116829856	-
SEQ ID NO 5802	GGCAGCAGGCACTGAGGACC	CAG	chr11	116829847	116829866	116829850	-
SEQ ID NO 5803	GCAGCAGGCACTGAGGACCC	AGG	chr11	116829846	116829865	116829849	-
SEQ ID NO 5804	CAGCAGGCACTGAGGACCCA	GGG	chr11	116829845	116829864	116829848	-
SEQ ID NO 5805	GCACTGAGGACCCAGGGCGC	TGG	chr11	116829839	116829858	116829842	-
SEQ ID NO 5806	CACTGAGGACCCAGGGCGCT	GGG	chr11	116829838	116829857	116829841	-
SEQ ID NO 5807	AGGACCCAGGGCGCTGGGCA	AAG	chr11	116829833	116829852	116829836	-
SEQ ID NO 5808	GGACCCAGGGCGCTGGGCAA	AGG	chr11	116829832	116829851	116829835	-
SEQ ID NO 5809	GGCAAAGGTCACCTGCTGAC	CAG	chr11	116829817	116829836	116829820	-
SEQ ID NO 5810	AAAGGTCACCTGCTGACCAG	TGG	chr11	116829814	116829833	116829817	-
SEQ ID NO 5811	AGGTCACCTGCTGACCAGTG	GAG	chr11	116829812	116829831	116829815	-
SEQ ID NO 5812	ACCTGCTGACCAGTGGAGAT	GAG	chr11	116829807	116829826	116829810	-
SEQ ID NO 5813	CCTGCTGACCAGTGGAGATG	AGG	chr11	116829806	116829825	116829809	-
SEQ ID NO 5814	CTGCTGACCAGTGGAGATGA	GGG	chr11	116829805	116829824	116829808	-
SEQ ID NO 5815	ACCAGTGGAGATGAGGGCCT	GAG	chr11	116829799	116829818	116829802	-
SEQ ID NO 5816	CCAGTGGAGATGAGGGCCTG	AGG	chr11	116829798	116829817	116829801	-
SEQ ID NO 5817	GTGGAGATGAGGGCCTGAGG	CAG	chr11	116829795	116829814	116829798	-
SEQ ID NO 5818	TGGAGATGAGGGCCTGAGGC	AGG	chr11	116829794	116829813	116829797	-
SEQ ID NO 5819	GGAGATGAGGGCCTGAGGCA	GGG	chr11	116829793	116829812	116829796	-
SEQ ID NO 5820	AGGGCCTGAGGCAGGGTGTC	CAG	chr11	116829786	116829805	116829789	-
SEQ ID NO 5821	TGAGGCAGGGTGTCCAGATG	CAG	chr11	116829780	116829799	116829783	-
SEQ ID NO 5822	GCAGGGTGTCCAGATGCAGC	AAG	chr11	116829776	116829795	116829779	-

SEQ ID NO 5823	GGGTGTCCAGATGCAGCAAG	CGG	chr11	116829773	116829792	116829776	-
SEQ ID NO 5824	GGTGTCCAGATGCAGCAAGC	GGG	chr11	116829772	116829791	116829775	-
SEQ ID NO 5825	GTCCAGATGCAGCAAGCGGG	CGG	chr11	116829769	116829788	116829772	-
SEQ ID NO 5826	TCCAGATGCAGCAAGCGGGC	GGG	chr11	116829768	116829787	116829771	-
SEQ ID NO 5827	CAGATGCAGCAAGCGGGCGG	GAG	chr11	116829766	116829785	116829769	-
SEQ ID NO 5828	GATGCAGCAAGCGGGCGGGA	GAG	chr11	116829764	116829783	116829767	-
SEQ ID NO 5829	CAGCAAGCGGGCGGGAGAGT	TGG	chr11	116829760	116829779	116829763	-
SEQ ID NO 5830	AGCAAGCGGGCGGGAGAGTT	GGG	chr11	116829759	116829778	116829762	-
SEQ ID NO 5831	CGGGAGAGTTGGGAAATCCC	TAG	chr11	116829749	116829768	116829752	-
SEQ ID NO 5832	GGGAGAGTTGGGAAATCCCT	AGG	chr11	116829748	116829767	116829751	-
SEQ ID NO 5833	GAGAGTTGGGAAATCCCTAG	GAG	chr11	116829746	116829765	116829749	-
SEQ ID NO 5834	TGGGAAATCCCTAGGAGACT	GAG	chr11	116829740	116829759	116829743	-

Figure 20

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 5835	GGTGACCTTTGCCCAGCGCC	CTGGGT	chr11	116829824	116829843	116829840	+
SEQ ID NO 5836	GAGGGGAAAGAGGAGGGGAG	GAGGAT	chr11	116829956	116829975	116829972	+
SEQ ID NO 5837	TAAGGAAGCCTCGGAGCTGG	ACGGGT	chr11	116830048	116830067	116830064	+
SEQ ID NO 5838	GAAGAACATGGAGGCCCGGG	AGGGGT	chr11	116830098	116830117	116830114	+
SEQ ID NO 5839	CACTTGCCCAAAGCTACACA	GGGGGT	chr11	116830126	116830145	116830142	+
SEQ ID NO 5840	GTGCCTTGATGTTCAGTCTG	GTGGGT	chr11	116830333	116830352	116830349	+
SEQ ID NO 5841	GCCACGCCACCTCCCCAGGG	AGGGGT	chr11	116830495	116830514	116830511	+
SEQ ID NO 5842	GGTCCAGAGGCATGGGGACC	TGGGGT	chr11	116830518	116830537	116830534	+
SEQ ID NO 5843	AACAGAGGTGCCATGCAGCC	CCGGGT	chr11	116830571	116830590	116830587	+
SEQ ID NO 5844	TGGTGGGACTGGGCTGGGGG	CAGGGT	chr11	116830647	116830666	116830663	+
SEQ ID NO 5845	GCGCCAGGAGGGCAACAACA	AGGAGT	chr11	116830603	116830622	116830606	-
SEQ ID NO 5846	CCCCTAAGGTAGAACCTTAG	CTGGGT	chr11	116830476	116830495	116830479	-
SEQ ID NO 5847	CCTTAGCTGGGTCTGCCAGA	AGGAGT	chr11	116830462	116830481	116830465	-
SEQ ID NO 5848	AGGGGGACTGGTGAGGGGCG	AGGGAT	chr11	116830402	116830421	116830405	-
SEQ ID NO 5849	GGATCGAGGCCCAAAGGGAG	GTGGGT	chr11	116830380	116830399	116830383	-
SEQ ID NO 5850	GAGGCCCAAAGGGAGGTGGG	TGGGAT	chr11	116830375	116830394	116830378	-
SEQ ID NO 5851	AGCCAACATGCTGTGTGTCT	TTGGGT	chr11	116830283	116830302	116830286	-
SEQ ID NO 5852	CAGGCCTCAGTTTCCCTGTC	TGGGGT	chr11	116830241	116830260	116830244	-
SEQ ID NO 5853	TTCCTCCAGCCCTAAGCCTG	AAGAAT	chr11	116830195	116830214	116830198	-
SEQ ID NO 5854	ATGTTCTTCAGGTTATGATG	AGGGGT	chr11	116830087	116830106	116830090	-
SEQ ID NO 5855	TACCTGGAGCAGCTGCCTCT	AGGGAT	chr11	116829924	116829943	116829927	-
SEQ ID NO 5856	TGAACTGAGCAGACAGGCAG	GAGGGT	chr11	116829899	116829918	116829902	-
SEQ ID NO 5857	GTGGAGATGAGGGCCTGAGG	CAGGGT	chr11	116829795	116829814	116829798	-
SEQ ID NO 5858	CAGATGCAGCAAGCGGGCGG	GAGAGT	chr11	116829766	116829785	116829769	-
SEQ ID NO 5859	GTTGGGAAATCCCTAGGAGA	CTGAGT	chr11	116829742	116829761	116829745	-

Figure 21

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 5860	AAACTGAGGCCTGGAGAGGG	CCAGAAA	chr11	116830248	116830267	116830264	+
SEQ ID NO 5861	AGGGAGGTGGGTGGGATGGA	GCAGAAA	chr11	116830366	116830385	116830369	-
SEQ ID NO 5862	CTTCCTCCAGCCCTAAGCCT	GAAGAAT	chr11	116830196	116830215	116830199	-

Figure 22

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 5863	CTGCTGCCCTGGAGATGATA	TAAAAC	chr11	116829859	116829878	116829875	+
SEQ ID NO 5864	GAGGTGGGTGGGATGGAGCA	GAAAAC	chr11	116830363	116830382	116830366	-

Figure 23

#	Sequence	PAM	Chr	Start	End	Cuts 5' of	Str
SEQ ID NO 5865	AGGGATTTCCCAACTCTCCC	GCCCGCTT	chr11	116829748	116829767	116829764	+
SEQ ID NO 5866	GCAGGTTCCCCCCTCATTCT	TCAGGCTT	chr11	116830174	116830193	116830190	+
SEQ ID NO 5867	GTGCCTTGATGTTCAGTCTG	GTGGGTTT	chr11	116830333	116830352	116830349	+
SEQ ID NO 5868	GCCCCCAGCCCAGTCCCACC	AAGTGCTT	chr11	116830648	116830667	116830651	-
SEQ ID NO 5869	CCAACATGCTGTGTGTCTTT	GGGTGATT	chr11	116830281	116830300	116830284	-
SEQ ID NO 5870	ATTTCTGGCCCTCTCCAGGC	CTCAGTTT	chr11	116830256	116830275	116830259	-
SEQ ID NO 5871	TGGGGTAGGACTGGGCTGTC	TAAGGCTT	chr11	116830221	116830240	116830224	-
SEQ ID NO 5872	ACTTCCAGCCCCACCCCCTG	TGTAGCTT	chr11	116830144	116830163	116830147	-
SEQ ID NO 5873	GGGGGGCACCCGTCCAGCTC	CGAGGCTT	chr11	116830061	116830080	116830064	-
SEQ ID NO 5874	GAGGCTTCCTTAGCTCTAGC	AAGTGCTT	chr11	116830040	116830059	116830043	-
SEQ ID NO 5875	TAGCTCTAGCAAGTGCTTCT	CCAGGCTT	chr11	116830030	116830049	116830033	-
SEQ ID NO 5876	AGACAGGCAGGAGGGTTCTG	ACCTGTTT	chr11	116829889	116829908	116829892	-

Figure 24

#	Sequence	PAM	Chr	Start	End	Cut site 1 (5' of)	Cut site 2 (5' of)	Str
SEQ ID NO 5877	AGTCTCCTAGGGATTTCCCAAC	CTC	chr11	116829740	116829761	116829757	116829762	+
SEQ ID NO 5878	CTAGGGATTTCCCAACTCTCCC	CTC	chr11	116829746	116829767	116829763	116829768	+
SEQ ID NO 5879	GGGATTTCCCAACTCTCCCGCC	CTA	chr11	116829749	116829770	116829766	116829771	+
SEQ ID NO 5880	CCCAACTCTCCCGCCCGCTTGC	TTT	chr11	116829756	116829777	116829773	116829778	+
SEQ ID NO 5881	CCAACTCTCCCGCCCGCTTGCT	TTC	chr11	116829757	116829778	116829774	116829779	+
SEQ ID NO 5882	TCCCGCCCGCTTGCTGCATCTG	CTC	chr11	116829764	116829785	116829781	116829786	+
SEQ ID NO 5883	CCGCCCGCTTGCTGCATCTGGA	CTC	chr11	116829766	116829787	116829783	116829788	+
SEQ ID NO 5884	GCTGCATCTGGACACCCTGCCT	CTT	chr11	116829776	116829797	116829793	116829798	+
SEQ ID NO 5885	CTGCATCTGGACACCCTGCCTC	TTG	chr11	116829777	116829798	116829794	116829799	+
SEQ ID NO 5886	CATCTGGACACCCTGCCTCAGG	CTG	chr11	116829780	116829801	116829797	116829802	+
SEQ ID NO 5887	GACACCCTGCCTCAGGCCCTCA	CTG	chr11	116829786	116829807	116829803	116829808	+
SEQ ID NO 5888	CCTCAGGCCCTCATCTCCACTG	CTG	chr11	116829795	116829816	116829812	116829817	+
SEQ ID NO 5889	AGGCCCTCATCTCCACTGGTCA	CTC	chr11	116829799	116829820	116829816	116829821	+
SEQ ID NO 5890	ATCTCCACTGGTCAGCAGGTGA	CTC	chr11	116829807	116829828	116829824	116829829	+
SEQ ID NO 5891	CACTGGTCAGCAGGTGACCTTT	CTC	chr11	116829812	116829833	116829829	116829834	+
SEQ ID NO 5892	GTCAGCAGGTGACCTTTGCCCA	CTG	chr11	116829817	116829838	116829834	116829839	+
SEQ ID NO 5893	TGCCCAGCGCCCTGGGTCCTCA	CTT	chr11	116829833	116829854	116829850	116829855	+
SEQ ID NO 5894	GCCCAGCGCCCTGGGTCCTCAG	TTT	chr11	116829834	116829855	116829851	116829856	+
SEQ ID NO 5895	CCCAGCGCCCTGGGTCCTCAGT	TTG	chr11	116829835	116829856	116829852	116829857	+
SEQ ID NO 5896	GGTCCTCAGTGCCTGCTGCCCT	CTG	chr11	116829847	116829868	116829864	116829869	+
SEQ ID NO 5897	AGTGCCTGCTGCCCTGGAGATG	CTC	chr11	116829854	116829875	116829871	116829876	+
SEQ ID NO 5898	CTGCCCTGGAGATGATATAAAA	CTG	chr11	116829862	116829883	116829879	116829884	+
SEQ ID NO 5899	CCCTGGAGATGATATAAAACAG	CTG	chr11	116829865	116829886	116829882	116829887	+
SEQ ID NO 5900	GAGATGATATAAAACAGGTCAG	CTG	chr11	116829870	116829891	116829887	116829892	+
SEQ ID NO 5901	CTGCCTGTCTGCTCAGTTCATC	CTC	chr11	116829899	116829920	116829916	116829921	+
SEQ ID NO 5902	CCTGTCTGCTCAGTTCATCCCT	CTG	chr11	116829902	116829923	116829919	116829924	+
SEQ ID NO 5903	TCTGCTCAGTTCATCCCTAGAG	CTG	chr11	116829906	116829927	116829923	116829928	+
SEQ ID NO 5904	CTCAGTTCATCCCTAGAGGCAG	CTG	chr11	116829910	116829931	116829927	116829932	+
SEQ ID NO 5905	AGTTCATCCCTAGAGGCAGCTG	CTC	chr11	116829913	116829934	116829930	116829935	+
SEQ ID NO 5906	ATCCCTAGAGGCAGCTGCTCCA	TTC	chr11	116829918	116829939	116829935	116829940	+
SEQ ID NO 5907	GAGGCAGCTGCTCCAGGTAATG	CTA	chr11	116829925	116829946	116829942	116829947	+
SEQ ID NO 5908	CTCCAGGTAATGCCCTCTGGGG	CTG	chr11	116829935	116829956	116829952	116829957	+
SEQ ID NO 5909	CAGGTAATGCCCTCTGGGGAGG	CTC	chr11	116829938	116829959	116829955	116829960	+
SEQ ID NO 5910	TGGGGAGGGGAAAGAGGAGGGG	CTC	chr11	116829952	116829973	116829969	116829974	+
SEQ ID NO 5911	GGGAGGGGAAAGAGGAGGGGAG	CTG	chr11	116829954	116829975	116829971	116829976	+
SEQ ID NO 5912	CCTGCCCAGCCCAGCCAGCAAG	CTC	chr11	116830003	116830024	116830020	116830025	+
SEQ ID NO 5913	CCCAGCCCAGCCAGCAAGCCTG	CTG	chr11	116830007	116830028	116830024	116830029	+
SEQ ID NO 5914	GAGAAGCACTTGCTAGAGCTAA	CTG	chr11	116830029	116830050	116830046	116830051	+
SEQ ID NO 5915	GCTAGAGCTAAGGAAGCCTCGG	CTT	chr11	116830040	116830061	116830057	116830062	+
SEQ ID NO 5916	CTAGAGCTAAGGAAGCCTCGGA	TTG	chr11	116830041	116830062	116830058	116830063	+
SEQ ID NO 5917	GAGCTAAGGAAGCCTCGGAGCT	CTA	chr11	116830044	116830065	116830061	116830066	+
SEQ ID NO 5918	AGGAAGCCTCGGAGCTGGACGG	CTA	chr11	116830050	116830071	116830067	116830072	+
SEQ ID NO 5919	GGAGCTGGACGGGTGCCCCCCA	CTC	chr11	116830060	116830081	116830077	116830082	+
SEQ ID NO 5920	GACGGGTGCCCCCCACCCCTCA	CTG	chr11	116830067	116830088	116830084	116830089	+
SEQ ID NO 5921	ATCATAACCTGAAGAACATGGA	CTC	chr11	116830088	116830109	116830105	116830110	+
SEQ ID NO 5922	AAGAACATGGAGGCCCGGGAGG	CTG	chr11	116830099	116830120	116830116	116830121	+
SEQ ID NO 5923	GCCCAAAGCTACACAGGGGGTG	CTT	chr11	116830131	116830152	116830148	116830153	+
SEQ ID NO 5924	CCCAAAGCTACACAGGGGGTGG	TTG	chr11	116830132	116830153	116830149	116830154	+
SEQ ID NO 5925	CACAGGGGGTGGGGCTGGAAGT	CTA	chr11	116830142	116830163	116830159	116830164	+
SEQ ID NO 5926	GAAGTGGCTCCAAGTGCAGGTT	CTG	chr11	116830159	116830180	116830176	116830181	+
SEQ ID NO 5927	CAAGTGCAGGTTCCCCCCTCAT	CTC	chr11	116830169	116830190	116830186	116830191	+
SEQ ID NO 5928	CCCCCTCATTCTTCAGGCTTAG	TTC	chr11	116830182	116830203	116830199	116830204	+
SEQ ID NO 5929	ATTCTTCAGGCTTAGGGCTGGA	CTC	chr11	116830189	116830210	116830206	116830211	+
SEQ ID NO 5930	TTCAGGCTTAGGGCTGGAGGAA	TTC	chr11	116830193	116830214	116830210	116830215	+
SEQ ID NO 5931	CAGGCTTAGGGCTGGAGGAAGC	CTT	chr11	116830195	116830216	116830212	116830217	+
SEQ ID NO 5932	AGGCTTAGGGCTGGAGGAAGCC	TTC	chr11	116830196	116830217	116830213	116830218	+
SEQ ID NO 5933	AGGGCTGGAGGAAGCCTTAGAC	CTT	chr11	116830202	116830223	116830219	116830224	+
SEQ ID NO 5934	GGGCTGGAGGAAGCCTTAGACA	TTA	chr11	116830203	116830224	116830220	116830225	+
SEQ ID NO 5935	GAGGAAGCCTTAGACAGCCCAG	CTG	chr11	116830209	116830230	116830226	116830231	+

SEQ ID NO 5936	AGACAGCCCAGTCCTACCCCAG	CTT	chr11	116830220	116830241	116830237	116830242	+
SEQ ID NO 5937	GACAGCCCAGTCCTACCCCAGA	TTA	chr11	116830221	116830242	116830238	116830243	+
SEQ ID NO 5938	CCCCAGACAGGGAAACTGAGGC	CTA	chr11	116830236	116830257	116830253	116830258	+
SEQ ID NO 5939	AGGCCTGGAGAGGGCCAGAAAT	CTG	chr11	116830254	116830275	116830271	116830276	+
SEQ ID NO 5940	GAGAGGGCCAGAAATCACCCAA	CTG	chr11	116830261	116830282	116830278	116830283	+
SEQ ID NO 5941	GCTGGACTGGACGGAGATCAGT	TTG	chr11	116830300	116830321	116830317	116830322	+
SEQ ID NO 5942	GACTGGACGGAGATCAGTCCAG	CTG	chr11	116830304	116830325	116830321	116830326	+
SEQ ID NO 5943	GACGGAGATCAGTCCAGACCGC	CTG	chr11	116830309	116830330	116830326	116830331	+
SEQ ID NO 5944	GATGTTCAGTCTGGTGGGTTTT	CTT	chr11	116830340	116830361	116830357	116830362	+
SEQ ID NO 5945	ATGTTCAGTCTGGTGGGTTTTC	TTG	chr11	116830341	116830362	116830358	116830363	+
SEQ ID NO 5946	AGTCTGGTGGGTTTTCTGCTCC	TTC	chr11	116830347	116830368	116830364	116830369	+
SEQ ID NO 5947	GTGGGTTTTCTGCTCCATCCCA	CTG	chr11	116830353	116830374	116830370	116830375	+
SEQ ID NO 5948	TCTGCTCCATCCCACCCACCTC	TTT	chr11	116830361	116830382	116830378	116830383	+
SEQ ID NO 5949	CTGCTCCATCCCACCCACCTCC	TTT	chr11	116830362	116830383	116830379	116830384	+
SEQ ID NO 5950	TGCTCCATCCCACCCACCTCCC	TTC	chr11	116830363	116830384	116830380	116830385	+
SEQ ID NO 5951	CTCCATCCCACCCACCTCCCTT	CTG	chr11	116830365	116830386	116830382	116830387	+
SEQ ID NO 5952	CATCCCACCCACCTCCCTTTGG	CTC	chr11	116830368	116830389	116830385	116830390	+
SEQ ID NO 5953	CCTTTGGGCCTCGATCCCTCGC	CTC	chr11	116830383	116830404	116830400	116830405	+
SEQ ID NO 5954	TGGGCCTCGATCCCTCGCCCCT	CTT	chr11	116830387	116830408	116830404	116830409	+
SEQ ID NO 5955	GGGCCTCGATCCCTCGCCCCTC	TTT	chr11	116830388	116830409	116830405	116830410	+
SEQ ID NO 5956	GGCCTCGATCCCTCGCCCCTCA	TTG	chr11	116830389	116830410	116830406	116830411	+
SEQ ID NO 5957	GATCCCTCGCCCCTCACCAGTC	CTC	chr11	116830395	116830416	116830412	116830417	+
SEQ ID NO 5958	GCCCCTCACCAGTCCCCCTTCT	CTC	chr11	116830403	116830424	116830420	116830425	+
SEQ ID NO 5959	ACCAGTCCCCCTTCTGAGAGCC	CTC	chr11	116830410	116830431	116830427	116830432	+
SEQ ID NO 5960	CTGAGAGCCCGTATTAGCAGGG	CTT	chr11	116830423	116830444	116830440	116830445	+
SEQ ID NO 5961	TGAGAGCCCGTATTAGCAGGGA	TTC	chr11	116830424	116830445	116830441	116830446	+
SEQ ID NO 5962	AGAGCCCGTATTAGCAGGGAGC	CTG	chr11	116830426	116830447	116830443	116830448	+
SEQ ID NO 5963	GCAGGGAGCCGGCCCCTACTCC	TTA	chr11	116830439	116830460	116830456	116830461	+
SEQ ID NO 5964	CTCCTTCTGGCAGACCCAGCTA	CTA	chr11	116830457	116830478	116830474	116830479	+
SEQ ID NO 5965	CTTCTGGCAGACCCAGCTAAGG	CTC	chr11	116830460	116830481	116830477	116830482	+
SEQ ID NO 5966	CTGGCAGACCCAGCTAAGGTTC	CTT	chr11	116830463	116830484	116830480	116830485	+
SEQ ID NO 5967	TGGCAGACCCAGCTAAGGTTCT	TTC	chr11	116830464	116830485	116830481	116830486	+
SEQ ID NO 5968	GCAGACCCAGCTAAGGTTCTAC	CTG	chr11	116830466	116830487	116830483	116830488	+
SEQ ID NO 5969	AGGTTCTACCTTAGGGGCCACG	CTA	chr11	116830479	116830500	116830496	116830501	+
SEQ ID NO 5970	TACCTTAGGGGCCACGCCACCT	TTC	chr11	116830485	116830506	116830502	116830507	+
SEQ ID NO 5971	CCTTAGGGGCCACGCCACCTCC	CTA	chr11	116830487	116830508	116830504	116830509	+
SEQ ID NO 5972	AGGGGCCACGCCACCTCCCCAG	CTT	chr11	116830491	116830512	116830508	116830513	+
SEQ ID NO 5973	GGGGCCACGCCACCTCCCCAGG	TTA	chr11	116830492	116830513	116830509	116830514	+
SEQ ID NO 5974	CCCAGGGAGGGGTCCAGAGGCA	CTC	chr11	116830508	116830529	116830525	116830530	+
SEQ ID NO 5975	GGGTGCCCCTCACAGGACACTT	CTG	chr11	116830540	116830561	116830557	116830562	+
SEQ ID NO 5976	ACAGGACACTTCCTTGCAGGAA	CTC	chr11	116830551	116830572	116830568	116830573	+
SEQ ID NO 5977	CCTTGCAGGAACAGAGGTGCCA	CTT	chr11	116830562	116830583	116830579	116830584	+
SEQ ID NO 5978	CTTGCAGGAACAGAGGTGCCAT	TTC	chr11	116830563	116830584	116830580	116830585	+
SEQ ID NO 5979	GCAGGAACAGAGGTGCCATGCA	CTT	chr11	116830566	116830587	116830583	116830588	+
SEQ ID NO 5980	CAGGAACAGAGGTGCCATGCAG	TTG	chr11	116830567	116830588	116830584	116830589	+
SEQ ID NO 5981	CTTGTTGTTGCCCTCCTGGCGC	CTC	chr11	116830601	116830622	116830618	116830623	+
SEQ ID NO 5982	GTTGTTGCCCTCCTGGCGCTCC	CTT	chr11	116830604	116830625	116830621	116830626	+
SEQ ID NO 5983	TTGTTGCCCTCCTGGCGCTCCT	TTG	chr11	116830605	116830626	116830622	116830627	+
SEQ ID NO 5984	TTGCCCTCCTGGCGCTCCTGGC	TTG	chr11	116830608	116830629	116830625	116830630	+
SEQ ID NO 5985	CCCTCCTGGCGCTCCTGGCCTC	TTG	chr11	116830611	116830632	116830628	116830633	+
SEQ ID NO 5986	CTGGCGCTCCTGGCCTCTGCCC	CTC	chr11	116830616	116830637	116830633	116830638	+
SEQ ID NO 5987	GCGCTCCTGGCCTCTGCCCGTA	CTG	chr11	116830619	116830640	116830636	116830641	+
SEQ ID NO 5988	CTGGCCTCTGCCCGTAAGCACT	CTC	chr11	116830625	116830646	116830642	116830647	+
SEQ ID NO 5989	GCCTCTGCCCGTAAGCACTTGG	CTG	chr11	116830628	116830649	116830645	116830650	+
SEQ ID NO 5990	TGCCCGTAAGCACTTGGTGGGA	CTC	chr11	116830633	116830654	116830650	116830655	+
SEQ ID NO 5991	CCCGTAAGCACTTGGTGGGACT	CTG	chr11	116830635	116830656	116830652	116830657	+
SEQ ID NO 5992	GGTGGGACTGGGCTGGGGGCAG	CTT	chr11	116830648	116830669	116830665	116830670	+
SEQ ID NO 5993	GTGGGACTGGGCTGGGGGCAGG	TTG	chr11	116830649	116830670	116830666	116830671	+
SEQ ID NO 5994	CCCCCAGCCCAGTCCCACCAAG	CTG	chr11	116830645	116830666	116830650	116830645	-
SEQ ID NO 5995	ACGGGCAGAGGCCAGGAGCGCC	CTT	chr11	116830618	116830639	116830623	116830618	-

SEQ ID NO 5996	CGGGCAGAGGCCAGGAGCGCCA	TTA	chr11	116830617	116830638	116830622	116830617	-
SEQ ID NO 5997	CATGGCACCTCTGTTCCTGCAA	CTG	chr11	116830564	116830585	116830569	116830564	-
SEQ ID NO 5998	TGTTCCTGCAAGGAAGTGTCCT	CTC	chr11	116830553	116830574	116830558	116830553	-
SEQ ID NO 5999	TTCCTGCAAGGAAGTGTCCTGT	CTG	chr11	116830551	116830572	116830556	116830551	-
SEQ ID NO 6000	CTGCAAGGAAGTGTCCTGTGAG	TTC	chr11	116830548	116830569	116830553	116830548	-
SEQ ID NO 6001	CAAGGAAGTGTCCTGTGAGGGG	CTG	chr11	116830545	116830566	116830550	116830545	-
SEQ ID NO 6002	TGAGGGGCACCCCAGGTCCCCA	CTG	chr11	116830530	116830551	116830535	116830530	-
SEQ ID NO 6003	TGGACCCCTCCCTGGGGAGGTG	CTC	chr11	116830502	116830523	116830507	116830502	-
SEQ ID NO 6004	GACCCCTCCCTGGGGAGGTGGC	CTG	chr11	116830500	116830521	116830505	116830500	-
SEQ ID NO 6005	CCTGGGGAGGTGGCGTGGCCCC	CTC	chr11	116830492	116830513	116830497	116830492	-
SEQ ID NO 6006	GGGAGGTGGCGTGGCCCCTAAG	CTG	chr11	116830488	116830509	116830493	116830488	-
SEQ ID NO 6007	AGGTAGAACCTTAGCTGGGTCT	CTA	chr11	116830468	116830489	116830473	116830468	-
SEQ ID NO 6008	AGCTGGGTCTGCCAGAAGGAGT	CTT	chr11	116830456	116830477	116830461	116830456	-
SEQ ID NO 6009	GCTGGGTCTGCCAGAAGGAGTA	TTA	chr11	116830455	116830476	116830460	116830455	-
SEQ ID NO 6010	GGTCTGCCAGAAGGAGTAGGGG	CTG	chr11	116830451	116830472	116830456	116830451	-
SEQ ID NO 6011	CCAGAAGGAGTAGGGGCCGGCT	CTG	chr11	116830445	116830466	116830450	116830445	-
SEQ ID NO 6012	CCTGCTAATACGGGCTCTCAGA	CTC	chr11	116830422	116830443	116830427	116830422	-
SEQ ID NO 6013	CTAATACGGGCTCTCAGAAGGG	CTG	chr11	116830418	116830439	116830423	116830418	-
SEQ ID NO 6014	ATACGGGCTCTCAGAAGGGGGA	CTA	chr11	116830415	116830436	116830420	116830415	-
SEQ ID NO 6015	TCAGAAGGGGGACTGGTGAGGG	CTC	chr11	116830405	116830426	116830410	116830405	-
SEQ ID NO 6016	AGAAGGGGGACTGGTGAGGGGC	CTC	chr11	116830403	116830424	116830408	116830403	-
SEQ ID NO 6017	GTGAGGGGCGAGGGATCGAGGC	CTG	chr11	116830390	116830411	116830395	116830390	-
SEQ ID NO 6018	AACATCAAGGCACCTGCGGTCT	CTG	chr11	116830324	116830345	116830329	116830324	-
SEQ ID NO 6019	CGGTCTGGACTGATCTCCGTCC	CTG	chr11	116830308	116830329	116830313	116830308	-
SEQ ID NO 6020	GACTGATCTCCGTCCAGTCCAG	CTG	chr11	116830301	116830322	116830306	116830301	-
SEQ ID NO 6021	ATCTCCGTCCAGTCCAGCCAAC	CTG	chr11	116830296	116830317	116830301	116830296	-
SEQ ID NO 6022	CGTCCAGTCCAGCCAACATGCT	CTC	chr11	116830291	116830312	116830296	116830291	-
SEQ ID NO 6023	TGTGTCTTTGGGTGATTTCTGG	CTG	chr11	116830268	116830289	116830273	116830268	-
SEQ ID NO 6024	TGGGTGATTTCTGGCCCTCTCC	CTT	chr11	116830260	116830281	116830265	116830260	-
SEQ ID NO 6025	GGGTGATTTCTGGCCCTCTCCA	TTT	chr11	116830259	116830280	116830264	116830259	-
SEQ ID NO 6026	GGTGATTTCTGGCCCTCTCCAG	TTG	chr11	116830258	116830279	116830263	116830258	-
SEQ ID NO 6027	CTGGCCCTCTCCAGGCCTCAGT	TTT	chr11	116830250	116830271	116830255	116830250	-
SEQ ID NO 6028	TGGCCCTCTCCAGGCCTCAGTT	TTC	chr11	116830249	116830270	116830254	116830249	-
SEQ ID NO 6029	GCCCTCTCCAGGCCTCAGTTTC	CTG	chr11	116830247	116830268	116830252	116830247	-
SEQ ID NO 6030	TCCAGGCCTCAGTTTCCCTGTC	CTC	chr11	116830241	116830262	116830246	116830241	-
SEQ ID NO 6031	CAGGCCTCAGTTTCCCTGTCTG	CTC	chr11	116830239	116830260	116830244	116830239	-
SEQ ID NO 6032	AGTTTCCCTGTCTGGGGTAGGA	CTC	chr11	116830231	116830252	116830236	116830231	-
SEQ ID NO 6033	CCCTGTCTGGGGTAGGACTGGG	TTT	chr11	116830226	116830247	116830231	116830226	-
SEQ ID NO 6034	CCTGTCTGGGGTAGGACTGGGC	TTC	chr11	116830225	116830246	116830230	116830225	-
SEQ ID NO 6035	TCTGGGGTAGGACTGGGCTGTC	CTG	chr11	116830221	116830242	116830226	116830221	-
SEQ ID NO 6036	GGGTAGGACTGGGCTGTCTAAG	CTG	chr11	116830217	116830238	116830222	116830217	-
SEQ ID NO 6037	GGCTGTCTAAGGCTTCCTCCAG	CTG	chr11	116830206	116830227	116830211	116830206	-
SEQ ID NO 6038	TCTAAGGCTTCCTCCAGCCCTA	CTG	chr11	116830201	116830222	116830206	116830201	-
SEQ ID NO 6039	AGGCTTCCTCCAGCCCTAAGCC	CTA	chr11	116830197	116830218	116830202	116830197	-
SEQ ID NO 6040	CCTCCAGCCCTAAGCCTGAAGA	CTT	chr11	116830191	116830212	116830196	116830191	-
SEQ ID NO 6041	CTCCAGCCCTAAGCCTGAAGAA	TTC	chr11	116830190	116830211	116830195	116830190	-
SEQ ID NO 6042	CAGCCCTAAGCCTGAAGAATGA	CTC	chr11	116830187	116830208	116830192	116830187	-
SEQ ID NO 6043	AGCCTGAAGAATGAGGGGGGAA	CTA	chr11	116830179	116830200	116830184	116830179	-
SEQ ID NO 6044	AAGAATGAGGGGGGAACCTGCA	CTG	chr11	116830173	116830194	116830178	116830173	-
SEQ ID NO 6045	CACTTGGAGCCACTTCCAGCCC	CTG	chr11	116830153	116830174	116830158	116830153	-
SEQ ID NO 6046	GGAGCCACTTCCAGCCCCACCC	CTT	chr11	116830148	116830169	116830153	116830148	-
SEQ ID NO 6047	GAGCCACTTCCAGCCCCACCCC	TTG	chr11	116830147	116830168	116830152	116830147	-
SEQ ID NO 6048	CCAGCCCCACCCCCTGTGTAGC	CTT	chr11	116830138	116830159	116830143	116830138	-
SEQ ID NO 6049	CAGCCCCACCCCCTGTGTAGCT	TTC	chr11	116830137	116830158	116830142	116830137	-
SEQ ID NO 6050	TGTAGCTTTGGGCAAGTGACAC	CTG	chr11	116830122	116830143	116830127	116830122	-
SEQ ID NO 6051	TGGGCAAGTGACACCCCTCCCG	CTT	chr11	116830114	116830135	116830119	116830114	-
SEQ ID NO 6052	GGGCAAGTGACACCCCTCCCGG	TTT	chr11	116830113	116830134	116830118	116830113	-
SEQ ID NO 6053	GGCAAGTGACACCCCTCCCGGG	TTG	chr11	116830112	116830133	116830117	116830112	-
SEQ ID NO 6054	CCGGGCCTCCATGTTCTTCAGG	CTC	chr11	116830095	116830116	116830100	116830095	-
SEQ ID NO 6055	CATGTTCTTCAGGTTATGATGA	CTC	chr11	116830086	116830107	116830091	116830086	-

SEQ ID NO 6056	TTCAGGTTATGATGAGGGGTGG	TTC	chr11	116830079	116830100	116830084	116830079	-
SEQ ID NO 6057	CAGGTTATGATGAGGGGTGGGG	CTT	chr11	116830077	116830098	116830082	116830077	-
SEQ ID NO 6058	AGGTTATGATGAGGGGTGGGGG	TTC	chr11	116830076	116830097	116830081	116830076	-
SEQ ID NO 6059	TGATGAGGGGTGGGGGGCACCC	TTA	chr11	116830070	116830091	116830075	116830070	-
SEQ ID NO 6060	CGAGGCTTCCTTAGCTCTAGCA	CTC	chr11	116830039	116830060	116830044	116830039	-
SEQ ID NO 6061	CCTTAGCTCTAGCAAGTGCTTC	CTT	chr11	116830031	116830052	116830036	116830031	-
SEQ ID NO 6062	CTTAGCTCTAGCAAGTGCTTCT	TTC	chr11	116830030	116830051	116830035	116830030	-
SEQ ID NO 6063	AGCTCTAGCAAGTGCTTCTCCA	CTT	chr11	116830027	116830048	116830032	116830027	-
SEQ ID NO 6064	GCTCTAGCAAGTGCTTCTCCAG	TTA	chr11	116830026	116830047	116830031	116830026	-
SEQ ID NO 6065	TAGCAAGTGCTTCTCCAGGCTT	CTC	chr11	116830022	116830043	116830027	116830022	-
SEQ ID NO 6066	GCAAGTGCTTCTCCAGGCTTGC	CTA	chr11	116830020	116830041	116830025	116830020	-
SEQ ID NO 6067	CTCCAGGCTTGCTGGCTGGGCT	CTT	chr11	116830010	116830031	116830015	116830010	-
SEQ ID NO 6068	TCCAGGCTTGCTGGCTGGGCTG	TTC	chr11	116830009	116830030	116830014	116830009	-
SEQ ID NO 6069	CAGGCTTGCTGGCTGGGCTGGG	CTC	chr11	116830007	116830028	116830012	116830007	-
SEQ ID NO 6070	GCTGGCTGGGCTGGGCAGGGAG	CTT	chr11	116830000	116830021	116830005	116830000	-
SEQ ID NO 6071	CTGGCTGGGCTGGGCAGGGAGC	TTG	chr11	116829999	116830020	116830004	116829999	-
SEQ ID NO 6072	GCTGGGCTGGGCAGGGAGCTCC	CTG	chr11	116829996	116830017	116830001	116829996	-
SEQ ID NO 6073	GGCTGGGCAGGGAGCTCCTCTT	CTG	chr11	116829992	116830013	116829997	116829992	-
SEQ ID NO 6074	GGCAGGGAGCTCCTCTTGCCCC	CTG	chr11	116829987	116830008	116829992	116829987	-
SEQ ID NO 6075	CTCTTGCCCCTCTTCATCCTCC	CTC	chr11	116829975	116829996	116829980	116829975	-
SEQ ID NO 6076	TTGCCCCTCTTCATCCTCCTCC	CTC	chr11	116829972	116829993	116829977	116829972	-
SEQ ID NO 6077	GCCCCTCTTCATCCTCCTCCCC	CTT	chr11	116829970	116829991	116829975	116829970	-
SEQ ID NO 6078	CCCCTCTTCATCCTCCTCCCCT	TTG	chr11	116829969	116829990	116829974	116829969	-
SEQ ID NO 6079	TTCATCCTCCTCCCCTCCTCTT	CTC	chr11	116829963	116829984	116829968	116829963	-
SEQ ID NO 6080	CATCCTCCTCCCCTCCTCTTTC	CTT	chr11	116829961	116829982	116829966	116829961	-
SEQ ID NO 6081	ATCCTCCTCCCCTCCTCTTTCC	TTC	chr11	116829960	116829981	116829965	116829960	-
SEQ ID NO 6082	CTCCCCTCCTCTTTCCCCTCCC	CTC	chr11	116829954	116829975	116829959	116829954	-
SEQ ID NO 6083	CCCTCCTCTTTCCCCTCCCCAG	CTC	chr11	116829951	116829972	116829956	116829951	-
SEQ ID NO 6084	CTCTTTCCCCTCCCCAGAGGGC	CTC	chr11	116829946	116829967	116829951	116829946	-
SEQ ID NO 6085	TTTCCCCTCCCCAGAGGGCATT	CTC	chr11	116829943	116829964	116829948	116829943	-
SEQ ID NO 6086	TCCCCTCCCCAGAGGGCATTAC	CTT	chr11	116829941	116829962	116829946	116829941	-
SEQ ID NO 6087	CCCCTCCCCAGAGGGCATTACC	TTT	chr11	116829940	116829961	116829945	116829940	-
SEQ ID NO 6088	CCCTCCCCAGAGGGCATTACCT	TTC	chr11	116829939	116829960	116829944	116829939	-
SEQ ID NO 6089	CCCAGAGGGCATTACCTGGAGC	CTC	chr11	116829934	116829955	116829939	116829934	-
SEQ ID NO 6090	CCTGGAGCAGCTGCCTCTAGGG	TTA	chr11	116829920	116829941	116829925	116829920	-
SEQ ID NO 6091	GAGCAGCTGCCTCTAGGGATGA	CTG	chr11	116829916	116829937	116829921	116829916	-
SEQ ID NO 6092	CCTCTAGGGATGAACTGAGCAG	CTG	chr11	116829907	116829928	116829912	116829907	-
SEQ ID NO 6093	TAGGGATGAACTGAGCAGACAG	CTC	chr11	116829903	116829924	116829908	116829903	-
SEQ ID NO 6094	GGGATGAACTGAGCAGACAGGC	CTA	chr11	116829901	116829922	116829906	116829901	-
SEQ ID NO 6095	AGCAGACAGGCAGGAGGGTTCT	CTG	chr11	116829890	116829911	116829895	116829890	-
SEQ ID NO 6096	TGACCTGTTTTATATCATCTCC	TTC	chr11	116829869	116829890	116829874	116829869	-
SEQ ID NO 6097	ACCTGTTTTATATCATCTCCAG	CTG	chr11	116829867	116829888	116829872	116829867	-
SEQ ID NO 6098	TTTTATATCATCTCCAGGGCAG	CTG	chr11	116829862	116829883	116829867	116829862	-
SEQ ID NO 6099	TATATCATCTCCAGGGCAGCAG	TTT	chr11	116829859	116829880	116829864	116829859	-
SEQ ID NO 6100	ATATCATCTCCAGGGCAGCAGG	TTT	chr11	116829858	116829879	116829863	116829858	-
SEQ ID NO 6101	TATCATCTCCAGGGCAGCAGGC	TTA	chr11	116829857	116829878	116829862	116829857	-
SEQ ID NO 6102	CAGGGCAGCAGGCACTGAGGAC	CTC	chr11	116829848	116829869	116829853	116829848	-
SEQ ID NO 6103	AGGACCCAGGGCGCTGGGCAAA	CTG	chr11	116829831	116829852	116829836	116829831	-
SEQ ID NO 6104	GGCAAAGGTCACCTGCTGACCA	CTG	chr11	116829815	116829836	116829820	116829815	-
SEQ ID NO 6105	CTGACCAGTGGAGATGAGGGCC	CTG	chr11	116829800	116829821	116829805	116829800	-
SEQ ID NO 6106	ACCAGTGGAGATGAGGGCCTGA	CTG	chr11	116829797	116829818	116829802	116829797	-
SEQ ID NO 6107	AGGCAGGGTGTCCAGATGCAGC	CTG	chr11	116829776	116829797	116829781	116829776	-
SEQ ID NO 6108	GGAAATCCCTAGGAGACTGAGT	TTG	chr11	116829736	116829757	116829741	116829736	-

Figure 25

#	Sequence	PAM	chr17	Start	End	Cuts 5' of	Str
SEQ ID NO 6109	TACCCCTTGCCCATCCCTGC	TGG	chr17	7108733	7108752	7108749	+
SEQ ID NO 6110	GGCCCCCGTGACCCTCACTT	TGG	chr17	7108754	7108773	7108770	+
SEQ ID NO 6111	GCCCCCGTGACCCTCACTTT	GGG	chr17	7108755	7108774	7108771	+
SEQ ID NO 6112	GTGACCCTCACTTTGGGACC	CAG	chr17	7108761	7108780	7108777	+
SEQ ID NO 6113	CACTTTGGGACCCAGTCACA	CAG	chr17	7108769	7108788	7108785	+
SEQ ID NO 6114	CCAGTCACACAGATGACCAC	CAG	chr17	7108780	7108799	7108796	+
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SEQ ID NO 6118	CCACCAGCAGCAGGATGTTG	AAG	chr17	7108796	7108815	7108812	+
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SEQ ID NO 6120	GCAGCAGGATGTTGAAGCTC	AGG	chr17	7108802	7108821	7108818	+
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SEQ ID NO 6199	ACGACTCAGGATATTCACAT	CAG	chr17	7109133	7109152	7109149	+
SEQ ID NO 6200	ATTCACATCAGCTGTGTGCA	AAG	chr17	7109145	7109164	7109161	+
SEQ ID NO 6201	CATCAGCTGTGTGCAAAGCC	CGG	chr17	7109150	7109169	7109166	+

DEMANDE OU BREVET VOLUMINEUX

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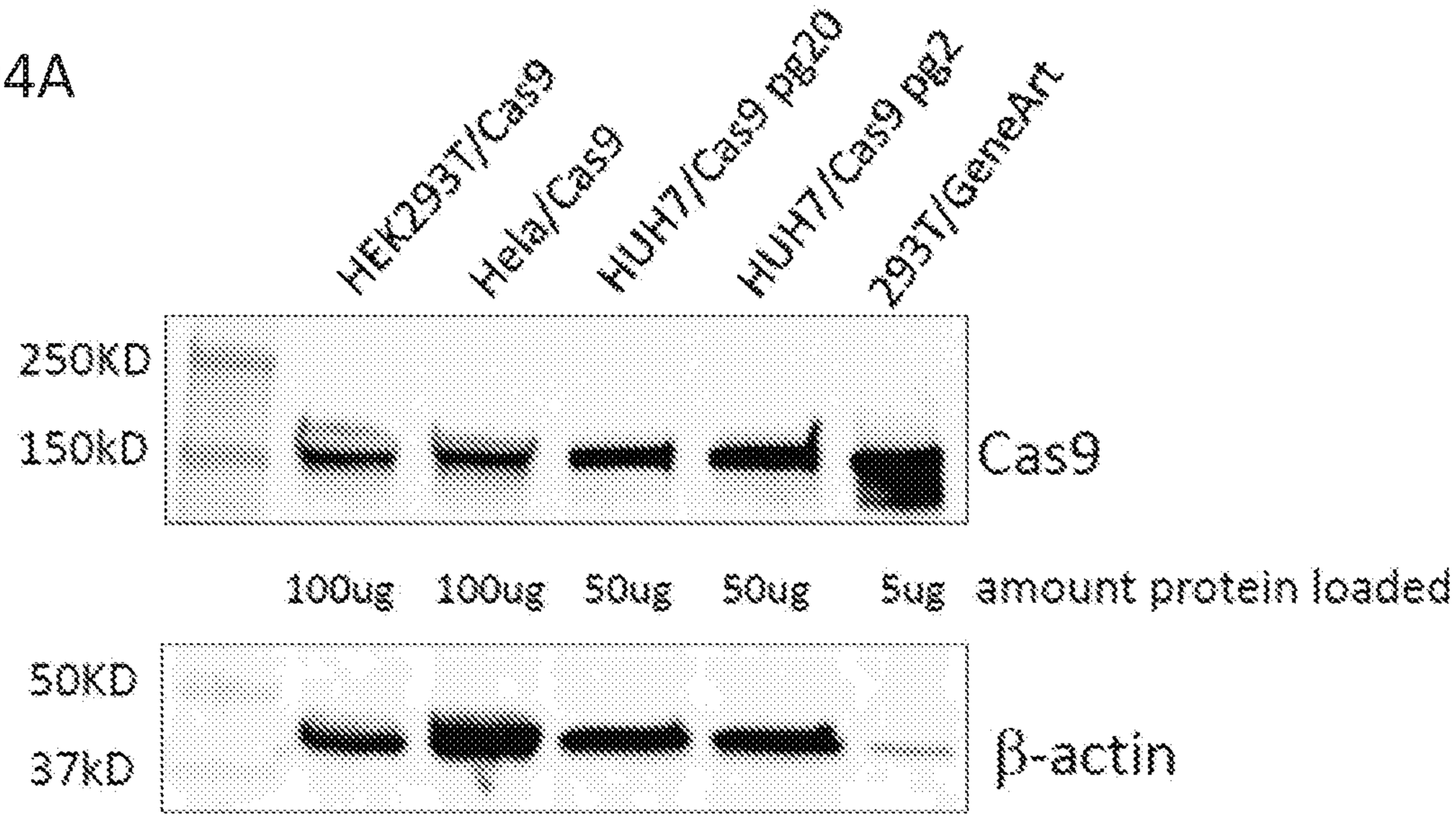
Fig. 94A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