ENGINEERED LEISHMANIA CELLS

[0001] This application claims priority to U.S. Provisional Application No. 62/958,088, filed on January 7, 2020, the entirety of which is incorporated herein by reference.

SEQUENCE LISTING

[0002] This application incorporates by reference in its entirety the Computer Readable Form (CRF) of a Sequence Listing in ASCII text format. The Sequence Listing text file is entitled "14197-011-228_SEQ_LISTING," was created on December 21, 2020, and is 1,115,773 bytes in size.

1. INTRODUCTION

[0003] The present application relates to a method of recombinantly engineering a *Leishmania* cell that involves homologous recombination of DNA fragments. Further provided herein are *Leishmania* cells recombinantly engineered using the method provided herein. Also provided herein are methods of making a polypeptide using a *Leishmania* cell described herein and polypeptides produced by the methods provided herein.

2. BACKGROUND

[0004] *Leishmania* sp. have unusual genetic properties, for example, a certain level of lacking transcriptional control. Genes are transcribed into polycistronic pre-mRNAs that are subsequently processed into mature mRNAs by trans splicing, which involves the addition of a spliced leader or miniexon, and polyadenylation. Control of gene expression does not occur at the transcriptional level but rather at the level of RNA stability, translation and protein turnover (Roberts, Sigrid C. (2011) Bioeng Bugs 2 (6), pp. 320–326). These processes are influenced by the non-coding DNA regions (intergenic regions, IRs) between the genes (Breitling, et al. (2002) Protein Expr. Purif. 25 (2), pp. 209–218). For this reason, all protein-coding sequences need to be separated by intergenic regions that may be originating from *Leishmania tarentolae* or closely related species. This is also the case when using recombinant DNA and vector plasmids.

[0005] Direct assembly of multiple linear DNA fragments via homologous recombination, also described as *in vivo* assembly or transformation associated recombination, has been successfully applied to assemble DNA constructs ranging in size from a few kilobases to full synthetic microbial genomes. It has also enabled the complete replacement of eukaryotic

chromosomes with heterologous DNA. Complex *in vivo* assembly of multiple DNA fragments is a routine procedure using *S. cerevisiae*, contributing to its extensive use as a synthetic biology and biotechnology host (Shao, et al. (2009) Nucleic acids research 37 (2), e16).

[0006] *Leishmania* sp. effectively undergo homologous recombination, which is used for example to exchange target genes with drug resistance markers where the introduced drug resistance markers provide a selection mechanism. Targeting constructs are designed in which upstream and downstream regions corresponding to the flanking sequences of the target gene are joined to a drug resistance cassette. Previously, time-consuming cloning steps were involved in the generation of targeting DNAs (Roberts, Sigrid C. (2011) Bioeng Bugs 2 (6), pp. 320–326). Some techniques have been developed that simultaneously assemble multiple DNA fragments and considerably simplify the assembly of targeting constructs. Examples include the use of a PCR fusion-based strategy (Mukherjee, et al. (2009) Mol Microbiol 74 (4), pp. 914–927) and a one-step multi-fragment ligation technique (Fulwiler, et al. (2011) Molecular and Biochemical Parasitology 175 (2), pp. 209–212). The general strategy was described to be adaptable to the generation of targeting constructs for other parasites and genetically manipulatable organisms by simply producing species-specific selectable markers flanked by the appropriate SfiI sites (Fulwiler, et al. (2011) Molecular and Biochemical Parasitology 175 (2), pp. 209–212). This multi-fragment ligation technique was described for generating deletion strains, but not for knock-in /insertion strains.

[0007] To use *Leishmania* as an expression host for glycoengineered therapeutic proteins (International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein), several recombinant elements may be inserted into the host cell genome and co-expressed at the same time. Regulatory DNA sequences flanking the recombinantly expressed genes of interest are required for efficient expression, i.e. for processing and splicing of the mature processed mRNA from a polycistronic pre-mRNA. The number of genes and regulatory sequences to be inserted becomes limiting in the case of multiple gene insertions, because inserting identical sequences into the same genome can lead to undesired recombination events. Provided herein are methods to address these concerns.

3. SUMMARY OF THE INVENTION

[0008] Provided herein are methods of recombinantly engineering a *Leishmania* cell, *Leishmania* cells, kits comprising the *Leishmania* cells, methods of making a polypeptide using a *Leishmania* cell, and polypeptides produced by such methods.

[0009] In one aspect, provided herein is a method of recombinantly engineering a *Leishmania* cell comprising

(a) introducing two or more DNA fragments into the *Leishmania* cell, and

(b) incubating the *Leishmania* cell to allow homologous recombination of the DNA fragments, wherein a first DNA fragment of the two or more DNA fragments comprises a 5' homologous region and/or a 3' homologous region; wherein the 5' homologous region is homologous to a 3' homologous region of a second DNA fragment of the two or more DNA fragments or the 3' homologous region of the first DNA fragment is homologous to a 5' homologous region of the second DNA fragment; and

wherein the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) are not homologous to each other; are not homologous to a sequence in the *Leishmania* cell's genome; and/or have no homologies within the respective DNA fragment.

[0010] In certain embodiments, each of the two or more DNA fragments comprises a 5' homologous region and/or a 3' homologous region; wherein the 5' homologous region of the each of the two or more DNA fragments is homologous to a 3' homologous region of another one of the two or more DNA fragments or the 3' homologous region of the each of the two or more DNA fragments is homologous to a 5' homologous region of another one of the two or more DNA fragments; and wherein the nucleotide sequences outside the homologous regions in each DNA fragment are not homologous to each other; are not homologous to a sequence in the *Leishmania* cell's genome; and/or have no homologies within the respective DNA fragment.

[0011] In certain embodiments, the two or more DNA fragments, optionally after the two or more DNA fragments are recombined with each other, are suitable for integration into a chromosome of the *Leishmania* cell. In certain embodiments, the two or more DNA fragments, optionally after the two or more DNA fragments are recombined with each other, are integrated into the chromosome of the *Leishmania* cell. In certain embodiments, the two or more DNA fragments are integrated in tandem into the paraflagellar rod protein (Pfr) locus. In certain

embodiments, the two or more DNA fragments are integrated at the start of the 18S coding region (Ssu-PolI).

[0012] In certain embodiments, the two or more DNA fragments, before and/or after recombination with each other, are not integrated in a chromosome of the *Leishmania* cell.

[0013] In certain embodiments, the homologous recombination of the two or more DNA fragments results in a circular plasmid.

[0014] In certain embodiments, the nucleotide sequence of the first DNA fragment outside the homologous region is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length. In certain embodiments, the nucleotide sequence of the second DNA fragment outside the homologous region is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of all of the two or more DNA fragments outside the homologous region are at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length.

[0015] In certain embodiments, the homologous recombination of the DNA fragments results in a nucleotide sequence that is 50 nucleotides to 100 nucleotides, 100 nucleotides to 500 nucleotides, 500 nucleotides to 1000 nucleotides, 1000 nucleotides to 5000 nucleotides, 5000 nucleotides to 10000 nucleotides, 10000 nucleotides to 15000 nucleotides, 15000 nucleotides to 20000 nucleotides, 20000 nucleotides to 25000 nucleotides, 25000 nucleotides to 30000

nucleotides, 30000 nucleotides to 35000 nucleotides, 35000 nucleotides to 40000 nucleotides, 40000 nucleotides to 45000 nucleotides, 45000 nucleotides to 50000 nucleotides, 50000 nucleotides to 55000 nucleotides, 55000 nucleotides to 60000 nucleotides, 60000 nucleotides to 65000 nucleotides, 65000 nucleotides to 70000 nucleotides, 70000 nucleotides to 75000 nucleotides, or 75000 nucleotides to 80000 nucleotides in length.

[0016] In certain embodiments, the 5' homologous region and/or the 3' homologous region of the first DNA fragment is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of the second DNA fragment is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of all of the two or more DNA fragments is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length.

[0017] In certain embodiments, the 5' homologous region and/or the 3' homologous region of the first DNA fragment is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of the second DNA fragment is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200

nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of all of the two or more DNA fragments is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length.

[0018] In certain embodiments, the 5' homologous region of the first DNA fragment and the 3' homologous region of the second DNA fragment have at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity. In certain embodiments, the 3' homologous region of the first DNA fragment and the 5' homologous region of the second DNA fragment have at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity.

[0019] In certain embodiments, the two or more DNA fragments are introduced by transfection. In certain embodiments, the two or more DNA fragments are introduced concurrently.

[0020] In certain embodiments, the number of DNA fragments is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 37, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50.

[0021] In certain embodiments, the nucleotide sequences of the two or more DNA fragments outside the homologous region are selected from a group consisting of intergenic regions (IRs), untranslated regions (UTRs), and open reading frames (ORFs) encoding polypeptides. In certain embodiments, the IRs, UTRs and ORFs are devoid of homologous sequences within itself, and/or homologous sequences to one another.

[0022] In certain embodiments, the nucleotide sequences of the two or more DNA fragments outside the homologous region encode the same polypeptide. In certain embodiments, the *Leishmania* cell is capable of expressing two or more copies of the same polypeptide. In certain embodiments, the method increases the expression level of the polypeptide.

[0023] In certain embodiments, the homologous recombination of the DNA fragments results in a nucleotide sequence comprising at least 50%, 60%, 70%, 80%, 90% or 100% of genetic information encoded by the two or more DNA fragments.

[0024] In certain embodiments, the undesired crossing out and/or crossing over occurs in at most 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or at most 10% of the *Leishmania* cells over a period of at least 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, or at least 10 days. In certain embodiments, the undesired crossing out and/or crossing over occurs in at most 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or at most 10% of the *Leishmania* cells over at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or at least 10 cell divisions.

[0025] In certain embodiments, the *Leishmania* cell is *Leishmania tarentolae*.

[0026] In another aspect, provided herein is a *Leishmania* cell recombinantly engineered using the methods provided herein. In certain embodiments, the *Leishmania* cell is recombinantly engineered using the method repeatedly. In certain embodiments, the *Leishmania* cell is *Leishmania tarentolae*.

[0027] In another aspect, provided herein is a kit comprising one or more containers and instructions for use, wherein said one or more containers comprise the *Leishmania* cell provided herein.

[0028] In another aspect, provided herein is a method of making a polypeptide comprising (a) culturing the *Leishmania* cell provided herein under suitable conditions for polypeptide production; and (b) isolating the polypeptide. In certain embodiments, the method further comprises introducing a nucleotide sequence encoding the polypeptide.

[0029] In yet another aspect, provided herein is a polypeptide produced by the method of making a polypeptide provided herein.

3.1 Definitions

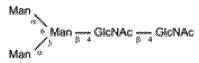
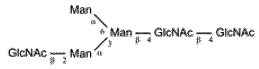
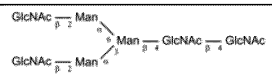
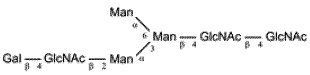
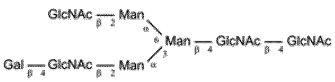
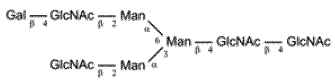
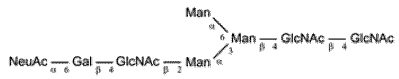
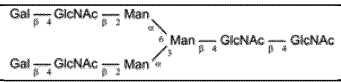
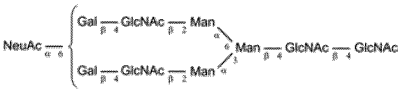
[0030] As used herein and unless otherwise indicated, the term "extremity" refers to a region at the 5' or 3' end of a DNA fragment.

[0031] As used herein and unless otherwise indicated, the term "about," when used in conjunction with a number, refers to any number within ±1, ±5 or ±10% of the referenced number.

[0032] As used herein and unless otherwise indicated, the term "subject" refers to an animal (e.g., birds, reptiles, and mammals). In another embodiment, a subject is a mammal including a non-primate (e.g., a camel, donkey, zebra, cow, pig, horse, goat, sheep, cat, dog, rat, and mouse) and a primate (e.g., a monkey, chimpanzee, and a human). In certain embodiments, a subject is a non-human animal. In some embodiments, a subject is a farm animal or pet (e.g., a dog, cat, horse, goat, sheep, pig, donkey, or chicken). In a specific embodiment, a subject is a human. The terms "subject" and "patient" may be used herein interchangeably.

[0033] As used herein and unless otherwise indicated, the term "effective amount," in the context of administering a therapy (e.g., a composition described herein) to a subject refers to the amount of a therapy which has a prophylactic and/or therapeutic effect(s). In certain embodiments, an "effective amount" refers to the amount of a therapy which is sufficient to achieve one, two, three, four, or more of the following effects: (i) reduce or ameliorate the severity of a disease/disorder or symptom associated therewith; (ii) reduce the duration of a disease/disorder or symptom associated therewith; (iii) prevent the progression of a disease/disorder or symptom associated therewith; (iv) cause regression of a disease/disorder or symptom associated therewith; (v) prevent the development or onset of a disease/disorder, or symptom associated therewith; (vi) prevent the recurrence of a disease/disorder or symptom associated therewith; (vii) reduce organ failure associated with a disease/disorder; (viii) reduce hospitalization of a subject having a disease/disorder; (ix) reduce hospitalization length of a subject having a disease/disorder; (x) increase the survival of a subject with a disease/disorder; (xi) eliminate a disease/disorder in a subject; and/or (xii) enhance or improve the prophylactic or therapeutic effect(s) of another therapy.

3.2 Conventions and Abbreviations

Abbreviation	Convention
bp	base pair
CDS	coding sequence
EPO	erythropoietin
GlcNAc-transferase	N-acetylglucosamine-transferase
IR	Intergenic region
mAb	monoclonal antibody
ORF	open reading frames
UTR	untranslated region
Man3	
G0-N	
G0	
G1-N	
G1	 or 
G1S1-N	
G2	
G1S1	or
G2S1	
G2S2	

4. BRIEF DESCRIPTION OF THE FIGURES

[0034] FIGs. 1A-1B: *Leishmania tarentolae* is able to assemble a chromosomal integration construct from multiple DNA fragments by homologous recombination. (FIG. 1A) Schematic representation of a full length monoclonal antibody (mAb) expression construct. The integration construct for Rituximab (top) comprises the homologous recombination sites for integration into the ssu locus (Lhr [ssu] and Rhr [ssu]), 4 intergenic regions ensuring correct transcription and splicing of the mRNA (IR1 = aprtIR; IR2 = aTubIR from *L. enrietti*; IR3 = CamIR from *L. tarentolae*; IR4 = dhfr-ts) and the open reading frames (ORF) for the light (ORF1) and heavy (ORF2) chains of Rituximab and the selection marker NTC (ORF3). The full construct is present on plasmid pLMTB5026, or split between fragments present on donor plasmids pLMTB5024 and pLMTB5025. Overlapping regions for homologous recombination into the genome (>500 bp; lower part of figure) and between the fragments (250 bp) are indicated as grey bars. (FIG. 1B) Western blot analysis of cell culture supernatants of strains generated by co-transfecting two DNA fragments that should recombine *in vivo* in order to form an expression construct for a monoclonal antibody (Rituximab). Positive control = Rituximab (Anti CD20, Lubio: A1049-100). Expression of full-length monoclonal antibody can be detected via light chain or heavy chain specific antibodies directly in the cell culture supernatant.

[0035] FIG. 2: Multiple homologous recombination events of heterologous coding sequences lead to function-engineered *Leishmania* host cells. Schematic representation of the integration constructs (top) comprising the homologous recombination sites for integration into the AQP locus (Lhr [AQP] and Rhr [AQP]), regulatory elements (PolA; promoter) and intergenic regions ensuring correct transcription and splicing of the mRNA (aTubIR from *L. enrietti*; Pfr IR = IR of paraflagellar rod protein from *L. tarentolae*; Val IR, IR from Valosin from *L. tarentolae*; Cam IR from *L. tarentolae* and UtrA = dhfr-ts) and the coding sequences for heterologous glycosyltransferases (sfGntI, rnMGAT2, drMGAT1, hsB4GalT1, see, e.g., International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein) and the selection marker hygromycin Sm[hyg]). The full construct is split between ten fragments, which were excised from ten donor plasmids. Overlapping regions for homologous recombination into the genome (500 bp) are within black boxes at the extremities and homologous recombination regions between the fragments (200 bp) are indicated as grey bars. Bottom graph shows the functional read out of glycoengineering efficiencies, indicated as relative % N-glycans, which

were released from cellular proteins and measured by routine N-glycan analysis such as RF-MS or PC- labeling.

[0036] FIGs. 3A-3C: Multiple homologous events of heterologous coding sequences interspaced by *Leishmania tarentolae* regulatory elements and intergenic regions (IRs). (FIG. 3A) Functional read out of glycoengineering efficiencies is indicated as relative % N-glycans, released from cellular proteins and measured by routine RF-MS, and shows activity of all enzymatic steps in St15368. Absent activities from second glycoengineering enzymatic step by MGAT2 in St15448 suggest phenotypic differences based on desired and undesired integration events. (FIG. 3B) Schematic representation of the integration (top) comprising the homologous recombination sites for counterclockwise disruption of aquaporin (AQP) (dark grey boxes, Lhr and Rhr), regulatory elements PolA, and intergenic regions (striped boxes) ensuring correct transcription and splicing of the mRNA (aTubIR from *L. enrietti*; Pfr IR = IR of paraflagellar rod protein from *L. tarentolae*; Val IR, IR from Valosin from *L. tarentolae*; 60S ribosomal protein L23 from *L. tarentolae* and a 3' UTR downstream of the selection marker gene (SmA). The coding sequences for heterologous glycosyltransferases are rnMGAT2 (GtD), hsB4GalT1 (GtE), sfGntI (GtA), drMGAT1 (GtB), and SmA for the selection marker hygromycin. Inserted genetic element regions are shaded with grey dotted background. Correct integration is exemplified for St15368 (top). Region marked with black background and white dots shows the Pfr IR that caused an undesired crossing over to the identical Pfr IR sequence in Chromosome 29, thereby omitting the recombinant genetic elements of rnMGAT2 (GtD), hsB4GalT1 (GtE) in St15448 (bottom) and (FIG. 3C) leading to a hybrid chromosome as identified by PacBio sequencing (PacBio raw subread m54073_181001_130829/9307006/0_32110).

[0037] FIG. 4: Schematic representation of the intended integration comprising the 500 bp homologous recombination sites (dark grey boxes) for counterclockwise disruption of Ptr1 in Chromosome 23 (Lhr and Rhr), regulatory element PolI ("PolA"), and intergenic regions (IRs, striped boxes) ensuring correct transcription and splicing of the mRNA and a 3' UTR downstream of the selection marker gene (SmA). The coding sequences for heterologous glycosyltransferases are hsB4GalT1 (ORF1), hsMGAT1 (ORF2) rnMGAT2 (ORF3), and SM for the selection marker hygromycin. The full expression cassette is split between eight fragments, which were excised from their donor plasmids. Overlapping regions for homologous recombination into the genome (500 bp at the extremities) and between the fragments (200 bp)

are indicated as grey boxes. Within black brackets, the region shaded dark grey with white dots marks an identical stretch of 93 bp derived from the 3x HA tag at the C-terminus of hsMGAT1 ORF in donor fragment GtC_5IrLmM(8081), and the identical sequence in IrLmO_5GtD (8085) derived from the 3x HA tag also present at the C-terminus of rnMGAT2 ORF. Homologous recombination of these fragments creates an undesired crossing out and omission of genetic information for IR2 and rnMGAT2. The phenotype is represented by glycoengineering activities of the GTs, and the absence of G0 and G2 glycans suggests absence of MGAT2 activity, shown as graph with relative % N-glycans (Top left).

[0038] FIG. 5: Schematic representation of different chromosomal integration strategies with light grey arrows indicating chromosomal coding sequences and dark grey arrows heterologous coding sequences that are inserted via homology ends at their extremities (shaded grey). The regulatory element PolI is a promoter region for PolI transcription and used for transcription initiation in counter clockwise integration constructs.

[0039] FIGs. 6A-6B: Heterologous and non-identical sequences ensure correct chromosomal integrations and internal fragment recombinations, while selected heterologous regulatory sequences are functional in *Leishmania tarentolae* CustomGlycan host cells. (FIG. 6A) Glycoengineering activities of the GTs are assessed as relative % N- glycans derived from total surface glycoproteins and compared between the different strains differing in their IRs but not in the GT and SM coding sequences. (FIG. 6B) Schematic representation of the Nanopore sequencing analysis results for the different integrations and resulting strains (St17212 = LmIR, St17311 = LdIR, St17176 = LiIR, St17180 = LmxIR). Each integration comprises the homologous recombination sites for integration into the GP63 locus of Chromosome 10 (LhrD [GP63] and RhrD [GP63]). The intergenic regions (Ir) derived from different *Leishmania* species *L. major (Lm), L. donovani (Ld), L. infantum (Li), L. mexicana (Lmx)* and ensuring correct transcription and splicing of the mRNA, are shown as striped boxes with indicated text description for each IR. The coding sequences for heterologous glycosyltransferases, GTs, (sfGntI, rnMGAT2, drMGAT1, hsB4GalT1) are depicted as white arrows and the selection marker hygromycin in grey and are identical in all four strains.

[0040] FIG. 7: Stepwise increase of N-glycan conversion efficiency by transfection of several genetic modules, shown as N-glycans (relative in %) from surface glycoproteins of three consecutively generated strains, St17238 (1st), St17294 (2nd) and St17826 (3rd). Increase in copy

numbers of glycosyltransferases was achieved by using codon diversified enzymes and homologs from different species (hs, *Homo sapiens*; rn, *Rattus norvegicus*, dr, *Danio rerio*, gj, *Gekko japonicus*, ag, *Anopheles gambiae*).

[0041] FIGs. 8A-8C: Generation of an N-glycan sialylation proficient cell line St17527 by multiple homologous recombination of 13 fragments into the parental glycosyltransferase containing cell line (St17311). (FIG. 8A) Schematic representation of the genomic modification of St17527. Top indicates genomically integrated expression cassette in gp63 locus (Chromosome 10) from parental cell line St17311. The new integration comprises the homologous recombination sites for the alpha tubulin locus of Chromosome 13 (Lhr [aTub] and Rhr [aTub]), the intergenic regions (Ir) derived from *L. infantum (IrLi) and L. major (IrLm)* for transcription and splicing of the mRNA, shown as striped boxes. The coding sequences for sialic acid (Neu5Ac) biosynthesis, Golgi import and transfer to N-glycans (such as $NeuC_{3xMyc}$: UDP-N-acetyl glucosamine 2-epimerase, CgNal : N-acetylneuraminic acid lyase favoring N-acetylneuraminic acid synthesis, $NeuB_{3xHA}$: CMP-sialic acid synthase, $_{3xHA}ST6$: Beta-galactoside alpha-2,6-sialyltransferase 1, $NeuA_{3xHA}$: CMP-sialic acid synthetase and CST_{3xmyc} CMP-Neu5Ac transporter) are depicted as white arrows and the selection marker, pac, in grey. (FIG. 8B) HPLC traces of DMB labelled total sialic acid (Neu5Ac + CMP-Neu5Ac) and CMP-Neu5Ac extracted from cell pellets of St17527 show presence of Neu5Ac and the activated sugar CMP-Neu5Ac and thus demonstrate functionality of sialic acid precursor biosynthesis. (FIG. 8C) Glycoengineering activities of the GTs is represented as relative % N-glycans derived from total surface glycoproteins. Total galactosylation and total sialylation is also indicated, demonstrating a function-customized *L. tarentolae* host cell.

[0042] FIGs. 9A-9C: Chromosomal integrations of the same glycoengineering construct into different chromosomal loci for high level glycoengineering activity of the expressed glycosyltransferases. (FIG. 9A) Schematic representation of chromosomal integration strategies targeting the Pfr locus on chromosome 29 as well as the rDNA expression locus on chromosome 27. Light grey arrows indicate chromosomal coding sequences and dark grey arrows indicate heterologous coding sequences that are inserted via homology ends at their extremities (shaded grey). Since the depicted chromosomal regions represent multi-copy loci, integration can occur in several different places, as indicated by the differently shaded grey bars. Regulatory elements ensuring correct processing of the pre-mRNA are shown as differently striped boxes flanking the

5' end of the first integrated heterologous coding sequence in the case of integrations into the rDNA locus (Ssu and Ssu-PolI) and the 3' end of the last heterologous coding sequence of the integration constructs. (FIG. 9B) Comparison of glycoengineering activities of the GTs encoded by the same G0 integration construct targeted to different chromosomal integration loci ("Pfr", "Ssu" or "Ssu-PolI"). Shown are relative % N- glycans derived from total surface glycoproteins of the respective strains. (FIG. 9C) Comparison of glycoengineering activities of the GTs encoded by the same G0 integration construct targeted to different variants of the rDNA chromosomal integration locus ("Ssu" vs. "Ssu-PolI"). Shown are relative % N- glycans released from the Fc N-glycosylation site of a coexpressed monoclonal antibody (Adalimumab).

[0043] FIGs. 10A-10C: Multiple homologous recombination events of heterologous coding sequences lead to function-engineered *Leishmania* host cells. (FIG. 10A) Schematic representation of the integration construct (top) comprising the homologous recombination sites for integration into the "Pfr" locus (LhrP and RhrP), intergenic regions ensuring correct transcription and splicing of the mRNA (15 different IRs from *L. major (Lm), L. donovani (Ld), L. infantum (Li), L. tarentolae (Lt)* and UtrA = dhfr-ts are shown as striped boxes) and the coding sequences for heterologous glycosyltransferases (different orthologs of MGAT1, MGAT2, hsB4GalT1 are shown as white boxes, see, e.g., International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein), the coding sequences for enzymes of the sialic acid biogenesis and transfer pathway (shown as dark grey boxes) and the selection marker for Puromycin resistance (SmD, shown as light grey box). The full construct is split between 25 fragments, which were excised from 25 donor plasmids. Overlapping regions for homologous recombination into the genome (500 bp) are within black boxes at the extremities and homologous recombination regions between the fragments (200 bp or longer) are indicated as grey bars. Bottom graph shows the functional read out of glycoengineering efficiencies, indicated as relative % N-glycans, which were released from cellular proteins and measured by routine N-glycan analysis (PC-labeling). (FIG. 10B) Increase of N-glycan conversion efficiency by transfection of several genetic modules, shown as N-glycans (relative in %) from total surface glycoproteins of three consecutively generated strains, St18700 (1st), St19084 (2nd) and St19384 (3rd). Increase in copy numbers of glycosyltransferases was achieved by using codon diversified enzymes and homologs from different species. (FIG. 10C) Alternative strains of different genetic composition that allow almost homogeneous N-glycan conversion to G2S2. Figure shows N-

glycans (relative in %) from total surface glycoproteins of three alternative strains, St20157, St20208 and St20224.

[0044] FIGs. 11A-11D: Assembly of a hybrid prokaryotic gene cluster on an *Escherichia coli* cosmid in *Leishmania tarentolae* (FIG. 11A) Schematic representation of the designed fragments and the expected recombination via 200 bp homologous regions shaded in grey or grey striped. (FIG. 11B) Western blot analysis on *E. coli* DH5a transformed with plasmids isolated from several polyclones for expression of *S. pneumoniae* serotype 1 polysaccharide. Lane 1: PageRuler™ Prestained Protein Ladder, 10 to 180 kDa (ThermoFischer scientific), lane 2: polyclone 1.2, lane 3: polyclone 1.3, lane 4: polyclone 1.4, lane 5: polyclone 1.5, lane 6: polyclone 1.6, lane 7: polyclone 1.7, lane 8: polyclone 1.8, lane 9: polyclone 2.3. (FIG. 11C) Control restriction of plasmids isolated from different polyclones. A: restrictions on polyclones from transfections #1 and #2. Upper panel: BstBI restriction (expected sizes for correct construct: 22210 bp, 9042 bp, 3787 bp; for empty vector: 20801 bp), lower panel: BsiWI restriction (expected sizes for correct construct: 32536 bp, 2503bp; for empty vector: undigested 20801 bp). Lane 1: GeneRuler™ 1kb DNA ladder (Thermo-Fischer scientific), lane 2: polyclone 1.1, lane 3: polyclone 1.7, lane 4: polyclone 2.1, lane 5: polyclone 2.2, lane 6: pGVXN775. (FIG. 11D) Restriction on polyclones from transfection #3. SacI restriction (expected sizes for correct construct: 19628 bp, 3723 bp; for empty vector: 20801 bp). Lane 1: polyclone 3.1, lane 2: polyclone 3.2, lane 3: pLMTB6412, lane 4: GeneRuler™ 1kb DNA ladder (Thermo-Fischer scientific).

5. DETAILED DESCRIPTION OF THE INVENTION

[0045] Provided herein are methods of recombinantly engineering a *Leishmania* cell, *Leishmania* cells engineered using the methods provided herein, methods of making a target polypeptide using a *Leishmania* cell provided herein, and target polypeptides produced by the methods. The methods of recombinantly engineering a *Leishmania* cell are described in Section 5.1. Properties of the resulting *Leishmania* cell are described in Section 5.2. Uses of such *Leishmania* cell as expression systems for target polypeptides, e.g., therapeutic proteins, are described in Section 5.3. Properties of the target polypeptides expressed in *Leishmania* host cells provided herein are described in Section 5.4.

[0046] Provided herein are i) a quick, multi-fragment homologous recombination to create large artificial chromosomal insertions of at least around 20 kb in *Leishmania tarentolae* hosts cells, ii) specific strategies to avoid undesired crossing out of recombinantly inserted genetic elements and iii) using multiple homologous recombination to assemble circular DNA adaptable for any heterologous shuttle vector use. Further, also provided herein is a method of increasing expression of a polypeptide by insertion of multiple expressed gene copies into the same host cell.

[0047] Problems using a multiple homologous recombination event for host cell engineering occur if the inserted DNA sequences are homologous/ identical. Even short stretches of less than 100 bp can lead to undesired crossing over due to the very efficient natural recombination of *Leishmania tarentolae*.

[0048] Without being bound by theory, the methods provided herein reduce or eliminate such undesired crossing over. Specifically, described herein are i) multiple regulatory DNA sequences that enable functional processing and splicing of polycistronic pre-mRNA to form mature processed mRNA for protein expression, while differing sufficiently from each other and from any chromosomal sequence to avoid undesired crossing over (such sequences were taken from related species but not from *Leishmania tarentolae*), and ii) strategies to diversify coding sequences for genes that are intended to be inserted in multiple copies in such a way that they are not recombining with themselves but still are efficiently expressed.

[0049] The multi-fragment ligation strategy described herein for creating engineered host cells is markedly faster than traditional approaches, it moreover allows simultaneous integration of multiple ORFs with only one selection marker and thus expands the previously limited capacity of genetic engineering possibilities. Furthermore, the selection of different insertion elements (intergenic regulatory sequences or codon-diversified genes of interest) enables expression of glycoengineered therapeutics and yield increases by increasing gene copy numbers. This application describes fully function-customized host cells, which were created by the genetic methods described.

[0050] Moreover, due to *L. tarentolae* very efficient innate homologous recombination system, *L. tarentolae* can be used to assemble multiple heterologous DNA fragments to a circular DNA, if homologous sites to the *L. tarentolae* chromosome are absent. *L. tarentolae* is able to propagate episomal (Plasmid) DNA in absence of origin of replication. These methods consist of

co-transfecting the donor plasmid and a series of DNA fragments which share homologies in their extremities and between their extremities and the recipient vector. A selection marker for *L. tarentolae* is added, which is as well separated into 2 fragments for selecting positive transfectants of *L. tarentolae* host cells. Nucleic acid from *L. tarentolae* PCR-positive cells can be extracted and the extracted material is transformed/transfected into target propagating microorganism on desired selection marker present in recipient vector. The technology can use any unmodified recipient circular DNA and no restriction site availability is necessary.

[0051] To summarize, multiple homologous recombination events, which efficiently occur in *Leishmania*, are exploited to introduce 2 to 20, and potentially even far more than 20, DNA fragments, which share homologies in their extremities, in order to create host cells that have site specifically integrated the genetic information containing coding sequences flanked by regulatory elements. Regulatory elements were identified from related species and remain functional when introduced in *Leishmania tarentolae*. Final genetic information comprises stretches of 20 kb/site specifically inserted into the chromosome of *Leishmania* host cells, and even larger insertions are possible. The application describes a novel tool using "plug and play" modules to efficiently create function-engineered *Leishmania* host cells. Additionally this efficient site-specific homologous recombination event is exploited to assemble multiple DNA fragments into an episomal construct, which can be adapted as shuttle vector for different unrelated host organisms, thereby representing an efficient cloning tool for complex shuttle vectors.

5.1 Methods of Recombinantly Engineering a *Leishmania* Cell

[0052] In one aspect, provided herein is a method of recombinantly engineering a *Leishmania* cell comprising (a) introducing two or more DNA fragments into the *Leishmania* cell, and (b) incubating the *Leishmania* cell to allow homologous recombination of the DNA fragments, wherein a first DNA fragment of the two or more DNA fragments comprises a 5' homologous region and/or a 3' homologous region; wherein the 5' homologous region is homologous to a 3' homologous region of a second DNA fragment of the two or more DNA fragments or the 3' homologous region of the first DNA fragment is homologous to a 5' homologous region of the second DNA fragment; and wherein the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) are not homologous to

each other; are not homologous to a sequence in the *Leishmania* cell's genome; and/or have no homologies within the respective DNA fragment.

5.1.1 DNA fragments

[0053] In certain embodiments, the DNA fragment described herein comprises a 5' homologous region or a 3' homologous region that is homologous to a 5' homologous region or a 3' homologous region of another DNA fragment. In certain embodiments, the DNA fragment described herein comprises a 5' homologous region that is homologous to a 3' homologous region of another DNA fragment. In certain embodiments, the DNA fragment described herein comprises a 3' homologous region that is homologous to a 5' homologous region of another DNA fragment. In certain embodiments, the DNA fragment described herein comprises a 5' homologous region that is homologous to a 3' homologous region of another DNA fragment, and a 3' homologous region that is homologous to a 5' homologous region of a third DNA fragment. In certain embodiments, the nucleotide sequences outside the homologous regions in the DNA fragment described herein are not homologous to each other. In certain embodiments, the nucleotide sequences outside the homologous regions in the DNA fragment described herein are not homologous to a sequence in the *Leishmania* cell's genome. In certain embodiments, the nucleotide sequences outside the homologous regions in the DNA fragment described herein have no homologies within the respective DNA fragment.

[0054] In certain embodiments, the first DNA fragment of the two or more DNA fragments comprises a 5' homologous region and/or a 3' homologous region. In certain embodiments, the 5' homologous region of the first DNA fragment is homologous to a 3' homologous region of a second DNA fragment of the two or more DNA fragments. In certain embodiments, the 3' homologous region of the first DNA fragment is homologous to a 5' homologous region of a second DNA fragment of the two or more DNA fragments. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) are not homologous to each other; are not homologous to a sequence in the *Leishmania* cell's genome; and/or have no homologies within the respective DNA fragment.

[0055] In certain embodiments, each of the two or more DNA fragments comprises a 5' homologous region and/or a 3' homologous region. In certain embodiments, the 5' homologous region of the each of the two or more DNA fragments is homologous to a 3' homologous region of another one of the two or more DNA fragments. In certain embodiments, the 3' homologous

region of the each of the two or more DNA fragments is homologous to a 5' homologous region of another one of the two or more DNA fragments. In certain embodiments, the nucleotide sequences outside the homologous regions in each DNA fragment are not homologous to each other; are not homologous to a sequence in the *Leishmania* cell's genome; and/or have no homologies within the respective DNA fragment.

[0056] In certain embodiments, the DNA fragment described herein comprises a 5' homologous region or a 3' homologous region that is homologous to a region in the chromosome of the *Leishmania* cell. In certain embodiments, such homologous region allows the integration of the DNA fragment into the chromosome of the *Leishmania* cell. In certain embodiments, the DNA fragment comprises a 5' homologous region that is homologous to a 3' homologous region of another DNA fragment, a region that is outside the homologous regions, and a 3' homologous region that is homologous to a 5' homologous region of another DNA fragment.

[0057] In certain embodiments, the two or more DNA fragments, optionally after the two or more DNA fragments are recombined with each other, are suitable for integration into a chromosome of the *Leishmania* cell. In certain embodiments, the two or more DNA fragments, optionally after the two or more DNA fragments are recombined with each other, are integrated into the chromosome of the *Leishmania* cell. In certain embodiments, the two or more DNA fragments are integrated in tandem into the paraflagellar rod protein (Pfr) locus. In certain embodiments, the two or more DNA fragments are integrated at the start of the 18S coding region (Ssu-PolI). In certain embodiments, the two or more DNA fragments, before and/or after recombination with each other, are not integrated in a chromosome of the *Leishmania* cell.

5.1.2 Homologous region

[0058] In certain embodiments, the 5' homologous region and/or the 3' homologous region may be 10 to 2000 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region may be at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 60 nucleotides, 70 nucleotides, 80 nucleotides, 90 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600

nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at least 5000 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region may be 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 60 nucleotides, 70 nucleotides, 80 nucleotides, 90 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or 5000 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region may be 200 nucleotides, 250 nucleotides or more than 500 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region may be of any length that is described in the Example section.

[0059] In certain embodiments, the 5' homologous region and/or the 3' homologous region of the first DNA fragment is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of the first DNA fragment is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of the first DNA fragment is 10 nucleotide to 50 nucleotides, 50 nucleotide to 100 nucleotides, 100 nucleotide to 150 nucleotides, 150 nucleotide to 200 nucleotides, 200 nucleotide to 250 nucleotides, 250 nucleotide to 300 nucleotides, 300

nucleotide to 350 nucleotides, 350 nucleotide to 400 nucleotides, 400 nucleotide to 450 nucleotides, 450 nucleotide to 500 nucleotides, 500 nucleotide to 550 nucleotides, 550 nucleotide to 600 nucleotides, 600 nucleotide to 650 nucleotides, 650 nucleotide to 700 nucleotides, 700 nucleotide to 750 nucleotides, 750 nucleotide to 800 nucleotides, 800 nucleotide to 850 nucleotides, 850 nucleotide to 900 nucleotides, 900 nucleotide to 950 nucleotides, 950 nucleotide to 1000 nucleotides, 1000 nucleotides to 1200 nucleotides, 1200 nucleotides to 1400 nucleotides, 1400 nucleotides to 1600 nucleotides, 1600 nucleotides to 1800 nucleotides, 1800 nucleotides to 2000 nucleotides, 2000 nucleotides to 2200 nucleotides, 2200 nucleotides to 2400 nucleotides, 2400 nucleotides to 2600 nucleotides, 2600 nucleotides to 2800 nucleotides, 2800 nucleotides to 3000 nucleotides, 3000 nucleotides to 3200 nucleotides, 3200 nucleotides to 3400 nucleotides, 3400 nucleotides to 3600 nucleotides, 3600 nucleotides to 3800 nucleotides, 3800 nucleotides to 4000 nucleotides, , 4000 nucleotides to 4200 nucleotides, 4200 nucleotides to 4400 nucleotides, 4400 nucleotides to 4600 nucleotides, 4600 nucleotides to 4800 nucleotides, or 4800 nucleotides to 5000 nucleotides in length.

[0060] In certain embodiments, the 5' homologous region and/or the 3' homologous region of the second DNA fragment is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of the second DNA fragment is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of the second DNA fragment is 10 nucleotide to 50 nucleotides, 50 nucleotide to 100 nucleotides, 100 nucleotide to 150 nucleotides, 150 nucleotide to 200 nucleotides, 200 nucleotide to 250 nucleotides, 250 nucleotide to 300 nucleotides, 300 nucleotide to 350 nucleotides, 350 nucleotide to 400 nucleotides, 400 nucleotide to 450 nucleotides, 450 nucleotide to 500 nucleotides, 500 nucleotide to 550 nucleotides, 550 nucleotide

to 600 nucleotides, 600 nucleotide to 650 nucleotides, 650 nucleotide to 700 nucleotides, 700 nucleotide to 750 nucleotides, 750 nucleotide to 800 nucleotides, 800 nucleotide to 850 nucleotides, 850 nucleotide to 900 nucleotides, 900 nucleotide to 950 nucleotides, 950 nucleotide to 1000 nucleotides, 1000 nucleotides to 1200 nucleotides, 1200 nucleotides to 1400 nucleotides, 1400 nucleotides to 1600 nucleotides, 1600 nucleotides to 1800 nucleotides, 1800 nucleotides to 2000 nucleotides, 2000 nucleotides to 2200 nucleotides, 2200 nucleotides to 2400 nucleotides, 2400 nucleotides to 2600 nucleotides, 2600 nucleotides to 2800 nucleotides, 2800 nucleotides to 3000 nucleotides, 3000 nucleotides to 3200 nucleotides, 3200 nucleotides to 3400 nucleotides, 3400 nucleotides to 3600 nucleotides, 3600 nucleotides to 3800 nucleotides, 3800 nucleotides to 4000 nucleotides, , 4000 nucleotides to 4200 nucleotides, 4200 nucleotides to 4400 nucleotides, 4400 nucleotides to 4600 nucleotides, 4600 nucleotides to 4800 nucleotides, or 4800 nucleotides to 5000 nucleotides in length.

[0061] In certain embodiments, the 5' homologous region and/or the 3' homologous region of all of the two or more DNA fragments is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of all of the two or more DNA fragments is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length. In certain embodiments, the 5' homologous region and/or the 3' homologous region of all of the two or more DNA fragments is 10 nucleotide to 50 nucleotides, 50 nucleotide to 100 nucleotides, 100 nucleotide to 150 nucleotides, 150 nucleotide to 200 nucleotides, 200 nucleotide to 250 nucleotides, 250 nucleotide to 300 nucleotides, 300 nucleotide to 350 nucleotides, 350 nucleotide to 400 nucleotides, 400 nucleotide to 450 nucleotides, 450 nucleotide to 500 nucleotides, 500 nucleotide to 550 nucleotides, 550 nucleotide to 600 nucleotides, 600 nucleotide to 650 nucleotides, 650 nucleotide to 700 nucleotides, 700 nucleotide to 750 nucleotides, 750 nucleotide

to 800 nucleotides, 800 nucleotide to 850 nucleotides, 850 nucleotide to 900 nucleotides, 900 nucleotide to 950 nucleotides, 950 nucleotide to 1000 nucleotides, 1000 nucleotides to 1200 nucleotides, 1200 nucleotides to 1400 nucleotides, 1400 nucleotides to 1600 nucleotides, 1600 nucleotides to 1800 nucleotides, 1800 nucleotides to 2000 nucleotides, 2000 nucleotides to 2200 nucleotides, 2200 nucleotides to 2400 nucleotides, 2400 nucleotides to 2600 nucleotides, 2600 nucleotides to 2800 nucleotides, 2800 nucleotides to 3000 nucleotides, 3000 nucleotides to 3200 nucleotides, 3200 nucleotides to 3400 nucleotides, 3400 nucleotides to 3600 nucleotides, 3600 nucleotides to 3800 nucleotides, 3800 nucleotides to 4000 nucleotides, , 4000 nucleotides to 4200 nucleotides, 4200 nucleotides to 4400 nucleotides, 4400 nucleotides to 4600 nucleotides, 4600 nucleotides to 4800 nucleotides, or 4800 nucleotides to 5000 nucleotides in length.

[0062] In certain embodiments, two homologous regions that are homologous to each other have at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity. In certain embodiments, two homologous regions that are homologous to each other have 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity. In certain embodiments, two homologous regions have enough level of homology to allow homologous recombination of the corresponding DNA fragments comprising the homologous regions.

[0063] In certain embodiments, the 5' homologous region of the first DNA fragment and the 3' homologous region of the second DNA fragment have at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity. In certain embodiments, the 3' homologous region of the first DNA fragment and the 5' homologous region of the second DNA fragment have at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity. In certain embodiments, the 5' homologous region of the first DNA fragment and the 3' homologous region of the second DNA fragment have 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity. In certain embodiments, the 3' homologous region of the first DNA fragment and the 5' homologous region of the second DNA fragment have 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity.

5.1.3 The DNA fragments outside the homologous region

[0064] In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 1200 nucleotides, 1500 nucleotides, 1800 nucleotides, 2000 nucleotides, 2500 nucleotides, 3000 nucleotides, 3500 nucleotides, 4000 nucleotides, 4500 nucleotides, 5000 nucleotides, 6000 nucleotides, 7000 nucleotides, 8000 nucleotides, 9000 nucleotides, 10000 nucleotides, 11000 nucleotides, 12000 nucleotides, 13000 nucleotides, 14000 nucleotides, 15000 nucleotides, 16000 nucleotides, 17000 nucleotides, 18000 nucleotides, 19000 nucleotides, 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are 10 to 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are 50 to 10000 nucleotides in length. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are 100 to 5000 nucleotides in length. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are 150 to 2500 nucleotides in length. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are 250 to 2000 nucleotides in length.

[0065] In certain embodiments, the nucleotide sequence of the first DNA fragment outside the homologous region is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of the first DNA fragment outside the homologous region are 10 to 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of the first DNA fragment outside the homologous region are 50 to 10000 nucleotides in length. In certain embodiments, the nucleotide sequences of the first DNA fragment outside the homologous region are 100 to 5000 nucleotides in length. In certain embodiments, the nucleotide sequences of the first DNA

fragment outside the homologous region are 150 to 2500 nucleotides in length. In certain embodiments, the nucleotide sequences of the first DNA fragment outside the homologous region are 250 to 2000 nucleotides in length.

[0066] In certain embodiments, the nucleotide sequence of the second DNA fragment outside the homologous region is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of the second DNA fragment outside the homologous region are 10 to 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of the first DNA fragment outside the homologous region are 50 to 10000 nucleotides in length. In certain embodiments, the nucleotide sequences of the second DNA fragment outside the homologous region are 100 to 5000 nucleotides in length. In certain embodiments, the nucleotide sequences of the second DNA fragment outside the homologous region are 150 to 2500 nucleotides in length. In certain embodiments, the nucleotide sequences of the second DNA fragment outside the homologous region are 250 to 2000 nucleotides in length.

[0067] In certain embodiments, the nucleotide sequences of all of the two or more DNA fragments outside the homologous region are at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of all of the two or more DNA fragments outside the homologous region are 10 to 50000 nucleotides in length. In certain embodiments, the nucleotide sequences of the first DNA fragment outside the homologous region are 50 to 10000 nucleotides in length. In certain embodiments, the nucleotide sequences of all of the two or more DNA fragments outside the homologous region are 100 to 5000 nucleotides in length. In certain embodiments, the nucleotide sequences of the second DNA fragment outside the homologous

region are 150 to 2500 nucleotides in length. In certain embodiments, the nucleotide sequences of all of the two or more DNA fragments outside the homologous region are 250 to 2000 nucleotides in length.

[0068] As used herein and unless otherwise indicated, when two nucleotide sequences have "no homologies" or are "not homologous to" each other, the two nucleotide sequences have at most 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or at most 80% sequence identity over a region of about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, about 500 nucleotides, about 525 nucleotides, about 550 nucleotides, about 575 nucleotides, about 600 nucleotides, about 625 nucleotides, about 650 nucleotides, about 675 nucleotides, about 700 nucleotides, about 725 nucleotides, about 750 nucleotides, about 775 nucleotides, about 800 nucleotides, about 825 nucleotides, about 850 nucleotides, about 875 nucleotides, about 900 nucleotides, about 925 nucleotides, about 950 nucleotides, about 975 nucleotides, about 1000 nucleotides, about 1025 nucleotides, about 1050 nucleotides, about 1075 nucleotides, or about 2000 nucleotides. In certain embodiments, the two nucleotide sequences may have regions with 90% or higher sequence identity, and such regions are at most about 10 nucleotide, about 20 nucleotide, about 30 nucleotide, or at most about 40 nucleotides in length. In certain embodiments, the two nucleotide sequences may have at most 70% or 80% sequence identity over a region of about 20 nucleotides, about 30 nucleotides, about 40 nucleotides, about 50 nucleotides, about 60 nucleotides, about 70 nucleotides, about 80 nucleotides, about 90 nucleotides, about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, or about 500 nucleotides. In certain embodiments, the level of homology in the two nucleotide sequences is not enough to allow homologous recombination of the two nucleotide sequences. In certain embodiments, the level of homology in the two nucleotide sequences may allow at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 undesired recombination events between the two nucleotide sequences per

10,000 copies of nucleotide sequences per 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days of incubation.

(i) The first and the second DNA fragments are not homologous to each other outside the 5' and/or 3' homologous region(s)

[0069] In certain embodiments, the nucleotide sequences of the first and the second DNA fragments are not homologous to each other outside the homologous region(s). In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) may have at most 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or at most 80% sequence identity over a region of about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, about 500 nucleotides, about 525 nucleotides, about 550 nucleotides, about 575 nucleotides, about 600 nucleotides, about 625 nucleotides, about 650 nucleotides, about 675 nucleotides, about 700 nucleotides, about 725 nucleotides, about 750 nucleotides, about 775 nucleotides, about 800 nucleotides, about 825 nucleotides, about 850 nucleotides, about 875 nucleotides, about 900 nucleotides, about 925 nucleotides, about 950 nucleotides, about 975 nucleotides, about 1000 nucleotides, about 1025 nucleotides, about 1050 nucleotides, about 1075 nucleotides, or about 2000 nucleotides. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) may have regions with 90% or higher sequence identity, and such regions are at most about 10 nucleotide, about 20 nucleotide, about 30 nucleotide, or at most about 40 nucleotides in length. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) may have at most 70% or 80% sequence identity over a region of about 20 nucleotides, about 30 nucleotides, about 40 nucleotides, about 50 nucleotides, about 60 nucleotides, about 70 nucleotides, about 80 nucleotides, about 90 nucleotides, about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, or about 500 nucleotides. In certain

embodiments, the level of homology in the nucleotide sequences of the first and the second DNA fragments outside the homologous region is not enough to allow homologous recombination of the DNA fragments in the regions that are outside the homologous region. In certain embodiments, the level of homology in the nucleotide sequences of the first and the second DNA fragments outside the homologous region may allow at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or at most 10 undesired recombination events between the first and the second DNA fragments in the regions that are outside the homologous region per 10,000 copies of each of the first and the second DNA fragments per 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days of incubation.

(ii) All DNA fragments are not homologous to each other outside the 5' and/or 3' homologous region(s)

[0070] In certain embodiments, the nucleotide sequences of all the DNA fragments are not homologous to each other outside the homologous region(s). In certain embodiments, the nucleotide sequences of all the DNA fragments outside the homologous region(s) may have at most 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or at most 80% sequence identity over a region of about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, about 500 nucleotides, about 525 nucleotides, about 550 nucleotides, about 575 nucleotides, about 600 nucleotides, about 625 nucleotides, about 650 nucleotides, about 675 nucleotides, about 700 nucleotides, about 725 nucleotides, about 750 nucleotides, about 775 nucleotides, about 800 nucleotides, about 825 nucleotides, about 850 nucleotides, about 875 nucleotides, about 900 nucleotides, about 925 nucleotides, about 950 nucleotides, about 975 nucleotides, about 1000 nucleotides, about 1025 nucleotides, about 1050 nucleotides, about 1075 nucleotides, or about 2000 nucleotides. In certain embodiments, the nucleotide sequences of all the DNA fragments outside the homologous region(s) may have regions with 90% or higher sequence identity, and such regions are at most about 10 nucleotide, about 20 nucleotide, about 30 nucleotide, or at most about 40 nucleotides in length. In certain embodiments, the nucleotide sequences of all the DNA fragments outside the homologous region(s) may have at most 70% or 80% sequence identity over a region of about 20 nucleotides, about 30 nucleotides, about 40 nucleotides, about 50 nucleotides, about 60

nucleotides, about 70 nucleotides, about 80 nucleotides, about 90 nucleotides, about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, or about 500 nucleotides. In certain embodiments, the level of homology in the nucleotide sequences of all the DNA fragments outside the homologous region is not enough to allow homologous recombination of the DNA fragments in the regions that are outside the homologous region. In certain embodiments, the level of homology in the nucleotide sequences of all the DNA fragments outside the homologous region may allow at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or at most 10 undesired recombination events of the DNA fragments in the regions that are outside the homologous region per 10,000 copies of each of the DNA fragments per 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days of incubation.

(iii) The first and the second DNA fragments outside the 5' and/or 3' homologous region(s) are not homologous to a sequence in the *Leishmania* cell's genome

[0071] In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) are not homologous to a sequence in the *Leishmania* cell's genome. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) and the *Leishmania* cell's genome may have at most 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or at most 80% sequence identity over a region of about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, about 500 nucleotides, about 525 nucleotides, about 550 nucleotides, about 575 nucleotides, about 600 nucleotides, about 625 nucleotides, about 650 nucleotides, about 675 nucleotides, about 700 nucleotides, about 725 nucleotides, about 750 nucleotides, about 775 nucleotides, about 800 nucleotides, about 825 nucleotides, about 850 nucleotides, about 875 nucleotides, about 900 nucleotides, about 925 nucleotides, about 950 nucleotides, about 975 nucleotides, about 1000 nucleotides, about 1025 nucleotides, about 1050 nucleotides, about 1075 nucleotides, or about 2000 nucleotides. In

certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) and the *Leishmania* cell's genome may have regions with 90% or higher sequence identity, and such regions are at most about 10 nucleotide, about 20 nucleotide, about 30 nucleotide, or at most about 40 nucleotides in length. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) and the *Leishmania* cell's genome may have at most 70% or 80% sequence identity over a region of about 20 nucleotides, about 30 nucleotides, about 40 nucleotides, about 50 nucleotides, about 60 nucleotides, about 70 nucleotides, about 80 nucleotides, about 90 nucleotides, about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, or about 500 nucleotides. In certain embodiments, the level of homology in the first and the second DNA fragments outside the homologous region and the *Leishmania* cell's genome is not enough to allow homologous recombination of the DNA fragments and the *Leishmania* cell's genome in the regions that are outside the homologous region. In certain embodiments, the level of homology in the first and the second DNA fragments outside the homologous region and the *Leishmania* cell's genome may allow at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or at most 10 undesired recombination events of the DNA fragments and the *Leishmania* cell's genome in the regions that are outside the homologous region per 10,000 copies of each of the first and the second DNA fragments per 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days of incubation.

(iv) All the DNA fragments outside the 5' and/or 3' homologous region(s) are not homologous to a sequence in the *Leishmania* cell's genome

[0072] In certain embodiments, the nucleotide sequences of all the DNA fragments outside the homologous region(s) are not homologous to a sequence in the *Leishmania* cell's genome. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) and the *Leishmania* cell's genome may have at most 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or at most 80% sequence identity over a region of about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250

nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, about 500 nucleotides, about 525 nucleotides, about 550 nucleotides, about 575 nucleotides, about 600 nucleotides, about 625 nucleotides, about 650 nucleotides, about 675 nucleotides, about 700 nucleotides, about 725 nucleotides, about 750 nucleotides, about 775 nucleotides, about 800 nucleotides, about 825 nucleotides, about 850 nucleotides, about 875 nucleotides, about 900 nucleotides, about 925 nucleotides, about 950 nucleotides, about 975 nucleotides, about 1000 nucleotides, about 1025 nucleotides, about 1050 nucleotides, about 1075 nucleotides, or about 2000 nucleotides. In certain embodiments, the nucleotide sequences of all the DNA fragments outside the homologous region(s) and the *Leishmania* cell's genome may have regions with 90% or higher sequence identity, and such regions are at most about 10 nucleotide, about 20 nucleotide, about 30 nucleotide, or at most about 40 nucleotides in length. In certain embodiments, the nucleotide sequences of all the DNA fragments outside the homologous region(s) and the *Leishmania* cell's genome may have at most 70% or 80% sequence identity over a region of about 20 nucleotides, about 30 nucleotides, about 40 nucleotides, about 50 nucleotides, about 60 nucleotides, about 70 nucleotides, about 80 nucleotides, about 90 nucleotides, about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, or about 500 nucleotides. In certain embodiments, the level of homology in the nucleotide sequences of all the DNA fragments outside the homologous region and the *Leishmania* cell's genome is not enough to allow homologous recombination of the DNA fragments and the *Leishmania* cell's genome in the regions that are outside the homologous region. In certain embodiments, the level of homology in the nucleotide sequences of all the DNA fragments outside the homologous region and the *Leishmania* cell's genome may allow at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or at most 10 undesired recombination events of the DNA fragments and the *Leishmania* cell's genome in the regions that are outside the homologous region per 10,000 copies of each of the DNA fragments per 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days of incubation.

(v) The first and the second DNA fragments have no homologies within the respective DNA fragment

[0073] In certain embodiments, the nucleotide sequences of the first and the second DNA fragments have no homologies within the respective DNA fragment. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments within the respective DNA fragment may contain nucleotide sequences that have at most 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or at most 80% sequence identity over a region of about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, about 500 nucleotides, about 525 nucleotides, about 550 nucleotides, about 575 nucleotides, about 600 nucleotides, about 625 nucleotides, about 650 nucleotides, about 675 nucleotides, about 700 nucleotides, about 725 nucleotides, about 750 nucleotides, about 775 nucleotides, about 800 nucleotides, about 825 nucleotides, about 850 nucleotides, about 875 nucleotides, about 900 nucleotides, about 925 nucleotides, about 950 nucleotides, about 975 nucleotides, about 1000 nucleotides, about 1025 nucleotides, about 1050 nucleotides, about 1075 nucleotides, or about 2000 nucleotides. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments within the respective DNA fragment may contain nucleotide sequences with 90% or higher sequence identity, and such regions are at most about 10 nucleotide, about 20 nucleotide, about 30 nucleotide, or at most about 40 nucleotides in length. In certain embodiments, the nucleotide sequences of the first and the second DNA fragments within the respective DNA fragment may contain nucleotide sequences that have at most 70% or 80% sequence identity over a region of about 20 nucleotides, about 30 nucleotides, about 40 nucleotides, about 50 nucleotides, about 60 nucleotides, about 70 nucleotides, about 80 nucleotides, about 90 nucleotides, about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, or about 500 nucleotides. In certain embodiments, the level of homology in the nucleotide sequences of the first and the second DNA fragments within the

respective DNA fragment is not enough to allow homologous recombination of the DNA fragments within itself. In certain embodiments, the level of homology in the nucleotide sequences of the first and the second DNA fragments within the respective DNA fragment may allow at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or at most 10 undesired recombination events within the DNA fragment itself per 10,000 copies of the DNA fragment per 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days of incubation.

(vi) All the DNA fragments have no homologies within the respective DNA fragment

[0074] In certain embodiments, the nucleotide sequences of all the DNA fragments have no homologies within the respective DNA fragment. In certain embodiments, the nucleotide sequences of all the DNA fragments within the respective DNA fragment may contain nucleotide sequences that have at most 1%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, or at most 80% sequence identity over a region of about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225 nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, about 500 nucleotides, about 525 nucleotides, about 550 nucleotides, about 575 nucleotides, about 600 nucleotides, about 625 nucleotides, about 650 nucleotides, about 675 nucleotides, about 700 nucleotides, about 725 nucleotides, about 750 nucleotides, about 775 nucleotides, about 800 nucleotides, about 825 nucleotides, about 850 nucleotides, about 875 nucleotides, about 900 nucleotides, about 925 nucleotides, about 950 nucleotides, about 975 nucleotides, about 1000 nucleotides, about 1025 nucleotides, about 1050 nucleotides, about 1075 nucleotides, or about 2000 nucleotides. In certain embodiments, the nucleotide sequences of all the DNA fragments within the respective DNA fragment may contain nucleotide sequences with 90% or higher sequence identity, and such regions are at most about 10 nucleotide, about 20 nucleotide, about 30 nucleotide, or at most about 40 nucleotides in length. In certain embodiments, the nucleotide sequences of all the DNA fragments within the respective DNA fragment may contain nucleotide sequences that have at most 70% or 80% sequence identity over a region of about 20 nucleotides, about 30 nucleotides, about 40 nucleotides, about 50 nucleotides, about 60 nucleotides, about 70 nucleotides, about 80 nucleotides, about 90 nucleotides, about 100 nucleotides, about 125 nucleotides, about 150 nucleotides, about 175 nucleotides, about 200 nucleotides, about 225

nucleotides, about 250 nucleotides, about 275 nucleotides, about 300 nucleotides, about 325 nucleotides, about 350 nucleotides, about 375 nucleotides, about 400 nucleotides, about 425 nucleotides, about 450 nucleotides, about 475 nucleotides, or about 500 nucleotides. In certain embodiments, the level of homology in the nucleotide sequences of all the fragments within the respective DNA fragment is not enough to allow homologous recombination of the DNA fragments within itself. In certain embodiments, the level of homology in the nucleotide sequences of all the DNA fragments within the respective DNA fragment may allow at most 1, 2, 3, 4, 5, 6, 7, 8, 9, or at most 10 undesired recombination events within the DNA fragment itself per 10,000 copies of the DNA fragment per 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, or 15 days of incubation.

[0075] In certain embodiments, the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) have no repetitive sequences.

[0076] In certain embodiments, the number of DNA fragments is at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, or at least 25. In certain embodiments, the number of DNA fragments is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 37, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50.

5.1.4 Translation product of the DNA fragments

[0077] In certain embodiments, the nucleotide sequences of the two or more DNA fragments outside the homologous region are selected from a group consisting of intergenic regions (IRs), untranslated regions (UTRs), and open reading frames (ORFs) encoding polypeptides. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are selected from a group consisting of intergenic regions (IRs), untranslated regions (UTRs), and open reading frames (ORFs) that are described in the Example section. In certain embodiments, the IRs, UTRs and ORFs are devoid of homologous sequences within itself, and/or homologous sequences to one another.

[0078] In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are ORFs that encode target polypeptides as described in Section 5.4. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are ORFs that encode enzymes related to the production of the target polypeptides. Non-limiting exemplary enzymes may be found in International Publication No. WO2019/002512 A2,

incorporated by reference in its entirety herein) and International Application entitled "Glycoengineering Using *Leishmania* Cells" filed even date herewith. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region are ORFs that encode heterologous glycosyltransferases. In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region may be transcribed to RNA products, for example ribozymes, regulating RNA, ncRNA, and crisprRNA). In certain embodiments, the nucleotide sequences of the DNA fragments outside the homologous region may be ORFs that encode polypeptides having the function that relates to catalyzing metabolic reactions and DNA replication, responding to stimuli, transporting molecules from one location to another, providing structure to cells and organisms, aggregation and adhesion to other cells, localization of molecules, utilization of carbon, carbohydrates, nitrogen, phosphorus and sulfur, biomineralization, growth, development and mitosis of cells, locomotion, biological regulation, protein folding, and/or toxins.

[0079] In certain embodiments, the nucleotide sequences of the two or more DNA fragments outside the homologous region encode the same polypeptide. In certain embodiments, the *Leishmania* cell is capable of expressing multiple copies of the same polypeptide. In certain embodiments, the method provided herein increases the expression level of the polypeptide. In certain embodiments, using multiple DNA fragments encoding the same polypeptide may increase the expression level of the polypeptide in comparison to the resulting expression level of the approach using one DNA fragment encoding the polypeptide.

(i) Nucleotide sequence resulted from the homologous recombination of the DNA fragments

[0080] In certain embodiments, the homologous recombination of the DNA fragments results in a nucleotide sequence that is 50 nucleotides to 100 nucleotides, 100 nucleotides to 500 nucleotides, 500 nucleotides to 1000 nucleotides, 1000 nucleotides to 5000 nucleotides, 5000 nucleotides to 10000 nucleotides, 10000 nucleotides to 15000 nucleotides, 15000 nucleotides to 20000 nucleotides, 20000 nucleotides to 25000 nucleotides, 25000 nucleotides to 30000 nucleotides, 30000 nucleotides to 35000 nucleotides, 35000 nucleotides to 40000 nucleotides, 40000 nucleotides to 45000 nucleotides, 45000 nucleotides to 50000 nucleotides, 50000 nucleotides to 55000 nucleotides, 55000 nucleotides to 60000 nucleotides, 60000 nucleotides to

65000 nucleotides, 65000 nucleotides to 70000 nucleotides, 70000 nucleotides to 75000 nucleotides, or 75000 nucleotides to 80000 nucleotides in length.

[0081] In certain embodiments, the homologous recombination of the DNA fragments results in a nucleotide sequence comprising at least 50%, 60%, 70%, 80%, 90% or 100% of genetic information encoded by the two or more DNA fragments. In certain embodiments, the nucleotide sequence resulted from the homologous recombination of the DNA fragments contains all the genetic information encoded in the two or more DNA fragments.

5.1.5 Undesired crossing out and/or crossing over

[0082] In general, the methods provided herein are capable of avoiding undesired genetic recombination events. In certain embodiments, the undesired genetic recombination events include crossing over and crossing out. In certain embodiments, the undesired genetic recombination events may be single-strand annealing (SSA) or micro homology mediated end joining (MMEJ) and non-homologous end joining (NHEJ) (Zhang (2019) Single-Strand Annealing Plays a Major Role in Double-Strand DNA Break Repair following CRISPR-Cas9 Cleavage in *Leishmania*. doi: 10.1128/mSphere.00408-19.) In certain embodiments, undesired crossing out and/or crossing over may lead to omission of genetic information of the DNA fragments in the nucleotide sequence resulted from the homologous recombination of the DNA fragments. In certain embodiments, undesired crossing out and/or crossing over may lead to omission of genetic information of the chromosomal endogenous DNA.

[0083] In certain embodiments, undesired crossing out and/or crossing over may be detected using gene sequencing technologies known in the art. In certain embodiments, undesired crossing out and/or crossing over may be detected by phenotypical testing of the resulting genetically engineered *Leishmania* cells, for example by testing of the activity of an enzyme that is encoded by one or more DNA fragments used in the method described herein. In certain embodiments, undesired crossing out and/or crossing over may be detected using methods as described in the Assay and Example sections of this application.

[0084] In certain embodiments, the method described herein results in low level of undesired crossing out and/or crossing over. In certain embodiments, the undesired crossing out and/or crossing over occurs in at most 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or at most 10% of the *Leishmania* cells over a period of at least 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, or at least 10 days. In certain embodiments, the undesired

crossing out and/or crossing over occurs in about 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or about 10% of the *Leishmania* cells over a period of at least 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, or at least 10 days.

[0085] In certain embodiments, the undesired crossing out and/or crossing over occurs in at most 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or at most 10% of the *Leishmania* cells over a period of 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, or 10 days. In certain embodiments, the undesired crossing out and/or crossing over occurs in about 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or about 10% of the *Leishmania* cells over a period of 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, or 10 days.

[0086] In certain embodiments, the undesired crossing out and/or crossing over occurs in at most 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or at most 10% of the *Leishmania* cells over at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or at least 10 cell divisions. In certain embodiments, the undesired crossing out and/or crossing over occurs in about 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or about 10% of the *Leishmania* cells over at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or at least 10 cell divisions.

[0087] In certain embodiments, the undesired crossing out and/or crossing over occurs in at most 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or at most 10% of the *Leishmania* cells over 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 cell divisions. In certain embodiments, the undesired crossing out and/or crossing over occurs in about 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or about 10% of the *Leishmania* cells over 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 cell divisions.

5.1.6 Chromosomal integration

[0088] In certain embodiments, the two or more DNA fragments are suitable for integration in the chromosome of the *Leishmania* cell.

[0089] In certain embodiments, the two or more DNA fragments are integrated into the chromosomes of the *Leishmania* cell. In certain embodiments, one of the DNA fragments comprises a 5' homologous region that is homologous to a region in the chromosome of the *Leishmania* cell, and a 3' homologous region that is homologous to a 5' homologous region of another DNA fragment. In certain embodiments, one of the DNA fragments comprises a 3' homologous region that is homologous to another region in the chromosome of the *Leishmania*

cell, and a 5' homologous region that is homologous to a 3' homologous region of another DNA fragment. In certain embodiments, the homologous regions that are homologous to regions in the chromosome of the *Leishmania* cell allow the integration of the DNA fragments into the chromosome of the *Leishmania* cell. Non-limiting examples of the chromosomal integration described herein may be found in the Example section and illustrated in at least FIGs. 1A, 3B, 4, 6B, and 8A.

5.1.7 Extrachromosomal plasmid

[0090] In certain embodiments, the two or more DNA fragments are not integrated in the chromosome of the *Leishmania* cell. In certain embodiments, the homologous recombination of the two or more DNA fragments results in a circular plasmid. In certain embodiment, the circular plasmid comprises a cos site. In certain embodiment, the circular plasmid is a cosmid. In certain embodiment, the plasmid is an *Escherichia coli* cosmid. Non-limiting examples of the extrachromosomal plasmid described herein include the *Escherichia coli* cosmid as described in Example 6 and illustrated in at least FIG. 11A.

5.1.8 Introduction of a DNA fragment into host cells

[0091] Any method known in the art can be used to introduce a DNA fragment (e.g., a gene fragment thereof) into the host cell, e.g., a *Leishmania* cell.

[0092] In certain embodiments, a DNA fragment is introduced into the host cells described herein using transfection, infection, or electroporation, chemical transformation by heat shock, natural transformation, phage transduction, or conjugation. In a further embodiment, a DNA fragment is introduced into integrated site-specifically into the host cell genome by homologous recombination.

[0093] In certain embodiments, a DNA fragment is introduced into the host cells described herein using a plasmid, e.g., a DNA fragment is expressed in the host cells by a plasmid (e.g., an expression vector), and the plasmid is introduced into the modified host cells by transfection, infection, or electroporation, chemical transformation by heat shock, natural transformation, phage transduction, or conjugation. In a specific embodiment, said plasmid is introduced into the modified host cells by stable transfection.

[0094] In certain embodiments, the two or more DNA fragments are introduced by transfection. In certain embodiments, the two or more DNA fragments are introduced concurrently.

5.1.9 Methods of culturing cells

[0095] Provided herein are methods for culturing host cells, for example *Leishmania* host cells. In one embodiment, host cells are cultured using any of the standard culturing techniques known in the art. For example, cells are routinely grown in rich media like Brain Heart Infusion, Trypticase Soy Broth or Yeast Extract, all containing 5 μg /ml Hemin. Additionally, incubation is done at 26°C in the dark as static or shaking cultures for 2-3 days. In some embodiments, cultures of recombinant cell lines contain the appropriate selective agents. Non-limiting exemplary selective agents are provided in Table 1. In some embodiments, cultures contain Biopterin at a final concentration of 10 μM to support growth. In certain embodiments, host cells may be cultured using the methods as described in the Assay and Examples Sections.

5.2 *Leishmania* Cell

[0096] Also provided herein are genetically engineered *Leishmania* cells. In certain embodiments, the *Leishmania* cells are genetically engineered using the method described herein in Section 5.1. In certain embodiments, the *Leishmania* cell is recombinantly engineered using the method described herein repeatedly. In certain embodiments, the *Leishmania* cells described herein may be used to express the DNA fragments as described in Section 5.1.1. In certain embodiments, the *Leishmania* cells described herein may be used as an expression system as described in Section 5.3. In certain embodiments, the *Leishmania* cells described herein may be used to make a polypeptide as described in Section 5.4.

5.2.1 Genetically engineered *Leishmania* cells

[0097] In certain embodiments, the *Leishmania* cells are genetically engineered such that they may be used to express the ORFs of the DNA fragments. In certain embodiments, the DNA fragments are integrated into the chromosomes of the *Leishmania* cell. In certain embodiments, the DNA fragments are not integrated into the chromosomes of the *Leishmania* cell. In certain embodiments, the homologous recombination of the DNA fragments are circularized to an extrachromosomal plasmid. In certain embodiment, the plasmid is a cosmid. In certain embodiment, the plasmid is an *E. coli* cosmid.

5.2.2 *Leishmania* and Kinetoplastida strains

[0098] In certain embodiments, the *Leishmania* cell is a *Leishmania tarentolae* cell. In certain embodiments, the *Leishmania* cell is a *Leishmania aethiopica* cell. In certain

embodiments, the *Leishmania* cell is part of the *Leishmania aethiopica* species complex. In certain embodiments, the *Leishmania* cell is a *Leishmania aristidesi* cell. In certain embodiments, the *Leishmania* cell is a *Leishmania deanei* cell. In certain embodiments, the *Leishmania* cell is part of the *Leishmania donovani* species complex. In certain embodiments, the *Leishmania* cell is a *Leishmania donovani* cell. In certain embodiments, the *Leishmania* cell is a *Leishmania chagasi* cell. In certain embodiments, the *Leishmania* cell is a *Leishmania infantum* cell. In certain embodiments, the *Leishmania* cell is a *Leishmania hertigi* cell. In certain embodiments, the *Leishmania* cell is part of the *Leishmania major* species complex. In certain embodiments, the *Leishmania* cell is a *Leishmania major* cell. In certain embodiments, the *Leishmania* cell is a *Leishmania martiniquensis* cell. In certain embodiments, the *Leishmania* cell is part of the *Leishmania mexicana* species complex. In certain embodiments, the *Leishmania* cell is a *Leishmania mexicana* cell. In certain embodiments, the *Leishmania* cell is a *Leishmania pifanoi* cell. In certain embodiments, the *Leishmania* cell is part of the *Leishmania tropica* species complex. In certain embodiments, the *Leishmania* cell is a *Leishmania tropica* cell.

[0099] In certain embodiments, other host cells may be genetically engineered using the method described herein. In certain embodiments, the host cell belongs to the bodonidae family of kinetoplasts. In a specific embodiment, the host cell is a *Bodo saltans* cell. In certain embodiments, the host cell belongs to the ichthyobodonidae family of kinetoplasts. In certain embodiments, the host cell belongs to the trypanosomatidae family of kinetoplasts. In certain embodiments, the host cell belongs to the blastocrithidia family of trypanosomatidae. In certain embodiments, the host cell belongs to the blechomonas family of trypanosomatidae. In certain embodiments, the host cell belongs to the herpetomonas family of trypanosomatidae. In certain embodiments, the host cell belongs to the jaenimonas family of trypanosomatidae. In certain embodiments, the host cell belongs to the lafontella family of trypanosomatidae. In certain embodiments, the host cell belongs to the leishmaniinae family of trypanosomatidae. In certain embodiments, the host cell belongs to the novymonas family of trypanosomatidae. In certain embodiments, the host cell belongs to the paratrypanosoma family of trypanosomatidae. In certain embodiments, the host cell belongs to the phytomonas family of trypanosomatidae. In certain embodiments, the host cell belongs to the sergeia family of trypanosomatidae. In certain embodiments, the host cell belongs to the strigomonadinae family of trypanosomatidae. In

certain embodiments, the host cell belongs to the trypanosoma family of trypanosomatidae. In certain embodiments, the host cell belongs to the wallacemonas family of trypanosomatidae. In certain embodiments, the host cell belongs to the blastocrithidia family of trypanosomatidae.

5.3 Uses of the *Leishmania* cell as Expression Systems

[00100] In certain embodiments, a *Leishmania* cell (as described in Section 5.2) may be used as an expression system for making of a polypeptide. In certain embodiments, the polypeptide may be a heterologous, non-*Leishmania* protein, such as a therapeutic protein (e.g., an antibody).

5.3.1 Compositions comprising host cells

[00101] In one aspect, provided herein are compositions comprising the host cells described herein, for example, compositions comprising the *Leishmania* cells as described in Section 5.2. Such compositions can be used in methods for generating a target polypeptide as described in Section 5.4. In certain embodiments, the compositions comprising host cells can be cultured under conditions suitable for the production of polypeptides. Subsequently, the polypeptides can be isolated from said compositions comprising host cells using methods known in the art.

[00102] The compositions comprising the host cells provided herein can comprise additional components suitable for maintenance and survival of the host cells described herein, and can additionally comprise additional components required or beneficial to the production of polypeptides by the host cells, e.g., inducers for inducible promoters, such as arabinose, IPTG, tetracycline, and doxycycline.

[00103] In certain embodiments, provided herein are kits comprising one or more containers and instructions for use, wherein said one or more containers comprise the *Leishmania* cell described herein.

5.3.2 Methods of Target Polypeptide Production

[00104] In one aspect, provided herein are methods of making a target polypeptide as described in Section 5.4. In one embodiment, provided herein is a method of producing a target polypeptide as described in Section 5.4 *in vivo*, using a host cell described herein. In a specific embodiment, provided herein is a method for producing a target polypeptide, said method comprising (i) culturing a host cell provided herein under conditions suitable for polypeptide production and (ii) isolating said target polypeptide. In a specific embodiment, the host cell comprises (a) a recombinant nucleic acid encoding a target polypeptide; and (b) a recombinant

nucleic acid encoding one or more heterologous glycosyltransferases. In certain embodiments, the heterologous glycosyltransferase is an N-acetyl glucosamine transferase; or a heterologous galactosyltransferase; or a heterologous sialyltransferase. In certain embodiments, the host cell is a *Leishmania* cell.

[00105] In one aspect, provided herein are methods of making a polypeptide as described in Section 5.4 comprising (a) culturing the *Leishmania* cell described herein in Section 5.2 under suitable conditions for polypeptide production; and (b) isolating the polypeptide. In certain embodiments, the method further comprises introducing a nucleotide sequence encoding the polypeptide.

[00106] In certain embodiments, the target polypeptide produced by the host cells provided is a therapeutic polypeptide, *i.e.*, a polypeptide used in the treatment of a disease or disorder. For example, the target polypeptide produced by the host cells provided herein can be an enzyme, a cytokine, or an antibody. A list of non-limiting exemplary target polypeptides is provided in Section 5.4.

5.4 Target Polypeptide

[00107] In one aspect, provided herein are polypeptides produced by the method as described in Section 5.3. In certain embodiments, the target polypeptide produced by the *Leishmania* cells provided is a therapeutic polypeptide, *i.e.*, a polypeptide used in the treatment of a disease or disorder. For example, the target polypeptide produced by the host cells provided herein can be an enzyme, a cytokine, or an antibody. In certain embodiments, the target the polypeptide is selected from the group consisting of adalimumab, rituximab and erythropoietin (EPO).

[00108] Any polypeptide (or peptide/polypeptide corresponding to the polypeptide) known in the art can be used as a target polypeptide in accordance with the methods described herein. One of skill in the art will readily appreciate that the nucleic acid sequence of a known polypeptide, as well as a newly identified polypeptide, can easily be deduced using methods known in the art, and thus it would be well within the capacity of one of skill in the art to introduce a nucleic acid that encodes any polypeptide of interest into a host cell provided herein (e.g., via an expression vector, e.g., a plasmid, e.g., a site specific integration by homologous recombination).

[00109] In certain embodiments, the target polypeptide is glycosylated, e.g., sialylated. One of skill in the art will further recognize that the target polypeptides may be glycosylated using the

methods described herein, e.g., either *in vivo* using a host cell provided herein or *in vitro*, possess therapeutic benefit (e.g., due to improved pharmacokinetics) and thus can be used in the treatment of subjects having diseases/disorders that will benefit from treatment with the glycosylated (e.g., polysialylated) target polypeptides.

[00110] In certain embodiments, the target polypeptide comprises the amino acid sequence of human Interferon-α (INF-α), Interferon-β (INF-β), Interferon-γ (INF-γ), Interleukin-2 (IL2), Chimeric diphteria toxin-IL-2 (Denileukin diftitox), Interleukin-1 (IL1), IL1B, IL3, IL4, IL11, IL21, IL22, IL1 receptor antagonist (anakinra), Tumor necrosis factor alpha (TNF-α), Insulin, Pramlintide, Growth hormone (GH), Insulin-like growth factor (IGF1), Human parathyroid hormone, Calcitonin, Glucagon-like peptide-1 agonist (GLP-1), Glucagon, Growth hormone-releasing hormone (GHRH), Secretin, Thyroid stimulating hormone (TSH), Human bone morphogenic polypeptide 2 (hBMP2), Human bone morphogenic proetin 7 (hBMP7), Gonadotropin releasing hormone (GnRH), Keratinocyte growth factor (KGF), Platelet-derived growth factor (PDGF), Fibroblast growth factor 7 (FGF7), Fibroblast growth factor 20 (FGF20), Fibroblast growth factor 21 (FGF21), Epidermal growth factor (EGF), Vascular endothelial growth factor (VEGF), Neurotrophin-3, Human follicle-stimulating hormone (FSH), Human chorionic gonadotropin (HCG), Lutropin-α, Erythropoietin, Granulocyte colony-stimulating factor (G-CSF), Granulocyte-macrophage colony-stimulating factor (GM-CSF), the extracellular domain of CTLA4 (e.g., an FC-fusion), or the extracellular domain of TNF receptor (e.g., an FC-fusion). In a specific embodiment, the target polypeptide used in accordance with the methods and host cells described herein is an enzyme or an inhibitor. Exemplary enzymes and inhibitors that can be used as a target polypeptide include, without limitation, Factor VII, Factor VIII, Factor IX, Factor X, Factor XIII, Factor VIIa, Antithrombin III (AT-III), Polypeptide C, Tissue plasminogen activator (tPA) and tPA variants, Urokinase, Hirudin, Streptokinase, Glucocerebrosidase, Alglucosidase-α, Laronidase (α-L-iduronidase), Idursulphase (Iduronate-2-sulphatase), Galsulphase, Agalsidase-β (human α-galactosidase A), Botulinum toxin, Collagenase, Human DNAse-I, Hyaluronidase, Papain, L-Asparaginase, Uricase (Urate oxidase), glutamate carboxypeptidase (glucarpidase), α1 Protease inhibitor (α1 antitrypsin), Lactase, Pancreatic enzymes (lipase, amylase, protease), and Adenosine deaminase.

[00111] In a specific embodiment, the target polypeptide used in accordance with the methods and host cells described herein is a cytokine. Exemplary cytokines that can be used as a target

polypeptide include, without limitation, Interferon-α (INF-α), Interferon-β (INF-β), Interferon-γ (INF-γ), Interleukin-2 (IL2), Chimeric diphteria toxin-IL-2 (Denileukin diftitox), Interleukin-1 (IL1), IL1B, IL3, IL4, IL11, IL21, IL22, IL1 receptor antagonist (anakinra), and Tumor necrosis factor alpha (TNF-α).

[00112] In a specific embodiment, the target polypeptide used in accordance with the methods and host cells described herein is a hormone or growth factor. Exemplary hormones and growth factors that can be used as a target polypeptide include, without limitation, Insulin, Pramlintide, Growth hormone (GH), Insulin-like growth factor (IGF1), Human parathyroid hormone, Calcitonin, Glucagon-like peptide-1 agonist (GLP-1), Glucagon, Growth hormone-releasing hormone (GHRH), Secretin, Thyroid stimulating hormone (TSH), Human bone morphogenic polypeptide 2 (hBMP2), Human bone morphogenic proetin 7 (hBMP7), Gonadotropin releasing hormone (GnRH), Keratinocyte growth factor (KGF), Platelet-derived growth factor (PDGF), Fibroblast growth factor 7 (FGF7), Fibroblast growth factor 20 (FGF20), Fibroblast growth factor 21 (FGF21), Epidermal growth factor (EGF), Vascular endothelial growth factor (VEGF), Neurotrophin-3, Human follicle-stimulating hormone (FSH), Human chorionic gonadotropin (HCG), Lutropin-α, Erythropoietin, Granulocyte colony-stimulating factor (G-CSF), and Granulocyte-macrophage colony-stimulating factor (GM-CSF).

[00113] In a specific embodiment, the target polypeptide used in accordance with the methods and host cells described herein is a receptor. Exemplary receptors that can be used as a target polypeptide include, without limitation, the extracellular domain of human CTLA4 (e.g., fused to an Fc) and the soluble TNF receptor (e.g., fused to an Fc).

[00114] In other embodiments, the target polypeptide is a therapeutic polypeptide. In other embodiments, the target polypeptide is an approved biologic drug. In another embodiment, the therapeutic polypeptide comprises the amino acid sequence of Abatacept (e.g., Orencia), Aflibercept (e.g., Eylea), Agalsidase beta (e.g., Fabrazyme), Albiglutide (e.g., Eperzan), Aldesleukin (e.g., Proleukin), Alefacept (e.g., Amevive), Alglucerase (e.g., Ceredase), Alglucosidase alfa (e.g., LUMIZYME), Aliskiren (e.g., Tekturna), Alpha-1-polypeptidease inhibitor (e.g., Aralast), Alteplase (e.g., Activase), Anakinra (e.g., Kineret), Anistreplase (e.g., Eminase), Anthrax immune globulin human (e.g., ANTHRASIL), Antihemophilic Factor (e.g., Advate), Anti-inhibitor coagulant complex (e.g., Feiba Nf), Antithrombin Alfa, Antithrombin III

human, Antithymocyte globulin (e.g., Antithymocyte globulin), Anti-thymocyte Globulin (Equine) (e.g., ATGAM), Anti-thymocyte Globulin (Rabbit) (e.g., ATG-Fresenius), Aprotinin (e.g., Trasylol), Asfotase Alfa, Asparaginase (e.g., Elspar), Asparaginase erwinia chrysanthemi (e.g., Erwinaze), Becaplermin (e.g., REGRANEX), Belatacept (e.g., Nulojix), Beractant, Bivalirudin (e.g., Angiomax), Botulinum Toxin Type A (e.g., BOTOXÊ), Botulinum Toxin Type B (e.g., Myobloc), Brentuximab vedotin (e.g., Adcetris), Buserelin (e.g., Suprecur), C1 Esterase Inhibitor (Human), C1 Esterase Inhibitor (Recombinant) (e.g., Ruconest), Certolizumab pegol (e.g., Cimzia), Choriogonadotropin alfa (e.g., Choriogonadotropin alfa), Chorionic Gonadotropin (Human) (e.g., Ovidrel), Chorionic Gonadotropin (Recombinant) (e.g., Ovitrelle), Coagulation factor ix (e.g., Alprolix), Coagulation factor VIIa (e.g., NovoSeven), Coagulation factor X human (e.g., Coagadex), Coagulation Factor XIII A-Subunit (Recombinant), Collagenase (e.g., Cordase), Conestat alfa, Corticotropin (e.g., H.P. Acthar), Cosyntropin (e.g., Cortrosyn), Darbepoetin alfa (e.g., Aranesp), Defibrotide (e.g., Noravid), Denileukin diftitox (e.g., Ontak), Desirudin, Digoxin Immune Fab (Ovine) (e.g., DIGIBIND), Dornase alfa (e.g., Pulmozyme), Drotrecogin alfa (e.g., Xigris), Dulaglutide, Efmoroctocog alfa (e.g., ELOCTA), Elosulfase alfa, Enfuvirtide (e.g., FUZEON), Epoetin alfa (e.g., Binocrit), Epoetin zeta (e.g., Retacrit), Eptifibatide (e.g., INTEGRILIN), Etanercept (e.g., Enbrel), Exenatide (e.g., Byetta), Factor IX Complex (Human) (e.g., AlphaNine), Fibrinolysin aka plasmin (e.g., Elase), Filgrastim (e.g., N.A.), Filgrastim-sndz, Follitropin alfa (e.g., Gonal-F), Follitropin beta (e.g., Follistim AQ), Galsulfase (e.g., Naglazyme), Gastric intrinsic factor, Gemtuzumab ozogamicin (e.g., Mylotarg), Glatiramer acetate (e.g., Copaxone), Glucagon recombinant (e.g., GlucaGen), Glucarpidase (e.g., Voraxaze), Gramicidin D (e.g., Neosporin), Hepatitis B immune globulin, Human calcitonin, Human clostridium tetani toxoid immune globulin, Human rabies virus immune globulin (e.g., Hyperab Rabies Immune Globulin Human), Human Rho(D) immune globulin (e.g., Hyp Rho D Inj 16.5%), Human Serum Albumin (e.g., Albuminar), Human Varicella-Zoster Immune Globulin (e.g., Varizig), Hyaluronidase (e.g., HYLENEX), Hyaluronidase (Human Recombinant), Ibritumomab tiuxetan (e.g., Zevalin), Idursulfase (e.g., Elaprase), Imiglucerase (e.g., Cerezyme), Immune Globulin Human, Insulin aspart (e.g., NovoLog), Insulin Beef, Insulin Degludec (e.g., Tresiba), Insulin detemir (e.g., LEVEMIR), Insulin Glargine (e.g., Lantus), Insulin glulisine (e.g., APIDRA), Insulin Lispro (e.g., Humalog), Insulin Pork (e.g., Iletin II), Insulin Regular (e.g., Humulin R), Insulin, porcine (e.g., vetsulin), Insulin, isophane (e.g.,

Novolin N), Interferon Alfa-2a, Recombinant (e.g., Roferon A), Interferon alfa-2b (e.g., INTRON A), Interferon alfacon-1 (e.g., INFERGEN), Interferon alfa-n1 (e.g., Wellferon), Interferon alfa-n3 (e.g., Alferon), Interferon beta-1a (e.g., Avonex), Interferon beta-1b (e.g., Betaseron), Interferon gamma-1b (e.g., Actimmune), Intravenous Immunoglobulin (e.g., Civacir), Laronidase (e.g., Aldurazyme), Lenograstim (e.g., Granocyte), Lepirudin (e.g., Refludan), Leuprolide (e.g., Eligard), Liraglutide (e.g., Saxenda), Lucinactant (e.g., Surfaxin), Lutropin alfa (e.g., Luveris), Mecasermin (e.g., N.A.), Menotropins (e.g., Menopur), Methoxy polyethylene glycol-epoetin beta (e.g., Mircera), Metreleptin (e.g., Myalept), Natural alpha interferon OR multiferon (e.g., Intron/ Roferon-A), Nesiritide (e.g., NATRECOR), Ocriplasmin (e.g., Jetrea), Oprelvekin (e.g., Neumega), OspA lipopolypeptide (e.g., Lymerix), Oxytocin (e.g., Pitocin), Palifermin (e.g., Kepivance), Pancrelipase (e.g., Pancrecarb), Pegademase bovine (e.g., Adagen), Pegaspargase (e.g., Oncaspar), Pegfilgrastim (e.g., Neulasta), Peginterferon alfa-2a (e.g., Pegasys), Peginterferon alfa-2b (e.g., PEG-Intron), Peginterferon beta-1a (e.g., Plegridy), Pegloticase (e.g., (Krystexxa)), Pegvisomant (e.g., SOMAVERT), Poractant alfa (e.g., Curosurf), Pramlintide (e.g., Symlin), Preotact (e.g., PreotactÊ), Protamine sulfate (e.g., Protamine Sulfate Injection, USP), Polypeptide S human (e.g., Polypeptide S human), Prothrombin (e.g., Feiba Nf), Prothrombin complex (e.g., Cofact), Prothrombin complex concentrate (e.g., Kcentra), Rasburicase (e.g., Elitek), Reteplase (e.g., Retavase), Rilonacept (e.g., Arcalyst), Romiplostim (e.g., Nplate), Sacrosidase (e.g., Sucraid), Salmon Calcitonin (e.g., Calcimar), Sargramostim (e.g., Leucomax), Satumomab Pendetide (e.g., OncoScint), Sebelipase alfa (e.g., Kanuma), Secretin (e.g., SecreFlo), Sermorelin (e.g., Sermorelin acetate), Serum albumin (e.g., Albunex), Serum albumin iodonated (e.g., Megatope), Simoctocog Alfa (e.g., Nuwiq), Sipuleucel-T (e.g., Provenge), Somatotropin Recombinant (e.g., NutropinAQ), Somatropin recombinant (e.g., BioTropin), Streptokinase (e.g., Streptase), Susoctocog alfa (e.g., Obizur), Taliglucerase alfa (e.g., Elelyso), Teduglutide (e.g., Gattex), Tenecteplase (e.g., TNKase), Teriparatide (e.g., Forteo), Tesamorelin (e.g., Egrifta), Thrombomodulin Alfa (e.g., Recomodulin), Thymalfasin (e.g., Zadaxin), Thyroglobulin, Thyrotropin Alfa (e.g., Thyrogen), Tuberculin Purified Polypeptide Derivative (e.g., Aplisol), Turoctocog alfa (e.g., Zonovate), Urofollitropin (e.g., BRAVELLE), Urokinase (e.g., Kinlytic), Vasopressin (e.g., Pitressin), Velaglucerase alfa (e.g., Vpriv), Abciximab (e.g., ReoPro), Adalimumab (e.g., Humira), Alemtuzumab (e.g., CAMPATH), Alirocumab (e.g., Praluent), Arcitumomab (e.g., CEA-Scan), Atezolizumab (e.g.,

Tecentriq), Basiliximab (e.g., Simulect), Belimumab (e.g., Benlysta), Bevacizumab (e.g., Avastin), Blinatumomab (e.g., Blincyto), Brodalumab (e.g., Siliq), Canakinumab (e.g., ILARISE), Canakinumab (e.g., Ilaris), Capromab (e.g., ProstaScint), Cetuximab (e.g., Erbitux), Daclizumab (e.g., Zenapax), Daratumumab (e.g., DARZALEX), Denosumab (e.g., Xgeva), Dinutuximab (e.g., unituxin), Eculizumab (e.g., Soliris), Efalizumab (e.g., RAPTIVA), Elotuzumab (e.g., EMPLICITI), Evolocumab (e.g., Repatha), Golimumab (e.g., Simponi Injection), Ibritumomab (e.g., Zevalin), Idarucizumab (e.g., Praxbind), Infliximab (e.g., REMICADE), Ipilimumab (e.g., YERVOY), Ixekizumab (e.g., Taltz), Mepolizumab (e.g., Nucala), Muromonab (e.g., ORTHOCLONE OKT3), Natalizumab (e.g., Tysabri), Necitumumab (e.g., Portrazza), Nivolumab (e.g., Opdivo), Obiltoxaximab (e.g., Anthim), Obinutuzumab (e.g., Gazyva), Ofatumumab (e.g., Arzerra), Omalizumab (e.g., Xolair), Palivizumab (e.g., Synagis), Panitumumab (e.g., Vectibix), Pembrolizumab (e.g., Keytruda), Pertuzumab (e.g., Perjeta), Ramucirumab (e.g., Cyramza), Ranibizumab (e.g., Lucentis), Raxibacumab (e.g., RAXIBACUMAB), Rituximab (e.g., Rituxan), Secukinumab (e.g., Cosentyx), Siltuximab (e.g., Sylvant), Tocilizumab (e.g., ACTEMRA), Tositumomab (e.g., Bexxar), Trastuzumab (e.g., Herceptin), Ustekinumab (e.g., Stelara), or Vedolizumab (e.g., Entyvio).

[00115] In other embodiments, the target polypeptide is an antibody. In further embodiments, the antibody has the amino acid sequence of adalimumab (Humira); Remicade (Infliximab); ReoPro (Abciximab); Rituxan (Rituximab); Simulect (Basiliximab); Synagis (Palivizumab); Herceptin (Trastuzumab); Mylotarg (Gemtuzumab ozogamicin); Campath (Alemtuzumab); Zevalin (Ibritumomab tiuxetan); Xolair (Omalizumab); Bexxar (Tositumomab-I-131); Erbitux (Cetuximab); Avastin (Bevacizumab); Tysabri (Natalizumab); Actemra (Tocilizumab); Vectibix (Panitumumab); Lucentis (Ranibizumab); Soliris (Eculizumab); Cimzia (Certolizumab pegol); Simponi (Golimumab); Ilaris (Canakinumab); Stelara (Ustekinumab); Arzerra (Ofatumumab); Prolia (Denosumab); Numax (Motavizumab); ABThrax (Raxibacumab); Benlysta (Belimumab); Yervoy (Ipilimumab); Adcetris (Brentuximab Vedotin); Perjeta (Pertuzumab); Kadcyla (Ado-trastuzumab emtansine); or Gazyva (Obinutuzumab).

[00116] In other embodiments, the antibody is a full length antibody, an Fab, an $F(ab')_2$, an Scfv, or a sdAb. In other embodiments, the target polypeptide comprises the amino acid sequence of an enzyme or an inhibitor thereof. In another embodiment, the target polypeptide comprises the amino acid sequence of Factor VII, Factor VIII, Factor IX, Factor X, Factor XIII,

Factor VIIa, Antithrombin III (AT-III), Polypeptide C, Tissue plasminogen activator (tPA) and tPA variants, Urokinase, Hirudin, Streptokinase, Glucocerebrosidase, Alglucosidase-α, Laronidase (α-L-iduronidase), Idursulphase (Iduronate-2-sulphatase), Galsulphase, Agalsidase-β (human α-galactosidase A), Botulinum toxin, Collagenase, Human DNAse-I, Hyaluronidase, Papain, L-Asparaginase, Uricase (Urate oxidase), glutamate carboxypeptidase (glucarpidase), α1 Protease inhibitor (α1 antitrypsin), Lactase, Pancreatic enzymes (lipase, amylase, protease), and Adenosine deaminase.

[00117] In a specific embodiment, the target polypeptide used in accordance with the methods and host cells described herein is a receptor. Exemplary receptors that can be used as a target polypeptide include, without limitation, the extracellular domain of human CTLA4 (e.g., fused to an Fc) and the soluble TNF receptor (e.g., fused to an Fc).

[00118] In another embodiment, the target polypeptide is secreted into the culture media. In certain embodiments, the target polypeptide is purified from the culture media. In another embodiment, the target polypeptide is purified from the culture media via affinity purification or ion exchange chromatography. In another embodiment, the target polypeptide contains an Fc domain and is affinity purified from the culture media via polypeptide-A. In another embodiment, the target polypeptide contains an affinity tag and is affinity purified.

[00119] In certain embodiments, the target polypeptide used in accordance with the methods and host cells described herein can be a full length polypeptide, a truncation, a polypeptide domain, a region, a motif or a peptide thereof.

[00120] In certain embodiments, the target polypeptide is an Fc-fusion polypeptide.

[00121] In certain embodiments, the target polypeptide is a biologic comprising an Fc domain of an IgG.

[00122] In certain embodiment, the target polypeptide could be modified. In another embodiment, the target polypeptide has been engineered to comprise a signal sequence from *Leishmania.* In other embodiments, the signal sequence is processed and removed from the target polypeptide. In another embodiment, the target polypeptide has been engineered to comprise one or more tag(s). In other embodiments, the tag is processed and removed from the target polypeptide.

5.4.1 Composition and/or formulation comprising the polypeptide

[00123] In another aspect, provided herein are compositions (e.g., pharmaceutical compositions) comprising one or more of the target polypeptides described herein. The compositions described herein are useful in the treatment and/or prevention of diseases/disorders in subjects (e.g., human subjects) (see Section 5.4.2).

[00124] In certain embodiments, in addition to comprising a target polypeptide described herein, the compositions (e.g., pharmaceutical compositions) described herein comprise a pharmaceutically acceptable carrier. As used herein, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeiae for use in animals, and more particularly in humans. The term "carrier," as used herein in the context of a pharmaceutically acceptable carrier, refers to a diluent, adjuvant, excipient, or vehicle with which the pharmaceutical composition is administered. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. Examples of suitable pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin.

[00125] In certain embodiments, the compositions described herein are formulated to be suitable for the intended route of administration to a subject. For example, the compositions described herein may be formulated to be suitable for subcutaneous, parenteral, oral, intradermal, transdermal, colorectal, intraperitoneal, and rectal administration. In a specific embodiment, the pharmaceutical composition may be formulated for intravenous, oral, intraperitoneal, intranasal, intratracheal, subcutaneous, intramuscular, topical, intradermal, transdermal or pulmonary administration.

[00126] In certain embodiments, the compositions described herein additionally comprise one or more buffers, e.g., phosphate buffer and sucrose phosphate glutamate buffer. In other embodiments, the compositions described herein do not comprise buffers.

[00127] In certain embodiments, the compositions described herein additionally comprise one or more salts, e.g., sodium chloride, calcium chloride, sodium phosphate, monosodium glutamate, and aluminum salts (e.g., aluminum hydroxide, aluminum phosphate, alum

(potassium aluminum sulfate), or a mixture of such aluminum salts). In other embodiments, the compositions described herein do not comprise salts.

[00128] The compositions described herein can be included in a kit, container, pack, or dispenser together with instructions for administration.

[00129] The compositions described herein can be stored before use, *e.g.*, the compositions can be stored frozen (*e.g.*, at about -20 ˚C or at about -70 ˚C); stored in refrigerated conditions (*e.g.*, at about 4 ˚C); or stored at room temperature.

5.4.2 Prophylactic and Therapeutic Uses

[00130] In one aspect, provided herein are methods of preventing or treating a disease or disorder in a subject comprising administering to the subject a target polypeptide described herein or a composition thereof. Further provided herein are methods of preventing a disease or disorder in a subject comprising administering to the subject a target polypeptide described herein or a composition thereof.

[00131] In one aspect, provided herein are methods of treating a disease or disorder in a subject comprising administering to the subject a target polypeptide described herein or a composition thereof. In another aspect, provided herein are methods of preventing a disease or disorder in a subject comprising administering to the subject a target polypeptide described herein or a composition thereof. In a specific embodiment, provided herein is a method for treating or preventing a disease or disorder in a subject comprising administering to the subject a polysialylated target polypeptide produced according to the methods described herein.

[00132] In certain embodiments, the disease or disorder may be caused by the presence of a defective version of a target polypeptide in a subject, the absence of a target polypeptide in a subject, diminished expression of a target polypeptide in a subject can be treated or prevented using the target polypeptides produced using the methods described herein. In certain embodiments, the diseases or disorder may be mediated by a receptor that is bound by a target polypeptide produced using the methods described herein, or mediated by a ligand that is bound by a target polypeptide produced using the methods described herein (e.g., where the target polypeptide is a receptor for the ligand).

[00133] In certain embodiments, the methods of preventing or treating a disease or disorder in a subject comprise administering to the subject an effective amount of a target polypeptide

described herein or a composition thereof. In certain embodiments, the effective amount is the amount of a therapy which has a prophylactic and/or therapeutic effect(s). In certain embodiments, an "effective amount" refers to the amount of a therapy which is sufficient to achieve one, two, three, four, or more of the following effects: (i) reduce or ameliorate the severity of a disease/disorder or symptom associated therewith; (ii) reduce the duration of a disease/disorder or symptom associated therewith; (iii) prevent the progression of a disease/disorder or symptom associated therewith; (iv) cause regression of a disease/disorder or symptom associated therewith; (v) prevent the development or onset of a disease/disorder, or symptom associated therewith; (vi) prevent the recurrence of a disease/disorder or symptom associated therewith; (vii) reduce organ failure associated with a disease/disorder; (viii) reduce hospitalization of a subject having a disease/disorder; (ix) reduce hospitalization length of a subject having a disease/disorder; (x) increase the survival of a subject with a disease/disorder; (xi) eliminate a disease/disorder in a subject; and/or (xii) enhance or improve the prophylactic or therapeutic effect(s) of another therapy.

5.5 Assay

5.5.1 Strains, Growth and Genetic Methods

[00134] Provided herein are methods for culturing host cells.

Host cells are cultured using any of the standard culturing techniques known in the art. For example, cells are routinely grown in rich media like Brain Heart Infusion, Trypticase Soy Broth or Yeast Extract, all containing 5 µg/ml Hemin. Additionally, incubation is done at 26°C in the dark as static or shaking cultures for 2-3d. In some embodiments, cultures of recombinant cell lines contain the appropriate selective agents.

[00135] A non-limiting list of selective agents is provided in Table 1.

Table 1: Selective agents used during transfection (50% concentration for preselection and 100% concentration for main selection) and standard culturing of *L. tarentolae*. Double amounts of the selective agents could be used if higher selection pressure was intended.

Selective agent	Resistance conferring gene	Concentration (100%)	Concentration (50%)
		main selection/ standard culturing	preselection
Nourseothricin	*sat*	50 µg/ml	25 µg/ml
Geneticin	*neo*	50 µg/ml	25 µg/ml

Selective agent	Resistance conferring gene	Concentration (100%)	Concentration (50%)
		main selection/ standard culturing	preselection
Paromomycin	*neo*	300 µg/ml	150 µg/ml
Zeocin	*ble*	150 µg/ml	75 µg/ml
Hygromycin	*hyg*	50 µg/ml	25 µg/ml
Blasticidin	*bsd*	5 µg/ml	2.5 µg/ml
Puromycin	*pac*	5 µg/ml	2.5 µg/ml

5.5.2 Plasmids

[00136] Plasmids were derived from a pUC57 vector backbone for *E. coli* propagation and contained an ampicillin or kanamycin section marker. The expression cassettes are flanked by restriction sites suitable for excision. The composition of the cassettes depends on the intended use and is described in the respective methods and examples. The genes of interest are included as ORFs that were codon usage optimized for *L. tarentolae* by backtranslation of the protein sequences to nucleotide sequences using a custom Python3 script that stochastically selects codons based on the *L. tarentolae* codon usage frequency while excluding rare codons (frequency <10%). The codon usage has been calculated using cusp (Rice, et al. (2000) Trends in genetics: TIG 16 (6), pp. 276–277) on all annotated *L. tarentolae* nucleotide coding sequences. Optimized sequences were manually curated for avoidance of restriction sites and deletion of repeats or homopolymer stretches.

[00137] To select new intergenic regions for the generation of artificial polycistrons, the genomes of *L. mexicana*, *L. donovani*, and *L. infantum* were searched for homologs to *L. major* genes that were shown to have high relative expression transcript levels (Rastrojo, et al. (2013) BMC Genomics 14, p. 223) and the associated 3' intergenic regions (Murray, et al. (2007) Molecular and Biochemical Parasitology 153 (2), pp. 125–132) were further filtered using blastn (Camacho, et al. (2009) BMC Bioinformatics 10, p. 421) to exclude those that have more than 80% identity to each other (using cd-hit (Li, et al. (2006) Bioinformatics 22 (13), pp. 1658–1659)) or identical stretches of more than 30 bp to the *L. tarentolae* genome.

[00138] For long integration constructs, the constructs were split into several pieces of usually less than 2500 bp that contained regions for homologous recombination with either other

fragments (usually 200 bp) or the chromosomal integration locus (usually 500 bp) in their extremities to allow assembly by the *Leishmania tarentolae* homologous recombination system.

[00139] The plasmids were generated and sequenced by a gene synthesis provider. Plasmids and descriptions are found in the sequence listings.

(i) Transfection method

(A) Preparation of DNA

[00140] Restriction digest (12 µg DNA in total volume of 240 µL) was performed using standard restriction enzymes (ThermoFisher, preferably FastDigest) according to the manufacturer's instructions. The restriction digest was performed until completion or o/n at 30°C and purified DNA by EtOH precipitation (2 volume 100% ice cold EtOH was added to 1 volume digested DNA, incubated 30min on ice, centrifuged for 30 min 17'500 x g at 4°C. Pellet was washed with 70% EtOH and subsequently dried for maximum 15 min before resuspension in ddH_2O. For optimized removal of circularized plasmid, 1 or 2 restriction enzymes with recognition sites in the vector backbones were chosen and a digest was done for 1h at 37°C and purified by EtOH as described above. The digest was analyzed by agarose gel electrophoresis in 0.7-2% agarose gels (TAE buffer). Optionally, gel extraction was performed with the NucleoSpin® Gel and PCR Clean-up kit (Macherey&Nagel) according to manufacturer's instructions to remove undigested plasmid from the preparation.

(B) DNA preparation for transfection

[00141] The linear DNA fragments for integration are mixed for transfection in the needed combinations at 1 µg per fragment. The volume of the mix was reduced to approximately 2 µl per transfection in a vacuum concentrator at 30°C. For episomal transfection of plasmids, 0.1-1 µg of plasmid DNA were directly used for transfection.

(C) Transfection with Nucleofector

[00142] One day before transfection, a densely grown culture of the parental strain was diluted 1:10 into fresh media (Brain Heart Infusion plus Hemin, "BHIH"; or Yeast Extract plus Hemin, "YEH") containing all antibiotics for which selection markers were previously integrated and cultured overnight at 26°C.

[00143] Transfection was performed using the 4D-Nucleofector™_Core_X with the P3 Primary Cell 4D-NucleofectorTM X Kit (Lonza). For this, DNA as prepared above was mixed

with 16.4 µl P3 Primary Cell solution and 3.6 µl Supplement Solution. The equivalent culture volume of 10^7 cells (OD should be around 0.3-1.0/ml, cell shape round to drop-like) was pelleted by centrifugation at 1800 g for 5 min and the supernatant was removed. The cell pellet was resuspended in the DNA mix and transfected using a 16-well electroporation strip with pulse FI-158 (in some examples alternative pulses FP167, CM150, EO115, DN100, FP158, FB158 were used). As negative control, an additional culture was transfected with ddH_2O only.

[00144] 80 µl of fresh media (BHIH or YEH plus parental cell line selection markers) was added to each well and 2x45 µl of the mix were transferred to individual wells of a 96 well culture plate that were prefilled with 200 µl of fresh medium. After incubation for 24 h at 26°C in the dark (recovery), the new selection marker was added at 50% concentration (preselection; see table 2). After further incubation for 1-2 days, the selection marker was topped up to 100% (main selection, see table) and several dilutions between 1:2 and 1:10 were performed in 96 well format (final volume 250 µl). Cultures were further incubated at 26°C in the dark for up to 7 days. If no growth was observed, the culture medium was replaced (centrifugation at 1800 g, 10 min, RT) and cultures were again incubated for up to 7 days. This step was repeated if necessary. Growing cultures were expanded in to higher culture volumes by dilutions in the range of 1:5 and 1:20 before analysis.

(D) Transfection with Gene Pulser Xcell™ (Biorad)

[00145] Preparation of the *Leishmania* culture for transfection was done by a 1:10 dilution of a densely grown culture in BHIH or YEH the day before transfection, static at 26°C. The OD was measured at 600 nm with photometer in single-use cuvettes and ranged be between 0.4-1.0 (4-6 x 10*7 cells) for optimal efficiency. The cells should be in log-phase, which is indicated by a mixed population out of round and drop-like shaped cells. More round shaped cells were preferred. 10 ml culture was used for one transfection and one culture was always electroporated with ddH_2O as negative control for the respective selection marker. For transfection the culture was spun at 1 '800 x g for 5 min, RT. The SN was removed and pellet resuspended in 5ml transfection buffer (200 mM Hepes pH 7.0, 137 mM NaCl, 5 mM KCl, 0.7 mM Na2HP04, 6 mM dextrose, anhydrous (glucose), sterile filtered 0.22 um). Cells were centrifuged again and the pellet was resuspended in 400 µl transfection buffer. 400 µl of cells were added to the DNA and transferred into the cuvettes and incubate on ice for 10 min. Electroporation was performed with a Gene Pulser Xcell™ (Biorad) using a low voltage protocol (µ exp. decay: 450 V, 450 µF,

5-6 ms, cuvette: d=2 mm) and immediately put on ice for exact 10 min. The whole content of cuvette was transferred into 10 ml BHIH or YEH without any selection marker and cells were grown at 26°C in dark, aerated, static for 20-24h. For the selection of a polyclonal cell line, half concentration of selection marker was added and cultures were incubated at 26°C for 1-2 days and then passaged 1:10 in 10 ml BHIH or YEH with full concentration of selection marker. Cells were grown further at 26°C in dark. If after 7 days cultures were turning into turbid culture, cells would be spun down at 1'800 x g for 5 min at RT and pellet is resuspended in new BHIH or YEH media containing full selection marker concentration.

(ii) Clonal selection

[00146] For clonal selection, cells were streaked on BHIH or YEH plates (containing 1.4% agar and the appropriate 100% selective agent) as soon as the liquid culture turned turbid. Plates were sealed with parafilm and incubated 7-10 days upside down in dark at 26°C. Single colonies (1-2 mm size) were transferred into 24-well plates containing l ml BHIH or YEH, sealed with parafilm and incubated in dark at 26°C for around 7-10 days. 1 ml culture was then transferred from 24-well plate into 10 ml BHI or YEH in a flask and further grown statically as usual.

(iii)Extraction of genomic DNA by gravity flow method for long read sequencing

[00147] Genomic DNA was extracted from 10 ml of dense *Leishmania* tarentolae culture (grown for 3 days; OD approx. 2) by using the Macherey Nagel NucleoBond CB 100 Kit #740508 (Nucleobond Buffer set IV #740604 with AXG 100 columns). For this, the cells were pelleted for 15 min at 1600 g and washed twice with 10 ml PBS. Next, the cell pellet was resuspended in 1 ml PBS and subjected to the extraction protocol according to manufacturer's instructions.

(iv)Nanopore sequencing

[00148] Construction of strains St16834, St17311, St17212, St17180 were verified by long read Nanopore sequencing. Library preparation was performed according to the manufacturer's instructions (Oxford Nanopore Technologies, Oxford, UK). Nanopore sequencing was performed on a GridION X5 instrument (Oxford Nanopore Technologies) with real-time base calling enabled. Sequencing runs were terminated after 48 h. Raw reads were assembled using Canu hierarchical assembler (version 1.8) (Koren, et al. (2017) Genome research 27 (5), pp. 722–736). Assembled contigs were compared to the target *in silico* reference sequence using

BLAST (Camacho, et al. (2009) BMC Bioinformatics 10, p. 421) and Artemis Comparison Tool (Carver, et al. (2005 Bioinformatics 21 (16), pp. 3422–3423).

(v) PacBio sequencing

[00149] PacBio long read genome sequencing was performed on 2 PacBio SMRT cell (v2.1 chemistry) for St15448 and 1 PacBio sequel SMRT cell for St17527 with the library preparation according to the manufacturer's specification).

[00150] PacBio raw reads were assembled into long contigs using HGAP [https://github.com/PacificBiosciences/Bioinformatics-Training/wiki/HGAP-in-SMRT-Analysis] and error corrected using two rounds of Arrow [https://github.com/PacificBiosciences/GenomicConsensus].

(vi)Illumina sequencing

[00151] Genomic DNA of St17527 was additionally sequenced on Illumina NextSeq (2 × 150 bp paired-end sequencing; TruSeq library preparation according to the manufacturer's specification). The resulting quality trimmed data consists of approximately 20M paired reads per strain. BWA-MEM (Li, Heng (2013) Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. Available online at http://arxiv.org/pdf/1303.3997v2) was used to align the reads to the reference sequence.

5.5.3 Expression analysis

(i) Sample preparation from *Leishmania tarentolae*

[00152] Cells were grown for 2-3 days at 26°C, static (e.g.in 3 ml in a 6-well plates). Whole cell extract (WCE) and cell free culture supernatants corresponding are analyzed by Western blot. For supernatant analysis, grown culture was centrifuged at 1800 g at RT for 5 min and cell free supernatant was transferred to a new tube and mixed with Laemmli dye under reducing or non-reducing conditions. Cell pellets for WCE were washed with 1x PBS, centrifuged again at 1800 g at RT for 5 min and frozen at -80°C for minimally 30 min. After thawing it again at RT pellet was then resolved in Laemmli (reducing) buffer, boiled again at 95°C for 10 min and vortexed intensively.

(ii) Expression analysis by Western Blot

[00153] Samples were run on 4-12% Bis-Tris SDS PAGE, using a MOPS running buffer with 200 V for 60 min. Gels were blotted using an Iblot device for 7 min on PVDF membranes.

Membranes were blocked for at least 30 min at RT in 10% milk. Primary antibodies (i.e. goat anti-Human IgG–HRP (A6029, Sigma) 1:2000 diluted, mouse anti-Human Kappa Light Chain (K4377, Sigma) 1:5000 diluted or rabbit anti *S. pneumoniae* serotype 1 polysaccharide (SSI, #16744) 1:100 diluted) were used diluted in 1% milk, 1x PBST for o/n incubation at 4°C. Afterwards, the blot was washed with 1x PBST three times for 5 min before detection with horse reddish peroxidase (HRP) coupled secondary antibodies (anti-mouse polyvalent-HRP (A0412, Sigma) 1:2000 diluted or anti-rabbit-HRP conjugate (Jackson ImmunoResearch #111-035-008) 1:2000 diluted) in 1% milk, 1x PBST for 3h rotating at 30°C, followed by three washes for 5 min in 1xPBST and one component 3,3',5,5'-tetramethylbenzidine (TMB) substrate staining for colorimetric detection (TMBM-1000-01, Surmodics).

5.5.4 Small scale expression, purification of Adalimumab

[00154] Host cells were routinely grown in 50 ml culture in BHIH or YEH for 48 h at 26°C shaking at 140 rpm. Cultures were harvested and centrifuged for 10 min at 1800×g at RT. Media SN was filtered through 0.22 µm filter (Steriflip, SCGP00525) and EDTA (0.5 M pH8) was added to each load in a 1:100 dilution. Media SNs of each strain were subjected to 4 h incubation with 100 µl of proteinA resin (ProteinA-Sepharose 4B Fast Flow, Sigma Aldrich, P9424) per Falcon tube in batch while rotating at RT. After treatment with protein A resin, the samples were centrifuged at 500×g for 5 min, the FT was discarded and the resin was transferred to spin columns. Washes were performed with 3× 5 CV using Buffer A (pH 7.2 20 mM Na_2HPO_4, 150 mM NaCl, pH was adjusted with HCl to 7.20) using 500 µl for 100 µl resin; with centrifugation at 1000×g, RT, 1 min between each step. Elution was performed with several CV of Buffer B (0.1 M acetic acid, 100 mM NaCl, pH was adjusted with 1 M NaOH to 3.20) using 100 µl for 100 µl resin, with centrifugation at 1000×g, RT, 1 min between each step (e.g. 3x1 CV and 1x0.5 CV). Elution fractions were pooled and immediately neutralized by adding 100 mM Tris-HCl (1 M pH8). Afterwards, the pooled elutions were buffer exchanged to PBS pH 6 using 2 ml 7K ZebaSpin desalting columns and optionally concentrated using Amicon 0.5 ml 30 K concentrators.

5.5.5 Analysis of N-glycans released from purified proteins and cells surfaces by HILIC-UPLC-MS

[00155] Enzymatic release of N-glycans from purified proteins was performed using Rapid PNGase F (New England Biolabs) as recommended by the supplier. 8 µl of sample (15 µg of

protein) were mixed with 2 µl Rapid Buffer and 1 µl of Rapid PNGase F. The mixture was incubated at 50 °C for 10 min followed by 1 min at 90 °C.

[00156] Enzymatic release of N-glycans from cell surfaces was performed using PNGase F (New England Biolabs). Cells (grown for 48 or 72 h at 26°C shaking at 140 rpm) were harvested and washed with PBS by centrifugation for 10 min at 1800×g at RT.50 mg of cell pellet were re-suspended in Glyco Buffer 2 and incubated with 1 µl PNGase F for 1 h at 37 °C and 650 rpm. Cells were again pelleted by centrifugation and 75 µl of the supernatant was dried down in a SpeedVac concentrator. Glycans were resuspended in 10 µl of water. Following release, glycans were directly labeled with procainamide as described previously (Behrens, et al. (2018) Glycobiology 28 (11), pp. 825–831). Briefly, released glycans were mixed with 1 µl acetic acid, 8 µl of a procainamide stock solution (550 mg/ml in DMSO) and 12 µl of a sodium cyanoborohydride stock solution (200 mg/ml in H_2O). Samples were incubated for 60 min at 65 °C and cleaned up using LC-PROC-96 clean up plates (Ludger Ltd) according to the manufacturer's instructions.

[00157] Procainamide-labeled N-glycans were analyzed by hydrophilic interaction chromatography-ultra performance liquid chromatography-mass spectrometry (HILIC-UPLC-MS) using am Acquity UPLC System (Waters) with fluorescence detection coupled to a Synapt G2-Si mass spectrometer (Waters). Glycans were separated using an Acquity BEH Amide column (130 Å, 1.7 µm, 2.1 mM × 150 mM; Waters) with 50 mM ammonium formate, pH 4.4 as solvent A and acetonitrile as solvent B. The separation was performed using a linear gradient of 72-55 % solvent B at 0.5 ml/min for 40 min. Fluorescence was detected at an excitation wavelength of 310 nm and a detection wavelength of 370 nm. The Synapt G2-Si mass spectrometer fitted with a Zspray electrospray source was used for mass detection in positive resolution mode using the following parameters: Scan range: *m/z* 300-3500; scan time: 1 sec; capillary: 2.2 kV; source temperature: 120 °C and sampling cone: 75 V. MassLynx 4.2 (Waters) was used for data acquisition. Data processing and analysis was performed using Unifi 1.9.4.053 (Waters). Glucose units were assigned using a fifth-order polynomial distribution curve based on the retention times of a procainamide-labeled dextran ladder (Ludger Ltd). Glycan structures were assigned based on their m/z values and their retention times and matched against a previously constructed N-glycan library. For individual samples the UPLC was coupled to a Synapt HDMS mass spectrometer using comparable settings.

[00158] For a few samples, Waters RapiFluor labelling kit, mostly following the Waters Application Note: «Quality control and Automation Friendly GlycoWorks RapiFluor-MS N-Glycan Sample Preparation» that were analyzed using the same instrumentation as the procainamide labelled glycans (RF-MS).

5.5.6 DMB labeling of Neu5Ac and CMP-Neu5Ac

[00159] A highly sensitive strategy to quantify the concentration of nucleotide-activated sialic acid by a combination of reduction and fluorescent labeling using the fluorophore 1, 2-diamino-4,5-methylenedioxybenzene (DMB) was applied. The labeling with DMB requires free keto as well as carboxyl groups of the sialic acid molecule. Reduction of the keto group prior to the labeling process precludes the labeling of non-activated sialic acids (Neu5Ac). Since the keto group is protected against reduction by the CMP-substitution, labeling of nucleotide-activated sialic acids is still feasible after reduction. Subsequent combination of the DMB-high-performance liquid chromatography (HPLC) applications allows identification of both total Neu5Ac and modified CMP-sialic acid and quantification in the femtomole range (Galuska, et al. (2010) Anal Chem 82 (11), pp. 4591–4598).

[00160] MeOH/Chloroform extraction procedure for *L. tarentolae* cell pellets was performed on 4 OD of each sample, which were harvested by centrifugation and washed 2x with 1xPBS and frozen. For extraction, pellets were thawed, resuspended in 480 µl MeOH , supplemented with 20 µl water and sonicated in a water bath at RT for 15 min. The samples were spun in a table-top centrifuge at 18000 g and 4°C for 10 min. The SN was transferred into a glass vial, supplemented with 268 µl chloroform and vortexed. Next, 500 µl H_2O (MS grade) was added and the sample was vortexed again. The MeOH/chloroform/H_2O (1/0.54/1) mixture was spun at 2200 g and RT for 20 min to remove proteins, lipids and DNA in the CHCl3 phase. Approximately half (525 µl) of the upper MeOH/H_2O phase was collected and transferred into Eppendorf tubes, corresponding to extracted material from 2 OD pellet. The samples were dried in a speed-vac, resuspended in 16 µl H_2O and split into two samples of 8 µl that were separately subjected to DMB labeling with and without reduction. As control, Neu5Ac in H_2O was dried in a SpeedVac and dried material was diluted in H_2O, split into two for both labelling procedures. One set of samples was supplemented with 10 µl of ice cold 0.4 M sodium borate buffer pH 6.8 and 2 µl of freshly thawed 2 M borohydride in 0.5 M NaOH (final = 0.2 M sodium borate buffer pH 8,8 containing 0.2 M borohydride) and incubated at RT for 2h (reduced samples). . The

second set of samples was supplemented with 10 µl of ice cold 0.4 M sodium borate buffer pH 6.8 and 2 µl of 0.5 M NaOH (final = 0.2 M sodium borate buffer pH 8,8) and incubated at RT for 2h (non-reduced samples). Afterwards, samples were dried in a speedVac, resuspended in 3 µl H_2O and subjected to standard DMB labelling using the Takara labeling kit (#4400) according to manufacturer's instructions. Finally, samples were analyzed by RP-C18-LC in duplicates. Quantification was performed using a defined standard curve for which the standard solutions were subjected to incubation in sodium borate buffer (non-reducing) and DMB labeling analogous to the procedure described for non-reduced samples above.

6. EXAMPLES

6.1 EXAMPLE 1

[00161] To analyze the capability of *Leishmania tarentolae* to assemble a chromosomal integration construct from multiple DNA fragments by homologous recombination, transfection of the same construct (for expression of a monoclonal antibody, Rituximab) was in parallel attempted by a 1-fragment and a 2-fragment version.

[00162] The 1-fragment version (pLMTB5026) contains the coding sequences for light chain, heavy chain and a selection marker (Nourseothricin, ntc) flanked and interspaced by intergenic regions. These intergenic regions are used as spacers (intergenic region, IR) in the construction of synthetic polycistrons, since they are central components of the native polycistronic gene clusters in *Leishmania* that ensure proper splicing of the pre-mRNA and furthermore are believed to influence gene expression by regulating transcript stability. In addition, the extremities of the DNA fragment contain (600-1000 bp) regions homologous to the *L. tarentolae* rDNA locus (ssu) in order to integrate the construct into the genome (FIG. 34 in International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein).

[00163] The 2-fragment version contains the same genetic elements, but distributed across two DNA fragments. Fragment P1 (pLMTB5024) contains the coding sequences for light and heavy chain as well as the intergenic regions upstream of these CDS. The 5' end of the fragment contains the homologous recombination site for integration into the ssu locus. The last 250 bp of the heavy chain CDS (3' end of P1 construct) are repeated in the first 250 bp of the second fragment (P2; pLMTB5025) in order to allow homologous recombination between the two fragments via their identical sequences. Furthermore, P2 comprises an intergenic region downstream of the heavy chain (CamIR), the selection maker (ntc) followed by another

intergenic region (3'UTR=dhfr-ts) and the 3' homologous recombination site for integration into the ssu locus (FIG. 1A).

[00164] The different constructs, either SwaI linearized pLMTB5026 or SwaI linearized pLMTB5024+pLMTB5025, were transfected (Biorad system) into *L. tarentolae* (St10569). For both versions, viable polyclones were obtained and Western blot analysis of the clones obtained by the 2-fragment version also showed significant monoclonal antibody expression upon detection with light or heavy chain specific antibodies (FIG. 1B). This demonstrates the feasibility of the formation of expression constructs from several DNA fragments.

6.2 EXAMPLE 2

[00165] To obtain a cell line expressing four different glycosyltransferases for conversion of the endogenous Man3 to G2 N-glycans (two functionally redundant enzymes for addition of the first glycoengineering step, SfGnt1 and drMGAT1, as well as rnMGAT2 and hsB4GalT1 for further extension to N-glycan "G2") (International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein), wild type *L. tarentolae* (St10569) were transfected with an expression construct formed by homologous recombination of ten DNA fragments. These DNA fragments were designed similar to the previously introduced constructs with intergenic regions interspersing the coding sequences in the assembled synthetic polycistron and a PolI promoter region that is derived from the well described ribosomal DNA locus and supports high-level expression of the counterclockwise-integrated construct. Usually, the aquaporin locus as most protein coding genes in *Leishmania* is transcribed by PolII, for which specific promoter regions are elusive. Homologous recombination in-between the fragments and between fragments and the aquaporin locus on the genome (AQP) was enabled by 200 bp and 500 bp homologous regions, respectively (FIG. 2, top). Furthermore, the overlaps were planned in a way that allows modular exchange of individual enzymes or intergenic regions by combination of linear fragments from different donor plasmids.

[00166] To improve the transfection efficiency for multi-fragment homologous recombinations a new transfection system (Nucleofector) was tested in parallel to the old one (BioRad).

Linear DNA fragments derived from plasmids (pLMTB6855, 6952, 6958, 6807, 6848, 6852, 6811, 6860, 6906, 6861) were transfected into wt *L. tarentolae* (St10569) by either transfection

method 1 using the Biorad system or Transfection method 2 using the Nucleofector system. For both methods, viable polyclones were obtained suggesting the successful recombination of the split selection marker.

The resulting polyclones were analyzed for their engineered N-glycans by RF-MS on whole cell protein level, exemplified for St15257 in FIG. 2 and demonstrated successful glycoengineering up to G2 (16%), which implies that an expression construct covering at least 3 of the enzymes had been assembled by *L. tarentolae*. This demonstrated the general feasibility of integrating multi-fragment assemblies into *L. tarentolae* for glycoengineering. For both transfection methods, clones exhibiting similar properties were obtained, demonstrating that the transfection was feasible independent of the applied transfection method. Nevertheless, the clones from the Nucleofector transfection grew up slightly faster than the ones from the BioRad system, suggesting better cell viability after transfection and thus potentially better transfection efficiency.

6.3 EXAMPLE 3

[00167] To obtain conversion of the endogenous Man3 to G2 N-glycans in a strain that was previously transfected with a Rituximab expression construct, St12427 was transfected with a second expression construct formed by homologous recombination of ten DNA fragments. The construct encodes for expression of four different glycosyltransferases, i.e. two functionally redundant enzymes for addition of the first GlcNAc, SfGnt1 and drMGAT1, as well as rnMGAT2 and hsB4GalT1 for further extension to G2.

[00168] DNA fragments derived from plasmids (pLMTB6950, 6956, 6808, 6849, 6852, 6811, 6816, 6873, 6855, 6861) were transfected into *L. tarentolae* St12427 by transfection method 2 using the Nucleofector system. Viable polyclones were obtained suggesting the successful recombination of the split selection marker.

[00169] The resulting polyclones were analyzed by RF-MS on whole cell protein level and demonstrated glycoengineering up to G2 (4%) in some strains (St15368), which implies that an expression construct covering at least 3 of the enzymes had been assembled by *L. tarentolae*. This corroborates the general feasibility of integrating multi-fragment assemblies into *L. tarentolae* for glycoengineering. Other clones however only showed conversion up to G0-N (e.g. St15448), which suggests an incomplete integration of the construct (FIG. 3A).

[00170] In order to assess the genetic composition in strain St15448, gDNA was prepared (Macherey&Nagel NucleoBond® CB100) and subjected to PacBio long read genome sequencing on 2 PacBio SMRT cell (v2.1 chemistry, library preparation according to the manufacturer's specification). Several of the long subreads demonstrated an incomplete integration of the construct that includes only the coding sequences for the glycosyltransferases drMGAT1 and SfGnt1, which both catalyze the addition of the first GlcNAc to Man3. Thus, the obtained sequencing data are in line with the observed phenotype of the N-glycan profile. The data furthermore support that the incomplete integration happened by correct integration of the 3' end of the construct into the AQP locus on chromosome 31, while instead of 5' end integration into AQP, the intergenic region PfrIR (native *L. tarentolae* ~2 Kb) recombined with the endogenous Pfr expression locus on chromosome 29. By this, a chromosomal crossing over (FIG. 3B) was created. Besides this, also native chromosomes 29 and 31 were detected, most likely in diploid form (data representative cartoon shown in FIG. 3C).

[00171] These sequencing data indicate that the wrong homologous recombination was favored over the intended integration locus. This might have been facilitated by the fact that the Pfr intergenic region is long (~2 Kb) and 100% identical to the native genetic locus and the fact that the AQP locus is very close the telomere of the chromosome.

[00172] Another example that corroborates the hypothesis that stretches of homology between the fragments should be avoided was identified in a construct where hsB4GalT1-Strep, hsMAGT1-3xHA and rnMGAT2-3xHA were transfected into *L. tarentolae* wild type background (St10569 + pLMTB6946, 6951, 8080, 8081, 8082, 8083, 8085, 6924). In the resulting strain St16834 almost no activity of hsMGAT1 was detectable along with a complete absence of MGAT2 activity (78% M3, 11% G0-N, and 11% G1-N). Long read sequencing with the Nanopore technology revealed that two fragments carrying the rnMGAT2-3xHA had not been integrated into the genomic locus since two adjacent glycosyltransferases were both triple HA-tagged and the nucleotide sequence of the tag region was 100% identical. This demonstrates that a stretch of 93 bp is sufficient for homologous recombination (FIG. 4).

6.4 EXAMPLE 4

[00173] The previous examples suggested that the use of homologous sequences between the different fragments for integration as well as between the fragments and the *L. tarentolae*

genome can lead to unwanted homologous recombination. This on one hand necessitates the use of codon-diversified variants or homologs of glycosyltransferases when increasing the gene dosage for a specific N-glycan conversion step. On the other hand, this finding prohibits the repeated use of the previously successfully tested intergenic regions. Data about the exact signals for splicing and mRNA stability in *L. tarentolae* are not available and thus design of synthetic intergenic regions is currently not feasible. To overcome this limitation, a new set of DNA fragments was designed that use intergenic regions from other *Leishmania* species and various codon usage variants as wells as different homologues of the different glycosyltransferases.

[00174] Genes from *L. mexicana*, *L. donovani*, and *L. infantum* that are believed to be highly expressed have been identified by looking for homologs to *L. major* genes that were shown to have high relative expression transcript levels (Rastrojo, et al. (2013) BMC Genomics 14, p. 223). The 3' untranslated region (UTR) of these genes are believed in turn to support high protein expression levels (Murray, et al. (2007) Molecular and Biochemical Parasitology 153 (2), pp. 125–132). To minimize the potential for unwanted homologous recombination, sequences with >80% identity to each other (using cd-hit (Li, et al. (2006) Bioinformatics 22 (13), pp. 1658–1659.) and more than 30 bp identical stretches to the *L. tarentolae* genome, using blastn (Camacho, et al. (2009) BMC Bioinformatics 10, p. 421), have been excluded.

[00175] Protein sequences were back-translated to nucleotide sequences using a custom Python3 script that stochastically selects codons based on the *L. tarentolae* codon usage frequency while excluding rare codons (frequency <10%). The codon usage has been calculated using cusp (Rice, et al. (2000) Trends in genetics: TIG 16 (6), pp. 276–277) on all annotated *L. tarentolae* nucleotide coding sequences.

[00176] Again, as in the previous multi-fragment homologous recombination constructs, 200 bp overlaps between the fragments and 500 bp homologous regions to the anticipated integration sites were included to allow assembly of the fragments in *Leishmania*. New integration loci were designed and either used in a "Tandem integration" approach (FIG. 5, bottom), in which the new construct is integrated between the 5'UTR and the coding sequence of a highly expressed or multi-copy gene such as alpha Tubulin (aTub). In this case, no additional promotor region (PolI) is included in the construct and thus the endogenous IR of the target locus will govern the PolII mediated transcription of the first coding sequence of the integration construct. Consequently, the integration construct needs to conclude with an intergenic region at its 3' end, which spaces

the last CDS of the construct and the endogenous gene of the target locus. Alternatively, new loci are used in a "disruptive integration" approach (FIG. 5, top) where the CDS of a target gene is exchanged for the integration construct. In order to profit from the high transcription efficiency of RNA PolI in *Leishmania*, this integration approach can be paired with use of the PolI promoter region from *L. tarentolae* and counterclockwise integration. The latter should avoid an imbalanced transcription of neighboring genes that are usually transcribed by PolII (FIG. 5).

[00177] In order to test the capability of the IRs from different species to support expression of the glycosyltransferases, a set of four different transfections was performed with the Nucleofector method. Herein, the glycosyltransferases, the selection marker as well as the integration locus (shown example targets GP63 locus) were kept constant and only the intergenic regions were varied. Each transfection construct combined four different IRs from the same species in order to identify whether compatibility is limited to specific species (*L. major, L. donovani, L. infantum, L. mexicana*). For St17212, these fragments were derived from pLMTB8234, 8235, 8250, 8295, 8297, 8301, 8302, 8303, 6933. For St17311, these fragments were derived from pLMTB 8234, 8235, 8250, 8306, 8307, 8310, 8311, 8312, 6933. For St17176 these fragments were derived from pLMTB 8250, 8334, 8234, 8335, 8235, 8336, 8328, 8330, 6933. For St17180, these fragments were derived from pLMTB 8250, 8322, 8234, 8323, 8235, 8324, 8316, 8318, 6933.

[00178] All transfections successfully produced viable clones that were grown in 50 ml shake flask cultures and subjected to N-glycan analysis of the surface protein fraction of *L. tarentolae* (St17212 = LmIR, St17311 = LdIR, St17176 = LiIR, St17180 = LmxIR; FIG. 6A). The N-glycan profiles demonstrated that all four transfections were mostly successful since in the variants containing IRs from *L. major, L. donovani, L. mexicana* conversion up to G2 and in the variant with *L. infantum* IRs at least G1-N was detected (FIG. 6A). This demonstrates that intergenic regions from all four *Leishmania* species can be used to support expression of recombinant glycosyltransferases in *L. tarentolae*, enabling fully function-customized host cells. The detectable activities for most GTs suggests that the majority of the used IRs are functional and only few, i.e. the ones supporting MGAT2 expression in St17176 were not efficient. Since the contribution of 5' and 3' UTRs cannot be clearly distinguished based on the available data, the "non-functional" IRs cannot be unambiguously pinpointed. In addition, heterologous coding sequences could contribute to sequence-mediated mRNA stability.

[00179] However, the quite different N-glycan profiles that are observed for the analyzed strains furthermore support the hypothesis that the intergenic regions actually influence the expression level of the genes they flank.

[00180] To corroborate correct integration Nanopore sequencing was performed for St17311, St17212 and St17180 and confirmed correct integration for all tested constructs (FIG. 6B).

[00181] Next, it was assessed whether multiple of these multi-fragment integrations can be combined within one strain to improve the glycoengineering activity and obtain more homogenous N-glycan conversion. For this, St17238 was created by transfection of linearized DNA fragments from plasmids (pLMTB8253, 8313, 8314, 8236, 8315, 8255, 8259, 6940, 8379) targeting the alpha tubulin locus of an Adalimumab expression strain (St15449). Then, in a second transfection a 9-fragment construct derived from plasmids pLMTB8389, 8301, 8234, 8302, 8235, 8303, 8295, 8297, 8392 was integrated into the pfr locus to generate St17294. Last, St17294 was transfected with DNA fragments obtained from plasmids pLMTB8247, 8285, 8237, 8286, 8238, 8287, 8383, 8282, 6936 to obtain a third GT expression construct in the GP63 locus. Comparison of the resulting strain St17826 with its predecessors by N-glycan analysis of surface proteins depicts a step-wise increase in GT activity resulting in almost homogenous G2 N-glycans (88%) for the final strain (FIG. 7). This corroborates the usefulness of the multi-fragment integration method to achieve integration of multiple enzyme copies into the *Leishmania* genome and that copy number increases of glycosyltransferases can be achieved by using codon diversified enzymes as well as homologs from different species (here: hs, *Homo sapiens*; rn, *Rattus norvegicus*, dr, *Danio rerio*, gj, *Gekko japonicus*, ag, *Anopheles gambiae*).

[00182] To summarize, for enabling correct multiple homologous recombination events in *Leishmania tarentolae*, heterologous intergenic regions derived from other *Leishmania* species were successfully used to site-specifically engineer host cells. Furthermore, these heterologous intergenic regions containing regulatory elements were sufficient to drive splicing and expression of the heterologous coding sequences.

6.5 EXAMPLE 5

[00183] Since the heterologous, non-identical sequences were successfully used for correct multiple recombination events by up to ten DNA fragments, generation of an even larger chromosomal integration cluster by using genetic elements from 13 donor fragments was tested.

Importantly, an even more engineered strain was subsequently created, by transfecting an existing strain that is capable of galactosylation, St17311 (described in Example 4 and in FIG. 6A), with an expression construct providing it with the proficiency in generating sialic acid needed for the sialylation engineering of N-glycans (International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein). DNA elements were used to target the alpha tubulin locus using a tandem insertion strategy. The intended expression cassette contained $NeuC_{3xMyc}$, IrLiH, CgNal, IrLiI, $NeuB_{3xHA}$, IrLmR, $_{3xHA}$mmST6, IrLiK $NeuA_{3xHA}$, IrLiL, $hsCST_{3xmyc}$, IrLiM and SM (pac) followed by 3'UTR, and was inserted into host cells by transfecting St17311 with thirteen donor fragments excised from pLMTB8443, 8528, 8448, 8529, 8509, 8507, 8505, 8531, 8449, 8532, 8517, 8520, 6939 (FIG. 8A). The resulting strain St17527 was further analyzed for its phenotype: 1) by DMB labeling of production of Neu5Ac and CMP-Neu5Ac (FIG. 8B) and 2) for its engineered N-glycan (FIG. 8C). St17527 produced 0.49 nmol/OD Neu5Ac, 0.17 nmol/OD CMP-Neu5Ac, calculated based on a standard curve (not shown). Moreover, protein linked N-glycans showed a significant amount of sialylated N-glycans, with a total of 11.6% sialylated glycoforms (FIG. 8C). These results demonstrate full functionality of the glycoengineering pathway, indicating that the genetic information is completely inserted in *L. tarentolae* host cells. This was finally confirmed by PacBio sequencing, clearly showing that the genetic system applied successfully generated fully function-customized *L. tarentolae* host cells.

6.6 EXAMPLE 6

[00184] As previously shown in Example 3, the unwanted integration into the native expression site of the paraflagellar rod protein 1D (Pfr) seemed to support high expression on the integrated construct. Thus, it was assessed whether targeting this locus on purpose in a non-disruptive "tandem" integration manner (in comparison to Example 4) would also lead to high level expression and how this compares to expression from the *L. tarentolae* rDNA locus ("ssu"). Additionally, a different type of integration into the rDNA locus was tested, in which the 5' integration site was moved 141 bp towards the transcription initiation site of the rDNA locus to the start of the 18S (ssu) coding sequence. For integration into this site ("Ssu-PolI"), protein expression constructs were equipped with an artificial spliced leader acceptor site to ensure

correct processing (FIG. 9A). The 3' integration site was kept the same as that in the case of the "ssu" locus and thus also caused disruption of one of the ssu expression region.

[00185] A glycoengineering construct for N-glycan conversion to G0 glycoform, encoding 3 orthologs of MGAT1 (drMGAT1, gjMGAT1 and agMGAT1) as well as 1 ortholog of MGAT2 (drMGAT2), was transfected into the three different loci of WT *L. tarentolae* strains by transfection of either pLMTB8389, 8301, 8234, 8629, 8238, 8287, 8383, 8282, 8822 (for St18332), pLMTB9299, 8301, 8234, 8629, 8238, 8287, 8383, 8384, 8994 (for St18621) or pLMTB8223, 8381, 8301, 8234, 8629, 8238, 8287, 8383, 8281, 9304. The efficiency of these integrations was compared by comparison of the N-glycan profiles released from *Leishmania* surface glycoproteins. All three integrations resulted in high level conversion to G0. While integration into the two ssu locus variants performed indistinguishably with 99% G0, integration into the new "Pfr" locus resulted in 92% G0 N-glycans (FIG. 9B). The resulting cell lines showed no significant difference in viability, growth or productivity. Thus, the "Pfr" locus represents an additional high expression locus for *Leishmania*.

[00186] In order to assess further whether there is a difference between the two integration variants for the ssu locus ("Ssu" vs. "Ssu-PolI", see FIG. 9A), another G0 glycoengineering construct composed of two functional homologs of MGAT1 (sfGNT1, drMGAT1B) and 2 codon usage variants of rat MGAT2 was integrated into the respective loci and combined with a target protein expression construct. The conversion of the sterically more constraint Fc N-glycan of the highly expressed monoclonal antibody serves as a more stringent measure of glycoengineering efficiency.

[00187] Strain St18703 was obtained by transfection of St18344 with linearized fragments from plasmids pLMTB9301, 9070, 8568, 9072, 9080, 9082, 9083, 8461 and 8994 into the "Ssu" locus and subsequent transfection of the resulting strain St18625 with an Adalimumab expression construct (pLMTB6737, 8698, 7084, 6681, 6683). For generation of strain St19042, an Adalimumab expression strain St18607 was transfected with linearized fragments from plasmids pLMTB8223, 8564, 9070, 8568, 9072, 9080, 9082, 9083, 8461 and 8994 to obtain integration of the G0 construct into the "Ssu-PolI" locus.

[00188] Comparison of the Fc N-glycan profiles of Adalimumab purified from these two strains clearly demonstrated a difference between the integration variants and supports superiority of the "Ssu-PolI" integration variant with conversion to 87% G0 while St18703 only

obtained 68% G0 (FIG. 9C). Thus, in order to achieve high level conversion the "Ssu-PolI" locus is the most suitable integration locus, but balanced high level expression can also be achieved by targeting the "Pfr" locus or the alternative "Ssu" integration variant.

6.7 EXAMPLE 7

[00189] In order to further explore the opportunities of extending the multiple homologous recombination method, transfection of a genetic element assembled from 25 different donor fragments was attempted. This genetic module combines expression constructs for enzymes of the sialic acid biogenesis pathway (NeuC3xMyc, 3xflagcgNal, NeuB3xHA, NeuA3xHA and 3 codon usage variants of Spinv-Δ88ST6) with expression constructs for glycosyltransferases. For efficient glycoengineering up to G2, 3 copies of MGAT1, 3 copies of MGAT2 and 2 copies of hsB4GalT were combined by using codon usage variants in the case of hsB4GalT1 and orthologs from different organisms in the cases of MGAT1 and MGAT2. Furthermore, 15 different intergenic regions from 4 previously described *Leishmania* species were used in this construct to avoid repeated usage of the same sequences. Finally, the selection marker (pac), a 3'UTR as well as flanking sequences for homologous integration in tandem into Pfr locus were included into the construct. Notably, in this case, the selection marker was not situated in the end of the construct, but in between the clusters for glycoengineering.

[00190] For the integration of this construct, WT *L. tarentolae* (St18344) were transfected with the twentyfive donor fragments excised from plasmids pLMTB8389, 8310, 8234, 8311, 8235, 8312, 8254, 9220, 8528, 8448, 8529, 8509, 9131, 9132, 8449, 9339, 9340, 8333, 8636, 8313, 8236, 8314, 8379, 8315, 9320 (FIG. 10A).

[00191] The phenotype of the resulting strain St18700 was analyzed by N-glycan profiling of its surface glycoproteins. The strain proved to be very proficient in N-glycan conversion up to G2S2, with 90% galactosylated N-glycan species and a total of 43% sialylated N-glycans (FIG. 10A). This suggests full functionality of the glycoengineering pathway, since previously galactosylation of around 90% of the surface glycans could only be obtained by combination of two galactosyltransferase containing modules in different expression loci (compare FIG. 7). Also, long read sequencing of a derived cell line (St19384, see below) confirmed the complete and correct integration of the 30 kbp construct assembled from 25 individual fragments in *L. tarentolae*. This further underlines the high potential of the novel method in this invention of

recombinantly engineering a *Leishmania* cell that involves homologous recombination of a multitude of DNA fragments.

[00192] Next, the resulting strain was further modified by integration of two additional glycoengineering constructs aiming at improving the conversion to G2S2. First, St18700 was transfected with linearized inserts from plasmids pLMTB8391, 8285, 8237, 8286, 8238, 8287, 8383, 8281 and 8821, which constitute another glycoengineering module with a different codon usage variant of hsB4GalT1, a codon usage variant of rnMGAT2 and two additional orthologs of MGAT1 from different organisms. This modification led to a marked increase in G2 in the surface N-glycan profile of the resulting strain St19084 (FIG. 10B).

[00193] In order to improve sialylation of theses N-glycan species, an additional glycoengineering module containing sfGNT1, a functional homolog of MGAT1, as well as additional codon usage variants of MGAT1 from zebrafish and MGAT2 from rat for boosting the conversion of Man3 to higher modified N-glycan variants was transfected into St19084. Additionally, the module contained another ortholog of the sialyltransferase ST6, $_{strep}$CMAS and the sialic acid transporter CST for improved activation and transfer of sialic acid to the protein acceptors. For this transfection, linearized fragments from plasmids pLMTB8223, 8564, 8567,8568,8823,8599, 9486, 8488, 8447, 8490 and 9205 were transfected into the parental strain to obtain strain St19384. In this case, two plasmids, 8223 and 9205 had to be cut with alternative restriction enzymes (HindIII+SmiI or BglII+SmiI) to create the wanted overhangs for homologous recombination. By this transfection, high sialylation of the N-glycans released from surface glycoproteins with 74% G2S2 was obtained (FIG. 10B).

[00194] In order to confirm that all the previously mentioned glycoengineering modules were correctly integrated into this highly modified strain, high molecular weight gDNA from St19384 was prepared and subjected to Nanopore sequencing. By this, correct integration of the three glycoengineering modules in the targeted loci could be confirmed.

[00195] This example ultimately demonstrated the high potential of genetic modifications of *L. tarentolae* by the techniques described herein for multiple homologous recombination events, in each of the subsequent rounds of engineering. In total 45 linearized fragments were transfected into the cells in order to establish 3 different glycoengineering modules comprised of 7 orthologs or functional homologs of MGAT1, 5 orthologs or codon usage variants of MGAT2, 3 codon usage variants of hsB4GalT1, 4 codon usage variants or orthologs of ST6 and 6

enzymes of the sialic acid biosynthesis pathway. Thus, avoiding repetition of identical sequences in the coding as well as non-coding regions of the constructs as described in detail in previous examples, allows extensive modification of *Leishmania* cells without unwanted recombinations.

[00196] Confirmation of the reproducibility of extensive strain engineering like the one described before was obtained with strains St20157, St20208 and St20224, which each contain 3 glycoengineering constructs as well as an O-glycosylation knock-out (see International Application entitled "Glycoengineering Using *Leishmania* Cells" filed even date herewith) and are derived from the common parental strain St19084 (FIG. 10C).

6.8 EXAMPLE 8

Assembly of a hybrid prokaryotic gene cluster on an *Escherichia coli* cosmid in *Leishmania tarentolae*.

[00197] The recombinant expression in *E. coli* of the *Streptococcus pneumoniae* serotype 1 capsular polysaccharide as lipid-linked oligosaccharide (LLO) requires 10 exogenous genes. Seven genes are present as a cluster in *S. pneumoniae*, while three genes are present elsewhere in its genome. As the orthologues of these three genes are widespread in prokaryotes, genes from *Plesiomonas shigelloides* O17, a closer *E. coli* relative, were chosen, as they were elsewhere proven efficient in their function when recombinantly expressed in *E. coli*.

[00198] The aim of the experiment is to obtain a functional hybrid cluster cloned into the *E. coli*-compatible cosmid pLAFR1 (Vanbleu, E. et al. (2004) DNA Seq 15 (3): 225–227) by exploiting *L. tarentolae* recombination machinery's ability to assemble DNA fragments sharing homologies at their ends. pLAFR1 contains a tetracycline resistance for its selection, and a broad range origin of replication for *Enterobacteriaceae*. pGVXN775 is a derivative of pLAFR1 in which a multiple cloning site, a constitutive promoter J23114 (Anderson collection), and a transcriptional terminator have been introduced. Its linearization via *AsiS*I and *Xho*I allows insertion of DNA fragments between the constitutive promoter and the terminator.

[00199] Eleven fragments were designed as described in FIG. 11A and their synthesis was performed at GENEWIZ Germany GmbH. The following aspects have been taken into account for the design: a) Fragments length should not exceed 2000 bp in order to increase synthesis speed, b) overlap between fragments and between fragment and vector to be 200 bp for optimal homologous recombination efficiency.

[00200] The final construct is designed to contain a selection marker usable in *L. tarentolae* to be inserted together with the necessary 5' and 3' regulatory elements at the 3' of the gene cluster. The selection marker gene, i.e. streptothricin acetyl transferase (sat), which confer resistance to nourseothricin (NTC), is intact only if recombination takes place as it is split in two fragments. The selection marker cassette is flanked by the restriction enzyme BsiWI for its excision.

[00201] Two sets of recombinations were performed. For one set, called "pLAFR_Sp1" set, the 10 genes needed for the biosynthetic pathway and the selection marker cassette are split into nine fragments and recombined into pGVXN775. The total size of the insert is 14789 bp. The product should be able to convert *E. coli* in a *S. pneumoniae* serotype 1 LLO producer. A second set, called "pLAFR_SM" set, is a control strategy in which the selection marker cassette is split into 2 fragments and recombined into pGVXN775. The total size of the insert is 2956 bp.

[00202] Three different transfections in *Leishmania tarentolae* St10569 have been carried out as summarized in Table 2. For all the transfections, the Biorad transfection method has been followed. In transfection #1 cells have been co-transfected with the *AsiS*I-*Xho*I-linearized pGVXN775 and the 9 fragments needed for "pLAFR_Sp1". Transfection #2 differs from the previous, as the target vector is not linearized. In transfection #3 not linearized pGVXN775 is co-transfected with the two fragment needed for the "pLAFR_SM" set.

[00203] Growing cultures were analyzed by colony PCR using DreamTaq DNA Polymerase (Thermo Fisher Scientific) according to manufacturer's instructions. PCR A uses oligonucleotides o4949 and o4978 and is a positive control for lysis; PCR B uses oligonucleotides o229 and o6775 and amplifies the intersection between pGVXN775 and the 5' part of the inserted "pLAFR_Sp1" set; PCR C uses oligonucleotides o228 and o6045 and amplifies the intersection between the 3' part of the inserted "pLAFR_Sp1" set and pGVXN775; PCR D uses oligonucleotides o6517 and o6521 and amplifies an internal sequence of the "pLAFR_Sp1" set; PCR E uses oligonucleotides o5976 and o6776 and amplifies the intersection between the 3' part of the inserted "pLAFR_SM" and pGVXN775. PCRs A, B, C, D have been applied to cells from transfections #1 and #2, while PCRs A and E have been applied to cells from transfection #3. A polyclone is defined positive when all the applied PCRs yield the expected product band. The number of positive polyclones per transfection is reported in Table 2.

[00204] DNA was isolated from eight PCR-positive *L. tarentolae* polyclones from transfection #1 (polyclones 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8), three PCR-positive polyclones from transfection #2 (polyclones 2.1, 2.2, 2.3), and two PCR-positive polyclones from transfection #3 (polyclones 3.1, 3.2) using Macherey Nagel NucleoSpin plasmid Miniprep kit, following manufacturer's instructions for low copy *E. coli* plasmid isolation. The eluted material likely contains episomal and chromosomal DNA. The DNA was used to transform chemical competent *E. coli* DH5α via heat shock. The transformed colonies were plated on LB-Agar tetracycline plates. The growing colony are able to express the tetracycline-resistance cassette encoded in pGVXN775. One single colony per polyclone was inoculated in liquid LB tetracycline, and plasmid DNA was isolated using Macherey Nagel NucleoSpin plasmid kit, according to manufacturer's instructions.

[00205] *E. coli* DH5α cells transformed with all plasmids derived from polyclones from transfections #1 and #2 were assessed for their capability to express *S. pneumoniae* serotype 1 polysaccharide as lipid linked oligosaccharide (LLO). 5 mL LB tetracycline cultures have been grown o/n at 37°C in shaking culture tubes. The volume corresponding to 2 ODs was centrifuged, the pellet resuspended in Lämmli buffer, incubated 10 minutes at 95°C, cooled, supplemented with 2 µL of Proteinase K from *Tritirachium album* ≥800 units/mL (Sigma-Aldrich P4850), incubated at 55°C for 1 hour, then at 70°C for 10 minutes. 10 µL (corresponding to 0.1 OD) have been loaded on 4-12% Bis-Tris polyacrylamide gels for an SDS page. After the run, gel material has been transferred onto a blotting membrane and was detected with an antibody specific for *S. pneumoniae* serotype 1 polysaccharides. The Western blot on a part of the strains is depicted in FIG. 11B. For transfection #1 8 out of 8 clones showed *S. pneumoniae* type 1 polysaccharide production, for transfection #2 1 out of 3, as reported in Table 2. The production of the glycan indicates that a correct assembly took place.

[00206] To confirm the correct assembly, and to investigate non-producers, restriction analyses were carried out using standard restriction enzymes (Thermo Fisher Scientific). Plasmids from polyclones 1.1, 1.7, 2.1 and 2.2 were separately digested with *Bst*BI or *Bsi*WI. The tested LLO-positive clones show the expected restriction pattern. A non-producer from transfection #2 (polyclone 2.2) shows also the right pattern, while the non-producer 2.1 shows a negative pattern (FIG. 11C). Polyclones 3.1 and 3.2 from transfection 3 were digested with *Sac*I. The expected pattern for selection marker cassette insertion is observed, as deduced from the

comparison with an identical plasmid obtained by conventional cloning, pLMTB6412 (FIG. 11D).

[00207] Plasmids from polyclones 1.1 and 2.2 were further investigated via primer walking Sanger sequencing of the entire cosmid. Polyclone 1.1 shows 100% sequence identity to the expected 35038-bp construct. Polyclone 2.2 showed right restriction pattern but lack of activity. The sequencing shows 99% identity, a GG is deleted causing a frameshift in wbzG, inactivating the production of polysaccharide. The inserted selection marker cassette and its intersections with pGVXN775 of the plasmid from polyclone 3.2 were analyzed via Sanger sequencing, confirming 100% identity to expected sequence.

Plasmid derived from polyclone 1.1 has been digested via *Bsi*WI in order to remove the selection marker cassette, and religated. The obtained plasmid retains its *S. pneumoniae* serotype 1 glycan production activity.

[00208] A correct gene assembly has been achieved in 100% of the analyzed plasmids when nine fragments and a linearized vector have been co-transfected (transfection #1). The efficiency of the assembly on a circularized vector seems to be inferior but still a valid option in case of absence of suitable restriction sites as 1 case out of 3 yielded a phenotypic positive with the pLAFR_Sp1 set (transfection #2) and 2 out of 2 positives with the pLAFR_SM set (transfection #3).

Table 2: Summary of the analyses on the assembled plasmids

Transfection ID	**Transfected DNA fragments**	**Colony PCR ($n_{positive}/n_{tested}$)**	**Polyclones for plasmid isolation**	**Phenotypic test**	**Restriction analysis**	**Sequencing**
#1	pLMTB7382(SEQ1), 7383(SEQ2), 7384(SEQ3), 7385(SEQ4), 7386(SEQ5), 7387(SEQ6), 7388(SEQ7), 7390(SEQ8), 7391(SEQ9),	14 /14	1.1	Positive	Positive	Whole plasmid, 100% correct
			1.2	Positive	NA	NA
			1.3	Positive	NA	NA
			1.4	Positive	NA	NA
			1.5	Positive	NA	NA
			1.6	Positive	NA	NA
			1.7	Positive	Positive	NA

Transfection ID	Transfected DNA fragments	Colony PCR ($n_{positive}/n_{tested}$)	Polyclones for plasmid isolation	Phenotypic test	Restriction analysis	Sequencing
	linearized pGVXN775		1.8	Positive	NA	NA
#2	pLMTB7382(SEQ1), 7383(SEQ2), 7384(SEQ3), 7385(SEQ4), 7386(SEQ5), 7387(SEQ6), 7388(SEQ7), 7390(SEQ8), 7391(SEQ9), circular pGVXN775	8 / 9	2.1	Negative	Negative	NA
			2.2	Negative	Positive	Whole plasmid, 2-bp insertion
			2.3	Positive	NA	NA
#3	pLMTB7392(SEQA), 7393(SEQB), circular pGVXN775	10 / 10	3.1	NA	Positive	NA
			3.2	NA	Positive	Insert, 100% correct

7. EQUIVALENTS

[00209] The viruses, nucleic acids, methods, host cells, and compositions disclosed herein are not to be limited in scope by the specific embodiments described herein. Indeed, various modifications of the viruses, nucleic acids, methods, host cells, and compositions in addition to those described will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

[00210] Various publications, patents and patent applications are cited herein, the disclosures of which are incorporated by reference in their entireties.

8. SEQUENCE LISTING

SEQ ID NO.	Description	Sequence
1	pGVXN775	CTAGATTTATGGCTAGCTCAGTCCTAGGTACAATGCTAGCTACTAGA GATTAGGAGGATCGATAGCGATCGCCTCGAGGGCCGGCCGGATCTGT TTTGGCGGATGAGAGAAGAAATTCGTCGCCCGCCATAAACTGCCAGG CATCAAATTAAGCAGAAGGCCATCCTGACGGATGGCCTTTTTGCGTT TCTACAAACTCTTCCTGTGGATCCGAGCTCCTTAAGCTGATAGCTAG CTCAGTCCTAGGGATTATGCTAGCTACTAGAGATTAGGAGGACTAGT CCTGAGGTACGTAGGCGCGCCGTGCACTGTTTTGGCGGATGAGAGAA GAAATTCGTCGCCCGCCATAAACTGCCAGGCATCAAATTAAGCAGAA GGCCATCCTGACGGATGGCCTTTTTGCGTTTCTACAAACTCTTCCTG TTGCACACATGTGAATTCACCCCCGAACACGAGCACGGCACCCGCGA CCACTATGCCAAGAATGCCCAAGGTAAAAATTGCCGGCCCCGCCATG AAGTCCGTGAATGCCCCGACGGCCGAAGTGAAGGGCAGGCCGCCACC CAGGCCGCCGCCCTCACTGCCCGGCACCTGGTCGCTGAATGTCGATG CCAGCACCTGCGGCACGTCAATGCTTCCGGGCGTCGCGCTCGGGCTG ATCGCCCATCCCGTTACTGCCCCGATCCCGGCAATGGCAAGGACTGC CAGCGCTGCCATTTTTGGGGTGAGGCCGTTCGCGGCCGAGGGGCGCA GCCCCTGGGGGGATGGGAGGCCCGCGTTAGCGGGCCGGGAGGGTTCG AGAAGGGGGGGCACCCCCCTTCGGCGTGCGCGGTCACGCGCACAGGG CGCAGCCCTGGTTAAAAACAAGGTTTATAAATATTGGTTTAAAAGCA GGTTAAAAGACAGGTTAGCGGTGGCCGAAAAACGGGCGGAAACCCTT GCAAATGCTGGATTTTCTGCCTGTGGACAGCCCCTCAAATGTCAATA GGTGCGCCCCTCATCTGTCAGCACTCTGCCCCTCAAGTGTCAAGGAT CGCGCCCCTCATCTGTCAGTAGTCGCGCCCCTCAAGTGTCAATACCG CAGGGCACTTATCCCCAGGCTTGTCCACATCATCTGTGGGAAACTCG CGTAAAATCAGGCGTTTTCGCCGATTTGCGAGGCTGGCCAGCTCCAC GTCGCCGGCCGAAATCGAGCCTGCCCCTCATCTGTCAACGCCGCGCC GGGTGAGTCGGCCCCTCAAGTGTCAACGTCCGCCCCTCATCTGTCAG TGAGGGCCAAGTTTTCCGCGAGGTATCCACAACGCCGGCGGCCGCGG TGTCTCGCACACGGCTTCGACGGCGTTTCTGGCGCGTTTGCAGGGCC ATAGACGGCCGCCAGCCCAGCGGCGAGGGCAACCAGCCCGGTGAGCG TCGGAAAGGCGCTGGAAGCCCCGTAGCGACGCGGAGAGGGGCGAGAC AAGCCAAGGGCGCAGGCTCGATGCGCAGCACGACATAGCCGGTTCTC GCAAGGACGAGAATTTCCCTGCGGTGCCCCTCAAGTGTCAATGAAAG TTTCCAACGCGAGCCATTCGCGAGAGCCTTGAGTCCACGCTAGATCT GCCTCGCTGGCCTGCCGCAGTTCTTCAACCTCCCGGCGCAGCTTTTC GTTCTCAATTTCAGCATCCCTTTCGGCATACCATTTTATGACGGCGG CAGAGTCATAAAGCACCTCATTACCCTTGCCACCGCCTCGCAGAACG GGCATTCCCTGTTCCTGCCAGTTCTGAATGGTACGGATACTCGCACC GAAAATGTCAGCCAGCTGCTTTTTGTTGACTTCCATTGTTCATTCCA CGGACAAAAACAGAGAAAGGAAACGACAGAGGCCAAAAAGCTCGCTT TCAGCACCTGTCGTTTCCTTTCTTTTCAGAGGGTATTTTAAATAAAA ACATTAAGTTATGACGAAGAAGAACGGAAACGCCTTAAACCGGAAAA TTTTCATAAATAGCGAAAACCCGCGAGGTCGCCGCCCCGTAACAAGG CGGATCGCCGGAAAGGACCCGCAAATGATAATAATTATCAATTGCAT ACTATCGACGGCACTGCTGCCAGATAACACCACCGGGGAAACATTCC ATCATGATGGCCGTGCGGACATAGGAAGCCAGTTCATCCATCGCTTT

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		CTTGTCTGCTGCCATTTGCTTTGTGACATCCAGCGCCGCACATTCAG CAGCGTTTTTCAGCGCGTTTTCGATCAACGTTTCAATGTTGGTATCA ACACCAGGTTTAACTTTGAACTTATCGGCACTGACGGTTACCTTGTT CTGCGCTGGCTCATCACGCTGGATACCAAGGCTGATGTTGTAGATAT TGGTCACCGGCTGAGGTGTTTCGATTGCCGCTGCGTGGATAGCACCA TTTGCGATAGCGGCGTCCTTGATGAATGACACTCCATTGCGAATAAG TTCGAAGGAGACGGTGTCACGAATGCGCTGGTCCAGCTCGTCGATTG CCTTTTGTGCAGCAGAGGTATCAATCTCAACGCCAAGCGTCATCGAA GCGCAATATTGCTGCTCACCAAAACGCGTATTGACCAGGTGTTCAAC GGCAAATTTCTGCCCTTCTGATGTCAGAAAGGTAAAGTGATTTTCTT TCTGGTATTCAGTTGCTGTGTGTCTGGTTTCAGCAAAACCAAGCTCG CGCAATTCGGCTGTGCCAGATTTAGAAGGCAGATCACCAGACAGCAA CGCGCCACGGAAAAACAGCGCATACAGAACATCCGTCGCCGCGCCGG ACAACGTGATAATTTTATGACCCATGATTTATTTCCTTTTAGACGTG AGCCTGTCGCACAGCAAAGCCGCCGAAAGTTAACGGTTTGCCCAGGC TCACAACTGAAAGACTTTCTACGGTGTGCGCGTGCGATGCGCGTAGA AGACTGATTTATCAACCTGTCTTTATATCAGGATTCATTACCTGACT ATTTGTGGGTAAAGTTCGTAGTGCGCTGATCGTGCAAAATGATTTTA GTTGGGAACAGTTCGCAACTCTGTCCCATAAAAATCAGCATATTCCC ATCTATCCCATATCCAGCGCATTGACCATCGGGATACTGAAGGGAGA TTCCATCATCTCTTAGAAAGATCACCATCTCTTTTGTTTCAATTTGC ATATAGCTACCTGGAGGATTTATGAATACAAGGATTTTCATGGACTA TTACCATGAGATTGATTTTCCATCTTTATTCGCGAGAGCAGTGGAAA GCGATGACGATGTGGGTACTACATTGCGCATTCACCTACTTTGTGAG CGCATGGTCGAAGCATGGATATGCGCATGCTGTGACTGCCAAGATCT ATCTCATCTGCGCAAGGCAGAACGTGAAGACGGCCGCCCTGGACCTC GCCCGCGAGCGCCAGGCGCACGAGGCCGGCGCGCGGACCCGCGCCAC GGCCCACGAGCGGACGCCGCAGCAGGAGCGCCAGAAGGCCGCCAGAG AGGCCGAGCGCGGCCGTGAGGCTTGGACGCTAGGGCAGGGCATGAAA AAGCCCGTAGCGGGCTGCTACGGGCGTCTGACGCGGTGGAAAGGGGG AGGGGATGTTGTCTACATGGCTCTGCTGTAGTGAGTGGGTTGCGCTC CGGCAGCGGTCCTGATCAATCGTCACCCTTTCTCGGTCCTTCAACGT TCCTGACAACGAGCCTCCTTTTCGCCAATCCATCGACAATCACCGCG AGTCCCTGCTCGAACGCTGCGTCCGGACCGGCTTCGTCGAAGGCGTC TATCGCGGCCCGCAACAGCGGCGAGAGCGGAGCCTGTTCAACGGTGC CGCCGCGCTCGCCGGCATCGCTGTCGCCGGCCTGCTCCTCAAGCACG GCCCCAACAGTGAAGTAGCTGATTGTCATCAGCGCATTGACGGCGTC CCCGGCCGAAAAACCCGCCTCGCAGAGGAAGCGAAGCTGCGCGTCGG CCGTTTCCATCTGCGGTGCGCCCGGTCGCGTGCCGGCATGGATGCGC GCGCCATCGCGGTAGGCGAGCAGCGCCTGCCTGAAGCTGCGGGCATT CCCGATCAGAAATGAGCGCCAGTCGTCGTCGGCTCTCGGCACCGAAT GCGTATGATTCTCCGCCAGCATGGCTTCGGCCAGTGCGTCGAGCAGC GCCCGCTTGTTCCTGAAGTGCCAGTAAAGCGCCGGCTGCTGAACCCC CAACCGTTCCGCCAGTTTGCGTGTCGTCAGACCGTCTACGCCGACCT CGTTCAACAGGTCCAGGGCGGCACGGATCACTGTATTCGGCTGCAAC TTTGTCATGCTTGACACTTTATCACTGATAAACATAATATGTCCACC AACTTATCAGTGATAAAGAATCCGCGCGTTCAATCGGACCAGCGGAG GCTGGTCCGGAGGCCAGACGTGAAACCCAACATACCCCTGATCGTAA

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		TTCTGAGCACTGTCGCGCTCGACGCTGTCGGCATCGGCCTGATTATG CCGGTGCTGCCGGGCCTCCTGCGCGATCTGGTTCACTCGAACGACGT CACCGCCCACTATGGCATTCTGCTGGCGCTGTATGCGTTGGTGCAAT TTGCCTGCGCACCTGTGCTGGGCGCGCTGTCGGATCGTTTCGGGCGG CGGCCAATCTTGCTCGTCTCGCTGGCCGGCGCCACTGTCGACTACGC CATCATGGCGACAGCGCCTTTCCTTTGGGTTCTCTATATCGGGCGGA TCGTGGCCGGCATCACCGGGGCGACTGGGGCGGTAGCCGGCGCTTAT ATTGCCGATATCACTGATGGCGATGAGCGCGCGCGGCACTTCGGCTT CATGAGCGCCTGTTTCGGGTTCGGGATGGTCGCGGGACCTGTGCTCG GTGGGCTGATGGGCGGTTTCTCCCCCCACGCTCCGTTCTTCGCCGCG GCAGCCTTGAACGGCCTCAATTTCCTGACGGGCTGTTTCCTTTTGCC GGAGTCGCACAAAGGCGAACGCCGGCCGTTACGCCGGGAGGCTCTCA ACCCGCTCGCTTCGTTCCGGTGGGCCCGGGGCATGACCGTCGTCGCC GCCCTGATGGCGGTCTTCTTCATCATGCAACTTGTCGGACAGGTGCC GGCCGCGCTTTGGGTCATTTTCGGCGAGGATCGCTTTCACTGGGACG CGACCACGATCGGCATTTCGCTTGCCGCATTTGGCATTCTGCATTCA CTCGCCCAGGCAATGATCACCGGCCCTGTAGCCGCCCGGCTCGGCGA AAGGCGGGCACTCATGCTCGGAATGATTGCCGACGGCACAGGCTACA TCCTGCTTGCCTTCGCGACACGGGGATGGATGGCGTTCCCGATCATG GTCCTGCTTGCTTCGGGTGGCATCGGAATGCCGGCGCTGCAAGCAAT GTTGTCCAGGCAGGTGGATGAGGAACGTCAGGGGCAGCTGCAAGGCT CACTGGCGGCGCTCACCAGCCTGACCTCGATCGTCGGACCCCTCCTC TTCACGGCGATCTATGCGGCTTCTATAACAACGTGGAACGGGTGGGC ATGGATTGCAGGCGCTGCCCTCTACTTGCTCTGCCTGCCGGCGCTGC GTCGCGGGCTTTGGAGCGGCGCAGGGCAACGAGCCGATCGCTGATCG TGGAAACGATAGGCCTATGCCATGCGGGTCAAGGCGACTTCCGGCAA GCTATACGCGCCCTAGGAGTGCGGTTGGAACGTTGGCCCAGCCAGAT ACTCCCGATCACGAGCAGGACGCCGATGATTTGAAGCGCACTCAGCG TCTGATCCAAGAACAACCATCCTAGCAACACGGCGGTCCCCGGGCTG AGAAAGCCCAGTAAGGAAACAACTGTAGGTTCGAGTCGCGAGATCCC CCGGAACCAAAGGAAGTAGGTTAAACCCGCTCCGATCAGGCCGAGCC ACGCCAGGCCGAGAACATTGGTTCCTGTAGGCATCGGGATTGGCGGA TCAAACACTAAAGCTACTGGAACGAGCAGAAGTCCTCCGGCCGCCAG TTGCCAGGCGGTAAAGGTGAGCAGAGGCACGGGAGGTTGCCACTTGC GGGTCAGCACGGTTCCGAACGCCATGGAAACCGCCCCCGCCAGGCCC GCTGCGACGCCGACAGGATCTAGCGCTGCGTTTGGTGTCAACACCAA CAGCGCCACGCCCGCAGTTCCGCAAATAGCCCCCAGGACCGCCATCA ATCGTATCGGGCTACCTAGCAGAGCGGCAGAGATGAACACGACCATC AGCGGCTGCACAGCGCCTACCGTCGCCGCGACCCCGCCCGGCAGGCG GTAGACCGAAATAAACAACAAGCTCCAGAATAGCGAAATATTAAGTG CGCCGAGGATGAAGATGCGCATCCACCAGATTCCCGTTGGAATCTGT CGGACGATCATCACGAGCAATAAACCCGCCGGCAACGCCCGCAGCAG CATACCGGCGACCCCTCGGCCTCGCTGTTCGGGCTCCACGAAAACGC CGGACAGATGCGCCTTGTGAGCGTCCTTGGGGCCGTCCTCCTGTTTG AAGACCGACAGCCCAATGATCTCGCCGTCGATGTAGGCGCCGAATGC CACGGCATCTCGCAACCGTTCAGCGAACGCCTCCATGGGCTTTTTCT CCTCGTGCTCGTAAACGGACCCGAACATCTCTGGAGCTTTCTTCAGG GCCGACAATCGGATCTCGCGGAAATCCTGCACGTCGGCCGCTCCAAG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		CCGCTAAAACGGCCCCTTCTCTGCGGGCCGTCGGCTCGCGCATCATA TCGACATCCTCAACGGAAGCCGTGCCGCGAATGGCATCGGGCGGGTG CGCTTTGACAGTTGTTTTCTATCAGAACCCCTACGTCGTGCGGTTCG ATTAGCTGTTTGTCTTGCAGGCTAAACACTTTCGGTATATCGTTTGC CTGTGCGATAATGTTGCTAATGATTTGTTGCGTAGGGGTTACTGAAA AGTGAGCGGGAAAGAAGAGTTTCAGACCATCAAGGAGCGGGCCAAGC GCAAGCTGGAACGCGACATGGGTGCGGACCTGTTGGCCGCGCTCAAC GACCCGAAAACCGTTGAAGTCATGCTCAACGCGGACGGCAAGGTGTG GCACGAACGCCTTGGCGAGCCGATGCGGTACATCTGCGACATGCGGC CCAGCCAGTCGCAGGCGATTATAGAAACGGTGGCCGGATTCCACGGC AAAGAGGTCACGCGGCATTCGCCCATCCTGGAAGGCGAGTTCCCCTT GGATGGCAGCCGCTTTGCCGGCCAATTGCCGCCGGTCGTGGCCGCGC CAACCTTTGCGATCCGCAAGCGCGCGGTCGCCATCTTCACGCTGGAA CAGTACGTCGAGGCGGGCATCATGACCCGCGAGCAATACGAGGTCAT TAAAAGCGCCGTCGCGGCGCATCGAAACATCCTCGTCATTGGCGGTA CTGGCTCGGGCAAGACCACGCTCGTCAACGCGATCATCAATGAAATG GTCGCCTTCAACCCGTCTGAGCGCGTCGTCATCATCGAGGACACCGG CGAAATCCAGTGCGCCGCAGAGAACGCCGTCCAATACCACACCAGCA TCGACGTCTCGATGACGCTGCTGCTCAAGACAACGCTGCGTATGCGC CCCGACCGCATCCTGGTCGGTGAGGTACGTGGCCCCGAAGCCCTTGA TCTGTTGATGGCCTGGAACACCGGGCATGAAGGAGGTGCCGCCACCC TGCACGCAAACAACCCCAAAGCGGGCCTGAGCCGGCTCGCCATGCTT ATCAGCATGCACCCGGATTCACCGAAACCCATTGAGCCGCTGATTGG CGAGGCGGTTCATGTGGTCGTCCATATCGCCAGGACCCCTAGCGGCC GTCGAGTGCAAGAAATTCTCGAAGTTCTTGGTTACGAGAACGGCCAG TACATCACCAAAACCCTGTAAGGAGTATTTCCAATGACAACGGCTGT TCCGTTCCGTCTGACCATGAATCGCGGCATTTTGTTCTACCTTGCCG TGTTCTTCGTTCTCGCTCTCGCGTTATCCGCGCATCCGGCGATGGCC TCGGAAGGCACCGGCGGCAGCTTGCCATATGAGAGCTGGCTGACGAA CCTGCGCAACTCCGTAACCGGCCCGGTGGCCTTCGCGCTGTCCATCA TCGGCATCGTCGTCGCCGGCGGCGTGCTGATCTTCGGCGGCGAACTC AACGCCTTCTTCCGAACCCTGATCTTCCTGGTTCTGGTGATGGCGCT GCTGGTCGGCGCGCAGAACGTGATGAGCACCTTCTTCGGTCGTGGTG CCGAAATCGCGGCCCTCGGCAACGGGGCGCTGCACCAGGTGCAAGTC GCGGCGGCGGATGCCGTGCGTGCGGTAGCGGCTGGACGGCTCGCCTA ATCATGGCTCTGCGCACGATCCCCATCCGTCGCGCAGGCAACCGAGA AAACCTGTTCATGGGTGGTGATCGTGAACTGGTGATGTTCTCGGGCC TGATGGCGTTTGCGCTGATTTTCAGCGCCCAAGAGCTGCGGGCCACC GTGGTCGGTCTGATCCTGTGGTTCGGGGCGCTCTATGCGTTCCGAAT CATGGCGAAGGCCGATCCGAAGATGCGGTTCGTGTACCTGCGTCACC GCCGGTACAAGCCGTATTACCCGGCCCGCTCGACCCCGTTCCGCGAG AACACCAATAGCCAAGGGAAGCAATACCGATGATCCAAGCAATTGCG ATTGCAATCGCGGGCCTCGGCGCGCTTCTGTTGTTCATCCTCTTTGC CCGCATCCGCGCGGTCGATGCCGAACTGAAACTGAAAAAGCATCGTT CCAAGGACGCCGGCCTGGCCGATCTGCTCAACTACGCCGCTGTCGTC GATGACGGCGTAATCGTGGGCAAGAACGGCAGCTTTATGGCTGCCTG GCTGTACAAGGGCGATGACAACGCAAGCAGCACCGACCAGCAGCGCG AAGTAGTGTCCGCCCGCATCAACCAGGCCCTCGCGGGCCTGGGAAGT

SEQ ID NO.	Description	Sequence
		GGGTGGATGATCCATGTGGACGCCGTGCGGCGTCCTGCTCCGAACTA CGCGGAGCGGGGCCTGTCGGCGTTCCCTGACCGTCTGACGGCAGCGA TTGAAGAAGAGCGCTCGGTCTTGCCTTGCTCGTCGGTGATGTACTTC ACCAGCTCCGCGAAGTCGCTCTTCTTGATGGAGCGCATGGGGACGTG CTTGGCAATCACGCGCACCCCCCGGCCGTTTTAGCGGCTAAAAAAGT CATGGCTCTGCCCTCGGGCGGACCACGCCCATCATGACCTTGCCAAG CTCGTCCTGCTTCTCTTCGATCTTCGCCAGCAGGGCGAGGATCGTGG CATCACCGAACCGCGCCGTGCGCGGGTCGTCGGTGAGCCAGAGTTTC AGCAGGCCGCCCAGGCGGCCCAGGTCGCCATTGATGCGGGCCAGCTC GCGGACGTGCTCATAGTCCACGACGCCCGTGATTTTGTAGCCCTGGC CGACGGCCAGCAGGTAGGCCGACAGGCTCATGCCGGCCGCCGCCGCC TTTTCCTCAATCGCTCTTCGTTCGTCTGGAAGGCAGTACACCTTGAT AGGTGGGCTGCCCTTCCTGGTTGGCTTGGTTTCATCAGCCATCCGCT TGCCCTCATCTGTTACGCCGGCGGTAGCCGGCCAGCCTCGCAGAGCA GGATTCCCGTTGAGCACCGCCAGGTGCGAATAAGGGACAGTGAAGAA GGAACACCCGCTCGCGGGTGGGCCTACTTCACCTATCCTGCCCGGCT GACGCCGTTGGATACACCAAGGAAAGTCTACACGAACCCTTTGGCAA AATCCTGTATATCGTGCGAAAAAGGATGGATATACCGAAAAAATCGC TATAATGACCCCGAAGCAGGGTTATGCAGCGGAAAAGCGCTGCTTCC CTGCTGTTTTGTGGAATATCTACCGACTGGAAACAGGCAAATGCAGG AAATTACTGAACTGAGGGGACAGGCGAGAGACGATGCCAAAGAGCTA CACCGACGAGCTGGCCGAGTGGGTTGAATCCCGCGCGGCCAAGAAGC GCCGGCGTGATGAGGCTGCGGTTGCGTTCCTGGCGGTGAGGGCGGAT GTCGAGGCGGCGTTAGCGTCCGGCTATGCGCTCGTCACCATTTGGGA GCACATGCGGGAAACGGGGAAGGTCAAGTTCTCCTACGAGACGTTCC GCTCGCACGCCAGGCGGCACATCAAGGCCAAGCCCGCCGATGTGCCC GCACCGCAGGCCAAGGCTGCGGAACCCGCGCCGGCACCCAAGACGCC GGAGCCACGGCGGCCGAAGCAGGGGGGCAAGGCTGAAAAGCCGGCCC CCGCTGCGGCCCCGACCGGCTTCACCTTCAACCCAACACCGGACAAA AAGGATCTACTGTAATGGCGAAAATTCACATGGTTTTGCAGGGCAAG GGCGGGGTCGGCAAGTCGGCCATCGCCGCGATCATTGCGCAGTACAA GATGGACAAGGGGCAGACACCCTTGTGCATCGACACCGACCCGGTGA ACGCGACGTTCGAGGGCTACAAGGCCCTGAACGTCCGCCGGCTGAAC ATCATGGCCGGCGACGAAATTAACTCGCGCAACTTCGACACCCTGGT CGAGCTGATTGCGCCGACCAAGGATGACGTGGTGATCGACAACGGTG CCAGCTCGTTCGTGCCTCTGTCGCATTACCTCATCAGCAACCAGGTG CCGGCTCTGCTGCAAGAAATGGGGCATGAGCTGGTCATCCATACCGT CGTCACCGGCGGCCAGGCTCTCCTGGACACGGTGAGCGGCTTCGCCC AGCTCGCCAGCCAGTTCCCGGCCGAAGCGCTTTTCGTGGTCTGGCTG AACCCGTATTGGGGGCCTATCGAGCATGAGGGCAAGAGCTTTGAGCA GATGAAGGCGTACACGGCCAACAAGGCCCGCGTGTCGTCCATCATCC AGATTCCGGCCCTCAAGGAAGAAACCTACGGCCGCGATTTCAGCGAC ATGCTGCAAGAGCGGCTGACGTTCGACCAGGCGCTGGCCGATGAATC GCTCACGATCATGACGCGGCAACGCCTCAAGATCGTGCGGCGCGGCC TGTTTGAACAGCTCGACGCGGCGGCCGTGCTATGAGCGACCAGATTG AAGAGCTGATCCGGGAGATTGCGGCCAAGCACGGCATCGCCGTCGGC CGCGACGACCCGGTGCTGATCCTGCATACCATCAACGCCCGGCTCAT GGCCGACAGTGCGGCCAAGCAAGAGGAAATCCTTGCCGCGTTCAAGG

SEQ ID NO.	Description	Sequence
		AAGAGCTGGAAGGGATCGCCCATCGTTGGGGCGAGGACGCCAAGGCC AAAGCGGAGCGGATGCTGAACGCGGCCCTGGCGGCCAGCAAGGACGC AATGGCGAAGGTAATGAAGGACAGCGCCGCGCAGGCGGCCGAAGCGA TCCGCAGGGAAATCGACGACGGCCTTGGCCGCCAGCTCGCGGCCAAG GTCGCGGACGCGCGGCGCGTGGCGATGATGAACATGATCGCCGGCGG CATGGTGTTGTTCGCGGCCGCCCTGGTGGTGTGGGCCTCGTTATGAA TCGCAGAGGCGCAGATGAAAAAGCCCGGCGTTGCCGGGCTTTGTTTT TGCGTTAGCTGGGCTTGTTTGACAGGCCCAAGCTCTGACTGCGCCCG CGCTCGCGCTCCTGGGCCTGTTTCTTCTCCTGCTCCTGCTTGCGCAT CAGGGCCTGGTGCCGTCGGGCTGCTTCACGCATCGAATCCCAGTCGC CGGCCAGCTCGGGATGCTCCGCGCGCATCTTGCGCGTCGCCAGTTCC TCGATCTTGGGCGCGTGAATGCCCATGCCTTCCTTGATTTCGCGCAC CATGTCCAGCCGCGTGTGCAGGGTCTGCAAGCGGGCTTGCTGTTGGG CCTGCTGCTGCTGCCAGGCGGCCTTTGTACGCGGCAGGGACAGCAAG CCGGGGGCATTGGACTGTAGCTGCTGCAAACGCGCCTGCTGACGGTC TACGAGCTGTTCTAGGCGGTCCTCGATGCGCTCCACCTGGTCATGCT TTGCCTGCACGTAGAGCGCAAGGGTCTGCTGGTAGGTCTGCTCGATG GGCGCGGATTCTAAGAGGGCCTGCTGTTCCGTCTCGGCCTCCTGGGC CGCCTGTAGCAAATCCTCGCCGCTGTTGCCGCTGGACTGCTTTACTG CCGGGGACTGCTGTTGCCCTGCTCGCGCCGTCGTCGCAGTTCGGCTT GCCCCCACTCGATTGACTGCTTCATTTCGAGCCGCAGCGATGCGATC TCGGATTGCGTCAACGGACGGGGCAGCGCGGAGGTGTCCGGCTTCTC CTTGGGTGAGTCGGTCGATGCCATAGCCAAAGGTTTCCTTCCAAAAT GCGTCCATTGCTGGACCGTGTTTCTCATTGATGCCCGCAAGCATCTT CGGCTTGACCGCCAGGTCAAGCGCGCCTTCATGGGCGGTCATGACGG ACGCCGCCATGACCTTGCCGCCGTTGTTCTCGATGTAGCCGCGTAAT GAGGCAATGGTGCCGCCCATCGTCAGCGTGTCATCGACAACGATGTA CTTCTGGCCGGGGATCACCTCCCCCTCGAAAGTCGGGTTGAACGCCA GGCGATGATCTGAACCGGCTCCGGTTCGGGCGACCTTCTCCCGCTGC ACAATGTCCGTTTCGACCTCAAGGCCAAGGCGGTCGGCCAGAACGAC CGCCATCATGGCCGGAATCTTGTTGTTCCCCGCCGCCTCGACGGCGA GGACTGGAACGATGCGGGGCTTGTCGTCGCCGATCAGCGTCTTGAGC TGGGCAACAGTGTCGTCCGAAATCAGGCGCTCGACCAAATTAAGCGC CGCTTCCGCGTCGCCCTGCTTCGCAGCCTGGTATTCAGGCTCGTTGG TCAAAGAACCAAGGTCGCCGTTGCGAACCACCTTCGGGAAGTCTCCC CACGGTGCGCGCTCGGCTCTGCTGTAGCTGCTCAAGACGCCTCCCTT TTTAGCCGCTAAAACTCTAACGAGTGCGCCCGCGACTCAACTTGACG CTTTCGGCACTTACCTGTGCCTTGCCACTTGCGTCATAGGTGATGCT TTTCGCACTCCCGATTTCAGGTACTTTATCGAAATCTGACCGGGCGT GCATTACAAAGTTCTTCCCCACCTGTTGGTAAATGCTGCCGCTATCT GCGTGGACGATGCTGCCGTCGTGGCGCTGCGACTTATCGGCCTTTTG GGCCATATAGATGTTGTAAATGCCAGGTTTCAGGGCCCCGGCTTTAT CTACCTTCTGGTTCGTCCATGCGCCTTGGTTCTCGGTCTGGACAATT CTTTGCCCATTCATGACCAGGAGGCGGTGTTTCATTGGGTGACTCCT GACGGTTGCCTCTGGTGTTAAACGTGTCCTGGTCGCTTGCCGGCTAA AAAAAAGCCGACCTCGGCAGTTCGAGGCCGGCTTTCCCTAGAGCCGG GCGCGTCAAGGTTGTTCCATCTATTTTAGTGAACTGCGTTCGATTTA TCAGTTACTTTCCTCCCGCTTTGTGTTTCCTCCCACTCGTTTCCGCG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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2	pLMTB3857	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT TGGATAACTTGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTG TTCTCCACTCCAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCG AATGAATGACAGTAAAACCAATGCCTTCACTGGCAGTAACACCCAGC AGTGTTGACTCAATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGT CTTTTGACGAACAACTGCCCTATCAGCTGGTGATGGCCGTGTAGTGG ACTGCCATGCATGGCGTTGACGGGAGCGGGGGATTAGGGTTCGATTC CGGAGAGGGAGCCTGAGAAATAGCTACCACTTCTACGGAGGGCAGCA GGCGCGCAAATTGCCCAATGTCAAAACAAAACGATGAGGCAGCGAAA AGAAATAGAGTTGTCAGTCCATTTGGATTGTCATTTCAATGGGGGAT ATTTAAACCCATCCAATATCGAGTAACAATTGGAGGACAAGTCTGGT GCCAGCACCCGCGGTAATTCCAGCTCCAAAAGCGTATATTAATGCTG TTGCTGTTAAAGGGTTCGTAGTTGAACTGTGGGCTGTGCAGGTTTGT TCCTGGTCGTCCCGTCCATGTCGGATTTGGTGACCCAGGCCCTTGCA GCCCGTGAACATTCAAAGAAACAAGAAACACGGGAGTGGTTCCTTTC CTGATTTACGCATGTCATGCATGCGTCGAAGATCCAGTCGCAGCCTG ACCGCATCACACATCAAGGCGTTACAGCCTCTCCGTCTTTGCTGCAC CCAAGTGTATTCGTGTGACCGCGTTGAGGGATCTAATGGATTCGGAA CTTTGGTCGTTTGGTCTCTCATGCTGCCCAATCCCATGCGCTTTTCT CCGTGCCTCTCTGTCTCCCCTTCCGTTCTATTTGGACAACGATGTGT ACTGTAATGCGTGCGCCATCTGACAACGAATAGATCAGCAGCATTCG CACACTTGCACATACCCAGTGAAGCTTTTGTGTCTGTCGTATTGACA ACACCGACTGCAACAAGGTGTAGATAGAAGTTGGCCTTCTCGCTCGC TCGCACGCTCTTCACGCTCCTGCTTTCCTTGCTGTGCCTTGCCACCA GATCTGCCATGGCCTCGAGGCTCGTCCGTGTGCTGGCCGCCGCCATG CTGGTTGCAGCGGCCGTGTCGGTCGACGCTGGCGCCTCTCTAGACAC AATATGTATAGGCTACCATGCGAACAATTCAACCGACACTGTTGACA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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3	pLMTB5024	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGGAGATCGGTACTTCGCGAATGC GTCGAGATGGTACCAAATTGGATAACTTGGCGAAACGCCAAGCTAAT ACATGAACCAACCGGGTGTTCTCCACTCCAGACGGTGGGCAACCATC GTCGTGAGACGCCCAGCGAATGAATGACAGTAAAACCAATGCCTTCA CTGGCAGTAACACCCAGCAGTGTTGACTCAATTCATTCCGTGCGAAA GCCGGCTTGTTCCGGCGTCTTTTGACGAACAACTGCCCTATCAGCTG GTGATGGCCGTGTAGTGGACTGCCATGCATGGCGTTGACGGGAGCGG GGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAATAGCTACCA CTTCTACGGAGGGCAGCAGGCGCGCAAATTGCCCAATGTCAAAACAA AACGATGAGGCAGCGAAAAGAAATAGAGTTGTCAGTCCATTTGGATT GTCATTTCAATGGGGGATATTTAAACCCATCCAATATCGAGTAACAA TTGGAGGACAAGTCTGGTGCCAGCACCCGCGGTAATTCCAGCTCCAA AAGCGTATATTAATGCTGTTGCTGTTAAAGGGTTCGTAGTTGAACTG TGGGCTGTGCAGGTTTGTTCCTGGTCGTCCCGTCCATGTCGGATTTG GTGACCCAGGCCCTTGCAGCCCGTGAACATTCAAAGAAACAAGAAAC ACGGGAGTGGTTCCTTTCCTGATTTACGCATGTCATGCATGCGTCGA AGATCCAGTCGCAGCCTGACCGCATCACACATCAAGGCGTTACAGCC TCTCCGTCTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTTGAGG GATCTAATGGATTCGGAACTTTGGTCGTTTGGTCTCTCATGCTGCCC AATCCCATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCCGTTCT ATTTGGACAACGATGTGTACTGTAATGCGTGCGCCATCTGACAACGA ATAGATCAGCAGCATTCGCACACTTGCACATACCCAGTGAAGCTTTT GTGTCTGTCGTATTGACAACACCGACTGCAACAAGGTGTAGATAGAA GTTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCTCCTGCTTTCCT TGCTGTGCCTTGCCACCAGATCTGCCATGATCGCGGGCAGCGTGCGC CGCGGCGTGATCCTGCTGCTGGTGGCGGTGGCGGTGGCGACGATGGC GGCGGCGGTGAGCGCGGCGCAGATCGTGCTGAGCCAGAGCCCGGCGA TCCTGAGCGCGAGCCCGGGCGAGAAGGTGACGATGACGTGCCGCGCG AGCAGCAGCGTGAGCTACATCCACTGGTTCCAGCAGAAGCCGGGCAG CAGCCCGAAGCCGTGGATCTACGCGACGAGCAACCTGGCGAGCGGCG TGCCGGTGCGCTTCAGCGGCAGCGGCAGCGGCACGAGCTACAGCCTG ACGATCAGCCGCGTGGAGGCGGAGGACGCGGCGACGTACTACTGCCA GCAGTGGACGAGCAACCCGCCGACGTTCGGCGGCGGCACGAAGCTGG AGATCAAGCGCACGGTGGCGGCGCCGAGCGTGTTCATCTTCCCGCCG AGCGACGAGCAGCTGAAGAGCGGCACGGCGAGCGTGGTGTGCCTGCT GAACAACTTCTACCCGCGCGAGGCGAAGGTGCAGTGGAAGGTGGACA ACGCGCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACGGAGCAGGAC AGCAAGGACAGCACGTACAGCCTGAGCAGCACGCTGACGCTGAGCAA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		CACAACCACTACACGCAGAAGAGCCTGAGCCTGAGCCCGGGCAAGTG GGTACCATCGGATGCCGGGACCGACGAGTGCAGAGGCGTGCAAGCGA GCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTAT CCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAA AGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGC GCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCAT TAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCG CTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGC TGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCC ACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCA GCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGT CAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC CCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTA CCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCT CATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTC CAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCG CCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG GTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA GTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAAC CACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGC GCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGG TCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT GAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAAT GAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGAC AGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCT ATTTCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTA CGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCG CGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCC AGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCT CCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCG CCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGT GGTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCC AACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCG GTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGC AGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTG TCATGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACC AAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCC GGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAG TGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATC TTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAA CTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAA AAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGG AAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCAT TTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTT AGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG

SEQ ID NO.	Description	Sequence
		CCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAA AAATAGGCGTATCACGAGGCCCTTTCGTC
4	pLMTB5025	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGGAGATCGGTACTTCGCGAATGC GTCGAGATGGTACCAGCCTGACGTGCCTGGTGAAGGGCTTCTACCCG AGCGACATCGCGGTGGAGTGGGAGAGCAACGGCCAGCCGGAGAACAA CTACAAGACGACGCCGCCGGTGCTGGACAGCGACGGCAGCTTCTTCC TGTACAGCAAGCTGACGGTGGACAAGAGCCGCTGGCAGCAGGGCAAC GTGTTCAGCTGCAGCGTGATGCACGAGGCGCTGCACAACCACTACAC GCAGAAGAGCCTGAGCCTGAGCCCGGGCAAGTGACCTCCTCCTCCTT TCTTGTTCCTTTCACGTCGCCTTCTCGGTTGTAGCTGGCAGACGACG AGTCTTACTTTTACGTGTACTTCTCTATAGATGATGTATGATCTCTC TGCATGCGTGTTCGTGCATGTGTCCGTGTGTTGTGTACGCGTGCGTC TCGCCTCAGCTCTCCGCGTGAAAGGGTTTGACTGCCCATGATGCGTG TGTATATCCACGCGCAGGCACGCACACACACACACACACACACACAC ACAGGCACACACAGGCACACAAACGCATCTCAGGCCGAGCCGCATAC GTCTCTCGCACGGTCTCGTTTATTTGATCATGTAGTTGAGTATTAAA TTGGGAAGACAAAAACATAATAGCACGAAGAGTCGGGCACGAAAAGC CCGATCTCTCTCTCTCTCTCGTGCGCGCAGGGGCGTGTGGGTGCA CGACGACGAGGACGGAGGGGGGAAGGGAGGCATAAACGGATCGATCC CCCATCGCACATGCGGGTACGAGCATTATCTGCTGTGTCTGGTCCTT TATCATATCGCTACCCGCCCGCCCCCCGCCCCCCTCCCCCCCCCCCC CCCGCGGCTCCTGTCACTGTCGTTCCTGCGACTCCCCACACACCCGC GCAACGCTCATGTCACGAAGAGAAAAGTAGAAGGCGTGGCGATGCGT TGCGCGGCCCCCTGTCCGCTGGCATGCAGACGTCGAGCCGTGGAACG GATGGTAGCGAGAGACAACGCGGCGATGCAGGAAAGGAGATTTACTG CAGGACGTCTACACACGCGCGCACACCACTGCGAATGGCACCGTGCT GAGGAAAATTGGGGGGGAGGGCGCACGGGGGCGGGGCAGGAAACGGT TGGATCAGCAGCACTCTCAACTTGTGTCCGTATTGCGAAGGAGGGAG AGGAGCCTGCCCGTATTATGGGCGCTGAAACGTCGGAACCACCTATG AATCCCACTTCTGCGTCGCGGAGGCGTACTGCTTCCGACCACCTCCG CAGCTCACGCGCGTCGAGCTCCCTCCCTTTCCCCTTCTTTCCGTTGT GTGTGTGTGTGTGTGTGTGTCTTGTCACGATGCATGGCCATCTCTCC TCCAACCCTCCACGCCTTCCTCTCCCCCGCCCATCAAACGCGCTACG GCCACAACCATTTCTTCAAGTATCACATCCACCACCACTCTTACCCA CCTACCCTCTTCGACTCTGACACAGCCACTGACGCCCTCTCCGCCTC TCTCGCTCGCTGCACATTGACTCTCCACAGCCCCCCCTCCCTCGCAC AGCCAGCCCCACCCACCCACCCACCCACCCACCGCTCTACACACCTC CACAGCAGCCGGATCCTAGTATGAAGATTTCGGTGATCCCTGAGCAG GTGGCGGAAACATTGGATGCTGAGAACCATTTCATTGTTCGTGAAGT GTTCGATGTGCACCTATCCGACCAAGGCTTTGAACTATCTACCAGAA

SEQ ID NO.	Description	Sequence
		GTGTGAGCCCCTACCGGAAGGATTACATCTCGGATGATGACTCTGAT GAAGACTCTGCTTGCTATGGCGCATTCATCGACCAAGAGCTTGTCGG GAAGATTGAACTCAACTCAACATGGAACGATCTAGCCTCTATCGAAC ACATTGTTGTGTCGCACACGCACCGAGGCAAAGGAGTCGCGCACAGT CTCATCGAATTTGCGAAAAAGTGGGCACTAAGCAGACAGCTCCTTGG CATACGATTAGAGACACAAACGAACAATGTACCTGCCTGCAATTTGT ACGCAAAATGTGGCTTTACTCTCGGCGGCATTGACCTGTTCACGTAT AAAACTAGACCTCAAGTCTCGAACGAAACAGCGATGTACTGGTACTG GTTCTCGGGAGCACAGGATGACGCCTAACTAGCCTCGGAGATCCACT AGTTCTAGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGC GGAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAA GGCGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTG TTCTTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCT CACCCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTC TGCCGTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGC GCGCGCATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGC GGCCCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTA GCGCGGATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCC CTCAAGAGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGATGA GGCCGGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCT ACGCCTTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTC TCTCTCTCTCACACACACACACACACACACACACACACACAAAGCTCCG GTTCGTCCGGCCGTAACGCCTTTTCAACTCACGGCCTCTAGGAATGA AGGAGGGTAGTTCGGGGGAGAACGTACTGGGGCGTCAGAGGTGAAAT TCTTAGACCGCACCAAGACGAACTACAGCGAAGGCATTCTTCAAGGA TACCTTCCTCAATCAAGAACCAAAGTGTGGAGATCGAAGATGATTAG AGACCATTGTAGTCCACACTGCAAACGATGACACCCATGAATTGGGG ATCTTATGGGCCGGCCTGCGGCAGGGTTTACCCTGTGTCAGCACCGC GCCCGCTTTTACCAACTTACGTATCTTTTCTATTCGGCCTTTACCGG CCACCCACGGGAATATCCTCAGCACGTTTTCTGTTTTTTCACGCGAA AGCTTTGAGGTTACAGTCTCAGGGGGGAGTACGTTCGCAAGAGTGAA ACTTAAAGAAATTGACGGAATGGCACCACAAGACGTGGAGCGTGCGG TTTAATTTGACTCAACACGGGGAACTTTACCAGATCCGGACAGGATG AGGATTGACAGATTGAGTGTTCTTTCTCGATTCCCTGAATGGTGGTG CATGGCCGCTTTTGGTCGGTGGAGTGATTTGTTTGGTTGATTCCGTC AACGGACGAGATCCAAGCTGCCCAGTAGAATTCAGAATTGCCCATAG AATAGCAAACTCATCGGCGGGTTTTACCCAACGGTGGGCCGCATTCG GTCGAATTCTTCTCTGCGGGATTCCTTTGTAATTGCACAAGGTGAAA TTTTGGGCAACAGCAGGTCTGTGATGCTCCTCAATGTTCTGGGCGAC ACGCGCACTACAATGTCAGTGAGAACAAGAAAAACGACTTTTGTCGA ACCTACTTGATCAAAAGAGTGGGGAAACCCCGGAATCACATAGACCC ACTTGGGACCGAGGATTGCAATTATTGGTCGCGCAACGAGGAATGTC TCGTAGGCGCAGCTCATCAAACTGTGCCGATTACGTCCCTGCCATTT GTACACACCGCCCGTCGTTGTTTCCGATGATGGTGCAATACAGGTGA TCGGACAGGCGGTGTTTTATCCGCCCGAAAGTTCACCGATATTTGGT ACCATCGGATGCCGGGACCGACGAGTGCAGAGGCGTGCAAGCGAGCT TGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCG CTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGC

SEQ ID NO.	Description	Sequence
		CTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCT CACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAA TGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTC TTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGC GGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCA AAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAG AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCC TGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCG GATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCT TATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTA TCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA TGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT ACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAC CGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCA GAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCT GACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAG ATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAA GTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGT TACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATT TCGTTCATCCATAGTTGCCTGACTCCCCGTCGTGTAGATAACTACGA TACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGA GACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGC CGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCCTCCA TCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCA GTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGT GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAAC GATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTT AGCTCCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGT GTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCA TGCCATCCGTAAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAG TCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGC GTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGC TCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTA CCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAACTG ATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAA CAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAA TGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTA TCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGA AAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCA CCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAA TAGGCGTATCACGAGGCCCTTTCGTC
5	pLMTB5026	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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6	pLMTB6411	AATTGGCGCGCCCGGGACTAGTCTTGGGAATTCAGCGGGTTCGTGCG ATCCGTCTGCATGATGGTGATAGCCGTCAGCATGATTTTCGTGTCGT CGAACTTGGTGAAGGGCATTCTCGGCGGCGATCACGACGCCGGCCCT GCGGAGCCTTCGCCGCGTGCGCGATTCATGGCGGCCGTGGAGGCCAA GGATTTCGCGCGAGTGCAAGAGCTGATCGAGGCGCGTGGAGCCAAGT CGGCGGCTGATTATGTCCTTGCGCAGCTCGCCGTGGCCGAAGGTCTG GACCGCAAGCCTGGTGCGCGCGTCGTGGTCGGGAAAGCGGCGGGCAG CATGGCAATGCCGCCTGCGGCGCTGGGTTTTACGCCAAGGGGAGAAG CGGCATACGCCATCGAGCGGTCAGCCTATGGTGAGCCGAGGTCCAGC ATTGCGAAGCAGTACCAGCAGGAATGGAACCGGAAGGCGGCGACCTG GTGGGCGATGGCCGGTGTGGCCGGCATCATCGGCGCGATCCTGGCGG CGGCGGCAACCGGCTTTGTTGGGCTGGCAGTGTCGATCCGCAACCGA GTGAAGCGCGTGCGCGACCTGTTGGTGATGGAGCCGGGTGCAGAGCC ATAAGCGGCAAGAGACGAAAGCCCGGTTTCCGGGCTTTTGTTTTGTT ACGCCAAGGACGAGTTTTAGCGGCTAAAGGTGTTGACGTGCGAGAAA TGTTTAGCTAAACTTCTCTCATGTGCTGGCGGCTGTCACCGCTATGT TCAACCAAGGCGCGGAGCAAATTATGGGTGTTATCCATGAAGAAACG GCTTACCGAAAGCCAGTTCCAGGAGGCGATCCAGGGGCTGGAAGTGG GGCAGCAGACCATCGAGATAGCGCGGGGCGTCTTAGTCGATGGGAAG CCACAGGCGACGTTCGCAACGTCGCTGGGACTGACCAGGGGCGCAGT GTCGCAAGCGGTGCATCGCGTGTGGGCCGCGTTCGAGGACAAGAACT TGCCCGAGGGGTACGCGCGGGTAACGGCGGTTCTGCCGGAACATCAG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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7	pLMTB6412	AACCGGTGAATTCAGCGGGTTCGTGCGATCCGTCTGCATGATGGTGA TAGCCGTCAGCATGATTTTCGTGTCGTCGAACTTGGTGAAGGGCATT CTCGGCGGCGATCACGACGCCGGCCCTGCGGAGCCTTCGCCGCGTGC GCGATTCATGGCGGCCGTGGAGGCCAAGGATTTCGCGCGAGTGCAAG AGCTGATCGAGGCGCGTGGAGCCAAGTCGGCGGCTGATTATGTCCTT GCGCAGCTCGCCGTGGCCGAAGGTCTGGACCGCAAGCCTGGTGCGCG CGTCGTGGTCGGGAAAGCGGCGGGCAGCATGGCAATGCCGCCTGCGG CGCTGGGTTTTACGCCAAGGGGAGAAGCGGCATACGCCATCGAGCGG TCAGCCTATGGTGAGCCGAGGTCCAGCATTGCGAAGCAGTACCAGCA GGAATGGAACCGGAAGGCGGCGACCTGGTGGGCGATGGCCGGTGTGG CCGGCATCATCGGCGCGATCCTGGCGGCGGCGGCAACCGGCTTTGTT GGGCTGGCAGTGTCGATCCGCAACCGAGTGAAGCGCGTGCGCGACCT GTTGGTGATGGAGCCGGGTGCAGAGCCATAAGCGGCAAGAGACGAAA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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9	pLMTB6807	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCACACGGGCAGGCGCACGCTCCTCTCTCTTCAGGGAGCGCC GCCCCGCTGGTGTCATTGGACGAGCATCCGCCGCGCATCTCTTCACC CCTCACCCCTCATCCCTCTCCCCTCTCCCCGCACACACACGCAGTCC TTCGCTTTCACTCTTCGAACAAACACCTCAACCATCTTATCACCTTT CTCTCTTCCTTGTCAACCATGCGGTTCCGGATCTATAAGCGGAAGGT CCTGATCCTGACCCTGGTCGTCGCCGCCTGCGGCTTCGTCCTGTGGT CCTCCAACGGCCGGCAGCGGAAGAACGACGCCCTGGCCCCCCCCCTG CTGGACTCCGAGCCCCTGCGGGGCGCCGGCCACTTCGCCGCCTCCGT CGGCATCCGGCGGGTCTCCAACGACTCCGCCGCCCCCCTGGTCCCCG CCGTCCCCCGGCCCGAGGTCGACAACCTGACCCTGCGGTATCGGTCC CTGGTCTATCAGCTGAACTTCGACCAGATGCTGCGGAACGTCGACAA GGACGGCACCTGGTCCCCCGGCGAGCTGGTCCTGGTCGTCCAGGTCC ACAACCGGCCCGAGTATCTGCGGCTGCTGATCGACTCCCTGCGGAAG GCCCAGGGCATCCGGGAGGTCCTGGTCATCTTCTCCCACGACTTCTG GTCCGCCGAGATCAACTCCCTGATCTCCTCCGTCGACTTCTGCCCCG TCCTGCAGGTCTTCTTCCCCTTCTCCATCCAGCTGTATCCCTCCGAG TTCCCCGGCTCCGACCCCCGGGACTGCCCCCGGGACCTGAAGAAGAA CGCCGCCCTGAAGCTGGGCTGCATCAACGCCGAGTATCCCGACTCCT TCGGCCACTATCGGGAGGCCAAGTTCTCCCAGACCAAGCACCACTGG TGGTGGAAGCTGCACTTCGTCTGGGAGCGGGTCAAGGTCCTGCAGGA CTATACCGGCCTGATCCTGTTCCTGGAGGAGGACCACTATCTGGCCC CCGACTTCTATCACGTCTTCAAGAAGATGTGGAAGCTGAAGCAGCAG GAGTGCCCCGGCTGCGACGTCCTGTCCCTGGGCACCTATACCACCAT CCGGTCCTTCTATGGCATCGCCGACAAGGTCGACGTCAAGACCTGGA AGTCCACCGAGCACAACATGGGCCTGGCCCTGACCCGGGACGCCTAT CAGAAGCTGATCGAGTGCACCGACACCTTCTGCACCTATGACGACTA TAACTGGGACTGGACCCTGCAGTATCTGACCCTGGCCTGCCTGCCCA AGGTCTGGAAGGTCCTGGTCCCCCAGGCCCCCCGGATCTTCCACGCC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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10	pLMTB6808	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCACACGGGCAGGCGCACGCTCCTCTCTCTTCAGGGAGCGCC GCCCCGCTGGTGTCATTGGACGAGCATCCGCCGCGCATCTCTTCACC CCTCACCCCTCATCCCTCTCCCCTCTCCCCGCACACACACGCAGTCC TTCGCTTTCACTCTTCGAACAAACACCTCAACCATCTTATCACCTTT CTCTCTTCCTTGTCAACCATGCGCCTGCGCGAGCCGCTGCTGAGCGG CAGCGCGGCGATGCCGGGCGCGAGCCTGCAGCGCGCGTGCCGCCTGC TGGTGGCGGTGTGCGCGCTGCACCTGGGCGTGACGCTGGTGTACTAC CTGGCGGGCCGCGACCTGAGCCGCCTGCCGCAGCTGGTGGGCGTGAG CACGCCGCTGCAGGGCGGCAGCAACAGCGCGGCGGCGATCGGCCAGA GCAGCGGCGAGCTGCGCACGGGCGGCGCGCGCCCGCCGCCGCCGCTG GGCGCGAGCAGCCAGCCGCGCCCGGGCGGCGACAGCAGCCCGGTGGT GGACAGCGGCCCGGGCCCGGCGAGCAACCTGACGAGCGTGCCGGTGC CGCACACGACGGCGCTGAGCCTGCCGGCGTGCCCGGAGGAGAGCCCG CTGCTGGTGGGCCCGATGCTGATCGAGTTCAACATGCCGGTGGACCT GGAGCTGGTGGCGAAGCAGAACCCGAACGTGAAGATGGGTGGTCGTT ACGCGCCGCGCGACTGCGTGAGCCCGCACAAGGTGGCGATCATCATC CCGTTCCGCAACCGCCAGGAGCACCTGAAGTACTGGCTGTACTACCT GCACCCGGTGCTGCAGCGCCAGCAGCTGGACTACGGCATCTACGTGA TCAACCAGGCGGGCGACACGATCTTCAACCGCGCGAAGCTGCTGAAC GTGGGCTTCCAGGAGGCGCTGAAGGACTACGACTACACGTGCTTCGT GTTCAGCGACGTGGACCTGATCCCGATGAACGACCACAACGCGTACC GCTGCTTCAGCCAGCCGCGCCACATCAGCGTGGCGATGGACAAGTTC GGCTTCAGCCTGCCGTACGTGCAGTACTTCGGCGGCGTGAGCGCGCT GAGCAAGCAGCAGTTCCTGACGATCAACGGCTTCCCGAACAACTACT GGGGCTGGGGCGGCGAGGACGACGACATCTTCAACCGCCTGGTGTTC CGCGGCATGAGCATCAGCCGCCCGAACGCGGTGGTGGGCCGCTGCCG CATGATCCGCCACAGCCGCGACAAGAAGAACGAGCCGAACCCGCAGC GCTTCGACCGCATCGCGCACACGAAGGAGACGATGCTGAGCGACGGC CTGAACAGCCTGACGTACCAGGTGCTGGACGTGCAGCGCTACCCGCT GTACACGCAGATCACGGTGGACATCGGCACGCCGAGCTGGTCCCACC CGCAGTTCGAGAAGTAAGGTACCATTTAAATATCCCAATGGCGCGCC GAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTT ATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGT

SEQ ID NO.	Description	Sequence
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11	pLMTB6811	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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12	pLMTB6816	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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13	pLMTB6848	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCTCATCGGCGAGAAGTTCCCCATGGCCGCCATCTCCCCCCCC CGGAAGAACGGCGGCTGGGGCGACATCCGGGACCACGAGCTGTGCAA GTCCTATCGGCGGCTGCAGGCGGGAGCGTATCCTTATGACGTCCCTG ATTACGCATATCCTTATGACGTCCCTGATTACGCATATCCTTATGAC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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14	pLMTB6849	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA

SEQ ID NO.	Description	Sequence
		AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCTCCGCCACAGCCGCGACAAGAAGAACGAGCCGAACCCGCAG CGCTTCGACCGCATCGCGCACACGAAGGAGACGATGCTGAGCGACGG CCTGAACAGCCTGACGTACCAGGTGCTGGACGTGCAGCGCTACCCGC TGTACACGCAGATCACGGTGGACATCGGCACGCCGAGCTGGTCCCAC CCGCAGTTCGAGAAGTAAGGAGACTGAGCTTTAGCGAGGGAACCCGC ATGGCATACGTTGCCATAACAAGTGACCATCTACTCTCCTTAAAGTC ATGGGGGTGCTGCTGCTTGGCCGGTGCTGATCACTCTTGTTGAGGTT CCTTCAGGTGCGGGGACTCTCTTTGGCGCCTTCCCTGCTTGCCGTGC TCTCTCGACTTGTTCTAATTCCCACGTGTGCTCTCTTCCGCTTTCGT TGTAGTGGTGTACGCTGCGGTTGAGCTTGTTGTGCTTGCGCTACATT TCTCTTCGAAGGCGGAGGCAGGCGCGCCTGCGCAGTGCCGTGACGAG AGCCACTGCCGTGTCGAGCTGCGAGCAAGAGCAGTTAAGGCAAAAGG GTAGGTGAGAAAGATGACTCTGTGCGGTGCTCTCTTGTCCATGCCTG TCCGTTGTTGTCTCCCCTGTCTCTCCCTTTTTTCGGCTTGAGTGACG TTTTGCTGCCTTTGTACGTTGTTGTAGTGTCCTTACTGCTCTCGATT GCCGTCACGTTGATGCCCCTATGTGTCTCCTTTTCTTGCCTCGCACA TTGCGGATGTGCTCCCTTCTCCGCCCCCTTTTTTTTTTTTTTGCCAC AGCCGGTGCTGCCTTGTTGCGAGAGCATGCGCATTTGGAACAAATGG CACATAGTCGTAGCATCTGCGCTCTGGCCTCGGCGCCTCTCTACACC TTTGCTCACCGTGCATCACGCCATCTACACCATGTTCTCTTCGTGTT CTGCCACTCTTTTAAATGCTTTGCCTTCCCTTGGAATCCCATGCTCA GCCCTCCCCTGCTTCTCACGGTGCCTGTGGCTCTCGGCTGCGCTCTC CTGTCGCCTGTTCTTCTTCTTCCGTCCCTGTGGATGCTGCCGATTTC CCGTCTGCCCCCGTCTTTCGTTTGCCGCCTCCCCCTTCTGTGACGAA TGCCGTCTCTGTATCCCGGACGCTCCCTCACGCCAACCCACTCCTCT TTTGCGTTCTTGCGTGTGCGTCGGGCTTCTCTCCCTCCCCCTCCCCC TCCCCCTCCCCTGCCTACCCCATCACCGATGGGTGTGTGGGAGAGAG GTGGCAGGGGAAGAGGGAGTGCAGATAATGTGAGACAGAATTGAAAT ATCTGCTCTCCGACACACAGGGAGTAAATGCATTCAACAGGGATGGT AAGGACACGCACTGGCGTGACATGGAGAAAAAATAATGGAGTAATGC ATGCAGGGCTGAACTCGGCACAGAGGTACGCACCCGTGGGCACCCTC TTCTCTACGGCCCTACCTCTTTGTCTCCAATCGTTTTGTCCCCGTAT GTCATTATTATTGCTCACCTCGCGGCATTCTTGATGTAGCCGCCTCT TGACATGTATAGTGTTGTTCATTAGTATCCACCGCAAGAAAAGAAAT CCTGCATACCACCAATCGCGCGCACTGGACGTTGCCGAAAGCAGTCA GTGGGCACCTTGGACGTTGCCGCCGGTGTGGAAGTGGCCGCGTCGCA AGCAGGCCTCCATGACGTTGACTGCACGTCCCTCCCGGAAAGGGGAT GGCTTTGGTGCCATTTAGGACACAAATGGAGCTTCTTGTCGACCCTT GCTTCGAGGAATGAGGCTGCGTGTATGTGTCTTGGTGACCCCTTTGG GCTGTGCAGCTTGTGGCGTGTGCGCACCGGCGTGTGCCAACGCCCAG GTACTGTGCGCACGTTCGTATCTCCATACGCTAGCTGACCGAGACGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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15	pLMTB6851	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCTATTCTGCGCCCGCGACCCGCGCTTCGACTGCTGTCGGGTC ATGCCTTGTGCTGCGCGTTCAGCTCTTCATTGCCCCTCGGCCTTGTA CATAGCGGCTCTCCGTCATCGACGTTTTCCTCTCTCTTCAGCTCTAT ACACTCCCTCCCTTGTCAACACACTACACTGTGTCTCCCCCTTTCAT CTCTCCTCCCCTGTCACAATGCGGCTCAACGTCAAGAAGGCGCTCAT CTTCGTCGGCTGCGTGGTCTTCCTCTGGGTCCTGCTCTCGTACGCGA GCGTGATTGAGGTGCCGCGCGCGGTCCCGCAGAAGGACCCGGCCGTG GAGATCGAGAAGAAAATCATTAAGCTGCAAAAGCAGGTGGACGCCCA GATGGCCGAGAGCAAATCGCTGCTGGCGAAGGTCAAGAAGCTGAAGA AGATTAGCGAGGGCGAGAACGTGGGTGGCGAAGAGGACAGCCTGAAG GACTCGGAGGTGATGCAGCACCTGTCGCAGCCGATCCTGCCGGTCCT CGTCATCGCGTGTGACCGGGTGACCGTCCAGCGCTGCCTGGACAACC TCGTCAAGTTCCGCCCCAGCAAGGAGACGTTCCCGATCATTGTGAGC CAAGACTGTGGCCACAACGCCACCTACGAAGTGATCACGAGCTACAC GGCGAGCGACCCGACGATCAGCGTGGTGCGCCAACCGGACCTCAGCG AGATCGTGCTGCCCCGCGTGAAGGTGAAGTTCCGGGGCTACTACAAG ATCGCCCGCCACTATAAGTTCGCGCTGAACCACGTCTTTGAGACGCT GGGCCATGAAGCGGTGATCATTGTGGAGGATGACCTGGACATCTCGC CGGACTTCTTCGAGTACTTTCTCGGCACGTACCCGCTGCTGCTGAAG GATCCGAGCCTGTGGTGCATCTCGGCGTGGAACGACAACGGCAAGAT GGAGGTCATTGATATGTCGCGCCCCGACCTCCTCCATCGCACGGACT TCTTCCCGGGCCTCGGTTGGGTCCTCCGGCGCGAAATGTGGCGCAAG CTGGCGCCGAAGTGGCCCACGGCCTTCTTCGACGACTGGCTGCGCAA CCCGGTGAATATCGACGGCAAGGCCTGCATCCGCCCGGAGATCAGCC GCACGTACAGCTTCGGCAAGGTCGGCGTGAGCAAGGGCCTGTTCTTT GACCTCCATCTGCGCAACATCCAGCTCAACATGGAGTACGTGGAGTT CACGAAGCTGAACCTGACGTACCTCCTGAAGGAGCACTACGACGACG CGCTGGTGAGCACGGTGTACAACCTGCCGGAAATGTCGGCGAGCGAG GTGGTGGCGGGCAGCGACCTGAGCGCCGACCCGGTGCGCGTCATGTA CTCGAACGCGAAGACCTACCAGCGCGCCGCCAAGAAGCTCGGCCTGA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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16	pLMTB6852	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCTATTCTGCGCCCGCGACCCGCGCTTCGACTGCTGTCGGGTC ATGCCTTGTGCTGCGCGTTCAGCTCTTCATTGCCCCTCGGCCTTGTA CATAGCGGCTCTCCGTCATCGACGTTTTCCTCTCTCTTCAGCTCTAT ACACTCCCTCCCTTGTCAACACACTACACTGTGTCTCCCCCTTTCAT CTCTCCTCCCCTGTCACAATGGTCCGGAAGAAGGGCTCCCTGATCCT GTGCGGCGCCTTCCTGTTCGTCGCCTGGAACGCCCTGCTGCTGCTGT TCCTGTGGGGCCGGCCCCCCATCGGCCGGCTGGGCGAGGGCGGCGGC GCCGAGCCCGGCGCCGGCGAGGAGTGGGGCGCCGGCAAGTCCAAGGT CGGCGGCGCCAACGGCCTGGCCGGCGAGGTCATCCGGCTGGCCGAGG AGGTCGAGTCCGAGCTGGAGACCCAGAAGAAGCTGCTGAAGCAGATC CAGTCCCACCGGGAGCTGTGGGAGCAGCGGAAGGAGCTGGAGAAGCG GGAGTCCGAGGACACCAAGGACGAGAAGATCGACGTCGAGCCCAAGA AGCCCCGGCAGATCCCCGCCGTCCACCTGTCCCACAAGGTCGTCGAG GACGCCCAGACCGTCACCAAGAAGATGCAGACCCTGATGGTCACCCC CCCCCAGCTGGTCATGAAGGAGCAGGAGACCGACCAGAAGAACAAGC AGATGATGGAGGACCAGCTGGGCCTGACCACCCCCTCCCCCCAGATC ATCATCCCCATCCTGGTCATCGCCTGCGACCGGGTCACCGTCAAGCG GTCCCTGGACCGGCTGATCCAGTATCGGCCCTCCGCCGAGCTGTATC CCATCATCGTCTCCCAGGACTGCGGCCACGCCGACACCGCCCGGGTC ATCGGCTCCTATGGCTCCCAGATCACCCACATCTCCCAGCCCGACCT GGCCGACATCCCCGTCCGGCCCGACCACCGGAAGTTCCAGGGCTATT ATAAGATCGCCCGGCACTATCGGTGGGCCCTGAACCAGGTCTTCAAC GTCTTCGCCTATTCCACCGTCGTCATCGTCGAGGACGACCTGGAGGT CGCCCCCGACTTCTTCGAGTATTTCCGGGCCCTGTATCCCATCCTGC GGTCCGACCCCACCCTGTGGTGCATCTCCGCCTGGAACGACAACGGC CGGGACGGCCTGGTCGACCCCGGCAAGGCCGAGCTGCTGTATCGGAC CGACTTCTTCCCCGGCCTGGGCTGGATGCTGCTGAAGGAGGTCTGGG CCGAGCTGGAGCCCAAGTGGCCCAAGGCCTTCTGGGACGACTGGATG CGGCACCCCGAGCAGCGGAAGAACCGGTCCTGCATCCGGCCCGAAAT TTCTCGGACCATCACCTTCGGCCGGAAGGGCGTCTCCCTGGGCCAGT TCTTCGACCAGTATCTGCGGTATATCAAGCTGAACACCGAGTTCGTC CCCTTCACCAAGCACGACCTGTCCTATCTGGTCCGGGAGAAGTATGA CGTCTCCTTCGAGAAGGACGTCTATTCCGCCCCCCTGGTCAAGGTCG AGGAGCTGCAGCACGGCGGCTCCCTGAAGGGCTCCGGCCCCTTCCGG GTCCAGTATTCCTCCCGGGACTCCTTCAAGGTCCTGGCCCGGAACCT GGGCGTCATGGACGACCTGAAGTCCGGCGTCCCCCGGGCCGGCTATC

SEQ ID NO.	Description	Sequence
		GGGGCGTCGTCTCCTTCATCTCCCGGGGCCGGCGGATCTATCTGGCC CCCCCCGAGGGCTGGACCAAGTATGACGTCTCCTGGTCCTAAGGTAC CATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCA TAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAA CATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAG TGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAG TCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGC GGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCA CTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCT CACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGC AGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC AGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTT CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTA TCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACG AACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGT CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGC CACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT TTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAA GAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCT TCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAA AGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAG CATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCAT ATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGG CAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGAC TCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAA GGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAG AATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTAT TCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTA AAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACAC TGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTA ATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCAT GCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCAT AAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCAT TGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCG GGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATT ATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAAT TTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATA CTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAA

SEQ ID NO.	Description	Sequence
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17	pLMTB6855	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCAGCAAGCAGGCGCTGTGGGGTTTATCCACACAGAAGAGAAA ATAGGGTCCGTGAAGCCTGCCTACAAAGGGCGTGGAATGATAAACAC GACGTACAAGAACATGCCGAGCAGGGCACCAACAAATGGGACGATAA GGGGTAACCAAAAGTAGTGGTCGTGCAACGTGAAGGGCTCTGAGCCC CAGAGCATCGCGGAGAGGACGCGAGGTGCAAAGTCACGTGCGGGATT GAGGCAATACCCTGAGTTAATGCCTGTAGTGGCACCAATAACCACCA GCAGCAGCCCAATAGCCACCGGCTTGTAGTTTGTAGCCGGCGTCATG CGGTCATCTGTAATGGCGAGAATGCCCATCAGTAGTGCCATGGTGTT GAACACCTCGCTCCACACCGCATAGCCGGTCGCCACCTTCGGGTAGG TGACGAAGATCCCGCCATACTTGGACGCCATCGTCTCTGTTGGAAGT AAGTTCCTCTCGCCCTCGTCAAAGTGGGACTTGAACGCGTGGGGATG GATCGCGAGGGACGCGGGGTTTGAGGGCCGTGGGTGGTGTGGAGAGT GTGGTTGATTATTGTATGGTGGTGAGGGTGGAAGGTGTGGCGGGGAT GGTGGTGCGGTGGTGTCGGAAGGGGTGTGTGAGAGGGCGCGGGTCCT TGAGGGAGGGTGGGTGTGTTGTTGTTTTGCGGGTGTTATCCGGGGCT TGGGTGTTGGTGTGATTGGTGACTATGTAGGGGTGAAGGGTGAGTGG AGGGGGTCGCCAGAGGCGTTCCGTTCTACGAAGCTTCATTCCTATGT CCGACTCCGAAGCATGCCTGCAGTTCTGCTGGCTATGTGGGCGTGTC TGGGCAACGACTGAATTGAGAAGGGGAGTCGAAACGGTGCGTGGATG CTGTGTTTGTGCTACACACAAGCAAAGGCAACAACACAAGCGCATCG AGCCAGACGAACCAACCCAATATTCACACAACTGTACGTGGCCGCGC GCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGCCACCACCACGT ACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCTTTTGCGTTGTG CTTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCGTATCCCGGGAC CTGCGGGCGGTGGGTGCCACACAACCCGTCACATTCAACATCACTCA TACATCTCACCGATGTGTGCGTGTGCTTGCTGTGTGCGTGTGTTGTG TGGCGTCAAACCTGTTTGAAAACACACCCCTAGCACTATTCGACCGC GAAAGCGCCCCCCCAAAGGGGCCGGTGTGCAATGCGAGCTACATGTA TGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTGCTGAACATGTT TTGTGTGTGCTGCCGTGTCTACACGTTTGCAGCGGAAACTCGGTTGA ACCAGAAACAGAACTTGATTGTTGCTGCATTTCGAGGAATTTCAGCC AAACAAGAGGTCAACAACCAAGCCGCGTGTACACATATACACACACC GCGTGTATGTATATATGCGTTTGTTTTGTTACCACAAATACTGAGTT GTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGGAAATACAACAA AATACAACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTG TGTGTGCGAGCGCACACACACATGCACACGACTCACGTTGTCACACA ATTGAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTC

SEQ ID NO.	Description	Sequence
		TCCAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCT CCAGAGCTCGAGCCACCGGTACCATTTAAATATCCCAATGGCGCGCC GAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTT ATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGT AAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT GCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGG CGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCG GCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTAT CCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAA GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT CCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCT TACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTT CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC TCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTG CGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACG ACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG AGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA CGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGC CAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAA ACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTAC GCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG GGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTC ATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAA ATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG ACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTC ATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAA TGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCT GGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATT AATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATG AGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTT TCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCA CTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAG ACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCG AATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCA CCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGG GATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAAT GCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTG ACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTT CAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTG TCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATAT AAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGT TTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAA GCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAA

SEQ ID NO.	Description	Sequence
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18	pLMTB6860	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCGCTGCCCACTCACCATCACCGGCCTCCTTCGTTGGCAGAGC AACATTTGTTCATGAGCAGCTCTCCGTACTGTGTGTGTGCCCACTAG CCGGTGCAGAGTAGGAGCCGCGCTTTTGTTGTTGTACGTATCTTTTG ACGTGGGTGTGCGTGCAAGCAAGGATCTACGCGCAACAAGTAGCAGG CAAGCGGATCTGTTCGCCATGCGCCTGCGCGAGCCGCTGCTGAGCGG CAGCGCGGCGATGCCGGGCGCGAGCCTGCAGCGCGCGTGCCGCCTGC TGGTGGCGGTGTGCGCGCTGCACCTGGGCGTGACGCTGGTGTACTAC CTGGCGGGCCGCGACCTGAGCCGCCTGCCGCAGCTGGTGGGCGTGAG CACGCCGCTGCAGGGCGGCAGCAACAGCGCGGCGGCGATCGGCCAGA GCAGCGGCGAGCTGCGCACGGGCGGCGCGCGCCCGCCGCCGCCGCTG GGCGCGAGCAGCCAGCCGCGCCCGGGCGGCGACAGCAGCCCGGTGGT GGACAGCGGCCCGGGCCCGGCGAGCAACCTGACGAGCGTGCCGGTGC CGCACACGACGGCGCTGAGCCTGCCGGCGTGCCCGGAGGAGAGCCCG CTGCTGGTGGGCCCGATGCTGATCGAGTTCAACATGCCGGTGGACCT GGAGCTGGTGGCGAAGCAGAACCCGAACGTGAAGATGGGTGGTCGTT ACGCGCCGCGCGACTGCGTGAGCCCGCACAAGGTGGCGATCATCATC CCGTTCCGCAACCGCCAGGAGCACCTGAAGTACTGGCTGTACTACCT GCACCCGGTGCTGCAGCGCCAGCAGCTGGACTACGGCATCTACGTGA TCAACCAGGCGGGCGACACGATCTTCAACCGCGCGAAGCTGCTGAAC GTGGGCTTCCAGGAGGCGCTGAAGGACTACGACTACACGTGCTTCGT GTTCAGCGACGTGGACCTGATCCCGATGAACGACCACAACGCGTACC GCTGCTTCAGCCAGCCGCGCCACATCAGCGTGGCGATGGACAAGTTC GGCTTCAGCCTGCCGTACGTGCAGTACTTCGGCGGCGTGAGCGCGCT GAGCAAGCAGCAGTTCCTGACGATCAACGGCTTCCCGAACAACTACT GGGGCTGGGGCGGCGAGGACGACGACATCTTCAACCGCCTGGTGTTC CGCGGCATGAGCATCAGCCGCCCGAACGCGGTGGTGGGCCGCTGCCG CATGATCCGCCACAGCCGCGACAAGAAGAACGAGCCGAACCCGCAGC GCTTCGACCGCATCGCGCACACGAAGGAGACGATGCTGAGCGACGGC CTGAACAGCCTGACGTACCAGGTGCTGGACGTGCAGCGCTACCCGCT GTACACGCAGATCACGGTGGACATCGGCACGCCGAGCTGGTCCCACC CGCAGTTCGAGAAGTAAGGTACCATTTAAATATCCCAATGGCGCGCC GAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTT ATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGT AAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT GCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGG CGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCG

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19	pLMTB6861	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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20	pLMTB6873	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT

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21	pLMTB6906	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCTCCGCCACAGCCGCGACAAGAAGAACGAGCCGAACCCGCAG CGCTTCGACCGCATCGCGCACACGAAGGAGACGATGCTGAGCGACGG CCTGAACAGCCTGACGTACCAGGTGCTGGACGTGCAGCGCTACCCGC TGTACACGCAGATCACGGTGGACATCGGCACGCCGAGCTGGTCCCAC CCGCAGTTCGAGAAGTAACCTCCTCCTCCTTTCTTGTTCCTTTCACG TCGCCTTCTCGGTTGTAGCTGGCAGACGACGAGTCTTACTTTTACGT GTACTTCTCTATAGATGATGTATGATCTCTCTGCATGCGTGTTCGTG CATGTGTCCGTGTGTTGTGTACGCGTGCGTCTCGCCTCAGCTCTCCG CGTGAAAGGGTTTGACTGCCCATGATGCGTGTGTATATCCACGCGCA

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22	pLMTB6924	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCGCAAGGAATCGGTCAATACACTACATGGCGTGATTTCATA TGCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGA

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SEQ ID NO.	Description	Sequence
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23	pLMTB6933	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCGCAAGGAATCGGTCAATACACTACATGGCGTGATTTCATA TGCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGA CGACACCGTCAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGC TTTGGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGAT

SEQ ID NO.	Description	Sequence
		TTCGGCTCCAACAATGTCCTGACGGACAATGGCCGCATAACAGCGGT CATTGACTGGAGCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCG CCAACATCTTCTTCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGCAG ACGCGCTACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCG GCTCCGGGCGTATATGCTCCGCATTGGTCTTGACCAACTCTATCAGA GCTTGGTTGACGGCAATTTCGATGATGCAGCTTGGGCGCAGGGTCGA TGCGACGCAATCGTCCGATCCGGAGCCGGGACTGTCGGGCGTACACA AATCGCCCGCAGAAGCGCGGCCGTCTGGACCGATGGCTGTGTAGAAG TACTCGCCGATAGTGGAAACCGACGCCCCAGCACTCGTCCGAGGGCA AAGGAATAGCTAGCCTCGGAGATCCACTAGTTCTAGTTCTAGGGGCC GAATTCAGATCCTCGTGTGAGCGTTCGCGGAATCGGTCGCTCGTGTT TATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAGCAGGATACC GTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAATTCGCGATCTC ACAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTTTTCCCACCT CTCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAGAAGGGACGG GCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCTTCTCTTGCT TGTGGCACTCACGCTCATGCGTCAAGGCGGCCCCACGCCGAGCCCCT GCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGATGCCGTCGATGC GCAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAGGGCACACTATC ATGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTCGGCGGAGAT GCGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCTTGACTTGCG CCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCACACACACA CACACACACACACACACACAAATGTCCGTCGACAGCAGCAGCACGCA CCGGCGCCGCAGCGTCGCCGCGCGCCTGGTGCGCCTCGCGGCTGCCA GCGCTGCAGCCGCCGTTGCCCTTGCCACAGCCGCCGCGTGGGCGCAC GGCGATGCGGCCCAGCACCGCTGCATCCACGACAGCATGCAGGCCCG TGTTGTGCAGTCTGTGGCGGAGCAGCGCCTCGACCCCAGCAGGGTTG CTCCCGTCGGCCTGCCCTACGTTGCCGTGGACGCCGACGATACCGCC GCTGAGAGGAGCAGCGGCGTGCACACTAAGCAGTGGGGCACGCCGCG CATCGCCGTTTTCACCTATGACTTCACGGACGAACACTATTTCTGTA GTCGTGTGGGGCAGAATGTGAGCATGCGCAACGGCAACTTTGCCATC TGCACAGCCGACGACGTCCTCACGTACGAGAAGCGCGACATAATCAG GGATTTCATCTTCCCGCAGGCACTGCAGCTGCACACGAGGCGGCTGA AGGTGGTACCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGA GCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAT TCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTG CCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCC GCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGG CCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCG GTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGG GGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA GGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT CCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTG TCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACG CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCT

SEQ ID NO.	Description	Sequence
		GTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGT AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACT GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGA AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG AAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTA GCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAA GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCA GTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAA AAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAA TCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAA CTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTAT CAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAAC TCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGC GATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGT CAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAA TCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTC AACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCA AACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGA TCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCG CAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGAT ATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTG AGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGG AAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTG TAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCT GGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTG CCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCA TGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATA TGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGG TTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATA AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCG TATCACGAGGCCCTTTCGTC
24	pLMTB6936	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCAGACGACGGCGCAGCGGTGGCAGTGTGGACGACACCAGAG AGCGTCGAGGCAGGCGCGGTGTTCGCAGAGATTGGCCCACGCATGGC GGAGCTGAGCGGCAGCCGCCTGGCAGCACAGCAGCAGATGGAGGGCC TGCTGGCACCGCACCGCCCAAAGGAGCCAGCCTGGTTTCTGGCGACA GTGGGCGTGTCCCCGGACCACCAGGGCAAGGGCCTGGGCAGCGCAGT GGTGCTCCCAGGCGTCGAGGCTGCAGAGCGCGCAGGCGTGCCGGCAT

SEQ ID NO.	Description	Sequence
		TCCTGGAGACAAGCGCGCCACGCAACCTGCCGTTCTACGAGCGCCTG GGCTTCACCGTGACGGCGGACGTCGAGGTGCCAGAGGGCCCACGCAC ATGGTGCATGACACGCAAGCCAGGCGCGTAGCTAGCCTCGGAGATCC ACTAGTTCTAGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTT CGCGGAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCG CAAGGCGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCT CTGTTCTTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTT CCTCACCCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCC GTCTGCCGTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCT CGCGCGCGCATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAA GGCGGCCCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCC GTAGCGCGGATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGT GCCCTCAAGAGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGA TGAGGCCGGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGC GCTACGCCTTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCA CTCTCTCTCTCTCACACACACACACACACACACACACACACAAATGT CCGTCGACAGCAGCAGCACGCACCGGCGCCGCAGCGTCGCCGCGCGC CTGGTGCGCCTCGCGGCTGCCAGCGCTGCAGCCGCCGTTGCCCTTGC CACAGCCGCCGCGTGGGCGCACGGCGATGCGGCCCAGCACCGCTGCA TCCACGACAGCATGCAGGCCCGTGTTGTGCAGTCTGTGGCGGAGCAG CGCCTCGACCCCAGCAGGGTTGCTCCCGTCGGCCTGCCCTACGTTGC CGTGGACGCCGACGATACCGCCGCTGAGAGGAGCAGCGGCGTGCACA CTAAGCAGTGGGGCACGCCGCGCATCGCCGTTTTCACCTATGACTTC ACGGACGAACACTATTTCTGTAGTCGTGTGGGGCAGAATGTGAGCAT GCGCAACGGCAACTTTGCCATCTGCACAGCCGACGACGTCCTCACGT ACGAGAAGCGCGACATAATCAGGGATTTCATCTTCCCGCAGGCACTG CAGCTGCACACGAGGCGGCTGAAGGTGGTACCATTTAAATATCCCAA TGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGT GAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATT AATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGT GCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTG CGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTC GGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCT GGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATC GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGAC CCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG TGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG GTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCC CGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGG TAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG GCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC TGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCC GGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA

SEQ ID NO.	Description	Sequence
		GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCT TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGG ATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAA CTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGC AATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCG TTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGG CAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATA CAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAA ATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTAT GCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGC CTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAA CAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACA ATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGT TTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTAC GGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAG TTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTT GCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATC GATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTA TACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGA GCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAAT ATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATA TTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATT TCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGA CATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
25	pLMTB6939	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCAGACGACGGCGCAGCGGTGGCAGTGTGGACGACACCAGAG AGCGTCGAGGCAGGCGCGGTGTTCGCAGAGATTGGCCCACGCATGGC GGAGCTGAGCGGCAGCCGCCTGGCAGCACAGCAGCAGATGGAGGGCC TGCTGGCACCGCACCGCCCAAAGGAGCCAGCCTGGTTTCTGGCGACA GTGGGCGTGTCCCCGGACCACCAGGGCAAGGGCCTGGGCAGCGCAGT GGTGCTCCCAGGCGTCGAGGCTGCAGAGCGCGCAGGCGTGCCGGCAT TCCTGGAGACAAGCGCGCCACGCAACCTGCCGTTCTACGAGCGCCTG GGCTTCACCGTGACGGCGGACGTCGAGGTGCCAGAGGGCCCACGCAC ATGGTGCATGACACGCAAGCCAGGCGCGTAGCTAGCCTCGGAGATCC ACTAGTTCTAGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTT CGCGGAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCG CAAGGCGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCT CTGTTCTTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTT

SEQ ID NO.	Description	Sequence
		CCTCACCCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCC GTCTGCCGTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCT CGCGCGCGCATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAA GGCGGCCCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCC GTAGCGCGGATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGT GCCCTCAAGAGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGA TGAGGCCGGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGC GCTACGCCTTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCA CTCTCTCTCTCTCACACACACACACACACACACACACACACAAATGC GTGAGGCTATCTGCATCCACATCGGCCAGGCCGGCTGCCAGGTCGGT AACGCGTGCTGGGAGCTGTTCTGCCTTGAGCACGGCATCCAGCCTGA TGGCTCCATGCCCTCTGACAAGTGCATCGGTGTTGAGGATGACGCGT TCAACACGTTCTTCTCGGAGACTGGCGCCGGCAAGCACGTTCCTCGC TGCCTCTTCCTGGACCTGGAGCCCACGGTCGTGGATGAGGTGCGCAC CGGCACGTACCGCCAGCTGTTCAACCCCGAGCAGCTGGTGTCTGGCA AGGAGGATGCGGCGAACAACTACGCTCGTGGCCACTACACGATCGGC AAGGAGATCGTCGACCTTGCGCTGGACCGCATTCGCAAGCTGGCGGA CAACTGCACTGGTCTCCAGGGCTTTATGGTGTTCCACGCGGTGGGTG GCGGCACGGGCTCTGGCCTCGGTGCGCTGCTGCTGGAGCGCCTGTCT GTGGACTACGGCAAGAAGTCGAAGCTGGTACCATTTAAATATCCCAA TGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGT GAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATT AATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGT GCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTG CGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTC GGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCT GGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATC GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGAC CCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG TGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG GTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCC CGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGG TAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG GCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC TGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCC GGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCT TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGG ATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAA CTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGC AATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCG TTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGG

SEQ ID NO.	Description	Sequence
		CAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATA CAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAA ATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTAT GCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGC CTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAA CAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACA ATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGT TTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTAC GGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAG TTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTT GCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATC GATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTA TACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGA GCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAAT ATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATA TTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATT TCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGA CATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
26	pLMTB6940	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAA TGTATATCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGG GCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCG ATCGGAAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCG ACAGGTGCTTCTCGATCTGCATCCTGGGATCAAAGCCATAGTGAAGG ACAGTGATGGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCC TCTGGTTATGTGTGGGAGGGCTAACTAGCCTCGGAGATCCACTAGTT CTAGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGCGGAA TCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCG GTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCT TCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCACC CTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCC GTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGC GCATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGCC CCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCGC GGATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTCA AGAGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCC GGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGC CTTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTC TCTCTCACACACACACACACACACACACACACACACAAATGCGTGAGGC

SEQ ID NO.	Description	Sequence
		TATCTGCATCCACATCGGCCAGGCCGGCTGCCAGGTCGGTAACGCGT GCTGGGAGCTGTTCTGCCTTGAGCACGGCATCCAGCCTGATGGCTCC ATGCCCTCTGACAAGTGCATCGGTGTTGAGGATGACGCGTTCAACAC GTTCTTCTCGGAGACTGGCGCCGGCAAGCACGTTCCTCGCTGCCTCT TCCTGGACCTGGAGCCCACGGTCGTGGATGAGGTGCGCACCGGCACG TACCGCCAGCTGTTCAACCCCGAGCAGCTGGTGTCTGGCAAGGAGGA TGCGGCGAACAACTACGCTCGTGGCCACTACACGATCGGCAAGGAGA TCGTCGACCTTGCGCTGGACCGCATTCGCAAGCTGGCGGACAACTGC ACTGGTCTCCAGGGCTTTATGGTGTTCCACGCGGTGGGTGGCGGCAC GGGCTCTGGCCTCGGTGCGCTGCTGCTGGAGCGCCTGTCTGTGGACT ACGGCAAGAAGTCGAAGCTGGTACCATTTAAATATCCCAATGGCGCG CCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTG TTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGT GTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCG TTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCT GCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTG GGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTT CGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAG GCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTC AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT TTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCG CTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCT TTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTC GCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGC TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACA CGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAG CGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC GGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAA AAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTC TGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTAT TCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGT AATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATC CTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTA TTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCA TGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTC TTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAAT CACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCG AGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAAT CGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTT CACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCA GGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAA

SEQ ID NO.	Description	Sequence
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27	pLMTB6946	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCTAGCCACCATCAACTTTGATGCACGTGCCGGTGATGTACTT CGCCTTGGGGGAGCACAGAAAGATAACAACGTCGCTCACCTCCTCGG CGGAGGAATTACGCTGGTACAGAGGCACCTTTCTTCGGTAGTCCTCC TGCACAGAGAATGGCATGTCATCGGGGAGCACCGACAGGCCCGGACT GACGCCGTTCACTCGAATCTGCAGCGACGCAAGCTCCAGCGCGGCAG ACCGTGTGAGCCCCTCCAACGCCTCTTTGGCCATGGTATACATGGTG TATCCGAGAAGGGGCTGGCTCGTCATGGCGTCGACCATGTTGACGAT CGAGTAGCTAGTGCCGCGCTGCTCGGCTCGGGTATCCGCAACGCGCT GCGCAAACGCCTTAATCAAGAAGTAGGGCGCAATCGCGTTAGAGCCG AAGAGGTCGGCCGCGGCAACCTCCAGTGACTCCTTATCACCCACGGA GGATCCGCCTTCACCGGCGTCTTTCCTCAGCAGCGGGCGTGGGGATG GATCGCGAGGGACGCGGGGTTTGAGGGCCGTGGGTGGTGTGGAGAGT GTGGTTGATTATTGTATGGTGGTGAGGGTGGAAGGTGTGGCGGGGAT GGTGGTGCGGTGGTGTCGGAAGGGGTGTGTGAGAGGGCGCGGGTCCT TGAGGGAGGGTGGGTGTGTTGTTGTTTTGCGGGTGTTATCCGGGGCT TGGGTGTTGGTGTGATTGGTGACTATGTAGGGGTGAAGGGTGAGTGG AGGGGGTCGCCAGAGGCGTTCCGTTCTACGAAGCTTCATTCCTATGT CCGACTCCGAAGCATGCCTGCAGTTCTGCTGGCTATGTGGGCGTGTC TGGGCAACGACTGAATTGAGAAGGGGAGTCGAAACGGTGCGTGGATG CTGTGTTTGTGCTACACACAAGCAAAGGCAACAACACAAGCGCATCG AGCCAGACGAACCAACCCAATATTCACACAACTGTACGTGGCCGCGC GCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGCCACCACCACGT ACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCTTTTGCGTTGTG CTTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCGTATCCCGGGAC CTGCGGGCGGTGGGTGCCACACAACCCGTCACATTCAACATCACTCA TACATCTCACCGATGTGTGCGTGTGCTTGCTGTGTGCGTGTGTTGTG TGGCGTCAAACCTGTTTGAAAACACACCCCTAGCACTATTCGACCGC GAAAGCGCCCCCCCAAAGGGGCCGGTGTGCAATGCGAGCTACATGTA TGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTGCTGAACATGTT

SEQ ID NO.	Description	Sequence
		TTGTGTGTGCTGCCGTGTCTACACGTTTGCAGCGGAAACTCGGTTGA ACCAGAAACAGAACTTGATTGTTGCTGCATTTCGAGGAATTTCAGCC AAACAAGAGGTCAACAACCAAGCCGCGTGTACACATATACACACACC GCGTGTATGTATATATGCGTTTGTTTTGTTACCACAAATACTGAGTT GTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGGAAATACAACAA AATACAACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTG TGTGTGCGAGCGCACACACACATGCACACGACTCACGTTGTCACACA ATTGAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTC TCCAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCT CCAGAGCTCGAGCCACCGGTACCATTTAAATATCCCAATGGCGCGCC GAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTT ATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGT AAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT GCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGG CGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCG GCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTAT CCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGC CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAA GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT CCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCT TACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTT CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC TCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTG CGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACG ACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG AGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTA CGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGC CAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAA ACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTAC GCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG GGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTC ATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAA ATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTG ACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTC ATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAA TGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCT GGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATT AATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATG AGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTT TCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCA CTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAG ACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCG AATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCA CCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGG GATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAAT GCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTG

SEQ ID NO.	Description	Sequence
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28	pLMTB6950	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCAACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGT GTGTGTGCGAGCGCACACACACATGCACACGACTCACGTTGTCACAC AATTGAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCT CTCCAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTC TCCAGAGCTCGAGCCACCATGCGGTTCCGGATCTATAAGCGGAAGGT CCTGATCCTGACCCTGGTCGTCGCCGCCTGCGGCTTCGTCCTGTGGT CCTCCAACGGCCGGCAGCGGAAGAACGACGCCCTGGCCCCCCCCCTG CTGGACTCCGAGCCCCTGCGGGGCGCCGGCCACTTCGCCGCCTCCGT CGGCATCCGGCGGGTCTCCAACGACTCCGCCGCCCCCCTGGTCCCCG CCGTCCCCCGGCCCGAGGTCGACAACCTGACCCTGCGGTATCGGTCC CTGGTCTATCAGCTGAACTTCGACCAGATGCTGCGGAACGTCGACAA GGACGGCACCTGGTCCCCCGGCGAGCTGGTCCTGGTCGTCCAGGTCC ACAACCGGCCCGAGTATCTGCGGCTGCTGATCGACTCCCTGCGGAAG GCCCAGGGCATCCGGGAGGTCCTGGTCATCTTCTCCCACGACTTCTG GTCCGCCGAGATCAACTCCCTGATCTCCTCCGTCGACTTCTGCCCCG TCCTGCAGGTCTTCTTCCCCTTCTCCATCCAGCTGTATCCCTCCGAG TTCCCCGGCTCCGACCCCCGGGACTGCCCCCGGGACCTGAAGAAGAA CGCCGCCCTGAAGCTGGGCTGCATCAACGCCGAGTATCCCGACTCCT TCGGCCACTATCGGGAGGCCAAGTTCTCCCAGACCAAGCACCACTGG TGGTGGAAGCTGCACTTCGTCTGGGAGCGGGTCAAGGTCCTGCAGGA CTATACCGGCCTGATCCTGTTCCTGGAGGAGGACCACTATCTGGCCC CCGACTTCTATCACGTCTTCAAGAAGATGTGGAAGCTGAAGCAGCAG GAGTGCCCCGGCTGCGACGTCCTGTCCCTGGGCACCTATACCACCAT CCGGTCCTTCTATGGCATCGCCGACAAGGTCGACGTCAAGACCTGGA AGTCCACCGAGCACAACATGGGCCTGGCCCTGACCCGGGACGCCTAT CAGAAGCTGATCGAGTGCACCGACACCTTCTGCACCTATGACGACTA TAACTGGGACTGGACCCTGCAGTATCTGACCCTGGCCTGCCTGCCCA AGGTCTGGAAGGTCCTGGTCCCCCAGGCCCCCCGGATCTTCCACGCC GGCGACTGCGGCATGCACCACAAGAAGACCTGCCGGCCCTCCACCCA GTCCGCCCAGATCGAGTCCCTGCTGAACAACAACAAGCAGTATCTGT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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29	pLMTB6952	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCAACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGT GTGTGTGCGAGCGCACACACACATGCACACGACTCACGTTGTCACAC AATTGAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCT CTCCAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTC TCCAGAGCTCGAGCCACCATGCGCTTGAACGTAAAGAAGGCACTCAT TTTCGTCGGCTGCGTTGTCTTTCTGTGGGTGCTCCTCTCCTACGCGA GCGTCATTGAAGTGCCGCGCGCTGTGCCACAGAAGGATCCCGCAGTA GAAATTGAGAAGAAGATCATAAAGCTGCAGAAGCAGGTGGATGCCCA GATGGCCGAGTCTAAGAGTCTGCTTGCGAAGGTCAAGAAGCTTAAGA AGATATCGGAGGGAGAGAACGTGGGTGGCGAGGAGGACTCCCTGAAA GACAGCGAAGTGATGCAGCACCTGTCCCAGCCGATTCTCCCTGTCCT TGTGATCGCGTGCGACCGTGTGACGGTGCAGCGATGCCTGGACAATC TCGTGAAGTTTCGCCCATCCAAGGAGACCTTTCCGATCATTGTGTCG CAGGACTGCGGCCACAACGCTACATACGAGGTGATAACTAGCTACAC GGCTTCAGATCCGACGATCTCGGTGGTACGACAACCGGACTTGTCCG AGATCGTGCTGCCGCGGGTGAAGGTGAAGTTCCGAGGGTACTATAAG ATCGCCCGCCACTACAAATTTGCCTTGAACCACGTTTTTGAGACACT GGGTCACGAGGCTGTGATCATCGTAGAGGACGACCTCGATATCAGCC CGGACTTCTTCGAATACTTTTTGGGCACGTACCCTTTGCTTCTCAAG GACCCGAGCCTTTGGTGTATCTCTGCCTGGAACGACAATGGTAAGAT GGAGGTGATCGATATGAGCCGGCCAGATCTGCTCCACCGGACAGATT TCTTCCCCGGTCTTGGGTGGGTTTTGCGCCGGGAGATGTGGCGGAAG CTTGCACCCAAGTGGCCTACAGCTTTTTTTGACGACTGGCTTCGGAA CCCAGTGAACATCGACGGCAAGGCATGTATTCGCCCAGAGATTAGCC GCACGTACTCATTCGGAAAAGTGGGAGTCTCGAAAGGGCTCTTTTTT GACCTTCATCTCCGGAACATTCAGCTCAATATGGAATATGTGGAGTT TACGAAGCTTAACCTGACCTACCTCCTGAAGGAGCACTACGACGACG CTCTCGTGAGTACGGTGTACAATCTGCCCGAGATGTCAGCCTCGGAA GTTGTGGCGGGGAGTGATCTCAGCGCAGACCCCGTGCGAGTCATGTA CTCGAACGCAAAGACATACCAGCGTGCCGCGAAGAAGCTCGGTCTGA TGGACGACTTTCGATCAGGTGTTCCCCGCACGGCGTACCGTGGGATA GTAACATGCTTCATTCGCGGCCGCCGGGTGTACCTTGCCCCCAGTTT CGAGTGGAACAAGTACGACCCGACTTGGGGCGCGGGTGCCTGGTCGC ATCCCCAATTTGAGAAGTAGGGTACCATTTAAATATCCCAATGGCGC GCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATT

SEQ ID NO.	Description	Sequence
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30	pLMTB6956	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA

SEQ ID NO.	Description	Sequence
		AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCTCATCGGCGAGAAGTTCCCCATGGCCGCCATCTCCCCCCCC CGGAAGAACGGCGGCTGGGGCGACATCCGGGACCACGAGCTGTGCAA GTCCTATCGGCGGCTGCAGGCGGGAGCGTATCCTTATGACGTCCCTG ATTACGCATATCCTTATGACGTCCCTGATTACGCATATCCTTATGAC GTCCCTGATTACGCATAATCGAGGGAGGAGGAGGAGGCGCGTAGCAT TGCGTGCGGGTTATGTGTGCGTGCGTGTGTGTGTGCGGTGCGCGCCT TTCCTCTTTTTTTTCTCCCTCTCGTCGGTTTTTTTTTTCTGAGGAGA CGGGGCGAAGACGCGAGCGGGGGGCGGCGTTTGTGTGTGTGTGTGCG CGTGTCGGGGGCAGCGGTGTTGGCGGAACGGCCAACGCCCTGCCCCC TCCCCGCCCTGCGACGTTTCTGCGCACCCGTTCTCTCCTTCCTGCGT GCGTGTCTGCGCGCATGCACATCTGTCCGCGTGTGCCGCAGCGCTGG TATTTTTGTGAGGGCAGAGCCCTGCCTCCCCGCCTCTCTGCCGTTGG CAGGTGAAGCGAAAACGAAGCGAGAGGGCAGTCTGCATGTGTGTGCG AGGGCATGCGGAGCCCCCCTCCCCCCGCCCCCTGCCGTGCTGCACCG CTATTGTGGCGTCTTCTCTCGTTGTGCGCAAGTGTGGCTGCACCACG GCCGCCTCATGTGCGTGTGTGCGCATGTACACACACACACACACACA CACACACACACGGGCAGGCGCACGCTCCTCTCTCTTCAGGGAGCGCC GCCCCGCTGGTGTCATTGGACGAGCATCCGCCGCGCATCTCTTCACC CCTCACCCCTCATCCCTCTCCCCTCTCCCCGCACACACACGCAGTCC TTCGCTTTCACTCTTCGAACAAACACCTCAACCATCTTATCACCTTT CTCTCTTCCTTGTCAACCGGTACCATTTAAATATCCCAATGGCGCGC CGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGT TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGT TGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTG CATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGG GCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTC GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTA TCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGG CCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTT TCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCA AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTT TCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCG CTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCT GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAG CCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACA

SEQ ID NO.	Description	Sequence
		AACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTA CGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACG GGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGT CATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAA AATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCT GACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATT CATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTA ATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCC TGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTAT TAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCAT GAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCT TTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATC ACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGA GACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATC GAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTC ACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAG GGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAA TGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCT GACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTT TCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATT GTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATA TAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACG TTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGA AGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATG TATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAA AAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACC TATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
31	pLMTB6958	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCAAAGACATACCAGCGTGCCGCGAAGAAGCTCGGTCTGATG GACGACTTTCGATCAGGTGTTCCCCGCACGGCGTACCGTGGGATAGT AACATGCTTCATTCGCGGCCGCCGGGTGTACCTTGCCCCCAGTTTCG AGTGGAACAAGTACGACCCGACTTGGGGCGCGGGTGCCTGGTCGCAT CCCCAATTTGAGAAGTAGTCGAGGGAGGAGGAGGAGGCGCGTAGCAT TGCGTGCGGGTTATGTGTGCGTGCGTGTGTGTGTGCGGTGCGCGCCT TTCCTCTTTTTTTTCTCCCTCTCGTCGGTTTTTTTTTTCTGAGGAGA CGGGGCGAAGACGCGAGCGGGGGGCGGCGTTTGTGTGTGTGTGTGCG CGTGTCGGGGGCAGCGGTGTTGGCGGAACGGCCAACGCCCTGCCCCC TCCCCGCCCTGCGACGTTTCTGCGCACCCGTTCTCTCCTTCCTGCGT GCGTGTCTGCGCGCATGCACATCTGTCCGCGTGTGCCGCAGCGCTGG TATTTTTGTGAGGGCAGAGCCCTGCCTCCCCGCCTCTCTGCCGTTGG

SEQ ID NO.	Description	Sequence
		CAGGTGAAGCGAAAACGAAGCGAGAGGGCAGTCTGCATGTGTGTGCG AGGGCATGCGGAGCCCCCCTCCCCCCGCCCCCTGCCGTGCTGCACCG CTATTGTGGCGTCTTCTCTCGTTGTGCGCAAGTGTGGCTGCACCACG GCCGCCTCATGTGCGTGTGTGCGCATGTACACACACACACACACACA CACACACACACGGGCAGGCGCACGCTCCTCTCTCTTCAGGGAGCGCC GCCCCGCTGGTGTCATTGGACGAGCATCCGCCGCGCATCTCTTCACC CCTCACCCCTCATCCCTCTCCCCTCTCCCCGCACACACACGCAGTCC TTCGCTTTCACTCTTCGAACAAACACCTCAACCATCTTATCACCTTT CTCTCTTCCTTGTCAACCGGTACCATTTAAATATCCCAATGGCGCGC CGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGT TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGT TGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTG CATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGG GCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTC GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTA TCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGG CCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTT TCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCA AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTT TCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCG CTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCT GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAG CCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACA AACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTA CGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACG GGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGT CATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAA AATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCT GACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATT CATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTA ATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCC TGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTAT TAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCAT GAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCT TTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATC ACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGA GACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATC GAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTC ACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAG GGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAA TGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCT GACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTT

SEQ ID NO.	Description	Sequence
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32	pLMTB7233	CTAGATTTATGGCTAGCTCAGTCCTAGGTACAATGCTAGCTACTAGA GATTAGGAGGATCGATAGCGCGCAGGAGGACAGCTATGAATTTACAA AAGAAAAAAATTATGTTAATAACTAATCATGACGATGATATCTATTG TTTTCGAAAAGAAGTTATAGAGTCACTAGTTGAGTATGGGTATGAAG TGCTAGTGTCATGTCCTTATGGAGATAAGATAGAGTTGATGAAGTCT ATTCAATTTGAGTATGAAGATATTACTATTGATAGAAGAGGAATAAA CCCTTTAAAAGATATTCGTCTATTTCTTAGTTATATAAGATTATTGA GAAAATATAGACCGGATGTAGTCTTGACATATACCGTGAAACCAAAT GTATATGCTAGCCTAGCTGCAACAATTTTAGGAATAAAATATATAAA TAACGTAACAGGTTTAGGTAGTGTCTTAACAATGGGTTCTTGTGTAA GAAGCCTGGTGTTATTACTGTTTAGAATTTCTTTTAGGAAATCAAAT TGTGTTTTTTTTCAAAATGAATATAATATGAAAATGTTAAAAACTCT TGGCTTGATTTTGGGTGACTCTAAGCTGATACCTGGGTCAGGAGTGA ACATTGAAAAGTATCCTGTGCAACAGTATCCAAATGGTGGAAATGGA ATTCAAGGAGAAACAATCGTTTTTAATTTTATTGGTAGGATATTAAA AGAAAAAGGTATAGATACTTATCTGGCTGCTGCCCAAATTATTAAGA GTCGATATCCCAAAACAGAGTTTAATATTATTGGCTTTATAGAACCG ACAGAGAGTAATTATGAACTTAAAATTTGTGACTTAGAAAAAAAAGG AATCGTTTATTATTTGGGACAACAAAAAGATGTGATACCTCATATTA CCCGTTCCCATGCAATTATCCATCCCAGTGTGTATGGTGAAGGAATG AGCAATGTATTACTAGAAAACGCTAGTTCAGGACGTGTTTTAATTAC GACAGATAATCCAGGTTGCAAAGAAATTGTTAAAGATAGAGAGACAG GCTATATATTTCAAGGGGGAAATGTTGAGGAACTAGTCTCTATATTG GAAGTTTTTTTAGGTCTAGAAAATGAAAAACGAAAAGAGATGGGACT TCAAGGGAGAATGTATATAGAGCAATATTTTTCTCGTCAAATTATTA TAGATGCTTATTTAGATAAAATAAAAGGAGCTTTAGATGAATAGGAT TATAAAAAATATTGTTGGTTTACTTCGTGCAAATATTTGCTTGATAT TATTAAAAGTGTGTCGAAACAAGGATCTTACTTTTCATTATTTTTTA AAATTTGGAAAGAATGTAACTGTCGAACAGGAATCTAATGCTAAATT AATCTTAGGAAAAAAGATTAGAGTAAACGCCGGGGGAGTATTGAAAG TTAGAAAAGGAGCAAAACTCAAGATTTCTGATGATGTATTTTTGAGT AATAATTGTATGATAGCTTGTCGTAAATACATAGATATTAAATCTGG AGTAAAATGTGGTCCTGGAGTACTTATATATGATCATGACTATGATG TTAGTGTTCCAGGTGGATTGAAAGCAAAAAAATTTAAGACGGCCCCA GTTATGATTGGAGAAAATGTTTGGATTGGAGCTAACAGCATTGTCTT GAAGGGAGTGAGTATTGGTGAGAATAGTGTGGTTGCAGCAGGAAGTG TTGTAACAAAGGATATTCCAGCTGATACTATATTTATTCAGAAACGT TTATCAAGGGAGATGAAATTATGAAAGTATTTATAGCGACTGAATTT AGATGTACAATCTATAAAAATGAAATATATTTAAAACCGAAAGCTTA TTTTATTTATGAGCGCTATGCTAAAGCATTTGGAGAGATTGTACTAT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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34	pLMTB7383	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAATTTATCGGTTAGGCCAGGGATAACTG ACTTAGCATCTATAGAAATGGTAGATGAAAATGAGATTTTGTCTAGT TATGATGACCCACGTAGGGCTTATATAGATATAATTCTTCCAATCAA GCAAAGATATTATTTGGATTATGTTGCTAACAATTCAGTAAAGTATG ATTGTGTGATAATTTGGAAAACTATTATTAAGATTTTGTCGCGATAA TAAGGTAGTGTAGGATGATTGATAGAATATTGGAGCTGCCAAGAATT GTTAAGAGAGGTATCATCATCTGCATTGATGTAGTTATGGTGATATT CTCATTTTGGTTGTCTTATTGGTTGAGGCTTGATGAGCAAACGGCTT TTCTTAGTGCACCGATGTGGTTTGCTGCAGCTATTCTTACCATATTT ACCGTGTTTATATTTATCAGGATTGGGCTTTATCGGGCAGTCTTACG GTATGTTAGTGCAAAGATAATGTTGCTAATATCAGTTGGTATTCTGG CCTCAACGTTATCTCTTGTCGTTATATCATATTCGCTATCCATAATG TTGCCGCGCACTGTTGTCGGAATTTATTTTTTGGTTTTACTTTTACT GACATCAGGCTCTAGATTGCTTTTTAGAATGATACTTAACTATGGAG TTAAGGGTAGTGCGCCTGTTTTGATTTATGGCGCTGGTGAATCTGGC CGACAATTATTGCCAGCATTAATGCAGGCAAAAGAATATTTTCCTGT GGCATTTGTGGATGATAATCCTCGCTTGCATAAGGCCGTCATTCATG GTGTAACAGTTTATCCCTCGGATAAACTGAGTTACCTAGTAGATCGC TATGGTATAAAGAAAATTCTTTTGGCGATGCCGAGCGTCAGTAAGTC ACAAAGGCAGAAAGTGATTACTCGTTTAGAGCATTTACCGTGTGAAG TTCTCTCTATTCCGGGCATGGTCGATTTAGTCGAAGGTCGAGCACAA ATCAGTAATCTCAAAAAAGTATCGATTGATGACTTGCTAGGCCGTGA TCCAGTTGCTCCTGATGCCAAATTGATGGCGGAGAACATTACAGGCA AAGCAGTTATGGTCACTGGGGCGGGAGGATCGATCGGCTCTGAGCTT TGTCGTCAAATTGTTCGATATAAGCCAGCCAAATTGGTTCTATTTGA ACTGTCTGAATATGCCCTGTATGCCATTGAGAAAGAGCTATCGACGC TGTGTGATAAAGAAGGTTTGGATGTCTCAGTGATCCCTCTGTTGGGC TCGGTGCAGCGTCAGAATCGCTTACAGATGGTGATGAAGTCCTTTGG TATTCAAACGGTTTATCATGCGGCTGCTTATAAACATGTGCCTCTGG TTGAGCATAATGTGGTGGAAGGGGTGCGTAATAATGTGTTTGGTACC TTGTACTGCGCTGAGTCGGCGATCGATAGTGGCGTTGAAACCTTTGT GTTGATTTCCACCGATAAAGCGGTGCGGCCGACCAACACTATGGGGA CAACCAAGCGCCTGGCTGAGTTGGTATTGCAGGCGTTGTCTGCACGG CAAAGCAAAACCCGTTTTTGTATGGTGCGATTTGGTAATGTGCTGGG ATCCTCGGGCTCAGTTGTACCATTGTTTGAAAAGCAGATTGCCCAAG GTGGGCCAGTTACCCTGACTCATCGTGACATTATTCGCTATTTTATG ACAATTCCTGAAGCATCGCAGTTGGTGATTTAATTAACCTGCAGGGG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
35	pLMTB7384	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAAGAGTTGGTATTGCAGGCGTTGTCTGC ACGGCAAAGCAAAACCCGTTTTTGTATGGTGCGATTTGGTAATGTGC TGGGATCCTCGGGCTCAGTTGTACCATTGTTTGAAAAGCAGATTGCC CAAGGTGGGCCAGTTACCCTGACTCATCGTGACATTATTCGCTATTT TATGACAATTCCTGAAGCATCGCAGTTGGTGATTCAAGCGGGGGCGA TGGGGCATGGCGGCGATGTCTTTGTCTTAGACATGGGCGATCCGGTT AAGATTTATGACTTAGCCAAACGCATGATCCGGTTAAGTGGCTTGAC TGTGCGGGATGATAAAAATCCAGATGGCGATATTGCCATTGAAGTTA CGGGATTACGTCCAGGTGAGAAACTGTATGAAGAATTACTGATTGGT GATTCAGTTCAAGGTACCTCTCATCCACGAATTATGACGGCCAACGA AGTGATGCTACCGTGGCAGGATCTATCGCTCTTACTTAAAGAGCTGG ATCAAGCCTGTCATGACTTTGATCATGAGCGCATTCGCAGCTTATTG TTACAAGCACCAGCGGCATTCAATCCAACTGATGATATTTGCGATCT AGTTTGGCAGCAGAAAAAATCGCTGTTATCACAAGCGAGCAATGTCA TACGCCTGTGAAGGAGGACAGCTATGAATTTACAAAAGAAAAAAATT ATGTTAATAACTAATCATGACGATGATATCTATTGTTTTCGAAAAGA AGTTATAGAGTCACTAGTTGAGTATGGGTATGAAGTGCTAGTGTCAT GTCCTTATGGAGATAAGATAGAGTTGATGAAGTCTATTCAATTTGAG TATGAAGATATTACTATTGATAGAAGAGGAATAAACCCTTTAAAAGA TATTCGTCTATTTCTTAGTTATATAAGATTATTGAGAAAATATAGAC CGGATGTAGTCTTGACATATACCGTGAAACCAAATGTATATGCTAGC CTAGCTGCAACAATTTTAGGAATAAAATATATAAATAACGTAACAGG TTTAGGTAGTGTCTTAACAATGGGTTCTTGTGTAAGAAGCCTGGTGT TATTACTGTTTAGAATTTCTTTTAGGAAATCAAATTGTGTTTTTTTT CAAAATGAATATAATATGAAAATGTTAAAAACTCTTGGCTTGATTTT GGGTGACTCTAAGCTGATACCTGGGTCAGGAGTGAACATTGAAAAGT ATCCTGTGCAACAGTATCCAAATGGTGGAAATGGAATTCAAGGAGAA ACAATCGTTTTTAATTTTATTGGTAGGATATTAAAAGAAAAAGGTAT AGATACTTATCTGGCTGCTGCCCAAATTATTAAGAGTCGATATCCCA AAACAGAGTTTAATATTATTGGCTTTATAGAACCGACAGAGAGTAAT TATGAACTTAAAATTTGTGACTTAGAAAAAAAAGGAATCGTTTATTA TTTGGGACAACAAAAAGATGTGATACCTCATATTACCCGTTCCCATG CAATTATCCATCCCAGTGTGTATGGTGAAGGAATGAGCAATGTATTA CTAGAAAACGCTAGTTCAGGACGTGTTTTAATTACGACAGATAATCC AGGTTGCAAAGAAATTGTTAAAGATAGAGAGACAGGCTATATATTTC AAGGGGGAAATGTTGAGGAACTAGTCTCTATATTGGAAGTTTTTTTA GGTCTAGAAAATGAAAAACGAAAAGAGATGGGACTTCAAGGGAGAAT GTATATAGAGCAATATTTTTCTCGTCAAATTATTATAGATGCTTATT TAGATAAAATAAAAGGAGCTTTAGATGAATAGGATTATAAAAAATAT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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36	pLMTB7385	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAAGGGACTTCAAGGGAGAATGTATATAG AGCAATATTTTTCTCGTCAAATTATTATAGATGCTTATTTAGATAAA ATAAAAGGAGCTTTAGATGAATAGGATTATAAAAAATATTGTTGGTT TACTTCGTGCAAATATTTGCTTGATATTATTAAAAGTGTGTCGAAAC AAGGATCTTACTTTTCATTATTTTTTAAAATTTGGAAAGAATGTAAC TGTCGAACAGGAATCTAATGCTAAATTAATCTTAGGAAAAAAGATTA GAGTAAACGCCGGGGGAGTATTGAAAGTTAGAAAAGGAGCAAAACTC AAGATTTCTGATGATGTATTTTTGAGTAATAATTGTATGATAGCTTG TCGTAAATACATAGATATTAAATCTGGAGTAAAATGTGGTCCTGGAG TACTTATATATGATCATGACTATGATGTTAGTGTTCCAGGTGGATTG AAAGCAAAAAAATTTAAGACGGCCCCAGTTATGATTGGAGAAAATGT TTGGATTGGAGCTAACAGCATTGTCTTGAAGGGAGTGAGTATTGGTG AGAATAGTGTGGTTGCAGCAGGAAGTGTTGTAACAAAGGATATTCCA GCTGATACTATATTTATTCAGAAACGTTTATCAAGGGAGATGAAATT ATGAAAGTATTTATAGCGACTGAATTTAGATGTACAATCTATAAAAA TGAAATATATTTAAAACCGAAAGCTTATTTTATTTATGAGCGCTATG CTAAAGCATTTGGAGAGATTGTACTATGTAGTCGTTATGAGAAGGTG GAATCATACCCTGAAGGATATCATAAAGCGAACTTTATTAATAAATT TATCCCTATAGAAGGTCTACATCAGGTTCTATTTGGTCAAAATAAAA ATAAGATTATTGAAGGAATGATTGATAGCGACTTAATAGTTGTTCGT ATTCCGTCTATAATTGGATCAAAAACTGCAGACTACGCATTGAAGAT AGGTAAGCCGTATCTGACAGAAATAATGGGGGATGCTTGGGATTCTT ACTGGTATCATAGTTTAAAGGGAAAATTATTAGCTCCATATATATAC GCCAAAACTAAATCAATTGTAAAAAACGCTAATTATTGCATATACGT GACAGAAAAATATTTACAAGATAGATATCCTAATATTAAATCTAATA TCGTTGCTTCAAATGTTAATATTACCTCTGTAGAGAATAGATCTTTG AAGAGCCGTCTTTATAAGTTGAAAAAATTTAATCCTCAAAAAATTTC AATAATGACAACAGCATCTGTGAATGTACGAGCCAAGGGCCATAGAT TTGTATTGGAAGCAATGAAGAGATTAGAAATACAAGGTATTTTGTTG GATTATTATTTAGCAGGTGATGGTGATCAAAGTTTCTTAAAAAAGAA AGCAGAGGAATTGGGAGTAGCGAATAGAATCCATTTTTTAGGGGAAT TGACTACATCACAAATTTATGAGTATTTGGATAAAGTTGATTTATAT ATACAACCAAGTTTACAAGAAGGGTTACCTCGTGCGGTAATTGAAGC TATGAGCCGTGCTTGCCCTTGTATAGGGTCTAATAAAGCAGGAATTC CAGAGTTGCTGGGGCCACATTGTCTATTTACTCCATCCTCTTCACAA GCGATTGCGGGATCTATTATAGATTTTATTAGTATGGATAAGGAAAA GATGGTGATAAAACAGTTTGAATTCTCAAAAAAATTTCTTTCGAGTG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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37	pLMTB7386	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAAAAAAATTTCTTTCGAGTGTATTAAAT AAACGCAGAAGTGACTATTTTGCTCAAATTAGAAGAGAATTAAATAA TTCTGATGGTTTAGATTAAAATGCGATGGAAAATCCGTTTCGATATA TTAAATATGCTATAAAAACTGACTACATAGCCAATCAAATTTTTGAA TACGCATTACGTTTAAATTATTAGTTAAAGGAAAAAAGTAAATGAAG TTTAGTCTACAATCAAATGATATAAAAAATAAAATAATACTTCTAGT AGGTGTAGTTTTTTCAGGGACTTTAATTTTATGCAGTGAAAATAATG ATGTTACAATTCCATTATTTTCAATGATTTTTTTAAGTTTTATGGCA ATGATAATTGTGAAATTTAATATTTTTCATCCCTATGTGTGGTATAG TAGCTTCTTTACTATTTATTCTATTTCTTACCCGCTACTCTATAGAA TGGAGTATATAAACTATGGTTATACAAAAGATTTGATTTTCATGCAA TGGCTGGCTTTGGCAACTTTGTTGTTAACTCTACCTTCTAAAGCCAT TGTGTTAAGCGAAAGGAAAATAAACCTAAATAACAATAACTATTTAT TATTTCTCAATAATATGAATACGTTTATCACAACAGTAGCAATTATA TATCTATTAGGAAGTGGTTTTAGAAATAAAGGGGAAATATATTCAGG TGCCAATATTGTGATAATGTTAGTATTTTCTTTGGTTTATTTTATGA TTCTCATTCATACATATCAGCTATTTATACAGTTGAGTACTAAAAAA TGGAGACTACTAAATTGTAATACTAACACAGCGATAGTTATCTGTCT CTTCTCTATCGTTACAGGGGAAAGAGATTATATGTTTACTTTATTCA TCCTTGATGTGATTATATTATTTTACTTTCACAAAATAAAACGTTTT TATCTTGTAATGTTAGTTCCGCTTGCGGCACTACTGATTCCGTTATC TGCAGTTTTTAAATATACTTTATTAAGTGGGCAAGTTTCATCTATAA ATACAAATAATATTTGGTTTGATTTGCTAGATGGTGAGTTTGTATCA GCTAGTCGTAATTTACAGATTCTGATATTACATAATATGGGCAATTA TTTCGAAGGTCGTTCTTTTTTTAATGACATAGTAAGAATTTTTTATA ATACGGGGTATTCTAATCAAACTTGGTTTATGGACACCTTTTTTCCA AACGTACATTCAACCAAATATGGTTTTACTCTTGTGGGAGAGGGATA TGTGAATGGAGGATACTTTGGAATTGTAATGATTTTTATGCTAACAG GCTTTTTGATGAGATTTCTTTATATAAACGCTCAAAGAAATATATAC GGGATGCTGATATATCTGTATATGATACCTATTTTTATTTATTCTAC TCGTGCTGATTTTGCTAACATATTATCTCCATTACTTAAATATGCTA TATTGGGAACATTGGTTATTGTTTTTATCAATAGAATGGTGTTGATA TCACCATTGGATGAAATGGGTGGTGAGTAGTTTATTTAAAAAGGTGG GGTATACTTTTTGATACTATAGTGGTTTGAAGTTGGAGTAGTACAAT GCAGCTTCTAAAGAATTTTTATAAATTACTTTAAATTCCCTAATCGT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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38	pLMTB7387	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAAGAGACTATCTAAGAAATATTGGTTTG CTTTAACGAGTAAATTTTTGTTAATCTTATTAACACTTTTATCCTCA ATTATAATTAATAGGGGATTAGGTGTTGAAAAAAAAGGAGATTATGC CTATGTAATGAACTTAGTAGAAATTTTTTATATTTTAGGTGGAGTTG GTTTAGGTCAGGCTTACTCGACCTTTAAAAGGAATCATTCTAATGAG TATCAGAATAAATTTGTTTTTTTAACTTTTATTCAAGGATTATTGTT TGGAATAATAGGTTTAATAATAGTTTTAGCTGATGTTCCGATAGATT ATGGTGGGGTAATAATAGTTTTGTCCAGTCTATCTATTATGAGAACA AATCTTACTATGATTGCAGTAATAGAAAATAGTATAAAGAGGAATAA GATTGTATTAGGAGTAAGCGTAGTATATTCCGTTATGCTAGTATTGT TGTTACTATTTCATTTAGTTTCTATAGAGATGGTATTTTTGGTATAT GCTATTAATGAATTTTTACGTATCATTTTATTTTTATACTATTACAA TATGTTCCCAGTTTTTGAACATATTAGTATTAAAGAATTTTTCACTA TATATAAGTTTGGATTTCTTTCTATGATTCTTACTCTATTAATTACA TTTAATTATAGTATTGATATCATAATGTTGAAGCAAATGTCTAGTAG TTATAATGTAGGTATATACAGTGTCGCAGTTACGTTTTCTAATATGT TTTTGATGGTTCCAGACTCATTTAAAGAGATTTTATTTGGTGATTCG GCTAAAAGAACTTTTGAGAAAAATAAAGCAATAAATGCAATAAAAGT ATCATTTCTATTTATGATTTTATTAATTATTGGATTTCTTTCTTTTG GAGAATTTGCGATTACGCTCCTTTATGGTTCCAGTTATATAAAGGCA TTTCCTATAACATTAGTCATTTTTTTAGGAAGCTTATCGATGATTTT CTTTAAAATTTTACAACCAATTTATATATCTCAGGGTAAACAGAGTG TAGCTATAAAAATTTTATCTGTGTCGGCTTTGATAAATATAAGTTTA AACTGGTACTTAATTCCTAACTACCAAATTACAGGAGCTGCGATAGC ATCAGCAATCTCTTATACTGTATGTGGTTTGTTTTTTATTATAGATT ATCTTAGAAATTGATTATAATAGTTGTTAAAGAATGTGTATTAGTGG ATGAAAATATAAAAATAACAAGAGGTATTATGATATGAGAGGAAAAA CAATTCTAATTACAGGAGTAGCTGGTTTTATTGGATCAAATCTGGTT AGGAAATTATTGGAATTAGAAGGAACGATGACAATCATTGGTTTGGA CAATTTGAATGATTACTATGATATTGCACTTAAAGATTATCGATTGC TTCAACTTAATAAGCTAATTCAGGATTATCCAGAAAAAAACTGGATA TTTATCAAGGGTGATATTGCAGATAAAATGCTTATTAATAAGATTTT TAAGAGTTATCATCCTCAGATTGTTGTTAATCTAGCTGCCCAGGCAG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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39	pLMTB7388	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAATTTGCAACAGAAGATAAGGTAGACAA TCCTATTTCACTATATGCTGCGACTAAAAAAACAAATGAACTTCAAG CGTATGCTTATTCAAAGATTTACAATATTCCTTCGACAGGCTTACGC TTTTTTACAGTTTATGGTCCTGCTGGGCGCCCAGATATGGCCTATTT TGGATTTACAGATAAATTGCGAAGTGGTTCCGATATTGAGATTTATA ATCATGGTAATTGTAAACGAGATTTTACTTATATAGATGATATCGTT GAGGGGATAGTAAGGGTCATGCAATCAGCTCCGAAGAAACTAGTGGG ATCTGATAATTTACCGTTAGCCCCATATAAAGTGTACAATATTGGGA ATAGTAAACCCGAAAATTTGTTAGATTTTGTGGATGTTCTTCAACAG GAGCTAATCAAGGCAGGAGTTTTGCCGGAAAATTATGATTTTGATAG TCATAAAAAATTAGTTCCTATGCAACCAGGCGATGTTCCTGTTACTT ATGCAGATACAAGTGATTTAGAGAGAGATTTTGGTTTTAAACCAAAA ACTTCTTTACGAGAAGGTTTGAGAAAGTTTGCAGAGTGGTATAAAGA CTACTATAATGTATAACGAGAGTGTTTTGAGAAAGGAAAAAATTATG AAAATAGCAGTAGCAGGTACAGGATATGTTGGATTATCTATTGCAAT CTTACTGGCTCAACATCATCAAGTTGTTGCCGTAGATATCATTCCTG AGAAAGTTGAGTTAATCAATAAAAAGAAGTCCCCTATCCAAGACGAT TATATAGAAAAATATCTCGCGGAAAAAGAATTGAATCTCGTAGCTAC ATTGAATGCAGAGGAAGCATATGAGAATGCGGATTTTATAGTTATTG CGGCTCCAACTAATTATGATCCGAAAAAAAATTTTTTCGATACATCT TCAGTCGAGGCTGTCATTGAAGCAGTTATGAAATATAATCCTGATGC AATTATAATAATTAAAAGTACTGTTCCTGTTGGATATACAAAGTCAG TACGGAGGAAATTTCTTACAGACAATATTATGTTTAGTCCTGAGTTT TTACGGGAGTCAAAAGCGTTATATGATAACCTATATCCGAGTCGAAT TATTATAGGTACAGATAAAGATGATAAAGATTTGGTAAAGTCTGCTG AAATTTTTGTAAAAATGCTTCAGGAAGGTGCAGTGAAAGAAAATATT GAAACATTGTATATGGATTTTACAGAAGCTGAAGCAGTAAAACTTTT TGCTAATACCTATCTTGCCCTCCGGGTTTCCTATTTTAACGAGTTAG ATACTTATTCTGAGATGAAAGGACTAGATACTCAAGCGATTATTGAT GGAGTTTGTTTAGATCCGAGAATAGGTTCTCACTACAATAATCCTTC TTTTGGTTATGGGGGTTACTGTCTTCCTAAAGATACCAAGCAACTTC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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40	pLMTB7390	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAAACGAACCAACTCTTGAAAGTGGTACT ACTTTCTATGGTAGTCAAGTAGTTAATGATTTTGAAATATTTAAGAA ATCTAGTCAAGTGATTGTTGCAAATCGTTTTGATGAGACTTTAGAAG ATGTGAGGGGTAAAGTTTATACTAGGGATATTTTTAAGAGAGATTAA GCCTCGAGGGCCGGCCCGTACGCCTCCTCCTCCTTTCTTGTTCCTTT CACGTCGCCTTCTCGGTTGTAGCTGGCAGACGACGAGTCTTACTTTT ACGTGTACTTCTCTATAGATGATGTATGATCTCTCTGCATGCGTGTT CGTGCATGTGTCCGTGTGTTGTGTACGCGTGCGTCTCGCCTCAGCTC TCCGCGTGAAAGGGTTTGACTGCCCATGATGCGTGTGTATATCCACG CGCAGGCACGCACACACACACACACACACACACACACACAGGCACACAC AGGCACACAAACGCATCTCAGGCCGAGCCGCATACGTCTCTCGCACG GTCTCGTTTATTTGATCATGTAGTTGAGTATTAAATTGGGAAGACAA AAACATAATAGCACGAAGAGTCGGGCACGAAAAGCCCGATCTCTCTC TCTCTCTCTCGTGCGCGCAGGGGCGTGTGGGTGCACGACGACGAGGA CGGAGGGGGGAAGGGAGGCATAAACGGATCGATCCCCCATCGCACAT GCGGGTACGAGCATTATCTGCTGTGTCTGGTCCTTTATCATATCGCT ACCCGCCCGCCCCCCGCCCCCCTCCCCCCCCCCCCCCCGCGGCTCCT GTCACTGTCGTTCCTGCGACTCCCCACACACCCGCGCAACGCTCATG TCACGAAGAGAAAAGTAGAAGGCGTGGCGATGCGTTGCGCGGCCCCC TGTCCGCTGGCATGCAGACGTCGAGCCGTGGAACGGATGGTAGCGAG AGACAACGCGGCGATGCAGGAAAGGAGATTTACTGCAGGACGTCTAC ACACGCGCGCACACCACTGCGAATGGCACCGTGCTGAGGAAAATTGG GGGGGAGGGCGCACGGGGGCGGGGCAGGAAACGGTTGGATCAGCAGC ACTCTCAACTTGTGTCCGTATTGCGAAGGAGGGAGAGGAGCCTGCCC GTATTATGGGCGCTGAAACGTCGGAACCACCTATGAATCCCACTTCT GCGTCGCGGAGGCGTACTGCTTCCGACCACCTCCGCAGCTCACGCGC GTCGAGCTCCCTCCCTTTCCCCTTCTTTCCGTTGTGTGTGTGTGTGT GTGTGTGTCTTGTCACGATGCATGGCCATCTCTCCTCCAACCCTCCA CGCCTTCCTCTCCCCCGCCCATCAAACGCGCTACGGCCACAACCATT

SEQ ID NO.	Description	Sequence
		TCTTCAAGTATCACATCCACCACCACTCTTACCCACCTACCCTCTTC GACTCTGACACAGCCACTGACGCCCTCTCCGCCTCTCTCGCTCGCTG CACATTGACTCTCCACAGCCCCCCCTCCCTCGCACAGCCAGCCCCAC CCACCCACCCACCCACCCACCGCTCTACACACCTCCACAGCAGCCGG ATCCTAGTATGAAGATTTCGGTGATCCCTGAGCAGGTGGCGGAAACA TTGGATGCTGAGAACCATTTCATTGTTCGTGAAGTGTTCGATGTGCA CCTATCCGACCAAGGCTTTGAACTATCTACCAGAAGTGTGAGCCCCT ACCGGAAGGATTACATCTCGGATGATGACTCTGATGAAGACTCTGCT TGCTATGGCGCATTCATCGACCAAGAGCTTGTCGGGAAGATTGAACT CAACTCAACATGGAACGATCTAGCCTCTATCGAACACATTGTTGTGT CGCACACGCACCGAGGCAAAGGAGTCGCGCACAGTCTCATCGAATTT GCGAAAAAGTGGGCACTAAGCAGACAGCTCCTTGGCATACGTTAATT AACCTGCAGGGGATCCCGGGCCCGTCGACTGCAGAGGCCTGCATGCA AGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTA AAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTG CGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGC GCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGG CTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATC CACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCC AGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTC CATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTC CCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTC TCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGC GCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGA CTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGA GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTAC GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCC AGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAA CCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACG CGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG GTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCA TGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAA TGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGA CAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCA TATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAAT GAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTG GTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTA ATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGA GTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTT CCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCAC TCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGA CGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGA ATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCAC

SEQ ID NO.	Description	Sequence
		CTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGG ATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATG CTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGA CCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTC AGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGT CGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATA AATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTT TCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAG CATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAA GTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTA TAAAAATAGGCGTATCACGAGGC
41	pLMTB7391	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAATCTGATGAAGACTCTGCTTGCTATGG CGCATTCATCGACCAAGAGCTTGTCGGGAAGATTGAACTCAACTCAA CATGGAACGATCTAGCCTCTATCGAACACATTGTTGTGTCGCACACG CACCGAGGCAAAGGAGTCGCGCACAGTCTCATCGAATTTGCGAAAAA GTGGGCACTAAGCAGACAGCTCCTTGGCATACGATTAGAGACACAAA CGAACAATGTACCTGCCTGCAATTTGTACGCAAAATGTGGCTTTACT CTCGGCGGCATTGACCTGTTCACGTATAAAACTAGACCTCAAGTCTC GAACGAAACAGCGATGTACTGGTACTGGTTCTCGGGAGCACAGGATG ACGCCTAACTAGCCTCGGAGATCCACTAGTTCTAGTTCTAGGGGCCG AATTCAGATCCTCGTGTGAGCGTTCGCGGAATCGGTCGCTCGTGTTT ATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAGCAGGATACCG TCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAATTCGCGATCTCA CAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTTTTCCCACCTC TCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAGAAGGGACGGG CATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCTTCTCTTGCTT GTGGCACTCACGCTCATGCGTCAAGGCGGCCCCACGCCGAGCCCCTG CGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGATGCCGTCGATGCG CAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAGGGCACACTATCA TGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTCGGCGGAGATG CGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCTTGACTTGCGC CCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCACACACACAC ACACACACACACACACACAACGTACGGGATCTGTTTTGGCGGATGAG AGAAGAAATTCGTCGCCCGCCATAAACTGCCAGGCATCAAATTAAGC AGAAGGCCATCCTGACGGATGGCCTTTTTGCGTTTCTACAAACTCTT CCTGTGGATCCGAGCTCCTTAAGCTGATAGCTAGCTCAGTCCTAGGG ATTATGCTAGCTACTAGAGATTAGGAGGACTAGTCCTGAGGTACGTA GGCGCGCCGTGCACTGTTTTGGCGGATGAGAGAAGAAATTCGTCGCC

SEQ ID NO.	Description	Sequence
		CGCCATAAACTGCCAGGCATCAAATTAAGCAGAAGGCCATCCTGACG GATGGCCTTTTTGCGTTTCTACAAACTCTTCCTGTTTAATTAACCTG CAGGGGATCCCGGGCCCGTCGACTGCAGAGGCCTGCATGCAAGCTTG GCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCT CACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCT GGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCA CTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATG AATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTT CCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGG CGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGA ATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG GAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGA TACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTA TCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATG TAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC ACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTAC CTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCG CTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGA CGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT TATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGT TTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTA GAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAG GATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGA GAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCG GTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCC CCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACG ACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGAC TTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCAT CAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAAT ACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAA CCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAAT CAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCA GTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGAT GGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCT CATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAAC AACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACC TGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAG CATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGT TGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTA TCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGA AAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCA

SEQ ID NO.	Description	Sequence
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42	pLMTB7392	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAACAGCAACTGAATACCAGAAAGAAAAT CACTTTACCTTTCTGACATCAGAAGGGCAGAAATTTGCCGTTGAACA CCTGGTCAATACGCGTTTTGGTGAGCAGCAATATTGCGCTTCGATGA CGCTTGGCGTTGAGATTGATACCTCTGCTGCACAAAAGGCAATCGAC GAGCTGGACCAGCGCATTCGTGACACCGTCTCCCACCAGGTGTACGT ACACCACCATCACCACCACTAGGCGGCCGCCCTCCTCCTCCTTTCTT GTTCCTTTCACGTCGCCTTCTCGGTTGTAGCTGGCAGACGACGAGTC TTACTTTTACGTGTACTTCTCTATAGATGATGTATGATCTCTCTGCA TGCGTGTTCGTGCATGTGTCCGTGTGTTGTGTACGCGTGCGTCTCGC CTCAGCTCTCCGCGTGAAAGGGTTTGACTGCCCATGATGCGTGTGTA TATCCACGCGCAGGCACGCACACACACACACACACACACACACACAG GCACACACAGGCACACAAACGCATCTCAGGCCGAGCCGCATACGTCT CTCGCACGGTCTCGTTTATTTGATCATGTAGTTGAGTATTAAATTGG GAAGACAAAAACATAATAGCACGAAGAGTCGGGCACGAAAAGCCCGA TCTCTCTCTCTCTCTCTCGTGCGCGCAGGGGCGTGTGGGTGCACGAC GACGAGGACGGAGGGGGGAAGGGAGGCATAAACGGATCGATCCCCCA TCGCACATGCGGGTACGAGCATTATCTGCTGTGTCTGGTCCTTTATC ATATCGCTACCCGCCCGCCCCCCGCCCCCCTCCCCCCCCCCCCCCG CGGCTCCTGTCACTGTCGTTCCTGCGACTCCCCACACACCCGCGCAA CGCTCATGTCACGAAGAGAAAAGTAGAAGGCGTGGCGATGCGTTGCG CGGCCCCCTGTCCGCTGGCATGCAGACGTCGAGCCGTGGAACGGATG GTAGCGAGAGACAACGCGGCGATGCAGGAAAGGAGATTTACTGCAGG ACGTCTACACACGCGCGCACACCACTGCGAATGGCACCGTGCTGAGG AAAATTGGGGGGGAGGGCGCACGGGGGCGGGGCAGGAAACGGTTGGA TCAGCAGCACTCTCAACTTGTGTCCGTATTGCGAAGGAGGGAGAGGA GCCTGCCCGTATTATGGGCGCTGAAACGTCGGAACCACCTATGAATC CCACTTCTGCGTCGCGGAGGCGTACTGCTTCCGACCACCTCCGCAGC TCACGCGCGTCGAGCTCCCTCCCTTTCCCCTTCTTTCCGTTGTGTGT GTGTGTGTGTGTGTGTCTTGTCACGATGCATGGCCATCTCTCCTCCA ACCCTCCACGCCTTCCTCTCCCCCGCCCATCAAACGCGCTACGGCCA CAACCATTTCTTCAAGTATCACATCCACCACCACTCTTACCCACCTA CCCTCTTCGACTCTGACACAGCCACTGACGCCCTCTCCGCCTCTCTC GCTCGCTGCACATTGACTCTCCACAGCCCCCCCTCCCTCGCACAGCC AGCCCCACCCACCCACCCACCCACCCACCGCTCTACACACCTCCACA GCAGCCGGATCCTAGTATGAAGATTTCGGTGATCCCTGAGCAGGTGG CGGAAACATTGGATGCTGAGAACCATTTCATTGTTCGTGAAGTGTTC GATGTGCACCTATCCGACCAAGGCTTTGAACTATCTACCAGAAGTGT

SEQ ID NO.	Description	Sequence
		GAGCCCCTACCGGAAGGATTACATCTCGGATGATGACTCTGATGAAG ACTCTGCTTGCTATGGCGCATTCATCGACCAAGAGCTTGTCGGGAAG ATTGAACTCAACTCAACATGGAACGATCTAGCCTCTATCGAACACAT TGTTGTGTCGCACACGCACCGAGGCAAAGGAGTCGCGCACAGTCTCA TCGAATTTGCGAAAAAGTGGGCACTAAGCAGACAGCTCCTTGGCATA CGTTAATTAACCTGCAGGGGATCCCGGGCCCGTCGACTGCAGAGGCC TGCATGCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGA AATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAA TTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGC CAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCG TATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGG TCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATA CGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGC AAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGG CGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGA CGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCA GGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCC TGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT CGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCG ACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGC CTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTG CTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGG CAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGC AGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTT TCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGAT TTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAA ATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACT TGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAA TTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTT TCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCA AGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACA ACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAAT CACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGC ATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATC AAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCT GAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACA GGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAAT ATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTT TCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGG ATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTT TAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGC CATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGA TAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATA CCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGC

SEQ ID NO.	Description	Sequence
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43	pLMTB7393	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTCGAGCTCGGTACCTCGCGAATGC ATCTACCTGCAGGTTAATTAATCTGATGAAGACTCTGCTTGCTATGG CGCATTCATCGACCAAGAGCTTGTCGGGAAGATTGAACTCAACTCAA CATGGAACGATCTAGCCTCTATCGAACACATTGTTGTGTCGCACACG CACCGAGGCAAAGGAGTCGCGCACAGTCTCATCGAATTTGCGAAAAA GTGGGCACTAAGCAGACAGCTCCTTGGCATACGATTAGAGACACAAA CGAACAATGTACCTGCCTGCAATTTGTACGCAAAATGTGGCTTTACT CTCGGCGGCATTGACCTGTTCACGTATAAAACTAGACCTCAAGTCTC GAACGAAACAGCGATGTACTGGTACTGGTTCTCGGGAGCACAGGATG ACGCCTAACTAGCCTCGGAGATCCACTAGTTCTAGTTCTAGGGGCCG AATTCAGATCCTCGTGTGAGCGTTCGCGGAATCGGTCGCTCGTGTTT ATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAGCAGGATACCG TCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAATTCGCGATCTCA CAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTTTTCCCACCTC TCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAGAAGGGACGGG CATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCTTCTCTTGCTT GTGGCACTCACGCTCATGCGTCAAGGCGGCCCCACGCCGAGCCCCTG CGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGATGCCGTCGATGCG CAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAGGGCACACTATCA TGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTCGGCGGAGATG CGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCTTGACTTGCGC CCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCACACACACAC ACACACACACACACACACAATACGTACACCAGGTGCTTATTCGCAAT GGAGTGTCATTCATCAAGGACGCCGCTATCGCAAATGGTGCTATCCA CGCAGCGGCAATCGAAACACCTCAGCCGGTGACCAATATCTACAACA TCAGCCTTGGTATCCAGCGTGATGAGCCAGCGCAGAACAAGGTAACC GTCAGTGCCGATAAGTTCAAAGTTAAACCTGGTGTTGATACCAACAT TTAATTAACCTGCAGGGGATCCCGGGCCCGTCGACTGCAGAGGCCTG CATGCAAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAA TTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATT GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTA TTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTC GTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACG

SEQ ID NO.	Description	Sequence
		GTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACG CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTG CCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCG TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCT GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCA AACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAG ATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC TACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTT TGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAAT TAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTG GTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATT TATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTC TGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAG ATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAAC CTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCA CCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCAT TTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAA AATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGA GCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGG AATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATAT TTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTC CCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGAT AAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTA GTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCA TGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATA GATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACC CATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAA GACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTA TTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTG AATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCC CGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATT AACCTATAAAAATAGGCGTATCACGAGGC
44	pLMTB8080	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG

SEQ ID NO.	Description	Sequence
		TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT TCCGCCACAGCCGCGACAAGAAGAACGAGCCGAACCCGCAGCGCTTC GACCGCATCGCGCACACGAAGGAGACGATGCTGAGCGACGGCCTGAA CAGCCTGACGTACCAGGTGCTGGACGTGCAGCGCTACCCGCTGTACA CGCAGATCACGGTGGACATCGGCACGCCGAGCTGGTCCCACCCGCAG TTCGAGAAGTAAATGCTCCTGGCTGCCGGTTGCAAGCACGTGTTTCT TCCATCTTGCCATGCGAAGCCCGCGCGGTATCTTCTCAGCGTGCCCT GTGTGTCGTGTTCGTAAGTTTTGTTTTCCTTTTCGATGGTTCTCATT TCCTTCTTTCTAACGACGCTCTACCAAACCTGTACACGTACTGCAAG CGCTATCGTGGAGGCAGCAGGGGCAGGTGAGAGGGAGCCGCGGACGG CGTCGGCGGAAGCGTTAATCCTGCTTCCGTACTCGTCGGGCTCATCA TCGTCGCGTATCCCGATGAGTCGTCCCAAACTCCCGCTCTGTGCCAG AGAGTGGACTGCCCTGCGCACCGGTGCATCGGTGCTCTGCGCGGCAT TGGCATTCTTGATTCGTGTGGCGGTGCTTGTCGACCACGCTCTCCGC ACCTCTATCCTCTCCTTGGCGCTCTCCCGATGTGGCGCGAGCCGGCA GGTCTCAAGAGGCGCATGTGAATGTTTGCCTGCAGGGAGTACACTAA ATTACTTTTCTCTGTCTCTCTCTTTCTCTGACTCCCTTTGGCCTCCC TTTTCGAAACTCCCCATGCTGCCATTGCGGCGACCCTCCTTGTGGGA TGTACCGACACCACAACCACACGACACTGCATCCTCCCTCGTCTACT CCTACCTCCTCACTGATGCGTGTGCAGTTAACTGGAAAATTTAAATA TCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTC CTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCC GGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACT CACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACC TGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGC GGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG CGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAAC ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGC GTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACA AAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA AGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGT TCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGG GAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCG GTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGT TCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCA ACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAA GTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCT GCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTG CAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTT TGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGT TAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGAT CCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATG AGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGA AACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAA AAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATA

SEQ ID NO.	Description	Sequence
		GGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACA TCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAG TGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAA GTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGC TCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGA TTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAAT TACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCA TCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAA TGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAG GAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTC AGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCT ACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCAT ACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCC CATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG CCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTT TTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGA TACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCG CACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTA TCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGT C
45	pLMTB8081	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCAT TTAAATTGCCTGCAGGGAGTACACTAAATTACTTTTCTCTGTCTCTC TCTTTCTCTGACTCCCTTTGGCCTCCCTTTTCGAAACTCCCCATGCT GCCATTGCGGCGACCCTCCTTGTGGGATGTACCGACACCACAACCAC ACGACACTGCATCCTCCCTCGTCTACTCCTACCTCCTCACTGATGCG TGTGCAGTTAACTGGAAAATGCTGAAGAAGCAGTCCGCCGGCCTGGT CCTGTGGGGCGCCATCCTGTTCGTCGCCTGGAACGCCCTGCTGCTGC TGTTCTTCTGGACCCGGCCCGCCCCCGGCCGGCCCCCCTCCGTCTCC GCCCTGGACGGCGACCCCGCCTCCCTGACCCGGGAGGTCATCCGGCT GGCCCAGGACGCCGAGGTCGAGCTGGAGCGGCAGCGGGGCCTGCTGC AGCAGATCGGCGACGCCCTGTCCTCCCAGCGGGGCCGGGTCCCCACC GCCGCCCCCCCCGCCCAGCCCCGGGTCCCCGTCACCCCCGCCCCCGC CGTCATCCCCATCCTGGTCATCGCCTGCGACCGGTCCACCGTCCGGC GGTGCCTGGACAAGCTGCTGCACTATCGGCCCTCCGCCGAGCTGTTC CCCATCATCGTCTCCCAGGACTGCGGCCACGAGGAGACCGCCCAGGC CATCGCCTCCTATGGCTCCGCCGTCACCCACATCCGGCAGCCCGACC TGTCCTCCATCGCCGTCCCCCCCGACCACCGGAAGTTCCAGGGCTAT TATAAGATCGCCCGGCACTATCGGTGGGCCCTGGGCCAGGTCTTCCG GCAGTTCCGGTTCCCCGCCGCCGTCGTCGTCGAGGACGACCTGGAGG TCGCCCCCGACTTCTTCGAGTATTTCCGGGCCACCTATCCCCTGCTG

SEQ ID NO.	Description	Sequence
		AAGGCCGACCCCTCCCTGTGGTGCGTCTCCGCCTGGAACGACAACGG CAAGGAGCAGATGGTCGACGCCTCCCGGCCCGAGCTGCTGTATCGGA CCGACTTCTTCCCCGGCCTGGGCTGGCTGCTGCTGGCCGAGCTGTGG GCCGAGCTGGAGCCCAAGTGGCCCAAGGCCTTCTGGGACGACTGGAT GCGGCGGCCCGAGCAGCGGCAGGGCCGGGCCTGCATCCGGCCCGAAA TTTCTCGGACCATGACCTTCGGCCGGAAGGGCGTCTCCCACGGCCAG TTCTTCGACCAGCACCTGAAGTTCATCAAGCTGAACCAGCAGTTCGT CCACTTCACCCAGCTGGACCTGTCCTATCTGCAGCGGGAGGCCTATG ACCGGGACTTCCTGGCCCGGGTCTATGGCGCCCCCCAGCTGCAGGTC GAGAAGGTCCGGACCAACGACCGGAAGGAGCTGGGCGAGGTCCGGGT CCAGTATACCGGCCGGGACTCCTTCAAGGCCTTCGCCAAGGCCCTGG GCGTCATGGACGACCTGAAGTCCGGCGTCCCCCGGGCCGGCTATCGG GGCATCGTCACCTTCCAGTTCCGGGGCCGGCGGGTCCACCTGGCCCC CCCCCTGACCTGGGAGGGCTATGACCCCTCCTGGAACGCGGGAGCGT ATCCTTATGACGTCCCTGATTACGCATATCCTTATGACGTCCCTGAT TACGCATATCCTTATGACGTCCCTGATTACGCATAAATTTAAATGGT ACCATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTG TTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACG AGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCT AACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGA AACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAG AGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACT CGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGG CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCAT CACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTC CTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCT TCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAG TTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCC CCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAG TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCT TGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGT ATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAG CTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTG TTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGAT CCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTC ACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCT AGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATA TATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAA ATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTT GAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTC CATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCC AACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTAT CAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGC AAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATT

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		ACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTC GTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGA CAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAG CGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCT GGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCA TCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTC CGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAA CGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTC CCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCG AGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATC GCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTC CTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAG CGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTC CGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATT ATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTT TCGTC
46	pLMTB8082	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCAT TTAAATGCGTCCCCCGGGCCGGCTATCGGGGCATCGTCACCTTCCAG TTCCGGGGCCGGCGGGTCCACCTGGCCCCCCCCCTGACCTGGGAGGG CTATGACCCCTCCTGGAACGCGGGAGCGTATCCTTATGACGTCCCTG ATTACGCATATCCTTATGACGTCCCTGATTACGCATATCCTTATGAC GTCCCTGATTACGCATAAGGGAAGGATAATGTGAACGGACAACTTCT CTGTCCTTTTTCGTTTTAATTTGTGATTGTTTCCCGAAGAAGAAAAG CAACAAAACCGAAAGGGGAAGGAGCGATGTGCGCTCGGCAGAATAGC CTGTGCAAAGTTGGCGGCAGCGCACGTGCGCACCTGGAGATGGCAAC AGCGGCGGCAGTATGCACGCATGCACACACCTGGCAGCGCCAGAGAT GGAAAGGGACGAGGATAGAGAGGGTAAAGTGTCGGAGGAGAACAAGC ACATAAAGGGAGGGGCGAGGTCGTGACGGCGCGCGTGCTTGTTTTGC CCCCCCCCCTTTCCTGTGGTTTTGCTCCGACCTCTCTCTTCCTGTGT GTTCCCACCCTCTCTCTGGATGCATATCTGCGCGTGTTTTGCATAGG CACACACGCGACCCGCGCTGTTGCTGTCCGCTGCCATCATGTCACCT CCCGCCTTTTCTCTCCTCTGCACCCGCTGTGCTCGACAATCGCAGTG GAAAAAAAGGCGTGTGCTCCTTTTACATGCTTCATGCCCGACCCCTC TCCGTGGCGTGTTTACACTTCAACGCTACCTCTTGCTCCTCCCCCAC CCCCGCCTTTGCGTGATCTGCCAGAGTCGGCAGTACACCACCCTCTC GCTCTCGTCCTCCCTTGCTGCTCAACATCCGCGCGGAGACACGCACC CACACAGGCACACCAGACGCCAAGAAGGTGAGAGGGCGAGTGAGAAT CAGCAGGGGAAACCTCTTGCCGCGGTGTGCGTCCGTCTGTCTGTCTG CTCCTTGCCTCTCTCGACGATTGGCGTTTGTTTGCTCTCTTAGTGCA TATACGATGCTTTACAGGTTTTCCAAATTTAAATGGTACCATCCCAA

SEQ ID NO.	Description	Sequence
		TGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGT GAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATT AATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGT GCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTG CGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTC GGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCT GGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATC GACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGAC CCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG TGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG GTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCC CGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGG TAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG GCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTC TGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCC GGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCT TTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGG ATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAA CTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGC AATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCG TTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGG CAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATA CAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAA ATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTAT GCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGC CTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAA CAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACA ATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGT TTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTAC GGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAG TTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTT GCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATC GATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTA TACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGA GCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAAT ATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATA TTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATT TCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGA CATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC

SEQ ID NO.	Description	Sequence
47	pLMTB8083	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCAT TTAAATTTGCTGCTCAACATCCGCGCGGAGACACGCACCCACACAGG CACACCAGACGCCAAGAAGGTGAGAGGGCGAGTGAGAATCAGCAGGG GAAACCTCTTGCCGCGGTGTGCGTCCGTCTGTCTGTCTGCTCCTTGC CTCTCTCGACGATTGGCGTTTGTTTGCTCTCTTAGTGCATATACGAT GCTTTACAGGTTTTCCAAATGCGGTTCCGGATCTATAAGCGGAAGGT CCTGATCCTGACCCTGGTCGTCGCCGCCTGCGGCTTCGTCCTGTGGT CCTCCAACGGCCGGCAGCGGAAGAACGACGCCCTGGCCCCCCCCCTG CTGGACTCCGAGCCCCTGCGGGGCGCCGGCCACTTCGCCGCCTCCGT CGGCATCCGGCGGGTCTCCAACGACTCCGCCGCCCCCCTGGTCCCCG CCGTCCCCCGGCCCGAGGTCGACAACCTGACCCTGCGGTATCGGTCC CTGGTCTATCAGCTGAACTTCGACCAGATGCTGCGGAACGTCGACAA GGACGGCACCTGGTCCCCCGGCGAGCTGGTCCTGGTCGTCCAGGTCC ACAACCGGCCCGAGTATCTGCGGCTGCTGATCGACTCCCTGCGGAAG GCCCAGGGCATCCGGGAGGTCCTGGTCATCTTCTCCCACGACTTCTG GTCCGCCGAGATCAACTCCCTGATCTCCTCCGTCGACTTCTGCCCCG TCCTGCAGGTCTTCTTCCCCTTCTCCATCCAGCTGTATCCCTCCGAG TTCCCCGGCTCCGACCCCCGGGACTGCCCCCGGGACCTGAAGAAGAA CGCCGCCCTGAAGCTGGGCTGCATCAACGCCGAGTATCCCGACTCCT TCGGCCACTATCGGGAGGCCAAGTTCTCCCAGACCAAGCACCACTGG TGGTGGAAGCTGCACTTCGTCTGGGAGCGGGTCAAGGTCCTGCAGGA CTATACCGGCCTGATCCTGTTCCTGGAGGAGGACCACTATCTGGCCC CCGACTTCTATCACGTCTTCAAGAAGATGTGGAAGCTGAAGCAGCAG GAGTGCCCCGGCTGCGACGTCCTGTCCCTGGGCACCTATACCACCAT CCGGTCCTTCTATGGCATCGCCGACAAGGTCGACGTCAAGACCTGGA AGTCCACCGAGCACAACATGGGCCTGGCCCTGACCCGGGACGCCTAT CAGAAGCTGATCGAGTGCACCGACACCTTCTGCACCTATGACGACTA TAACTGGGACTGGACCCTGCAGTATCTGACCCTGGCCTGCCTGCCCA AGGTCTGGAAGGTCCTGGTCCCCCAGGCCCCCCGGATCTTCCACGCC GGCGACTGCGGCATGCACCACAAGAAGACCTGCCGGCCCTCCACCCA GTCCGCCCAGATCGAGTCCCTGCTGAACAACAACAAGCAGTATCTGT TCCCCGAGACCCTGGTCATCGGCGAGAAGTTCCCCATGGCCGCCATC TCCCCCCCCCCGGAAGAACGGCGGCTGGGGCGACATCCGGGACCACGA GCTGTGCAAGTCCTATCGGCGGCTGCAGGCGGGAGCGTATCCTTATG ACGTCCCTGATTACGCATATCCTTATGACGTCCCTGATTACGCATAT CCTTATGACGTCCCTGATTACGCATAAATTTAAATGGTACCATCCCA ATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTG TGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAG CATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACAT TAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG

SEQ ID NO.	Description	Sequence
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48	pLMTB8085	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG

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SEQ ID NO.	Description	Sequence
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49	pLMTB8234	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT

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50	pLMTB8235	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCTGAAGAAGCAGTCCGCCGGGTTGGTGCTGTGGGGCGCAATAAT CTTTGTTGGCTGGAACGCGCTCCTTCTGCTTTTTTTCTGGACCCGCC CTGCCCCCGGACGCCTCCCTTCGGACAGCGCTCTCGGGGACGACCCC GCAAGCCTTACGCGTGAAGTCATTCACCTGGCAGAGGATGCTGAGGC GGAGCTTGAGCGCCAACGTGGCTTGCTTCAACAGATTAAGGAACACT ACAGCCTGTGGCGCCAGCGCTGGCGGGTGCCAACAGTCGCTCCACCG GCCTGGCCACGCGTACCAGGAACACCGAGCCCCGCTGTAATTCCTAT ATTGGTGATTGCGTGCGATCGATCTACAGTCCGCCGCTGCCTTGATA AGTTGCTCCACTATCGTCCATCCGCCGAGCACTTCCCCATCATCGTC TCGCAAGACTGCGGTCATGAGGAGACGGCCCAGGTCATTGCAAGCTA CGGCACTGCGGTTACGCATATCCGTCAACCCGACCTCTCCAATATCG

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SEQ ID NO.	Description	Sequence
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51	pLMTB8236	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGTTGAAGAAGCAGTCAGCGGGGCTTGTGCTCTGGGGAGCGATCCT CTTCGTGGCCTGGAACGCTCTTCTGCTCCTGTTTTTCTGGACCCGTC CGGCCCCGGGCCGCCCGCCGTCGGTCTCCGCACTGGACGGCGATCCT GCTTCTCTCACCCGGGAGGTAATTCGCTTGGCTCAGGATGCGGAGGT GGAATTGGAGCGTCAGCGGGGCCTCCTCCAGCAGATTGGCGACGCAC TTAGCTCGCAGCGGGGGCGTGTGCCAACGGCGGCCCCTCCAGCGCAG CCCCGCGTGCCCGTGACCCCGGCACCGGCAGTCATCCCGATCCTCGT GATTGCGTGCGACCGTAGCACGGTCCGCCGCTGTTTGGATAAGCTTT TGCACTATCGGCCGTCAGCGGAGCTTTTCCCAATCATCGTGTCCCAG GATTGCGGACATGAGGAAACAGCGCAAGCTATCGCGTCTTACGGCAG CGCAGTGACGCATATTCGACAGCCGGATCTGAGTTCTATCGCCGTCC CTCCTGATCATCGAAAGTTCCAGGGATACTATAAGATTGCCCGTCAT TATCGATGGGCCCTTGGCCAGGTATTCCGCCAGTTCCGTTTCCCTGC CGCCGTCGTAGTTGAAGACGACCTCGAGGTGGCGCCGGATTTCTTCG AGTACTTTCGTGCCACGTATCCTCTGCTTAAGGCAGACCCGTCGCTG TGGTGCGTGTCTGCGTGGAATGACAATGGGAAGGAGCAGATGGTGGA TGCCTCACGTCCGGAGTTGCTTTATCGAACCGACTTTTTCCCCGGCC TCGGTTGGTTGCTTCTCGCCGAACTGTGGGCGGAGCTTGAACCTAAA TGGCCGAAGGCGTTCTGGGACGACTGGATGCGCCGTCCGGAGCAGCG TCAGGGTCGCGCCTGCATCCGGCCCGAGATCTCGCGTACAATGACCT TCGGGCGAAAAGGGGTATCCCATGGCCAGTTTTTTGATCAGCATCTC AAGTTCATTAAGCTGAACCAACAATTTGTGCATTTTACGCAACTCGA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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52	pLMTB8237	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCGTTTCCGAATTTACAAGCGTAAGGTGCTGATCCTCACCCTTGT CGTCGCTGCGTGCGGTTTTGTGCTTTGGAGCTCGAACGGGCGACAGC GTAAGAACGACGCGCTTGCACCACCGCTCCTGGATTCCGAGCCGCTC CGCGGCGCGGGGCATTTCGCAGCTAGCGTAGGGATCCGGCGTGTGAG TAACGACAGCGCAGCTCCGCTGGTCCCGGCGGTGCCGCGCCCTGAGG TCGACAACCTGACACTGCGATACCGGTCCCTGGTGTACCAGCTGAAC TTCGACCAAATGCTTCGGAACGTCGACAAGGACGGTACGTGGAGCCC TGGGGAGCTGGTGTTGGTGGTGCAGGTTCACAATCGCCCGGAGTACT TGCGTCTCCTTATTGACTCGCTCCGCAAGGCACAGGGCATCCGCGAG GTGCTGGTTATCTTCTCGCACGATTTCTGGAGCGCGGAAATCAACAG CCTGATTAGCTCAGTTGATTTCTGCCCGGTGCTGCAGGTGTTCTTCC CGTTCTCCATCCAGTTGTACCCATCCGAGTTCCCCGGCTCAGATCCC CGGGACTGCCCACGCGATCTGAAGAAAAACGCTGCTCTGAAACTGGG CTGCATCAACGCCGAGTACCCTGACTCTTTCGGGCACTACCGGGAGG CGAAGTTCAGCCAAACGAAGCATCACTGGTGGTGGAAGCTGCACTTT GTGTGGGAGCGCGTGAAGGTCCTGCAGGACTACACGGGCCTCATCTT GTTCCTGGAGGAGGACCACTATCTTGCACCCGACTTCTACCATGTGT TTAAGAAAATGTGGAAGCTGAAACAGCAGGAGTGTCCGGGCTGCGAC GTGCTTTCTCTGGGCACTTACACAACTATCCGCTCTTTCTACGGCAT CGCCGACAAAGTGGATGTGAAGACCTGGAAGTCCACTGAGCACAACA TGGGATTGGCGCTCACCCGAGATGCCTACCAGAAACTGATCGAGTGC ACCGACACATTCTGCACCTATGACGACTATAACTGGGACTGGACTCT CCAGTACCTGACATTGGCGTGCCTGCCGAAGGTCTGGAAGGTGCTGG TGCCACAGGCCCCTCGCATTTTTCACGCTGGCGACTGCGGCATGCAC CACAAAAAGACATGCCGCCCTTCCACCCAGAGCGCTCAAATTGAGTC GCTGCTCAATAACAACAAACAGTACCTTTTCCCGGAGACACTCGTAA TAGGGGAAAAGTTTCCAATGGCGGCTATCTCTCCCCCACGCAAGAAT GGTGGCTGGGGCGATATACGCGACCATGAGCTGTGTAAAAGTTACCG GCGCCTGCAAGCCGGCGCCTAGATTTAAATATCCCAATGGCGCGCCG AGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTA AAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTG CGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA

SEQ ID NO.	Description	Sequence
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53	pLMTB8238	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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54	pLMTB8247	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCGCGCAGCGCACAGCCGTCTTCTCCCGCCTCCGCGTGCCGCCTTAC TGGGTACTGCGCACGTCCGTCGTGCGACCATCAAGATACGATCCCCA CGGCAAGGTTAAGGCCCCCCGCTCGTGTCTCTTTCCTCTGCCGTGGA CTGCCTCTCGTCCCGTTTCTCCGTCTTCCTTTGCCCCACCTCCCCGA GCGACGGCGGTGGCGTGCGGTAGGGCGACGTGCTGGGCTGCCATCCC CCCTAGCCTCTGCACTCCCCAGCTCTACTGCCGATCTGCAGTCACGT GCCCGTCGCCTCCCCGCTGCCCACTGGCCCAACGCGCTCTCCGCCCA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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55	pLMTB8250	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCGCGCAGCGCACAGCCGTCTTCTCCCGCCTCCGCGTGCCGCCTTAC TGGGTACTGCGCACGTCCGTCGTGCGACCATCAAGATACGATCCCCA CGGCAAGGTTAAGGCCCCCCGCTCGTGTCTCTTTCCTCTGCCGTGGA CTGCCTCTCGTCCCGTTTCTCCGTCTTCCTTTGCCCCACCTCCCCGA GCGACGGCGGTGGCGTGCGGTAGGGCGACGTGCTGGGCTGCCATCCC CCCTAGCCTCTGCACTCCCCAGCTCTACTGCCGATCTGCAGTCACGT GCCCGTCGCCTCCCCGCTGCCCACTGGCCCAACGCGCTCTCCGCCCA CCTCTCCTCGCACTCCCTTCCTGCTTCCTCCTTCTACACATTCGCCA GCGCCCCCATCCTGCCCCCCCCCCTCTACGCACACCCACACTCACGC GCACACCGCCGTGCACAAGTCCTCGTCCTAGCTACCACGAACCATAC

SEQ ID NO.	Description	Sequence
		AGTCCACAGCACCCCTGCGCCCCGAGAGTCATGGTCCGCAAGAAGGG ATCTCTGATCCTGTGTGGGGCGTTTCTGTTCGTGGCCTGGAACGCGC TCTTGCTCCTTTTTTTGTGGGGCCGCCCGCCCATTGGTCGACTCGGC GAGGGTGGGGGGGCGGAGCCGGGCGCGGGCGAGGAGTGGGGTGCGGG GAAGAGCAAAGTGGGTGGCGCTAACGGCCTGGCGGGTGAGGTTATCC GCCTGGCGGAGGAGGTCGAGAGTGAGCTGGAGACGCAGAAGAAGCTT CTGAAACAGATACAGTCGCACCGCGAGCTTTGGGAACAGCGTAAGGA ACTGGAGAAGCGTGAAAGCGAGGATACCAAGGACGAGAAGATTGACG TTGAGCCTAAGAAGCCCCGCCAGATCCCGGCCGTGCACCTGTCCCAC AAGGTGGTGGAAGACGCCCAGACAGTAACCAAGAAAATGCAAACGCT GATGGTGACACCGCCTCAGCTGGTGATGAAGGAGCAGGAGACAGATC AGAAGAATAAGCAGATGATGGAGGACCAGCTGGGGCTCACCACGCCA TCTCCGCAAATCATCATCCCGATTCTCGTGATCGCGTGCGATCGCGT GACCGTGAAGCGGTCCCTCGACCGTCTGATCCAGTACCGGCCAAGCG CAGAGTTGTACCCAATTATCGTCAGCCAGGATTGTGGCCACGCTGAC ACAGCCCGCGTGATCGGGTCCTATGGCAGCCAGATCACGCACATAAG CCAGCCTGACCTTGCAGATATACCGGTGCGGCCAGATCATCGCAAGT TTCAGGGGTACTACAAGATCGCCCGCCATTACCGTTGGGCGCTCAAC CAGGTGTTCAACGTGTTTGCCTACTCAACGGTGGTGATAGTCGAGGA CGACCTGGAGGTGGCGCCTGACTTCTTCGAGTACTTTCGAGCTCTCT ATCCGATCTTGCGCTCAGATCCTACCTTGTGGTGCATTTCGGCTTGG AACGATAACGGGCGTGATGGTCTCGTGGATCCCGGGAAGGCCGAGCT CCTCTACCGCACGGACTTCTTTCCTGGACTGGGTTGGATGTTGCTTA AGGAGGTGTGGGCGGAACTCGAACCCAAGTGGCCAAAGGCGTTCTGG GACGACTGGATGCGACACCCGGAGCAGCGTAAAAATCGCTCTTGCAT CCGACCGGAAATTAGTCGGACGATCACATTCGGTCGTAAAGGTGTGT CCTTGGGGCAGTTCTTCGACCAGTATCTCCGTTACATTAAGCTCAAC ACTGAATTCGTCCCTTTCACGAAGCACGACCTCAGCTATCTTGTGCG AGAGAAGTACGATGTTAGCTTTGAAAAAGATGTATACTCGGCTCCCC TCGTAAAGGTAGAGGAGCTGCAGCACGGCGGCAGCCTTAAGGGCAGC GGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCAAGGTCCT TGCCCGCAACCTCGGGGTGATGGATGACCTGAAGTCAGGCGTGCCAC GCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCCGGCGC ATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATACGACGTGAGCTG GAGCTAAATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCA TGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCT TTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCA ACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCT CGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGA TAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA ACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCC CCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAA CCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCC TCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG

SEQ ID NO.	Description	Sequence
		TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAAC TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTG CTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA ACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAA AAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCG GTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGA TCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTG GAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAA GGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCA ATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTC ATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAA TACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCA CCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGAT TCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAA AAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCC GGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAAC AGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAAC CGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCG CTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAG GAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATT CTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGT AACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAG AGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAA CATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGC GCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCC GACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGT TGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGG CTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTA TTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAAC AAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC TAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTAT CACGAGGCCCTTTCGTC
56	pLMTB8253	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT AGTGGTGCGCGTGCGTGTCTCCGCTGTCTGGAGCTCCTTCCCTGCCA CGCAACTGCGAGCCTTCACGGCGGCCCACCCGCCCGCACACGGGAGC GGAGACTGTGCGTGTGTGCGTGTGTGCGTGTGGAGCGGGTAATGTCG GCACACACACACACACACACACACACACACACATGCACGCTGAGAGAAT GAGCAGCCCCAGAGGAGAACATGGGGCTCATGCGCGCAGACGGAAGG

SEQ ID NO.	Description	Sequence
		GCACACACGAGGAGGGGCACACCCCTCTGTCTTCAGGGAGCACGGCC CTGCTGCTGCCATGTGACGGGCGTCTGCCACGCGACTCTTCCCCACA CCTTGCTCCTTTCCTCCCTCCCCTCCTGGCGCACACGAAACACGCGC GATGCACACACGCACGCGCCCACCCCCCAAAATAAATAAAATGAAAC GCGCAGCTCTTCGCTCTCGTTCTTCGAACAAACACATCTAAACCCCC TTCCAACCCCTCTTTCTTCTTTTTTCAACCATGCGGTTTCGGATCTA CAAGCGCAAGGTATTGATTCTTACTCTCGTGGTGGCGGCGTGCGGCT TTGTGCTGTGGTCTAGCAATGGCCGGCAGCGTAAGAATGACGCGTTG GCTCCGCCGCTGTTGGACAGCGAGCCGCTTCGCGGGGCGGGCCATTT TGCCGCTTCGGTGGGCATCCGTCGTGTGTCTAACGATTCAGCCGCGC CGCTCGTGCCGGCCGTCCCTCGTCCGGAGGTGGACAACCTCACCTTG CGATACCGCAGCCTGGTCTACCAACTCAATTTCGACCAGATGCTGCG CAACGTAGATAAGGACGGGACATGGTCGCCCGGCGAGCTGGTACTGG TCGTGCAGGTGCACAATCGTCCAGAGTACCTGCGGCTCCTGATCGAC TCACTGCGCAAGGCTCAGGGCATCCGGGAGGTGCTGGTGATCTTTTC TCACGACTTCTGGTCCGCTGAGATTAACAGCCTGATAAGCTCTGTGG ACTTTTGCCCAGTACTTCAGGTATTCTTTCCATTCAGCATTCAGCTG TACCCCTCCGAGTTTCCGGGTAGTGACCCGCGCGATTGCCCGCGCGA TCTCAAAAAGAATGCCGCATTGAAGTTGGGCTGCATCAATGCGGAGT ATCCAGACAGCTTCGGCCACTACCGTGAGGCCAAGTTCTCTCAGACG AAACACCATTGGTGGTGGAAGTTGCATTTCGTCTGGGAGCGCGTGAA GGTCCTGCAGGATTACACAGGCCTGATTCTGTTCCTTGAGGAGGATC ACTACCTGGCGCCCGACTTCTACCATGTGTTCAAGAAGATGTGGAAG CTGAAACAACAAGAGTGCCCTGGTTGTGATGTGCTCAGTCTCGGGAC CTACACCACCATTCGTAGTTTCTACGGCATCGCTGACAAGGTGGACG TGAAGACATGGAAATCGACAGAGCACAACATGGGTCTGGCATTGACA CGGGATGCGTATCAGAAGCTGATTGAGTGCACCGACACATTCTGCAC GTACGACGATTATAACTGGGACTGGACGCTGCAGTACCTTACGCTGG CGTGCCTTCCGAAGGTATGGAAGGTCCTGGTGCCGCAGGCCCCGCGA ATCTTCCACGCGGGTGATTGCGGCATGCACCACAAGAAGACGTGCCG CCCTTCCACTCAGTCAGCCCAGATCGAAAGCCTGCTCAATAACAACA AACAGTACCTCTTCCCAGAAACCCTCGTGATCGGCGAGAAGTTCCCT ATGGCGGCGATCTCCCCGCCCCGTAAGAACGGGGGGTGGGGCGACAT ACGTGATCATGAGCTCTGTAAGTCGTATCGCCGCCTCCAAGCTGGGG CCTAGATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATG GTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCAC ACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAA TGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTT CCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAAC GCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCG CTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATC AGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATA ACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAAC CGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCC TGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACC CGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTC GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGC CTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTA

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		GGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTA TCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAG CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCT ACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAA GAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGT GGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATC TCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGA ACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGG ATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAAT CTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCAT CGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATA CCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACC GAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTC CGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAA ATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGG TGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAG GCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCG TTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCT GTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGA ACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCT TCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAA CCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAG GCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACA TCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGC ATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGA CATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTG GAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCT CATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATT GTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAA ATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTA AGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCA CGAGGCCCTTTCGTC
57	pLMTB8255	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCGCCTCCGAGAACCCCTGCTGAGCGGATCAGCCGCGATGCCGGG TGCCTCCCTCCAACGCGCCTGTCGCCTCCTTGTGGCGGTATGCGCAC TGCACCTTGGTGTAACACTGGTCTACTACCTGGCCGGGCGGGACCTT AGCCGGCTCCCGCAATTGGTCGGTGTGTCGACCCCACTGCAGGGTGG CTCCAATTCAGCGGCCGCTATAGGCCAGTCGTCTGGCGAGTTGCGAA

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		CAGGTGGCGCGCGCCCCCCGCCACCGTTGGGCGCCAGCTCTCAGCCG CGCCCCGGTGGCGATTCAAGCCCAGTGGTTGACAGCGGCCCGGGCCC AGCTAGCAACCTGACATCGGTCCCGGTGCCTCACACGACCGCGCTGT CCCTCCCCGCATGCCCGGAGGAGAGCCCACTCCTTGTGGGCCCCATG CTCATCGAGTTCAACATGCCCGTAGATCTCGAGCTCGTGGCTAAGCA GAACCCCAACGTCAAGATGGGTGGACGCTATGCACCGCGAGACTGTG TTAGCCCACACAAGGTGGCTATCATCATTCCGTTCCGCAACCGCCAG GAGCATCTGAAGTACTGGCTGTACTACCTGCACCCCGTGCTCCAGCG GCAGCAGCTGGACTACGGTATCTACGTAATCAACCAGGCGGGCGACA CCATCTTCAATCGCGCAAAGCTTCTTAACGTCGGTTTTCAGGAGGCT CTCAAGGACTATGACTACACCTGCTTCGTGTTCTCGGACGTCGACCT CATTCCAATGAACGACCACAACGCGTACCGCTGCTTTTCCCAGCCCC GCCACATCTCAGTTGCAATGGATAAGTTCGGGTTCTCGCTCCCCTAC GTTCAGTACTTTGGTGGTGTGTCCGCCCTCAGCAAGCAACAGTTTCT GACAATCAATGGCTTTCCGAACAACTACTGGGGCTGGGGCGGCGAGG ACGACGACATTTTCAACCGATTGGTGTTCCGCGGAATGTCTATCTCT CGTCCCAACGCGGTCGTAGGGCGATGCCGAATGATACGACATTCGCG GGATAAGAAGAATGAGCCGAATCCGCAGCGCTTTGACCGGATCGCCC ATACCAAGGAGACGATGCTGAGCGACGGACTGAATAGTCTCACCTAC CAGGTACTCGACGTGCAGCGCTACCCACTGTATACGCAGATCACGGT AGACATCGGAACGCCGAGCTGATTAGCGCTCCGTAGCTCGCTGCGTA TGAGAGGTACTGAGCTCCAATGCATCACACGGCGTACGGCAACACAC ACTATCTTTTCAGTTTATTTTTTTAATTATCCCTCCAAAAAGAAGCA ACTGACACTTCAAAATATTCCCAACAAGGAGCGTGAGGTCAGTGACC AGTCTCGGACTTCACACCGCGCATGTAGAAGCACATTTAAATATCCC AATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGT GTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA GCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTC GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGC TCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG CTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAA TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGAT ACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCG ACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAG CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGT AGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG TGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGC TCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT CCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAG

SEQ ID NO.	Description	Sequence
		GGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTT TTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTA AACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACT GCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGC CGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGAT GGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAA TACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAG AAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTT ATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGT CATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGC GCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACA AACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAA CAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCT GTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGT ACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCC AGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCT TTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAA TCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATT TATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTA GAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCA ATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACA TATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACA TTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCAT GACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
58	pLMTB8259	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT TTAGCGCTCCGTAGCTCGCTGCGTATGAGAGGTACTGAGCTCCAATG CATCACACGGCGTACGGCAACACACACTATCTTTTCAGTTTATTTTT TTAATTATCCCTCCAAAAAGAAGCAACTGACACTTCAAAATATTCCC AACAAGGAGCGTGAGGTCAGTGACCAGTCTCGGACTTCACACCGCGC ATGTAGAAGCACGCGGCTTGCGCGCCAGGCTTCTTTTGGCAAACCAC GCTGCACAGAATGTCTGTGTACAGCAGCCAGGCTGTGATCGATCTAT TATGCTCGCCCCTCGCTCCTCCGGCATTCTCGAGTCCATGTCGAGCT TGTCTGGCTCCGTGCACATGCAAGCGTTTGTGCGCGCCTCTAATGTA ACCACACGTCAAAACATTGTGTGTCTTCCGAAGTGGGAGACACCGGG GCCACCAACTCCGGTGGTTTACAGCCTCCTCCCTCAACCAACGCTGC CGATTGTACCACCTTTCATTGCGTCTTTGTGCCCCTCCCTATCTTCA TGTTTCCACTGCGCTTCGTTTCCGAATACTATTTTCGTGTACTGTTT CATCACTTTCTCACAACAGCTCTTTTTTTTCACCCGCAGAAGATGGC CAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGAAAGAGCAACGG CTACAATCAACAGCATCCCCATCTCTGAAGACTACAGCGTCGCCAGC

SEQ ID NO.	Description	Sequence
		GCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATA TCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTG CTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGA AATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGT GCTTCTCGATCTGATTTAAATATCCCAATGGCGCGCCGAGCTTGGCT CGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGG GTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTG CCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAAT CGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCG CTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGA GCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATC AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG CCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTC CGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAA GCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTC ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCC GGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCC ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG GCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACT AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTG GTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAA AAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC TCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTAT CAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAA AAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGAT TATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAA AACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTC TGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCT CGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACT GAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTG TTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAA CCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACG CGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCG GCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAG GATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTG GTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGT CGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCAT CTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAAC TCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGA TTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCAT CCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGA ATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCA

SEQ ID NO.	Description	Sequence
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59	pLMTB8282	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTAGACTCGTGCCGCGCGCTGATGATGTAGGTGCACGCGTGCGTGT GCTGCAGCGGAGCCGCCGCCACCGCGACTGTGTGTGTGTGCGCGCGT GACGACCGGCTCGAGGAAGGAGGAGCGCGCGTGTGCGTGCGATGCGC CTCCTCTTTTTTTTTCGCCCTCGTCGGTTTTTTTTTTTCTGAGAGGA CGGCGGCGGCGGATGGCGGGGCGGCGGCGCTGACGGAGCGGCCACGC TCTGCACCTCCCCGCCCTCCGCCGTCTCTCCGTTCGCCGTCCTCTCC TTCCTCGTGCGTGCGTCTGCCGCGCATGCACACGCGCGCGCGTTGCC GTAGCGCTGTGTATCTGTGGAGGAGGGCCTTGTCTCTCCCTCCCCGT CGCTGAGAGATGAAGGGGCAAAAAGAGAGAGCAGTGCGCATGTGTGC CTCCGCTCCCTGGAGCTCCCCACGAGCCCCCTGCGCCACGCACCTGC GAACCTGCACAGCGGCCCACCTGCCCGCACACGTGAGCAGAAATGGG TGTGTGGAGCGGGTGATGTCGGCGCGCACACGCGCGCGCGCTGACCA CTCCGACGTGAAAACACGGAAGAGCGAGGCTGGCAAGGCAGGGCAGG AACCTGATCACGTGCGCGCGCACAAACGGAATGAGCAGCTCCTGAAG AGGAGATGGGGCTCATGCACGCAGACACGCACGTGCACACTCCTCCG TCTTCACGGAGCGCGGCCCTGCTGCTGCTGCCATGTGCCGGACGTCT GCCACGCGTCTCTTCCCCACACCTTGCTCTTCCCCCCCCCCCTTCCC TCCCGGCGAACACAAAACACGCGCACGCCCACCGAAACAACAACGCG CAGCTCTTCGCTCTCGTTCTTCGAACAAACACCTTTAAACCGCCTTC CAACCCCTCTTTCTTCTTTTTCAGCCATGACCGAGTACAAGCCGACC GTGCGCCTGGCGACACGCGACGACGTGCCACGCGCAGTGCGCACACT GGCGGCAGCGTTTGCGGACTACCCGGCGACACGCCACACAGTGGACC CGGACCGCCACATCGAGCGCGTGACAGAGCTGCAGGAGCTGTTCCTG ACGCGCGTGGGCCTGGACATCGGCAAGGTCTGGGTGGCAGACGACGG CGCAGCGGTGGCAGTGTGGACGACACCAGAGAGCGTCGAGGCAGGCG CGGTGTTCGCAGAGATTGGCCCACGCATGGCGGAGCTGAGCGGCAGC CGCCTGGCAGCACAGCAGCAGATGGAGGGCCTGCTGGCACCGCACCG CCCAAAGGAGCCAGCCTGGTTTCTGGCGACAGTGGGCGTGTCCCCGG ACCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGT CATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACAC AACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATG AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCC AGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGC GCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCT CACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAG

SEQ ID NO.	Description	Sequence
		CTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAAC GCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCG TAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTG ACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGT GCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCT TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGG TATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCA GCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTAC AGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAG TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGA GTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGG TTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTC AAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAC GAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGAT CTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCT AAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCG AGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACC ATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGA GGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCG ACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAAT AAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTG AGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGC CAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTT ATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGT TAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAAC ACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTC TAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACC ATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGC ATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATC ATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCAT CGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACA TTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGA ATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCA TACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGT CTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAT AGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAG AAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACG AGGCCCTTTCGTC
60	pLMTB8285	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT

SEQ ID NO.	Description	Sequence
		GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CAGTCGTCGGTCGCTGCCGTATGATCCGACATTCTCGTGATAAGAAG AACGAGCCTAACCCACAGCGCTTCGACCGAATCGCTCATACTAAGGA AACGATGCTCTCCGACGGGCTCAACTCTCTCACATACCAGGTCCTCG ACGTGCAGCGCTATCCACTTTACACGCAGATTACGGTCGACATCGGC ACCCCGTCGTGAGTCCTCCGGCTTGACAGCGCACACGCGCCGCTGTA TGTGCGCGTGCGCGCGGGTCCCGACTGGGGCCGGCGATGAGGCGCAT CATACCTCCATAGAGACCCTATTTTTTGTTTTATGGCTTCTCAGATG ACCACTTGGTTTCTTCCTTCCTTCGTTTGGTTTGTTTATCTCCTCCC CTTCGTTGAGGGTACGAGTCAGGGTAGGCTCGGACAAAACTTACCGC ACCCGCGATGGGCCACAGCTGTCTATCGCTCTCGCTCTCTCGGTCTC CTGACCGGGACAGGTTGTCGCCCCGTCACGCGTACCGGCGTGCGCGC CCGCTCTTGCGCCCTGCCCCACCATTCGTCGAATGATGCGCGACGCG CATGACAGGCGCTGCTGCAGCACTGCTCCCTGCGGTTGCTGAGTGCG TACATGGCGTTGCTACTGATGTGTTTGCACTGCATCTCACCTCGCTC TCTTCACGCATCCGCTCGCCCTTCTTCCCTCTTCACGAGACTGCGTC GGTCTTTTGGTGCTGCTGTGGCGCAGCCCGCCGCCTTCCACTCCCCC CAAACACACACGTTCATACGTCCACACAGCACTCGTGCGCACCGACA CACCCACACCCCCTCCTCTCTCTCCTCTCCCCAACCATGCGTTTCCG AATTTACAAGCGTAAGGTGCTGATCCTCACCCTTGTCGTCGCTGCGT GCGGTTTTGTGCTTTGGAGCTCGAACGGGCGACAGCGTAAGAACGAC GCGCTTGCACCACCGCTCCTGGATTCCGAGCCGCTCCGCGGCGCGGG GCATTTCGCAGCTAGCGTAGGGATCCGGCGTGTGAGTAACGACAGCG CATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCA TAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAA CATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAG TGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAG TCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGC GGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCA CTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCT CACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGC AGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC AGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTT CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTA TCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACG AACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGT CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGC CACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT TTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAA GAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCT

SEQ ID NO.	Description	Sequence
		TCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAA AGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAG CATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCAT ATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGG CAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGAC TCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAA GGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAG AATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTAT TCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTA AAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACAC TGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTA ATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCAT GCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCAT AAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCAT TGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCG GGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATT ATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAAT TTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATA CTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAA ACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAG GCCCTTTCGTC
61	pLMTB8286	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CATGCCGCCCTTCCACCCAGAGCGCTCAAATTGAGTCGCTGCTCAAT AACAACAAACAGTACCTTTTCCCGGAGACACTCGTAATAGGGGAAAA GTTTCCAATGGCGGCTATCTCTCCCCCACGCAAGAATGGTGGCTGGG GCGATATACGCGACCATGAGCTGTGTAAAAGTTACCGGCGCCTGCAA GCCGGCGCCTAGGCCTGTGTGCTGCCTCCTCATTTCCGGCGGCTCGC ACGCGCTCGCATGCTTCGCCACACAGACGTCCTCGTGTCTACTGAAC AGCTAACGGATTTCCATGTCATTTCTCGTTTCCCATCTTCAAACACA AGAGCACCACTGCAACGTCAGCAGTGAACGCCCAACACTGCGGAGAG CGTGGTCACGCCCCTTCTGACTTGCACCATGAAAAACGATGTGAGGC AGCGGCGCGTCCTCTCTCCCGTTCGCTGACTTGCCCCACGCGAGTAT CTGCGCGCCGGCACCCCTCTCCGCAGCTCGGTTTGCCTGCAGGTGTG CGCTCTCGATACCTCCCGCCTCTGTCATTCTGTTTGTCTCTTCCTCC CAGCTCCACTCTTCTTCTTTTCCTGCTTCTCCGTTTGTTTGTGCGGC GCAGTGCCGCGACCAGCACATTTTGGCTCTCTCTCCGTTGCTAGCAC CAGGGGTCGGGATCGACGTGCGCGTTGCTCCTCCGCTCTCCCCATTT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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62	pLMTB8287	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCTGGGCACGGTGCGAGTGCAGTACACAACTCGCGACTCCTTCAAGG CGTTCGCTAAGGCGCTGGGTGTCATGGACGACCTTAAGTCCGGTGTG CCGCGTGCCGGTTACCGTGGCATCGTTTCGTTTCTCTATCAGAGCCG CCGGGTCTATCTGGCCCCGCCTTCCGACTGGACAGGATACGATCCCA GCTGGAGCTAGTTCCTTTCACCTATACACGTGGTTCATATATTATCG GCTTTTTACCTGAGAGAGCAAAGAAAGCTTATTAGCACGGAAAAACG TAATGTGCTGATAGGGGAAAGAAACAAAAACAACCGCAGCCGAGACA TTTTGTTTGTGTTGGAGGAAGTAGAGGAGGCCCATCGGTGTCTAGAA GACAATACCGCAGTGTGAGACAGTGACAGAGGTGGCAGAGGAGAGGT AGGGGGAAGCTCAAATGAGTGCTGTATCATGTATGCATGTCTCTCTG GCTGCTTCTCAGCTTTTCGTTCCGGCTTCCACTGGACTGTGGCCCTG CTCCAAACCTTCGACGTGGGATGATTCGATGACTCTTTCTTTTATCA GTGACTGATACCGATACTGTGCTGCAGAGAATCGAGAAAAAAAGCGG AAAAGGCGGCAGGGCCTCGATGGCAAATCGTTTAGTTGTGTGTGTCA GTGATGCCTCTCTAGGTGGCGGAGTGGGGCTGCACGTGATGGACGAC GACGTAGCGCAATACGCGCCTTCAGTCGACAGATCGAACAAGCACCG TGCTGGTTTCAGTATCCCTGCGCACTCTCCTGGTTATGGGCGCCTTG AATGCGAGCCTTTGTTTGAGCTCCACTTGCTGCTCATCAAATGGCCA CACTTCCGACCTCCCTTGCTCTTTTTTTTTGCACTTTTGTGGCACCT GTGTCCTTGCTGTCGGTCCTTTCCAACTTCAGCACACGGAGAAACCA CCCTGACTGTAGCAATCACGATCCAGTGGGGACAAAGGAGACGAGGT GTCGAGTGCCATTTCGACGATCGGAATGCGACCACGTAAGACCATAC TGCTCGTGGGTGTCCTGGTGATATGGGTGCTTATGACCTACCTTGCC TTTATGCGGAGCGTTCGGGGCACAGACGGGTCGCGCCCACGCCCGGC TTTCGCCAGTAATAAGCTCATGCTCGAGAAGGTACAGGATTTCGAGC AGAACCTGAAGTCGTTCGCCGACAGCCGTCAGAATCTATTTAAATAT CCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCC TGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCG GAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTC ACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCT GTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCG GTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTG CGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGC

SEQ ID NO.	Description	Sequence
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63	pLMTB8295	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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64	pLMTB8297	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT TCAGCGTTCCGTAGCGCGCTGCACATCCGGTACTGCGTTCCAGCGCA TCACGCGACGCACAGCAACACAAATTTTCGTTTTGTTTCTCTTCCAT TCGAAAAAAAAAAAGATAACACCCACCCCACTTAACCTCCATAACAAG AGAGCGTGAGAGGAGAGTCTGCTCTTGGCCTTCACACCGCAAATGCA GCAAAACGCGGCTTGTACGCAACGCATCTCTTAGCACGTCAAGCTAA GCAGAATCTTTGCGTACGGCAACCAGGCTCTCATCGACCCGTCGTTC GCTCCTCGCTCCTCCGGCATTCTTGAGCCACGACGCGTATGCTTGGC TCCGTGCGTCTGCGAGCGTTTGTGCGTTTCTCAAATACAAGCCGAGG GGCCACCACGTTTATCTTTGCCGCTCGACGCACCTCCTTCAACTACA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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65	pLMTB8301	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCAGCGGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCAAG GTCCTTGCCCGCAACCTCGGGGTGATGGATGACCTGAAGTCAGGCGT GCCACGCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCC GGCGCATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATACGACGTG AGCTGGAGCTAATGAACTGCCTGTCGCAACGACCACGGCCCTCTCGC TTTCCCTTGGTTGGTTCGTCAAACGGCTGAACCGGCTTCTCTTCCTC TGTCGCTCCTTGTCCTCATTTCTGTTTCACACGACATACTTGTCTAT TATGTCGCTGCCTGTATGTGTGTGTGTGTGTGCTGCAATGACGGGTA GGGGGCTGAGGCGGCAAGGTAAGCAGGGGCGCCGAGGCACGGGTAGA GGCCAAAGGCAGGCGTCGGCGATGATGGACCTTCCTCGACTTTCTTC GTTGTGGTCTTATCTTTGCTCGTTTCAATTCTTGTTTTCATTTCTCG TCGTCTGAAAAGAAAGGCAAAAAAAAACAAAGAAGGGGCGCAGAAGA GCGGGATCGCGACGTGCGTACACGTATCGAGGTCGCTTCCCTTTTTT GCGAAGTCTTTTCGACCTCTCGTACACATCTTTCGTGGGCTGTTGTG CACCATGTTCAGCGCGCGACGTCGAGCTGTGCTCGCTTCCTGCAATG ACTTCCCGCCCTTCGTCTTTGTCTTCCACTGGAAGAGTGTGGCACTT CACTCGCCAGTGATGAGGGGAAGGGGGAGCGGACCAACACCGTCTTT TTTATAGCGATAAGGAGGTGAGGAGGTGGTCTGTGTGGCGTTCCTCG TGATGATAGGCTTCATGGTCGACTTACTTACCGCGTGAGGAGCAGCA TATCCATCCACCTCCAAGTTCCTCGAAGAGGTCAGGAAACGCCACTT CTCATGCCCCGCCAGTCTCTTGTGTAACCTTCGTCCCTCTTATTCTT CATCTCACTCATCCGTGCCTCGTTGACCACTTCACCGTAACCCGCTC CCTCCCTTTCAATCTCTCCTGCCCCCCCCCCCCCCACACACACACTA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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66	pLMTB8302	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CTGCATGCCGAGCGGCCAGAAGACAAAGATTGAGAACGTGCTCCAGA ATAGCGGTAATCAGCTCTTCCCTAAGCAGCTCTTGATCACGAAGCGA CTGCCCGCGTCGGGGGCGAAGGGCGTAGCCCCCCATGTGAAGAACGG CGGTTGGGGCGACATCCGGGACCACGAACTGTGCAAGTCTTACCTGC GCCTTCAGTAGCGAGCGCGTTGCCTCTGCGCTGGTGAACGTGCCTGC GCACTTACATCTCAGCCGTGCTTTCTGGGAAGACCTTCTGCGACGCG GGGCGCTGTGCTGGTACAGATGGAAAGATGTGCGCCATCACGGATGC ATCCTTGCATGGTGCGTGCTCACGTGCTCACCACAGTTTGTGTGTGT GTGTGTGTGAGTGTGAGTGTGAGTGAGAGAGAGAGTGTGTTTCGGCG CACCTCCCATCCAACAGTGGCGTGAACGGCTTTCTCTGTATGCGCCC TTTCGTTTTAACTCTTTCTTTTTCCGCCTTTGTTTTTTGTGATTTTT GATGAACTCAAACACAAAATGAACATCCATGCTGAAGAAGCAGTCCG CCGGGTTGGTGCTGTGGGGCGCAATAATCTTTGTTGGCTGGAACGCG CTCCTTCTGCTTTTTTTCTGGACCCGCCCTGCCCCCGGACGCCTCCC TTCGGACAGCGCTCTCGGGGACGACCCCGCAAGCCTTACGCGTGAAG TCATTCACCTGGCAGAGGATGCTGAGGCGGAGCTTGAGCGATTTAAA TATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTT TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG CCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAA CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAA CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAG GCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAA GGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCA CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT AAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCT GTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC GGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT CGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA

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		ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCC TTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCAC GTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAG ATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATA TGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAAT GAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGA AAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCA TAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAA CATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCA AGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAA AAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTAC GCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGT GATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACA ATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCG CATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGG AATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATC AGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCG TCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACG CTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCC ATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAG CCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGC GGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCT TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCG GATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCG CGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTAT TATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTC GTC
67	pLMTB8303	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCTTGGCGAGGTGCGTGTCCAGTATACGTCCCGCGACAGCTTTAAGG CATTTGCTAAAGCCTTGGGTGTCATGGATGATCTGAAGTCTGGCGTG CCCCGTGCAGGCTACCGTGGAATCGTGACCTTCCAGTTCCGGGGTCG CCGGGTCCACCTCGCCCCGCCGGAGACCTGGAACGGCTACGACCCGT CCTGGAATTGAAGCGGCTTGCCGGATGCCGCGTGAGTAGGAGGGTGG CTGCCGCAAACGCTGACCTCGGCGACTGCGGCGTGGCGCTCCCCTTC TCCTCCTTTTCCGGCGGTGTGTGTCATGCATCTGCGTGACTCCTCCC TCTCATAGATGCAAGTTTTTCTTTTTGACCCCTCCCTGTTTGACCTG

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		CAGCCACACGGATCGCTGTGCGACGTGGACGGTGCGTGCTGACCGCA GAGCAAAACACAAGACACATTCTGCACCGCCGTTGGTGCCACCTGCG GCCTGCGACGCCGCCAGTGATGCCCATCTCGCCCCGTTGCCCTATAC ACCCTGTGAAGAGAGGCGCCGCGGTGCCGACGCCTTCTAGCATCTCT TCCTTTCCCGTGACCACTGCATGCTTCCTCGCTTTGCCTTCCTGCCA CGCCGGCTTCCTCAACTTTCCCTTCCCTCGCCACCTGCTTTTTCTCC TCATGGGTTCTGCGGCAGCTTCCCAGCCCACCTTCGCTATCCAGCCA CTCTCGCTCTTCTACATCTCCCACCCCCTCACACCGCCATGCGCCTG CGTGAGCCTCTTTTGTCAGGATCGGCGGCTATGCCCGGAGCCAGTCT CCAGCGGGCCTGCCGGTTGCTCGTTGCCGTCTGCGCGTTGCACCTGG GGGTCACCCTGGTCTACTACCTGGCTGGCCGTGACCTTTCCCGCTTG CCGCAGTTGGTCGGTGTATCCACCCCGCTCCAGGGGGGCTCGAACAG CGCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGT CATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACAC AACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATG AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCC AGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGC GCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCT CACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAG CTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAAC GCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCG TAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTG ACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCG ACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGT GCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCT TTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGG TATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCA CGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCA GCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTAC AGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAG TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGA GTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGG TTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTC AAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAC GAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGAT CTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCT AAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCG AGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACC ATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGA GGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCG ACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAAT AAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTG AGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGC CAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTT ATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGT TAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAAC ACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTC

SEQ ID NO.	Description	Sequence
		TAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACC ATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGC ATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATC ATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCAT CGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACA TTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGA ATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCA TACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGT CTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAT AGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAG AAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACG AGGCCCTTTCGTC
68	pLMTB8306	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCGCCTGCGTGAGCCTCTTTTGTCAGGATCGGCGGCTATGCCCGG AGCCAGTCTCCAGCGGGCCTGCCGGTTGCTCGTTGCCGTCTGCGCGT TGCACCTGGGGGTCACCCTGGTCTACTACCTGGCTGGCCGTGACCTT TCCCGCTTGCCGCAGTTGGTCGGTGTATCCACCCCGCTCCAGGGGGG CTCGAACAGCGCAGCGGCGATAGGACAGTCTTCGGGCGAGCTGCGAA CCGGCGGAGCGCGCCCACCCCCACCCCTGGGCGCGAGTTCCCAGCCC CGCCCGGGTGGTGACAGCTCGCCGGTGGTAGATTCAGGACCAGGGCC CGCCAGTAACCTCACGTCAGTGCCAGTACCCCACACCACGGCTTTGA GCCTGCCTGCTTGCCCGGAGGAGAGTCCTCTGCTTGTAGGACCAATG TTGATTGAATTTAACATGCCTGTGGACCTGGAGCTGGTGGCGAAGCA GAATCCAAACGTGAAAATGGGCGGTCGGTACGCGCCTCGCGATTGCG TCTCACCGCACAAGGTAGCGATTATAATACCCTTTCGCAACCGACAA GAACACCTGAAGTACTGGCTCTACTATCTCCACCCTGTCCTGCAGCG CCAGCAGCTGGACTACGGCATTTACGTGATCAACCAGGCGGGCGATA CTATCTTTAACCGTGCGAAGCTCCTCAATGTAGGGTTTCAGGAGGCT CTGAAGGACTACGACTACACATGCTTTGTCTTTAGCGACGTGGATCT CATTCCAATGAATGACCATAACGCCTACCGCTGCTTTTCCCAGCCGC GCCATATCTCTGTGGCCATGGACAAGTTCGGCTTCTCGCTGCCATAC GTGCAGTACTTCGGAGGCGTGTCTGCACTGAGTAAGCAACAGTTCCT GACCATTAACGGCTTCCCCAACAACTATTGGGGCTGGGGCGGGGAAG ACGATGACATCTTTAACCGGCTGGTCTTCCGAGGTATGAGCATTTCG CGCCCAAACGCCGTCGTGGGACGCTGCCGGATGATACGACACAGCCG AGACAAAAAGAACGAGCCTAATCCGCAGCGCTTCGACCGCATAGCTC ACACGAAGGAGACTATGTTGAGCGACGGCCTCAATAGCTTGACGTAT CAGGTTTTGGATGTGCAGCGTTACCCACTGTACACACAGATCACTGT GGATATCGGTACGCCTTCTTAAACCTGTGCGCCGCTCCCTCATTTCC GGCGGCTCGCACGCGCTCGCATACTTTGCCACACAGACGTCCTCGTG

SEQ ID NO.	Description	Sequence
		TCTACTGAACAACTAACGGATTTCCATGTCATTTCTCGTTTATCATC TTCAAACACAAGAGCACAACTGCAACGTCAGCAGTGAACGCCCGACA CAATCGGAGAGCGTGGTCACGCCCCTTCTGACTTATTTAAATATCCC AATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGT GTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA GCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTC GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGC TCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG CTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAA TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGAT ACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCG ACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAG CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGT AGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG TGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGC TCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT CCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAG GGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTT TTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTA AACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACT GCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGC CGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGAT GGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAA TACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAG AAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTT ATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGT CATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGC GCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACA AACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAA CAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCT GTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGT ACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCC AGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCT TTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAA TCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATT TATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTA GAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCA ATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACA TATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACA

SEQ ID NO.	Description	Sequence
		TTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCAT GACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
69	pLMTB8307	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ACCTGTGCGCCGCTCCCTCATTTCCGGCGGCTCGCACGCGCTCGCAT ACTTTGCCACACAGACGTCCTCGTGTCTACTGAACAACTAACGGATT TCCATGTCATTTCTCGTTTATCATCTTCAAACACAAGAGCACAACTG CAACGTCAGCAGTGAACGCCCGACACAATCGGAGAGCGTGGTCACGC CCCTTCTGACTTGCGCCATGAAAAACGATGTGAGGCAGCGGCGCGTC CTCTCCTCCGCCAGCTTCAAAGCGCTCGTGCGGTTTCGCGTGCTTTG CTCGGTGTTCCTCTCCCGCTCGCTGACTTGCCCCACGCGCGTATCTG CGCGCCGGTACCCCTCTGCGCAGCTCGGCTCGCCTGCAGGCGCGCGC TCTCGACACCCCCCTCGTCTCTGTAACTCTGTCTCTTCCTCCCAGCC CCACCCTTCTTTTTTCCTGCTTTTCCGTTTGTTTGTACGGCGCAGTG CCGCGACCAGCCCGTTTTGGCTCTTTCTCCGCGTTGCCAGCACCAGG GGGTTGGGGTCACCGTGCGCGTTGCTCCTCCGCTCTCTCTATTTCCA TCTCCTTGCTTTGTTTTGCGATCTCGCCGACGGACGCTGTCAAACCC TCATAGGTTGCTTTTCTCCCTTTCTCGCGGAACGCCGGCGTGTCAAG ACGAGGCCATGAAAAAGCCTGAACTCACCGCGACGTCTGTCGAGAAG TTTCTGATCGAAAAGTTCGACAGCGTCTCCGACCTGATGCAGCTCTC GGAGGGCGAAGAATCTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTG GATATGTCCTGCGGGTAAATAGCTGCGCCGATGGTTTCTACAAAGAT CGTTATGTTTATCGGCACTTTGCATCGGCCGCGCTCCCGATTCCGGA AGTGCTTGACATTGGGGAATTCAGCGAGAGCCTGACCTATTGCATCT CCCGCCGTGCACAGGGTGTCACGTTGCAAGACCTGCCTGAAACCGAA CTGCCCGCTGTTCTGCAGCCGGTCGCGGAGGCGATGGATGCGATCGC TGCGGCCGATCTTAGCCAGACGAGCGGGTTCGGCCCATTCGGACCGC AAGGAATCGGTCAATACACTACATGGCGTGATTTCATATGCGCGATT GCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACACCGT CAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTTGGGCCG AGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGCTCC AACAATGTCCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGA GCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAT TCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTG CCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCC GCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGG CCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCG GTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGG GGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA GGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC

SEQ ID NO.	Description	Sequence
		CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT CCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTG TCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACG CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCT GTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGT AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACT GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGA AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG AAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTA GCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAA GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCA GTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAA AAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAA TCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAA CTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTAT CAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAAC TCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGC GATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGT CAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAA TCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTC AACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCA AACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGA TCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCG CAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGAT ATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTG AGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGG AAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTG TAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCT GGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTG CCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCA TGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATA TGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGG TTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATA AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCG TATCACGAGGCCCTTTCGTC
70	pLMTB8310	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCAGCGGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCAAG

SEQ ID NO.	Description	Sequence
		GTCCTTGCCCGCAACCTCGGGGTGATGGATGACCTGAAGTCAGGCGT GCCACGCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCC GGCGCATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATACGACGTG AGCTGGAGCTAAATTGCACGGCTCTTATTTGTCCTTTGAAGTATATA TATATATATATATATTCTGTTTTCGACTTCACTGAGAAGCGGAGAAA TATCATTAAAAAATTTCAGTGGGCTTGAATGTCGCTGACTAAATGTG ATGCACATCTCGAAAGAGATGCGTAGGAGATCGAGTGGCTGACAGTT TTTGTGTTCAACCACTTCCCCTCCGTTACAAATGTGCGGATAACTCC GTATTTTCCGGATGTGGCACAATGAAAACGATATGTGGATATAGAGC TGTTTTCCTTGCCTGTGCTCGTTATGTTTGTTTTCTTGTCTCTCTTC TGTCTTCCTCTCGAGATTACTGTGAGGAGGAAAGCTATCATCTGTGA TCTTACATACCTAGCCTCTTTTCGCGATTACAAAGGTACTGCAGGCT CAGCGCACATAGATTTACTCTCTGAAGGGACTGTGCTCAGTCCATTT TTAGACTAACTGAGGAGCACTGACGACAACAAGGATACATAAACATG CGGTTCCGGATTTACAAGCGCAAAGTGGTCATCTTGACCCTCGTCGT GATTATATGCGGTTTTGCAGTGTGGAACAGTGGCAAACCGAAGAAGG CCAGCACGGTGTTTCCGAAAGAGGTGGAGACAGTGAAGCGCAGTAGT GTGGGCAGCCAAATCCAGGCGACCATTCCTGTCACGCGGAAGCCGAT CAACGAGTCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAG CATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGC CTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCG CTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGC CAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTC CTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGG TATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGG GATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAG GAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCC CCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGA AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTC CCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGT CCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTG TGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTG GCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGG TGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAA GAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAG CGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAG GATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAG TGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAA AAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAAT CAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAAC TCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATC AATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACT CACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCG ATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTC

SEQ ID NO.	Description	Sequence
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71	pLMTB8311	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CTGCATGCCGAGCGGCCAGAAGACAAAGATTGAGAACGTGCTCCAGA ATAGCGGTAATCAGCTCTTCCCTAAGCAGCTCTTGATCACGAAGCGA CTGCCCGCGTCGGGGGCGAAGGGCGTAGCCCCCCATGTGAAGAACGG CGGTTGGGGCGACATCCGGGACCACGAACTGTGCAAGTCTTACCTGC GCCTTCAGTAGGTCCTCCGGCCTGACAGCGCGCGCGCCGCTGTATGT GCGCGTGTGCGCGGCTTCCCACTGGGGCCAGCGATGAGGCGCATCAT ACCTCCATAGAGACCCTATCTTTTGTTTTCTGGGCTTCCCAGATGAC CACTTGATTCCTTCCTTCCTTTGATTTGTTTCTCTCCTCCCCTCCGC AGAGGGTACGAGTCAGGGTAGGCTCGGAGAAAGCTTGCCGCATCCAC GATGAGCCACGGCTGTCTCTCTCTCTCTCTTGACCGGGACAGGCTGT TGCCCAGTCACGCGTATCGGCGTGCACACCCGCTCTTGCGCCCTGCC CCACTATTCGTCGAATGATGCGCTACGCGCATGACAGGCGCTGCTGC AGCGCTGCTCCCTGCGGTTGCTGAGTGCGTACATGCCGTTGCTACTG ATGTGTTTGCACTGCATCTCACCTCGCTCTCTTTGCGCATGCGCTTG CCCTTCCTCCCTCCTCGCGACCGTGTCGGTCCTCTCGCGCCGCTGTG GCGCAGCTCGCCGCCTTCCACTCCCCCAAACACACACGCTCATACGC TCATATAGCACTCGTGCGCACCGACACACCCACACCCCCTCCTCTCT CTCTTCTCCCCAACCTACCCATCGCAGCCATGCTGAAGAAGCAGTCC GCCGGGTTGGTGCTGTGGGGCGCAATAATCTTTGTTGGCTGGAACGC GCTCCTTCTGCTTTTTTTCTGGACCCGCCCTGCCCCCGGACGCCTCC CTTCGGACAGCGCTCTCGGGGACGACCCCGCAAGCCTTACGCGTGAA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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72	pLMTB8312	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCTTGGCGAGGTGCGTGTCCAGTATACGTCCCGCGACAGCTTTAAGG CATTTGCTAAAGCCTTGGGTGTCATGGATGATCTGAAGTCTGGCGTG CCCCGTGCAGGCTACCGTGGAATCGTGACCTTCCAGTTCCGGGGTCG CCGGGTCCACCTCGCCCCGCCGGAGACCTGGAACGGCTACGACCCGT CCTGGAATTGAGTGACTATAAAGTGCTATTGAATTTTTTTTTCTTTT CCTTTCACGAAACAAAAATCTGTGTGTGCGCATTTTCTTACTCTCCA TTTGGTGCGCACCCTTCTGGGGGTATGACCTTCAGCACACACAAAGA ACGTGTGCTGCGCATATGTGTTCAATGCATGTGCTTTTCCTCTCTTT GTTTCTATCAAGGAGGTTCATATGAGAGGGCATGCTCACAGCAGCTT CCCTTATGCATATGTAGCCTTCTGAGTTCAGATGTGATACTGCTCCC TTGATCTCCCTTTTGTGTTTTTGTTCGAAACAACAATGACGCTCTTA CATTCTCTCTACCTATTATCGTTTCTTTCGCATCTGAAAGCGTGGTA CTAGTTAGCTTTATCTTAGTAAAACAGTTACCATTCACTGCCACCAA AAATGCGCCTGCGTGAGCCTCTTTTGTCAGGATCGGCGGCTATGCCC GGAGCCAGTCTCCAGCGGGCCTGCCGGTTGCTCGTTGCCGTCTGCGC GTTGCACCTGGGGGTCACCCTGGTCTACTACCTGGCTGGCCGTGACC TTTCCCGCTTGCCGCAGTTGGTCGGTGTATCCACCCCGCTCCAGGGG GGCTCGAACAGCGCATTTAAATATCCCAATGGCGCGCCGAGCTTGGC TCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCA CAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGG GGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACT GCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAA TCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCC GCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCG AGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT CCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGA AGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATA CCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCT CACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTG GGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATC CGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGC CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA GGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC TAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT

SEQ ID NO.	Description	Sequence
		TCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCT GGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAA AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG CTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTA TCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTT TAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGA AAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGA TTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGA AAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGT CTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCC TCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC TGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTT GTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCA ACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATAC GCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACC GGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCA GGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGT GGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGG TCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCA TCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAA CTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTG ATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCA TCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTG AATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATC AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAA AATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACC TGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATA GGCGTATCACGAGGCCCTTTCGTC
73	pLMTB8313	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CGTGCCGCCCTTCCACTCAGTCAGCCCAGATCGAAAGCCTGCTCAAT AACAACAAACAGTACCTCTTCCCAGAAACCCTCGTGATCGGCGAGAA GTTCCCTATGGCGGCGATCTCCCCGCCCCGTAAGAACGGGGGGTGGG GCGACATACGTGATCATGAGCTCTGTAAGTCGTATCGCCGCCTCCAA GCTGGGGCCTAGAGTCGTAGGCCGATGCTCATATCTTCCCCTTTTTT CACGGTGCCGTTCCTTTTCTTCTTTCATTTCTTCCCTTCCGAGACAA CAAATAAACGCAACACATAGAAGTATAGACAGGAACTGCGCCAAGCT GTGTATTGCCCTTCTCCCCCCTCCCACAACGACACAGTGTGTGCGCT GTTCATGGACGCTTCATGTGAGGAGGAACGCGACGAGAGACGGACAG GGATGGAGAGCCGCGCTGAACACGCAAAGCGCCCGCCCACAGGGACA CAAACAGAGGCACAGATGGCCCGCTACTGGCTTCCTTTTCGCCGCCA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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74	pLMTB8314	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT AGGTGCGGGTTCAGTACACCGGTCGCGACAGTTTTAAGGCATTCGCG AAGGCACTGGGGGTGATGGACGACCTGAAGTCCGGCGTGCCCCGCGC GGGTTACCGCGGAATCGTGACGTTCCAGTTCCGCGGCCGCCGAGTGC ACCTGGCGCCGCCACTTACGTGGGAAGGCTACGACCCTTCATGGAAC GCGGGCGCGTAGGGTCCTTGTGACCGCGCGTTTGGCGGACTGCTCAA CAGAGCGGGCTAACGCTGACGAAGATATGCTGGTTTCCCTGTGTTTG TGATTTGCCATCCTTTCGTGTCAAAAAGAAACAACAACAACAGCAAC CCGTTTAGGCCAAGAAGCGGGCGCTCGGACTCTTTCCCTGCCTGCCC CATCCCCATGAAGCACGCCGGCTGTCGCACTGGGCACCTCATGACCC TGTTGATAGCGCTGGAGGCCTTCATTGCGTGCTGGTTGTGGGGGGGG GTGGAAGGGGGAGAGGCGTGTTGTATTCATGTGAGGTGGTGGTGGCA TTGCGCAGCGGTGGGAAAAGCAGGGTCTTTTCCGTACTCCGTGACAG AGCTGCCGTGCTCATCTTTTCCCGGTTCACTGCTTGCACTGTTGGCT GCCTCGCCTTCTCCCCTCCCCCTGCCCCCACGAAACGCGGTTACCGC GTCTCCTTCGTGGGAGAAGTGGAGTGGCACAGTTAAGGCGACTACAA GGAGTTCCCCCTACCCTGGAGGGAGACTTGCGGGCGCGGGACGCCTT GTCTACGTGAGCGTCTCTTCCCAAGTAGACGACTCCCTCGACTTTGT CCCCTCCGTCGCATTCCGCCCCTCTCCGCCCTCCTTTCGTGTACGTC TCTGCATTGTACACTTCCTTTCGCCTGCTTTCCCACGCTCGCGCGCA ACAACGTGGACGCACCACATCGCTCGCTGGAGAAGAGAGAAAAGTGG TGAGTACGTGTTCCGCTCTTTCCCTTCTCCCCTCCGCTCGCGTCGCA CCTCTCCGCAGCTTTACCGCTCTCTTCCCTTCCATCATCCGCGTCGT GCACCACTTCCCTCATTTTCCGTGCGGCAGTAGAAAATGCGGTTCCG CATTTATAAGCGCAAGGTCTTGATCCTGACGCTGGTCGTCGCCGCAT GCGGATTTGTGCTGTGGAGCTCGAACGGTCGCCAGCGCAAGAACGAA

SEQ ID NO.	Description	Sequence
		GCGCTCGCCCCGCCGCTGCTTGACGCGGAGCCTGCACGAGGCGCGGG TGGCCGTGGCGGCGACCACCCGAGCGTGGCGGTGGGTATCCGCCGCG TATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCA TAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAA CATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAG TGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAG TCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGC GGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCA CTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCT CACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGC AGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC AGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGC GCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTT CTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTA TCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACG AACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGT CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGC CACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGT TGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTT TTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAA GAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCT TCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAA AGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAG CATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCAT ATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGG CAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGAC TCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAA GGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAG AATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTAT TCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTA AAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACAC TGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTA ATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCAT GCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCAT AAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCAT TGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCG GGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATT ATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAAT TTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATA CTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAA

SEQ ID NO.	Description	Sequence
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75	pLMTB8315	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ACAAAAAGACGTGTCGTCCATCGACGCAATCTGCCCAAATCGAGTCG CTTCTGAACAATAACAAGCAGTACATGTTTCCCGAAACGCTCACTAT CTCGGAGAAGTTTACCGTCGTGGCCATATCACCGCCACGCAAGAATG GCGGCTGGGGCGACATACGCGATCATGAATTGTGTAAGTCGTATCGC CGCCTGCAGTGATTCGCTTCGCGGTGCCGGCCATTGGCGTACTCTCG CTTTTTCTTATTTTGCCTTTCCTTTTCATTTCATGAAGAAACAAACT GCAAACGAATCGGACAGCGGCACGACCTGCACTCGCCGCTTACTAGA CTATCAGCAGCACAGCTCCGGGGAAGGATTCTCTCTGCCACAGAGAA CAATCTCTTGGTTTTCTTCCCTTACCTCACCGCAACTTAACCGTTGG TGCCGTCTTCTCGCTTGTGTGTGCGTGTAAGTGTGCTCTTGCCACTG CTCCCGCACAGCCTGCCTGATTCTGCGCTGCGGGCGAAATGAAGCCG AGGGTCTTCGACCCAGCCTCGTGCCACGTCCGTTGCATCTGCTCGCT TGTAAGATGGCTGTTGATCGCCTCCTCCTCCCCATTTCTTCATTTGA TTGGCTTCTGGGGCACTGTTCAGCTCCCTTCACACATACCGGAACTC AACCAGGTATCCGTCGACACCGCTCGCCATCGTGCGCGTTCACCGGC CGCACGGCGCCTCAGTCAGCCTTCTTTGCCACTCACTCGATCACCAC AGACAGAGTGCAGGGTGTCGTGTCGCACAGGACTACCTCGCGGATCG TGTCTTGCGACTTTGGTTGCGCTCACACCTTCTCGTCTTCTTCGTTC TCTCGCGAGGAGCTGCAAATCGTGGTTTCTACGCCTTTTTCTCTTTC CCGGTTTGACAGCGTCTCGGCGTGTGCTGCTGTTATCCCAGTCCAGG GCTCTCTTCCACACCTCTTCGGAAGAGTCTTGTCAACGTTGACGGTG CCACGTAGGAAGTAGGCTTGAGGCTTTTCGCGCTTCTTTTTGTCCTA GCCAGAAGAAGCCGCAATGCGCCTCCGAGAACCCCTGCTGAGCGGAT CAGCCGCGATGCCGGGTGCCTCCCTCCAACGCGCCTGTCGCCTCCTT GTGGCGGTATGCGCACTGCACCTTGGTGTAACACTGGTCTACTACCT GGCCGGGCGGGACCTTAGCCGGCTCCCGCAATTGGTCGGTGTGTCGA CCCCACTGCAGGGTGGCTCCAATTCAGCATTTAAATATCCCAATGGC GCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAA TTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATT GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTA TTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTC GTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACG GTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACG

SEQ ID NO.	Description	Sequence
		CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTG CCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCG TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCT GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCA AACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAG ATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC TACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTT TGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAAT TAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTG GTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATT TATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTC TGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAG ATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAAC CTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCA CCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCAT TTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAA AATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGA GCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGG AATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATAT TTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTC CCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGAT AAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTA GTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCA TGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATA GATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACC CATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAA GACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTA TTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTG AATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCC CGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATT AACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
76	pLMTB8316	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCGCCTGCGTGAGCCTCTTTTGTCAGGATCGGCGGCTATGCCCGG AGCCAGTCTCCAGCGGGCCTGCCGGTTGCTCGTTGCCGTCTGCGCGT

SEQ ID NO.	Description	Sequence
		TGCACCTGGGGGTCACCCTGGTCTACTACCTGGCTGGCCGTGACCTT TCCCGCTTGCCGCAGTTGGTCGGTGTATCCACCCCGCTCCAGGGGGG CTCGAACAGCGCAGCGGCGATAGGACAGTCTTCGGGCGAGCTGCGAA CCGGCGGAGCGCGCCCACCCCCACCCCTGGGCGCGAGTTCCCAGCCC CGCCCGGGTGGTGACAGCTCGCCGGTGGTAGATTCAGGACCAGGGCC CGCCAGTAACCTCACGTCAGTGCCAGTACCCCACACCACGGCTTTGA GCCTGCCTGCTTGCCCGGAGGAGAGTCCTCTGCTTGTAGGACCAATG TTGATTGAATTTAACATGCCTGTGGACCTGGAGCTGGTGGCGAAGCA GAATCCAAACGTGAAAATGGGCGGTCGGTACGCGCCTCGCGATTGCG TCTCACCGCACAAGGTAGCGATTATAATACCCTTTCGCAACCGACAA GAACACCTGAAGTACTGGCTCTACTATCTCCACCCTGTCCTGCAGCG CCAGCAGCTGGACTACGGCATTTACGTGATCAACCAGGCGGGCGATA CTATCTTTAACCGTGCGAAGCTCCTCAATGTAGGGTTTCAGGAGGCT CTGAAGGACTACGACTACACATGCTTTGTCTTTAGCGACGTGGATCT CATTCCAATGAATGACCATAACGCCTACCGCTGCTTTTCCCAGCCGC GCCATATCTCTGTGGCCATGGACAAGTTCGGCTTCTCGCTGCCATAC GTGCAGTACTTCGGAGGCGTGTCTGCACTGAGTAAGCAACAGTTCCT GACCATTAACGGCTTCCCCAACAACTATTGGGGCTGGGGCGGGGAAG ACGATGACATCTTTAACCGGCTGGTCTTCCGAGGTATGAGCATTTCG CGCCCAAACGCCGTCGTGGGACGCTGCCGGATGATACGACACAGCCG AGACAAAAAGAACGAGCCTAATCCGCAGCGCTTCGACCGCATAGCTC ACACGAAGGAGACTATGTTGAGCGACGGCCTCAATAGCTTGACGTAT CAGGTTTTGGATGTGCAGCGTTACCCACTGTACACACAGATCACTGT GGATATCGGTACGCCTTCTTAATCCGCGTGCCGTAGCTCGCTGCGTA TGAGGTACTCGGTTCCAGTGCATCACGCGGCGCAGGGCAACACAAAC TTTCTTTTTGTTTCTCTTCAAGTCAAAAAAGAAAAAGAAAACAGCCA TACCGCACACCATCCATAACAAGGGGCGTGTGAGGGGCGGCGGCTCT CGGGCTTTACCCCGCCAATGCAGCAACACGCGGCATTTAAATATCCC AATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGT GTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA GCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTC GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGC TCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG CTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAA TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGAT ACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCG ACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAG CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGT AGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG TGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGC TCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT

SEQ ID NO.	Description	Sequence
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77	pLMTB8318	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT TCCGCGTGCCGTAGCTCGCTGCGTATGAGGTACTCGGTTCCAGTGCA TCACGCGGCGCAGGGCAACACAAACTTTCTTTTTGTTTCTCTTCAAG TCAAAAAAGAAAAAGAAAACAGCCATACCGCACACCATCCATAACAA GGGGCGTGTGAGGGGCGGCGGCTCTCGGGCTTTACCCCGCCAATGCA GCAACACGCGGCTTGTACGCAACGCTTCTTTTGGCATGTCACGCTGA ACAGAATCTCTGCGTACAGCAACCACGTTGCCATCGGCCCGTCACTC GCTCCTCTCTCCTCCAGCATTCTTGAGTGACTACAGGTATGTTTGGT TCAGTGCGTATGCGAGCGTTAGTGCATCCCCTATACAAGCACGTGCC GCCAGGGCGCGTATCTTCGCAGTGAGACGCACTTGCTTTACCGACTA CCTGTGCTTAAGTCCCCCCCACTGACCTAAACAAACTCTGACCATCG CATCACCTCTCGTTTCGTCGTCGTGCCTCTCTCCCTTTCTCTGCCGA TTGTGATTCCTCTCCTCATGCCATTCTCCTGAAATCCCTCATCACTC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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78	pLMTB8322	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCAGCGGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCAAG GTCCTTGCCCGCAACCTCGGGGTGATGGATGACCTGAAGTCAGGCGT GCCACGCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCC GGCGCATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATACGACGTG AGCTGGAGCTAAGGTTTATCAGCTCCAGGAACGAATGTACTTTTATT ATTATTGTTTCGTGTCATGTAATTGACTCTATTTAAAACCAAGCAAA GCAACTCTTTACCAGGGAAGCCGACAAGGCTTTCTATTCCCGAAGAA CCTTTGCGGCTTTCCAACTCATAGGAGAGCCGTCTCTTCCCCACTTC GGCTTCAATAAAGGAAAATGGCGTCTTTCGAGTAGAAAAGGGCAGAT GCGGCGCATTGCGTGCTTTGCACCTATATCCGCCACAGCTCGCATTT CGACTGCGTAGAAAGTAGTGGAAATATGTTCTTCACCAAGACCGTGC CTGTTTGCTCTCTCAATTCTCGTTTCGCTATAACATCCCTTCCTCTT TAAAAAAAAATCTGTTGTGTCTCTGCAGCATTTCTGGTACCCGAGCT GTTTCCTCTCGCTAGGGAAGCAACAACAGCTACTGCTTGTTGTTATT AGTGCGAAATAGAGCATCTGAAACGGAAAATGCGGTTCCGGATTTAC AAGCGCAAAGTGGTCATCTTGACCCTCGTCGTGATTATATGCGGTTT TGCAGTGTGGAACAGTGGCAAACCGAAGAAGGCCAGCACGGTGTTTC CGAAAGAGGTGGAGACAGTGAAGCGCAGTAGTGTGGGCAGCCAAATC CAGGCGACCATTCCTGTCACGCGGAAGCCGATCAACGAGTCATTTAA ATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGT TTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGA GCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAA ACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGA GGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTC GCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAA

SEQ ID NO.	Description	Sequence
		AGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGC CGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATC ACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTA TAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCC TGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTT CGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT TCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTT GAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTA TCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGC TCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT TTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATC CTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCA CGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTA GATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATAT ATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAA TGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTG AAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCC ATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCA ACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATC AAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCA AAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTA CGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCG TGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGAC AATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGC GCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTG GAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCAT CAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCC GTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAAC GCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCC CATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGA GCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCG CGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCC TTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGC GGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCC GCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTA TTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTT CGTC
79	pLMTB8323	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		TTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAG TAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAA CTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAA GCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGG ATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATC AATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTG AGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGT TTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTC GTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATT GCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTA CAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATC AACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATG CTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGA GTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAG CCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTAC CTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATAC AATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCA TTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCC TAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTT CAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATA CATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCA CATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATC ATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
80	pLMTB8324	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCTTGGCGAGGTGCGTGTCCAGTATACGTCCCGCGACAGCTTTAAGG CATTTGCTAAAGCCTTGGGTGTCATGGATGATCTGAAGTCTGGCGTG CCCCGTGCAGGCTACCGTGGAATCGTGACCTTCCAGTTCCGGGGTCG CCGGGTCCACCTCGCCCCGCCGGAGACCTGGAACGGCTACGACCCGT CCTGGAATTGAAGTGTGCGGGGCAACCACACGCGAGGGACGAAGACA AGGATAACAGAAGGCAACGCGGCAAAACGGAGGACGGCCGCATACAA AAACAAACAAACAAACAGGTGAGCGGACGCACACCTGCCTGAGAAGT GCGCTGCCGCAGCGTGTGTGTGTGTGTCGCCGCGTTGCGGTCTGTAC CCTCCCCCCCACTTCCCCTGTCTGCGTCTCTCTCTCTCTGTGTGTGCG TGGGCTCATTTTCTCCGTTTCTTTTTTTCGTTTTGTTTTGTTTTATT TCTCTTCGAAAATGAGAAAAACGACCCGAAAATGGTCTCCGCCGGCG TTGTATCTCTGCCCCCCCCCCGCTGTCCCAGAGCGTAGGGTGCACCG TCTGCTGCTTCCCCAGACGGCGCGCAGGATGGGGCGGCAGTCTCGGA GGCTGCGACGTGTGTCATGATAGCTGTGACGGCGGGTGCGTACGGCT GCTTCTATCTCTGCGGCGATGCACCGCCTCGTGTTGCGTTGGATTTC CATCCAACTCCTCTCCCCACCCCCACCCGAGGCGTGCGTGTGCGGCG

SEQ ID NO.	Description	Sequence
		GTGTGCGGTGGCTCGCACACGACACCTTGTGTTTCCATCGCATGTTG CGTCGCTCGCTGCAGTTGGTGCTCTGAGCGTTTTCTTCCCCCTTCTC GCAGTCTTTTTACCCCTTGCTTTCATACTCCACAGAGAAAAACCGCT CCCGTCTTGCAGCCGGGGCGTGCCTGCGCTGCCCACCCCGCACCCAT TTCCTTTCCTGCCGTTGTGCGTTCTGCACATCGTTACTCATGCGCCT GCGTGAGCCTCTTTTGTCAGGATCGGCGGCTATGCCCGGAGCCAGTC TCCAGCGGGCCTGCCGGTTGCTCGTTGCCGTCTGCGCGTTGCACCTG GGGGTCACCCTGGTCTACTACCTGGCTGGCCGTGACCTTTCCCGCTT GCCGCAGTTGGTCGGTGTATCCACCCCGCTCCAGGGGGGCTCGAACA GCGCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGG TCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACA CAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAAT GAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC CAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGC TCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAA CGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACC GTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCT GACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCC GACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCG TGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC TTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG GTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGC ACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGC AGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA CAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG GTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCT CAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAA CGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGA TCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATC TAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATC GAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATAC CATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCG AGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCC GACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAA TAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGT GAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGG CCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGT TATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTG TTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAA CACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTT CTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAAC CATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGG CATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACAT

SEQ ID NO.	Description	Sequence
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81	pLMTB8328	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCGCCTGCGTGAGCCTCTTTTGTCAGGATCGGCGGCTATGCCCGG AGCCAGTCTCCAGCGGGCCTGCCGGTTGCTCGTTGCCGTCTGCGCGT TGCACCTGGGGGTCACCCTGGTCTACTACCTGGCTGGCCGTGACCTT TCCCGCTTGCCGCAGTTGGTCGGTGTATCCACCCCGCTCCAGGGGGG CTCGAACAGCGCAGCGGCGATAGGACAGTCTTCGGGCGAGCTGCGAA CCGGCGGAGCGCGCCCACCCCCACCCCTGGGCGCGAGTTCCCAGCCC CGCCCGGGTGGTGACAGCTCGCCGGTGGTAGATTCAGGACCAGGGCC CGCCAGTAACCTCACGTCAGTGCCAGTACCCCACACCACGGCTTTGA GCCTGCCTGCTTGCCCGGAGGAGAGTCCTCTGCTTGTAGGACCAATG TTGATTGAATTTAACATGCCTGTGGACCTGGAGCTGGTGGCGAAGCA GAATCCAAACGTGAAAATGGGCGGTCGGTACGCGCCTCGCGATTGCG TCTCACCGCACAAGGTAGCGATTATAATACCCTTTCGCAACCGACAA GAACACCTGAAGTACTGGCTCTACTATCTCCACCCTGTCCTGCAGCG CCAGCAGCTGGACTACGGCATTTACGTGATCAACCAGGCGGGCGATA CTATCTTTAACCGTGCGAAGCTCCTCAATGTAGGGTTTCAGGAGGCT CTGAAGGACTACGACTACACATGCTTTGTCTTTAGCGACGTGGATCT CATTCCAATGAATGACCATAACGCCTACCGCTGCTTTTCCCAGCCGC GCCATATCTCTGTGGCCATGGACAAGTTCGGCTTCTCGCTGCCATAC GTGCAGTACTTCGGAGGCGTGTCTGCACTGAGTAAGCAACAGTTCCT GACCATTAACGGCTTCCCCAACAACTATTGGGGCTGGGGCGGGGAAG ACGATGACATCTTTAACCGGCTGGTCTTCCGAGGTATGAGCATTTCG CGCCCAAACGCCGTCGTGGGACGCTGCCGGATGATACGACACAGCCG AGACAAAAAGAACGAGCCTAATCCGCAGCGCTTCGACCGCATAGCTC ACACGAAGGAGACTATGTTGAGCGACGGCCTCAATAGCTTGACGTAT CAGGTTTTGGATGTGCAGCGTTACCCACTGTACACACAGATCACTGT GGATATCGGTACGCCTTCTTAAGCAGAATTTGGATGATGCGATTACT TGAGATAATTTCATTTTCATCAGCAAAAACGAAGTGCAACGGTATCT TTGGTTCACCAGAGGCCGGCAAAGCTCTTAGGGTGGTGTAATGGGCT GTTAGCGCTACGGTACACTGAAGCGATCAGCTGCGGTATCTGTGTGA GCGTCAAGGGTGCGCTGGTTTCTGCATCTCCGAGATTTAAATATCCC

SEQ ID NO.	Description	Sequence
		AATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGT GTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA GCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTC GTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGC TCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGT AATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGT GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG CTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAA TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGAT ACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCG ACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAG CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGT AGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGA TTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGG TGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGC TCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT CCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAG GGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTT TTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTA AACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACT GCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGC CGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGAT GGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAA TACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAG AAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTT ATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGT CATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGC GCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACA AACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAA CAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCT GTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGT ACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCC AGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCT TTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAA TCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATT TATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTA GAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCA ATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACA TATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACA TTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCAT GACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC

SEQ ID NO.	Description	Sequence
82	pLMTB8330	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCAGAATTTGGATGATGCGATTACTTGAGATAATTTCATTTTCATCA GCAAAAACGAAGTGCAACGGTATCTTTGGTTCACCAGAGGCCGGCAA AGCTCTTAGGGTGGTGTAATGGGCTGTTAGCGCTACGGTACACTGAA GCGATCAGCTGCGGTATCTGTGTGAGCGTCAAGGGTGCGCTGGTTTC TGCATCTCCGAGTTTTTGATTCGCTCTGAGGATGTATCGCAAAAAGC ACGCTGCGGTGCTGCTTTACTACTCCTGCGCTGCTGCTCCTTCAAAT GCGTCGACATGTCCGATTTTCTGCAGCTACTCGCCTCCACTTTCATC TCTCCCTCTTCCTTGTTGTTTTCTGTGTGTCCATGCGCCTTGTGTGC GTCTCAACTTGCGACAACTTTTCTTTCGCGTCTCTGTGGAATAACAT CTGAACAGCTTTAGGGCTTCATTCGCAACGGATCATGAAAAAGCCTG AACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCGAAAAGTTCGAC AGCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGTGC TTTCAGCTTCGATGTAGGAGGGCGTGGATATGTCCTGCGGGTAAATA GCTGCGCCGATGGTTTCTACAAAGATCGTTATGTTTATCGGCACTTT GCATCGGCCGCGCTCCCGATTCCGGAAGTGCTTGACATTGGGGAATT CAGCGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCA CGTTGCAAGACCTGCCTGAAACCGAACTGCCCGCTGTTCTGCAGCCG GTCGCGGAGGCGATGGATGCGATCGCTGCGGCCGATCTTAGCCAGAC GAGCGGGTTCGGCCCATTCGGACCGCAAGGAATCGGTCAATACACTA CATGGCGTGATTTCATATGCGCGATTGCTGATCCCCATGTGTATCAC TGGCAAACTGTGATGGACGACACCGTCAGTGCGTCCGTCGCGCAGGC TCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGC ACCTCGTGCACGCGGATTTCGGCTCCAACAATGTCCATTTAAATATC CCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCT GTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGG AAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTG TCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGG TTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGC GCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGT TGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAA AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG ATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTC CGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGT GTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTC AGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAAC

SEQ ID NO.	Description	Sequence
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83	pLMTB8334	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCAGCGGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCAAG GTCCTTGCCCGCAACCTCGGGGGTGATGGATGACCTGAAGTCAGGCGT GCCACGCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCC GGCGCATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATACGACGTG AGCTGGAGCTAAGCGGTCATTACGATGATGAGAGAATACGTGGTCGG GGGAAGGAAGAGGACAGTGGTACTCTGCATGTGCTTGGGCACCGTGT CTTTTGGACGAGTAGACGGTGCCAGGTGGGGGAAGGGGGAAGGGAGT TTGGGCGATGAGGTAGTCGAGGCACAGCACACGTTCATGTGGCTGTC

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SEQ ID NO.	Description	Sequence
		CATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCG AGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCC GACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAA TAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGT GAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGG CCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGT TATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTG TTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAA CACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTT CTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAAC CATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGG CATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACAT CATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCA TCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGG AATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTC ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTG TCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAA TAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAA GAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCAC GAGGCCCTTTCGTC
84	pLMTB8335	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CTGCATGCCGAGCGGCCAGAAGACAAAGATTGAGAACGTGCTCCAGA ATAGCGGTAATCAGCTCTTCCCTAAGCAGCTCTTGATCACGAAGCGA CTGCCCGCGTCGGGGGCGAAGGGCGTAGCCCCCCATGTGAAGAACGG CGGTTGGGGCGACATCCGGGACCACGAACTGTGCAAGTCTTACCTGC GCCTTCAGTAGGCTCTCGCAGCAGCGTGAAACGCGTGGGGAAACGGG TGCGTGCGTCTGTGTGTGCGTGTTCAAATGGCATCCGCAGCGTGCCG CGCGCACCCGTGCCCGAGCACCTCTGGGATGAACGACCTCTCTCGTC GATTGAACGCGATGTCACCAATGGCAGTCATCTTTTTTCCCCCTTTT TTCACGGGCGCTCTGTGGCGTGCGCCTTTCATTTCTTGTTTTGACCC CTCGGCAAAGAACCAAAAGAAGCAGGGGTCGGCCGTGTAGCAGGCAC CCACCCGCTCCGCCTCCGTCCCCTCTCGCACGCACCGCCTCAAGACG CGGTGCATCGCCTGCGCGCCGTCTTGCGCACACAACTGCGTTCTGTT GTCACGGCTGTTCCTTGCGCGCGCGCGCGTGCGTCGTTGACGACTCT CTCCGACGCACCACCGATGAGCACCCTCTGGATGAGGGCACGCACGT ATGTATACACGCATGTTGTGTGCCTATGCACGTATGTATGCTCCTGC GCAGTCTCTCTCGCCTCGCCTCTTACGTCATTGCTTCGCCCTCGCCA TACCTGCAGCGGTGCGTGCGTGTATTGTGTAAGTTTTCGCACGCGAG CGGAGAGCTGCTACGCAGCAGCGACGCAGTCGAGTGCGTGACTACGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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85	pLMTB8336	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCTTGGCGAGGTGCGTGTCCAGTATACGTCCCGCGACAGCTTTAAGG CATTTGCTAAAGCCTTGGGTGTCATGGATGATCTGAAGTCTGGCGTG CCCCGTGCAGGCTACCGTGGAATCGTGACCTTCCAGTTCCGGGGTCG CCGGGTCCACCTCGCCCCGCCGGAGACCTGGAACGGCTACGACCCGT CCTGGAATTGAGGAGGTGGTCATTCCATGATTATCTTGGTTTCCTTC ATTTTTTTTATGCGTGTGCTTACTTTAAAAAAGAAGCAAAGAAGTAG TCAGTAGAATCAGTACGACCACGTCGGGAACTGACACGCGCCGTGAC GGATTTCGGCTATGTTTGTGGAGCACACCTGTAGGGGAAAAAAGGAC ATCTCTCCGCAGGCACACCGGCGATTTCCCTCGACAGCGTTCAGTGA ACCCCCTGGCGAGTCTCGTTGAAACCACAGGCACGTCCTAGACGCGT TGGGTCCCTTCGACGAGAAGCTCTCTCTCTCATTCCCTGCAACTCAT CCTCTGTGACTTCTCTTACTTGTTTTTATTCTCACCGGGCCGCCCCC CCCCCCCTCACACTCCCCCTTCCCTCTCTCCCTGAGGATGGCAAAAG CGCTTAACAAGCAAACGGCATCCAAGCCTCTCCTCCGCACGGCAGTT ATCCTGGAAGGAACGGGGCCGTACCTTGACCTAAGACACTCATACAC GGTGCAGGGCGTTGCGTAGAAGGGCTGTTGAACAAGGCGGGTTCAAC CCGGTCACACCGTTGTGTCGCCGCTGTAGACGCCCTGGTAGAGGCGA TGCGCCTGCGTGAGCCTCTTTTGTCAGGATCGGCGGCTATGCCCGGA GCCAGTCTCCAGCGGGCCTGCCGGTTGCTCGTTGCCGTCTGCGCGTT GCACCTGGGGGTCACCCTGGTCTACTACCTGGCTGGCCGTGACCTTT CCCGCTTGCCGCAGTTGGTCGGTGTATCCACCCCGCTCCAGGGGGGC TCGAACAGCGCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCG AGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAA TTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCC CGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCG GCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT TCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGC GGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAG

SEQ ID NO.	Description	Sequence
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86	pLMTB8379	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG

SEQ ID NO.	Description	Sequence
		TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCGGTTCCGCATTTATAAGCGCAAGGTCTTGATCCTGACGCTGGT CGTCGCCGCATGCGGATTTGTGCTGTGGAGCTCGAACGGTCGCCAGC GCAAGAACGAAGCGCTCGCCCCGCCGCTGCTTGACGCGGAGCCTGCA CGAGGCGCGGGTGGCCGTGGCGGCGACCACCCGAGCGTGGCGGTGGG TATCCGCCGCGTGTCAAACGTCTCAGCCGCATCATTGGTGCCAGCCG TGCCCCAGCCAGAGGCGGACAACCTCACATTGCGCTACCGATCCTTG GTCTACCAACTTAACTTTGACCAAACGTTGCGCAACGTCGACAAGGC AGGTACTTGGGCTCCACGCGAGCTTGTGTTGGTCGTCCAGGTGCATA ATCGTCCGGAGTACCTTCGCCTCCTGCTGGACTCCCTTCGCAAGGCA CAAGGCATCGACAACGTGCTGGTTATTTTCAGCCACGACTTTTGGTC CACCGAGATCAATCAACTTATCGCGGGCGTGAACTTCTGTCCAGTGC TCCAGGTTTTCTTCCCGTTCTCCATCCAGCTGTACCCCAACGAATTC CCAGGATCCGACCCGCGAGACTGTCCACGGGACCTCCCGAAGAACGC CGCTTTGAAGCTTGGTTGCATTAACGCGGAATACCCGGATAGCTTCG GTCACTACCGAGAGGCCAAATTCTCTCAGACGAAGCACCACTGGTGG TGGAAATTGCACTTCGTGTGGGAACGTGTTAAGATCCTGCGTGACTA CGCCGGCCTCATATTGTTCTTGGAGGAGGACCACTACCTCGCCCCCG ATTTTTACCACGTGTTCAAGAAAATGTGGAAACTGAAGCAGCAGGAG TGTCCTGAGTGTGATGTGCTGAGTCTCGGAACCTACTCAGCCAGCCG CTCTTTCTACGGCATGGCCGACAAGGTTGACGTGAAAACCTGGAAGA GCACTGAGCACAATATGGGTCTGGCACTTACGCGCAACGCGTACCAG AAGTTGATAGAGTGCACCGACACGTTCTGTACGTACGACGATTATAA CTGGGACTGGACGCTCCAGTACCTGACCGTGAGCTGCCTCCCTAAGT TTTGGAAAGTGCTGGTTCCGCAGATCCCACGTATCTTCCACGCAGGG GACTGCGGCATGCACCACAAAAAGACGTGTCGTCCATCGACGCAATC TGCCCAAATCGAGTCGCTTCTGAACAATAACAAGCAGTACATGTTTC CCGAAACGCTCACTATCTCGGAGAAGTTTACCGTCGTGGCCATATCA CCGCCACGCAAGAATGGCGGCTGGGGCGACATACGCGATCATGAATT GTGTAAGTCGTATCGCCGCCTGCAGTGAATTTAAATATCCCAATGGC GCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAA TTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATT GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTA TTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTC GTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACG GTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACG CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTG CCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCG TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT

SEQ ID NO.	Description	Sequence
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87	pLMTB8383	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCGACCACGTAAGACCATACTGCTCGTGGGTGTCCTGGTGATATG GGTGCTTATGACCTACCTTGCCTTTATGCGGAGCGTTCGGGGCACAG ACGGGTCGCGCCCACGCCCGGCTTTCGCCAGTAATAAGCTCATGCTC GAGAAGGTACAGGATTTCGAGCAGAACCTGAAGTCGTTCGCCGACAG CCGTCAGAATCTGTATCGCGACATCATTAACATCCTGCGCCGGACAG ACAAGGTGAGTTCTGTGCCAGCTCAGCCGATACCGGCTGTACCGTCG CAAGAGTCCCCTGGCGCGGCCGTGCAGGAGAGCGAGGTCCCGAAGGA GCGCCAAGCGCCGCCGCAACGCTACCTGAACAACGATCCAGCCTTCC CGGTGATCCCTGTGGTCGTTTTTGCTTGCAACCGCATTTCTGTCAAC AAGTGCCTTGACGATCTTATCCGCTATCGACCCTCGGCCGAACAATT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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88	pLMTB8389	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGCGTGTGCGCACCGGCGTGTGCCAACGCCCAGGTACTGTGCGCACG TTCGTATCTCCATACGCTAGCTGACCGAGACGCATGCCCTCCGCCAC CCTCAGTGGCGCGCACCTTCTCTCGTTTGAGCTCTTTATGCTCTCGT GAATGGCACACAACATCCCGTGACTATCACGATGATCCTTCTCAAGC CACACCGCTTGCCTTTTCTACAGCTCTGCGTTCTCTGGCCCATCCTC CTCTTGTTTGCTTTCCCTCTTTGCACATCCGTGTGCGCGTCCTTGTT CTTCTCTTCTGCGCACACTATTCTGCGCCCGCGACCCGCGCTTCGAC TGCTGTCGGGTCATGCCTTGTGCTGCGCGTTCAGCTCTTCATTGCCC CTCGGCCTTGTACATAGCGGCTCTCCGTCATCGACGTTTTCCTCTCT CTTCAGCTCTATACACTCCCTCCCTTGTCAACACACTACACTGTGTC TCCCCCTTTCATCTCTCCTCCCCTGTCACAATGGTCCGCAAGAAGGG ATCTCTGATCCTGTGTGGGGCGTTTCTGTTCGTGGCCTGGAACGCGC TCTTGCTCCTTTTTTTGTGGGGCCGCCCGCCCATTGGTCGACTCGGC GAGGGTGGGGGGGCGGAGCCGGGCGCGGGCGAGGAGTGGGGTGCGGG GAAGAGCAAAGTGGGTGGCGCTAACGGCCTGGCGGGTGAGGTTATCC

SEQ ID NO.	Description	Sequence
		GCCTGGCGGAGGAGGTCGAGAGTGAGCTGGAGACGCAGAAGAAGCTT CTGAAACAGATACAGTCGCACCGCGAGCTTTGGGAACAGCGTAAGGA ACTGGAGAAGCGTGAAAGCGAGGATACCAAGGACGAGAAGATTGACG TTGAGCCTAAGAAGCCCCGCCAGATCCCGGCCGTGCACCTGTCCCAC AAGGTGGTGGAAGACGCCCAGACAGTAACCAAGAAAATGCAAACGCT GATGGTGACACCGCCTCAGCTGGTGATGAAGGAGCAGGAGACAGATC AGAAGAATAAGCAGATGATGGAGGACCAGCTGGGGCTCACCACGCCA TCTCCGCAAATCATCATCCCGATTCTCGTGATCGCGTGCGATCGCGT GACCGTGAAGCGGTCCCTCGACCGTCTGATCCAGTACCGGCCAAGCG CAGAGTTGTACCCAATTATCGTCAGCCAGGATTGTGGCCACGCTGAC ACAGCCCGCGTGATCGGGTCCTATGGCAGCCAGATCACGCACATAAG CCAGCCTGACCTTGCAGATATACCGGTGCGGCCAGATCATCGCAAGT TTCAGGGGTACTACAAGATCGCCCGCCATTACCGTTGGGCGCTCAAC CAGGTGTTCAACGTGTTTGCCTACTCAACGGTGGTGATAGTCGAGGA CGACCTGGAGGTGGCGCCTGACTTCTTCGAGTACTTTCGAGCTCTCT ATCCGATCTTGCGCTCAGATCCTACCTTGTGGTGCATTTCGGCTTGG AACGATAACGGGCGTGATGGTCTCGTGGATCCCGGGAAGGCCGAGCT CCTCTACCGCACGGACTTCTTTCCTGGACTGGGTTGGATGTTGCTTA AGGAGGTGTGGGCGGAACTCGAACCCAAGTGGCCAAAGGCGTTCTGG GACGACTGGATGCGACACCCGGAGCAGCGTAAAAATCGCTCTTGCAT CCGACCGGAAATTAGTCGGACGATCACATTCGGTCGTAAAGGTGTGT CCTTGGGGCAGTTCTTCGACCAGTATCTCCGTTACATTAAGCTCAAC ACTGAATTCGTCCCTTTCACGAAGCACGACCTCAGCTATCTTGTGCG AGAGAAGTACGATGTTAGCTTTGAAAAAGATGTATACTCGGCTCCCC TCGTAAAGGTAGAGGAGCTGCAGCACGGCGGCAGCCTTAAGGGCAGC GGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCAAGGTCCT TGCCCGCAACCTCGGGGTGATGGATGACCTGAAGTCAGGCGTGCCAC GCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCCGGCGC ATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATACGACGTGAGCTG GAGCTAAATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCA TGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCT TTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCA ACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCT CGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTA TCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGA TAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGA ACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCC CCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAA CCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCC TCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTG TAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTG TGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAAC TATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTG CTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGA

SEQ ID NO.	Description	Sequence
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89	pLMTB8392	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CGCAAGGAATCGGTCAATACACTACATGGCGTGATTTCATATGCGCG ATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACAC CGTCAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTTGGG CCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGC TCCAACAATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTGA CTGGAGCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACA TCTTCTTCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGC TACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCG GGCGTATATGCTCCGCATTGGTCTTGACCAACTCTATCAGAGCTTGG TTGACGGCAATTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGAC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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90	pLMTB8443	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT AGTGGTGCGCGTGCGTGTCTCCGCTGTCTGGAGCTCCTTCCCTGCCA CGCAACTGCGAGCCTTCACGGCGGCCCACCCGCCCGCACACGGGAGC GGAGACTGTGCGTGTGTGCGTGTGTGCGTGTGGAGCGGGTAATGTCG GCACACACACACACACACACACACACACACACATGCACGCTGAGAGAAT GAGCAGCCCCAGAGGAGAACATGGGGCTCATGCGCGCAGACGGAAGG GCACACACGAGGAGGGGCACACCCCTCTGTCTTCAGGGAGCACGGCC CTGCTGCTGCCATGTGACGGGCGTCTGCCACGCGACTCTTCCCCACA CCTTGCTCCTTTCCTCCCTCCCCTCCTGGCGCACACGAAACACGCGC GATGCACACACGCACGCGCCCACCCCCCAAAATAAATAAAATGAAAC GCGCAGCTCTTCGCTCTCGTTCTTCGAACAAACACATCTAAACCCCC TTCCAACCCCTCTTTCTTCTTTTTTCAACCATGAAGCGCATCCTTTG CATCACAGGGACTCGAGCTGATTTCGGCAAGCTGAAGCCACTTCTGG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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91	pLMTB8448	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGGACTACAAGGACCACGACGGCGACTACAAGGATCACGATATCGA CTACAAGGATGACGATGACAAGGGTGGTAGCGGAGGTGCTAGCGCCA CATTTACGGGAGTCATACCTCCTGTGATGACGCCGCTTCACGCTGAC GGTTCTGTGGACGTAGAGAGCCTCCGGAAGCTCGTCGACCATCTGAT CAACGGCGGTGTCGATGGCCTGTTCGCACTCGGAAGCAGCGGCGAGG CAGCATTTCTGACACGTGCGCAGCGCAAACTCGCGCTGACCACGATC ATCGAGCACACCGCGGGCCGAGTGCCAGTTACGGCGGGGGTGATAGA GACCACAACTGCCCGAGTCATTGAATTGGTCGAGGACGCGCTCGAGG CTGGGGCCGAGGGCCTGGTGGCGACTGCGCCATTCTACACCCGGACT CACGATGTGGAGATTGAGGAGCACTTCCGTAAGATCCACGCTGCAGC GCCGGAGCTCCCGCTCTTCGCCTACAACATTCCAGTGTCTGTTCACT CGAACTTGAATCCTGTGATGCTCCTCACTCTTGCTAAAGACGGCGTT TTGGCCGGAACCAAGGATTCGAGTGGCAATGATGGCGCAATCCGTTC GCTGATCGAGGCGCGCGACGACGCTGGCCTGACCGAGCAGTTCAAGA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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92	pLMTB8449	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGGAGAAACAGAACATCGCGGTCATCCTCGCGCGGCAGAACTCCAA GGGGCTGCCACTCAAGAACCTGCGTAAGATGAACGGAATCAGTCTCC TCGGCCACACGATCAATGCGGCGATCTCGTCTAAGTGCTTCGACCGC ATCATTGTGTCTACGGACGGAGGGCTTATTGCGGAGGAGGCTAAGAA CTTCGGGGTTGAGGTTGTACTTCGGCCCGCGGAGCTGGCGTCTGACA CCGCGTCCTCCATCAGTGGGGTTATTCACGCACTGGAGACCATCGGA TCTAACAGTGGAACTGTTACACTTCTGCAACCTACCTCACCCCTGCG GACTGGTGCACACATTCGAGAGGCATTCAGCCTCTTTGACGAGAAGA TCAAAGGAAGCGTTGTAAGCGCGTGCCCCATGGAGCACCATCCACTT AAGACATTGCTCCAGATTAACAACGGAGAGTACGCCCCGATGCGCCA CCTGTCGGATCTGGAGCAGCCACGCCAGCAGCTGCCCCAAGCATTCC GCCCGAACGGCGCGATCTACATCAACGACACCGCGAGCCTGATCGCG AACAATTGTTTTTTTATTGCTCCCACGAAACTCTACATCATGTCCCA TCAAGATTCGATTGATATCGACACGGAGTTGGATCTGCAGCAGGCGG AGAACATACTGAATCACAAGGAGTCCGGAGGGAGTGGCGGTTACCCG TACGACGTGCCCGACTACGCCTACCCGTACGATGTGCCGGATTACGC GTATCCATATGACGTGCCAGACTATGCGTAGATTTAAATATCCCAAT GGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTG AAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCA TAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTA ATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTG CCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGC GTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAAT ACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTG GCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCG ACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACC AGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGG TCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCC

SEQ ID NO.	Description	Sequence
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93	pLMTB8505	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGATCCACACTAACCTTAAGCGAAAGTTCAGTTGCTTCGTGTTGGT GTTCCTTCTCTTTGCAATTATCTGTGTGTGGAAGAAGGGCTCCGACT ACGAGGCGCTGACACTTCAGGCCAAGGTGTTCCAGATGCCTAAGTCG CAGGAAAAGGTGGCCGTGGGCCCGGCCCCGCAGGCAGTGTTCTCGAA CTCGAAGCAGGACCCGAAGGAAGGCGTGCAAATACTGTCGTATCCGC GTGTGACGGCGAAAGTGAAACCACAGCCTAGCCTCCAGGTGTGGGAC AAGGATTCGACCTACAGCAAGCTCAACCCACGGCTTCTGAAAATATG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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94	pLMTB8507	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGAACGGTGATTTCTCCGTGAACGAATACGAGACTCTGTTTGGCAAA GTCGCCGCATGTAACATTCGTAAAGGCGCGCAGATCAAGAAAACTGA TATCGAGGGTGGTTCGGGCGGTTATCCTTACGACGTCCCGGATTACG CGTACCCTTACGACGTCCCGGACTACGCATACCCTTACGACGTCCCT GATTACGCCTAAGACGTGCACGCAGTCCTGTCCCCACCCCCGACAGC AGGAGTGCGGGACTGGGTGCTCTAACAAGCGCATGGTACGAGCTATG TGCTGGTGTGTAGCCAGCGGGGCTGTCATGCCATGTCGATCTCTCCC CGTGAGCAGCCCCCCAAAAAGACAACCTGATTTCTCCCTTTTTCCGA TATTTCTCCCTTTGTGCTAAGGGGACCCTTCAGCAGCTCCCAGCGCC GCACATGCACACACTGGCGCGTGCTTCCGAGGTCCTCGGTGCACATA TTTTCTATTATCTCACACACCCGGTTGCAGGGCGGCTCAATGTCACG GCGCGCGCACGCACTGCCTTGAGTACGGAACGGCGAGCGATACGACC GAGACGGCGCTGCCAGTAGGGTGTAGGACGCTGCGCATCTCATGAAT GTATGAAGCATGCAGCCAACCACACAAACATATGGGCGCACGAGTCT TCCCTCACAGACAGCGCGGCTGGTGAGGCGGCAGAAGGTCGGCCGCG GAAGGGCACACACTACGTTTCACGCGTACATGACCCCGTCCGCTTTC CGCGCTATTTTAGGCGCACACCCGTTCACCAGCCTCTCCGATCCTGC TTCCACTCCTCCTCCGCCTCCGCCCTCCCTCTCCCCGTCATGACGCC GCACGCACCGCGATCGCACACAAGCTCTCTCTCTCTCAACACAAC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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95	pLMTB8509	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATAGCTCGGC GCGCCATTGGGATATTTAAATTTAGGCGTAATCAGGGACGTCGTAAG GGTATGCGTAGTCCGGGACGTCGTAAGGGTACGCGTAATCCGGGACG TCGTAAGGATAACCGCCCGAACCACCCTCGATATCAGTTTTCTTGAT CTGCGCGCCTTTACGAATGTTACATGCGGCGACTTTGCCAAACAGAG TCTCGTATTCGTTCACGGAGAAATCACCGTTCCCGGGTCGCTTAACC CACAGATTATCTCCGCTCAACAGCTCACCCTTCTTGATATCCTTGTC GGCGACCACGGAGGCAAACGCGAAATCTTTGGTCGGCTTCTCGCCCG CAATAATGGTGTCTTTCTTGCCACCTCGCGCGAGTTTCAATGCGTGC GCACCCTGCTTCAGCTCCTTGAATGTATCCGGATTCATGCTGCACAC GATGTCTGGGCCTGGCCGGTCCATGCGGTCCGTGAAGTGGCGCTCGA GGATTGACCCGCCAAGAGCCACTGCGCCGAGACAAGCGTAGTTATCC AGCGTGTGGTCGCTCAGGCCAATAATTGCATCCGGGAAGGCTTCACT AAGGTCGTTCATGCCGCCCAGTCGGACGTCTTCGTACGGAGTCGGGT AGATATTTGTGCAGTGCAACAACGCGTAAGGCACACCGGCCTCACGG ATGATTTCGACAGACTTCTTGATTGATTCGATACTATTCATGCCGGT GGACAAGATGATCGGTTTACCAAACGATGCAACCAACTTAATGAGTG GATAATTATTGCACTCGCCGGAGCCTATCTTATAGGCGGGAATATCC ATGCGCTGCAATCGGAGAGCTGCGGCGCGCGAAAACGGGGTAGAAAT GAAAATCATGCCTTTCGATTCCACATACTCCTTCAGCTTGATCTCAT CTTCCTCGTTCAGGGCGCAGCGCTCCATGATCTCGTAAATCGACACG TCAGCATTACCTGGGATCACTTGCTTGGCTTCGTCGCTCATTTCGTC CTCAACAATGTGGGTTTGGTGTTTCACCACCTCTGCCCCAGCGTTAT AGGCGGCATCCACCATCTCAAAAGCCGTCTTCAGGCTGCCTTCGTGA TTGATGCCAATCTCGCAGATAATCAGCGGCTCATGGTTGTAGCCTAC AGAGCGGTTGCCGATCTTAAATTCGTTGTTATTCTGCATATTTAAAT ATCCCAATACGCGTCAATTCAATCCCAATGGCGCGCCGAGCTTGGCT CGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGG GTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTG CCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAAT CGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCG CTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGA GCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATC AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG

SEQ ID NO.	Description	Sequence
		CCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTC CGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAA GCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTC ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCC GGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCC ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG GCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACT AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTG GTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAA AAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGC TCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTAT CAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAA AAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGAT TATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAA AACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTC TGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCT CGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACT GAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTG TTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAA CCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACG CGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCG GCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAG GATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTG GTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGT CGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCAT CTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAAC TCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGA TTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCAT CCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGA ATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCA GGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAA ATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT GACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAG GCGTATCACGAGGCCCTTTCGTC
96	pLMTB8517	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATTGAATTGA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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97	pLMTB8520	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT TCAGCGCTCCGTAGCTCGCTGCACATGCGGTACTGCGTTCCAGAGCA TCACGCGACGCACAGCAACACAAACTTTCTTTATCTTTCTCTTCCAT TCGAAAAAAAAAAAAGATAACACCCACCTCACATAACGTCCATAACAA GAGAGCGTGAGAGGAGAGTCTGCTCTTCGACTTCACACCGCGAATGC GGCAACACGTGGCTTATGCGCAACGCTTCTTTTGGCACGTCATGCTA AACAGAATCTCTGCGTAGGGCAACCAGGCTTTCATCGACCCGTCGTT CGATCCTCGCTCCTCCGGCATTCTTGAGTCACGACACGAATGCTTGG CTCCGTGCGTCTGCGAGCGTTTGTGCGTTCCTCTAAAGCAAGAACGC GGGGACACGACGTTTATCTCCGCCTCGCGACGCACTTTCTTTACCAA CTACGTGCACTTACAACCCCCCGATCTCAAAACCTCTGCTCATCGCA TCACTTCTCATTCCGTCGTTGTGCCTCTCTCTACCTTCATCTCCCGC

SEQ ID NO.	Description	Sequence
		TTGTGCTTGGTTTCCTAATACCGTTCTCGTGTAATGCCTCATCCCTT TTCCACTACAGCTCTTTTTTTCCCCTCGCCGAAGATGACCGAGTACA AGCCGACCGTGCGCCTGGCGACACGCGACGACGTGCCACGCGCAGTG CGCACACTGGCGGCAGCGTTTGCGGACTACCCGGCGACACGCCACAC AGTGGACCCGGACCGCCACATCGAGCGCGTGACAGAGCTGCAGGAGC TGTTCCTGACGCGCGTGGGCCTGGACATCGGCAAGGTCTGGGTGGCA GACGACGGCGCAGCGGTGGCAGTGTGGACGACACCAGAGAGCGTCGA GGCAGGCGCGGTGTTCGCAGAGATTGGCCCACGCATGGCGGAGCTGA GCGGCAGCCGCCTGGCAGCACAGCAGCAGATGGAGGGCCTGCTGGCA CCGCACCGCCCAAAGGAGCCAGCCTGGTTTCTGGCGACAGTGGGCGT GTCCCCGGACCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCG AGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAA TTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCC CGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCG GCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT TCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGC GGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAG GGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCC AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCG CCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGC TCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCT GTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAC GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGG TAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC GGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGT AGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAA AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTC AGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCA AAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAA ATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAA ACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTA TCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAA CTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTG CGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCG TCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGA ATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTT CAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACC AAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCG ATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGC GCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGA TATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGT GAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCG

SEQ ID NO.	Description	Sequence
		GAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCT GTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTC TGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATT GCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCC ATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAAT ATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGG GTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAAT AAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGA CGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGC GTATCACGAGGCCCTTTCGTC
98	pLMTB8528	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CCCGCACCTCAACGGAGCGCTTTGCCGAGGTTATCAACAACCCCGAG ACCTGGAACGTGAGCGCACAAAAGCGCTTTATCGACCTGAACCTGGG CGGGTCCGGGGGCGAGCAGAAGCTCATCTCGGAAGAAGACCTCGAGC AGAAACTCATTAGTGAGGAGGACTTGGAGCAGAAGCTGATCTCGGAG GAAGATCTCTGAACTTTTGATGGCACTGTTTTTCTTTACTTTTATTT CTCTCAAAACATCAGAAGCAGTAATGTAAATATTCATTTTGTTTCAG CGCTCGTGCCAAACATCACGCGCTTGTTCAAGAGGCTATGCGAAGTG ATCATTGCCGTTTTTTTTTTCCTCAGCGTAAGCGGTGCATATGCTCA AAATGCATGTGCTTGTGGAAAATCAAGGCAACTTTGCATCTCCTGTT GAGAGTTCTAGTCCAGCAATCTATCCATGGCCTTTTCTTCTTTGGGA TACTTTTATCGCGATGCTTTGCGCTTCGTCTCTACCCCTTCTGTATC CTACAAAAATATCATAACGCCGATTATGTGCTCGATGCGCTGCTTCG AATAGCTCTGTTTTCTTCATTTAACACGATGGACTACAAGGACCACG ACGGCGACTACAAGGATCACGATATCGACTACAAGGATGACGATGAC AAGGGTGGTAGCGGAGGTGCTAGCGCCACATTTACGGGAGTCATACC TCCTGTGATGACGCCGCTTCACGCTGACGGTTCTGTGGACGTAGAGA GCCTCCGGAAGCTCGTCGACCATCTGATCAACGGCGGTGTATTTAAA TATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTT TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG CCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAA CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAA CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAG GCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAA GGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCA CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT AAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCT

SEQ ID NO.	Description	Sequence
		GTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC GGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT CGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCC TTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCAC GTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAG ATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATA TGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAAT GAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGA AAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCA TAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAA CATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCA AGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAA AAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTAC GCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGT GATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACA ATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCG CATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGG AATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATC AGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCG TCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACG CTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCC ATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAG CCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGC GGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCT TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCG GATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCG CGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTAT TATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTC GTC
99	pLMTB8529	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ACCACCTGTTTCACATCGTGTTCGTGGGAGATACGTCGCACATGTCG GGCTCAAGCGCTGGCCTCGGCGGCTTTAAAACTGCCCTCGCGCACCT TGGAATCATCGAGTCTAACGCGATGGCCGTGCCGCACCAGTCGCTCT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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100	pLMTB8531	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CCCTTCTTTTCGAGAAGAATATGGTCAAGCACCTCAACGAGGGTACG GATGAGGACATTTACCTGTTTGGGAAGGCAACACTCTCCGGATTTCG TAACAACCGTTGCGCAGGAGCATACCCCTACGACGTGCCAGATTACG CCTACCCTTACGATGTACCGGACTACGCTTACCCGTACGACGTGCCG GACTACGCGTAGAGAGCAATTGAGCGCGTGCGTGTCGGTGTTCGGGT GTGTTTATGGTCACTGAGGAGGGAGGAGAGAAATGCAGGGCTTCCTC CTCGTGTGTTGCTCTCTGTTTCGTTCTCCCTTCCCCGTAGCCTGCTG CCGCACTCTGCTCGTCCCGTGCGTCCAGACCTCTGTAGCCTTTCGAT TCCTTTATCTTTTTTGTTTTAATTTTCTTTTTTGTCCGTATGCTTCC CAGAAACGAAAAAAAGAACAAGAAAGGACGAAGTACAAGTGGATGTG CGCCGAGAGCACGTCTGCCCCCCTGTGAAGGAGCGCAGCGGATGCGT GCTCCGCTCCACTCGGTCATCTCTGCCGTCCCTCAGGCACGGCAGGC CCAGGAGAGTTCAAGGAGCTTGATGCTGCATTGCAAGGCGAATGCGT TTTTTTTTTCGTTCGCCCTCCGCCAGCGGTGCTCATGAACTGCGATG CACTCGAGTTCCCGAAAGAGCAGCGAGCCACTGTTTCTTCGTCGAGA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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101	pLMTB8532	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CTCCCACGAAACTCTACATCATGTCCCATCAAGATTCGATTGATATC GACACGGAGTTGGATCTGCAGCAGGCGGAGAACATACTGAATCACAA GGAGTCCGGAGGGAGTGGCGGTTACCCGTACGACGTGCCCGACTACG CCTACCCGTACGATGTGCCGGATTACGCGTATCCATATGACGTGCCA GACTATGCGTAGGTCGAACGCTCACTTTTGAGCACACGACTCTCTAC TTGTCTCCCGCTCTGATGTCTCTTTCCTTATTTCTGCGCCTGCAGGT AAAAGAAGTGCATCCGCATGGCTGTCTTTTAACGGGGACAGCGAGGC GTGCTGGCGGCAACTGTGTGCGCTTGTGTGCGCGCACGTTACGCTGA GAGAACCTCACATTTCCTTTTTGTTTTTACTGTTAATTTTCTGTATG TCCTTTTCTCGGCCTCTTGTCGCGTCTGCTCCCCCCCCGATGGGGCG CTGGCGAGGCGGAGAGGTCATAGGTTCCTCGTTATAAGCCAGTAGCG GTGCTGCACGGGCATGCCCTATGGAGGGAGAAGGGGTGCTGCGTGGA AAAGGGAGCGCAGTGCGCCAGAACACAAGCGTGCGCGCTTGTAGGTG CGCACATGTTTGCTACTTTTTTTTCTCTCCGTTCCGCTCTGGCTAGT GATCTTCGCCACTGCCGAGTGGGTGTTGGCCTGCTGCAGAGACTGCA ACATTGCTCCCGGTGCGGGCTGTGTGCGGTCATCGCGTGTGCGCAGC TGCAGTGTGCGGAGGGGCCGTCCAGGCACGGTCTTACTTCAATCTCC GCTGCTATGGGTGCGTCCTGATGAAGGCCCTGCCTACGGATCGCCTT TCTGTAGGCGCTCTTGTCCATCTCTGCTGTAGCTCAACTTTCTGCGC TTGTTTTTCCTCTTTTTGTTCTTCGGCATCTCCGCCTTTGTTGGTGA CTGGTACTGCCTTGCGTCTCCATGAACTAAAACAACGGCTGCATATC TTCCCCTTCCCTTGCGGATATAAAACTCGTACCTGTGCGACTTTCTC ACGTTCGCCGCACGCTCACGGACGTTCGACGTCCAATCGATGCGCGC ATGCGCACCATGACGCTTTTTCGAAGTTTCTACGCCTCGCCATCGTA CAGACACTTAAGCTAACAACTCGCTCACACACTCGAGATGGCTGCCC CTCGCGATAACGTCACACTCCTGTTTAAGCTTTATTGCCTGGCCGTG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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102	oLMTB228	CTTCACTTCGGCCGTCGG
103	oLMTB229	GATCGCCGCCGAGAATGC
104	oLMTB4949	GATCTGGTTGATTCTGCCAGTAG
105	oLMTB4978	GTGGGAAAGGTATCCTCTC
106	oLMTB5976	AAGTGGGCACTAAGCAGACAGCTCCTTGGCATACG
107	oLMTB6045	ACTATCATGCCCTACGTGGGCCACGCAGCGATGAG
108	oLMTB6517	CTGTGAATGTACGAGCCAAGG
109	oLMTB6521	GAATCAGTAGTGCCGCAAGC
110	oLMTB6775	ATCATCGCGATTAATAGCCGAATCAGTTT
111	oLMTB6776	ACATAGGAAGCCAGTTCATCCATCGCTT
112	IrA	TCGAGGGAGGAGGAGGAGGCGCGTAGCATTGCGTGCGGGTTATGTGT GCGTGCGTGTGTGTGTGCGGTGCGCGCCTTTCCTCTTTTTTTTCTCC CTCTCGTCGGTTTTTTTTTCTGAGGAGACGGGGCGAAGACGCGAGC GGGGGGCGGCGTTTGTGTGTGTGTGTGCGCGTGTCGGGGGCAGCGGT GTTGGCGGAACGGCCAACGCCCTGCCCCCTCCCCGCCCTGCGACGTT TCTGCGCACCCGTTCTCTCCTTCCTGCGTGCGTGTCTGCGCGCATGC ACATCTGTCCGCGTGTGCCGCAGCGCTGGTATTTTTGTGAGGGCAGA GCCCTGCCTCCCCGCCTCTCTGCCGTTGGCAGGTGAAGCGAAAACGA AGCGAGAGGGCAGTCTGCATGTGTGTGCGAGGGCATGCGGAGCCCCC CTCCCCCCGCCCCCTGCCGTGCTGCACCGCTATTGTGGCGTCTTCTC TCGTTGTGCGCAAGTGTGGCTGCACCACGGCCGCCTCATGTGCGTGT GTGCGCATGTACACACACACACACACACACACACACACACGGGCAGG CGCACGCTCCTCTCTCTTCAGGGAGCGCCGCCCCGCTGGTGTCATTG GACGAGCATCCGCCGCGCATCTCTTCACCCCTCACCCCTCATCCCTC TCCCCTCTCCCCGCACACACACGCAGTCCTTCGCTTTCACTCTTCGA ACAAACACCTCAACCATCTTATCACCTTTCTCTCTTCCTTGTCAACC
113	IrB	GAGACAAACGTGGCGGATGTGATGTTTTCAGTTTACTTCGCCTCTTT TCGTTTTCCTTTCAGGCGACTTCCCTTTTGAGTTTTCGTGTATGCAA TTGTTGCTGTTCTACTGTGCAGTTGTCACCAGCGCCGCTTTTGGGCT TGTGGCGTCGGTGATTCTGCCTACGTGATTCTTCTCCACGTTAACCA CACGTGTTATTGCCCTTCGCTTTTGCGTGCGCGGTCTGGGCAGCCAC TAGGTATAGGGGTGTGGTGGAGTGCACCCGTGACGGTGACATCCCTT CGACCCGCGTCTGCTGCCTCAGACGTTCGTGGAGAGCTGACATGTCG ACATCCCTTTGGTGTGAGCATTTGTGAGCGTGTGGGTGTTTAGTGTT

SEQ ID NO.	Description	Sequence
		TTTGTTACCGGTTTTGTTGCGCTTGTGTGCTCTAGTAGTGTTTGTGC GCGTGCGTGGGGCACTATGAAGCAAGCTGCGGTAGATGCGCTGCGTG GGGTGGTAGGCTGCAGGACTACAACCATTAAGATTCCTCTCTCTCTC CTTGGCTCGCTCTACATTGACCCTCTGCGGTGGTCTGCTTCTCTACA ATCGATATGCCCGACACCTCCCGTTGTGTGTTCGTTCTCCTTTATCA CTAGGCCATTGCATTCGGCCCTGTTGATGTGGCTACGGTCTTAGACA CGCACAAATGGTTTGCATTATTTATCGGCCATGGTGTGTGTCACACT CGCTTGATTGATTTTGTTCTGATGTGCAGCATGAAATGTCGGGAGAA TAAAACATAGTGCCTTCATCATAGGATGACGGATGCTTGAATCCGTC TTTGTCTTCTGAACAACTCTCTGCAGAGGGCGCGGGTGGCTGACTTC TCTCCCCCTTCGTATGGCGAAAGGATGGCTTTGGCGTCCTTCCGGGC TTCGCGCGCATAGGGGAGCAGAATATGTGCTGCAAAGAAGACGCCTG GCGGCTGCGTGCGTGCGTACGTGTGAGTGTGTGTGTGTGAGGGCT ACGCTGCCGGCACCACTACTCGTGCCTATCTTCACCACCTTCTCGTT CTCCTCCGTCTTCTCTTTTGCCTGGTGAGCATTTGTGTTCACCATAC CTCAACGCGCTTCGCATAGCTGCCCAACCTCCTACTACTCTGTTTGG CTAATCTCAGCTCGTTAGTTTCTCTCGTTAATCATAACGAGTTTGCC CCTCCCCCCCCATTGTGTGTGTGTGTCTTGTAAAAAAAAAAAAAAAAC ATTATCTTCTACCTTTCCGCGCCTCACATCCGCATCTTTCGTGTGCT GCCCACTCACCATCACCGGCCTCCTTCGTTGGCAGAGCAACATTTGT TCATGAGCAGCTCTCCGTACTGTGTGTGTGCCCACTAGCCGGTGCAG AGTAGGAGCCGCGCTTTTGTTGTTGTACGTATCTTTTGACGTGGGTG TGCGTGCAAGCAAGGATCTACGCGCAACAAGTAGCAGGCAAGCGGAT CTGTTCGCC
114	IrC	CCTCCTCCTCCTTTCTTGTTCCTTTCACGTCGCCTTCTCGGTTGTAG CTGGCAGACGACGAGTCTTACTTTTACGTGTACTTCTCTATAGATGA TGTATGATCTCTCTGCATGCGTGTTCGTGCATGTGTCCGTGTGTTGT GTACGCGTGCGTCTCGCCTCAGCTCTCCGCGTGAAAGGGTTTGACTG CCCATGATGCGTGTGTATATCCACGCGCAGGCACGCACACACACACA CACACACACACACACAGGCACACACAGGCACACAAACGCATCTCAGG CCGAGCCGCATACGTCTCTCGCACGGTCTCGTTTATTTGATCATGTA GTTGAGTATTAAATTGGGAAGACAAAAACATAATAGCACGAAGAGTC GGGCACGAAAAGCCCGATCTCTCTCTCTCTCTCGTGCGCGCAGGG GCGTGTGGGTGCACGACGACGAGGACGGAGGGGGGAAGGGAGGCATA AACGGATCGATCCCCCATCGCACATGCGGGTACGAGCATTATCTGCT GTGTCTGGTCCTTTATCATATCGCTACCCGCCCGCCCCCCGCCCCCC TCCCCCCCCCCCCCCCCGCGGCTCCTGTCACTGTCGTTCCTGCGACTC CCCACACACCCGCGCAACGCTCATGTCACGAAGAGAAAAGTAGAAGG CGTGGCGATGCGTTGCGCGGCCCCCTGTCCGCTGGCATGCAGACGTC GAGCCGTGGAACGGATGGTAGCGAGAGACAACGCGGCGATGCAGGAA AGGAGATTTACTGCAGGACGTCTACACACGCGCGCACACCACTGCGA ATGGCACCGTGCTGAGGAAAATTGGGGGGGAGGGCGCACGGGGGCGG GGCAGGAAACGGTTGGATCAGCAGCACTCTCAACTTGTGTCCGTATT GCGAAGGAGGGAGAGGAGCCTGCCCGTATTATGGGCGCTGAAACGTC GGAACCACCTATGAATCCCACTTCTGCGTCGCGGAGGCGTACTGCTT CCGACCACCTCCGCAGCTCACGCGCGTCGAGCTCCCTCCCTTTCCCC TTCTTTCCGTTGTGTGTGTGTGTGTGTGTGTCTTGTCACGATGCA TGGCCATCTCTCCTCCAACCCTCCACGCCTTCCTCTCCCCCGCCCAT

SEQ ID NO.	Description	Sequence
		CAAACGCGCTACGGCCACAACCATTTCTTCAAGTATCACATCCACCA CCACTCTTACCCACCTACCCTCTTCGACTCTGACACAGCCACTGACG CCCTCTCCGCCTCTCTCGCTCGCTGCACATTGACTCTCCACAGCCCC CCCTCCCTCGCACAGCCAGCCCCACCCACCCACCCACCCACCCACCG CTCTACACACCTCCACAGCAGCC
115	IrD	GGAGACTGAGCTTTAGCGAGGGAACCCGCATGGCATACGTTGCCATA ACAAGTGACCATCTACTCTCCTTAAAGTCATGGGGGTGCTGCTGCTT GGCCGGTGCTGATCACTCTTGTTGAGGTTCCTTCAGGTGCGGGGACT CTCTTTGGCGCCTTCCCTGCTTGCCGTGCTCTCTCGACTTGTTCTAA TTCCCACGTGTGCTCTCTTCCGCTTTCGTTGTAGTGGTGTACGCTGC GGTTGAGCTTGTTGTGCTTGCGCTACATTTCTCTTCGAAGGCGGAGG CAGGCGCGCCTGCGCAGTGCCGTGACGAGAGCCACTGCCGTGTCGAG CTGCGAGCAAGAGCAGTTAAGGCAAAAGGGTAGGTGAGAAAGATGAC TCTGTGCGGTGCTCTCTTGTCCATGCCTGTCCGTTGTTGTCTCCCCT GTCTCTCCCTTTTTTCGGCTTGAGTGACGTTTTGCTGCCTTTGTACG TTGTTGTAGTGTCCTTACTGCTCTCGATTGCCGTCACGTTGATGCCC CTATGTGTCTCCTTTTCTTGCCTCGCACATTGCGGATGTGCTCCCTT CTCCGCCCCCTTTTTTTTTTTTTTGCCACAGCCGGTGCTGCCTTGTT GCGAGAGCATGCGCATTTGGAACAAATGGCACATAGTCGTAGCATCT GCGCTCTGGCCTCGGCGCCTCTCTACACCTTTGCTCACCGTGCATCA CGCCATCTACACCATGTTCTCTTCGTGTTCTGCCACTCTTTTAAATG CTTTGCCTTCCCTTGGAATCCCATGCTCAGCCCTCCCCTGCTTCTCA CGGTGCCTGTGGCTCTCGGCTGCGCTCTCCTGTCGCCTGTTCTTCTT CTTCCGTCCCTGTGGATGCTGCCGATTTCCCGTCTGCCCCCGTCTTT CGTTTGCCGCCTCCCCCTTCTGTGACGAATGCCGTCTCTGTATCCCG GACGCTCCCTCACGCCAACCCACTCCTCTTTTGCGTTCTTGCGTGTG CGTCGGGCTTCTCTCCCTCCCCCTCCCCCTCCCCCTCCCCTGCCTAC CCCATCACCGATGGGTGTGTGGGAGAGAGGTGGCAGGGGAAGAGGGA GTGCAGATAATGTGAGACAGAATTGAAATATCTGCTCTCCGACACAC AGGGAGTAAATGCATTCAACAGGGATGGTAAGGACACGCACTGGCGT GACATGGAGAAAAAATAATGGAGTAATGCATGCAGGGCTGAACTCGG CACAGAGGTACGCACCCGTGGGCACCCTCTTCTCTACGGCCCTACCT CTTTGTCTCCAATCGTTTTGTCCCCGTATGTCATTATTATTGCTCAC CTCGCGGCATTCTTGATGTAGCCGCCTCTTGACATGTATAGTGTTGT TCATTAGTATCCACCGCAAGAAAAGAAATCCTGCATACCACCAATCG CGCGCACTGGACGTTGCCGAAAGCAGTCAGTGGGCACCTTGGACGTT GCCGCCGGTGTGGAAGTGGCCGCGTCGCAAGCAGGCCTCCATGACGT TGACTGCACGTCCCTCCCGGAAAGGGGATGGCTTTGGTGCCATTTAG GACACAAATGGAGCTTCTTGTCGACCCTTGCTTCGAGGAATGAGGCT GCGTGTATGTGTCTTGGTGACCCCTTTGGGCTGTGCAGCTTGTGGCG TGTGCGCACCGGCGTGTGCCAACGCCCAGGTACTGTGCGCACGTTCG TATCTCCATACGCTAGCTGACCGAGACGCATGCCCTCCGCCACCCTC AGTGGCGCGCACCTTCTCTCGTTTGAGCTCTTTATGCTCTCGTGAAT GGCACACAACATCCCGTGACTATCACGATGATCCTTCTCAAGCCACA CCGCTTGCCTTTTCTACAGCTCTGCGTTCTCTGGCCCATCCTCCTCT TGTTTGCTTTCCCTCTTTGCACATCCGTGTGCGCGTCCTTGTTCTTC TCTTCTGCGCACACTATTCTGCGCCCGCGACCCGCGCTTCGACTGCT GTCGGGTCATGCCTTGTGCTGCGCGTTCAGCTCTTCATTGCCCCTCG

SEQ ID NO.	Description	Sequence
		GCCTTGTACATAGCGGCTCTCCGTCATCGACGTTTTCCTCTCTCTTC AGCTCTATACACTCCCTCCCTTGTCAACACACTACACTGTGTCTCCC CCTTTCATCTCTCCTCCCCTGTCACA
116	IrE	TTAGCGCTCCGTAGCTCGCTGCGTATGAGAGGTACTGAGCTCCAATG CATCACACGGCGTACGGCAACACACACTATCTTTTCAGTTTATTTTT TTAATTATCCCTCCAAAAAGAAGCAACTGACACTTCAAAATATTCCC AACAAGGAGCGTGAGGTCAGTGACCAGTCTCGGACTTCACACCGCGC ATGTAGAAGCACGCGGCTTGCGCGCCAGGCTTCTTTTGGCAAACCAC GCTGCACAGAATGTCTGTGTACAGCAGCCAGGCTGTGATCGATCTAT TATGCTCGCCCCTCGCTCCTCCGGCATTCTCGAGTCCATGTCGAGCT TGTCTGGCTCCGTGCACATGCAAGCGTTTGTGCGCGCCTCTAATGTA ACCACACGTCAAAACATTGTGTGTCTTCCGAAGTGGGAGACACCGGG GCCACCAACTCCGGTGGTTTACAGCCTCCTCCCTCAACCAACGCTGC CGATTGTACCACCTTTCATTGCGTCTTTGTGCCCCTCCCTATCTTCA TGTTTCCACTGCGCTTCGTTTCCGAATACTATTTTCGTGTACTGTTT CATCACTTTCTCACAACAGCTCTTTTTTTTCACCCGCAGAAG
117	PolB	GCGTGGGGATGGATCGCGAGGGACGCGGGGTTTGAGGGCCGTGGGTG GTGTGGAGAGTGTGGTTGATTATTGTATGGTGGTGAGGGTGGAAGGT GTGGCGGGGATGGTGGTGCGGTGGTGTCGGAAGGGGTGTGTGAGAGG GCGCGGGTCCTTGAGGGAGGGTGGGTGTGTTGTTGTTTTGCGGGTGT TATCCGGGGCTTGGGTGTTGGTGTGATTGGTGACTATGTAGGGGTGA AGGGTGAGTGGAGGGGGTCGCCAGAGGCGTTCCGTTCTACGAAGCTT CATTCCTATGTCCGACTCCGAAGCATGCCTGCAGTTCTGCTGGCTAT GTGGGCGTGTCTGGGCAACGACTGAATTGAGAAGGGGAGTCGAAACG GTGCGTGGATGCTGTGTTTGTGCTACACACAAGCAAAGGCAACAACA CAAGCGCATCGAGCCAGACGAACCAACCCAATATTCACACAACTGTA CGTGGCCGCGCGCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGC CACCACCACGTACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCT TTTGCGTTGTGCTTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCG TATCCCGGGACCTGCGGGCGGTGGGTGCCACACAACCCGTCACATTC AACATCACTCATACATCTCACCGATGTGTGCGTGTGCTTGCTGTGTG CGTGTGTTGTGTGGCGTCAAACCTGTTTGAAAACACACCCCTAGCAC TATTCGACCGCGAAAGCGCCCCCCCAAAGGGGCCGGTGTGCAATGCG AGCTACATGTATGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTG CTGAACATGTTTTGTGTGTGCTGCCGTGTCTACACGTTTGCAGCGGA AACTCGGTTGAACCAGAAACAGAACTTGATTGTTGCTGCATTTCGAG GAATTTCAGCCAAACAAGAGGTCAACAACCAAGCCGCGTGTACACAT ATACACACACCGCGTGTATGTATATATGCGTTTGTTTTGTTACCACA AATACTGAGTTGTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGG AAATACAACAAAATACAACACTTGATCATCAATGCGCAATGTGCGCG TGTTGTGTGTGTGTGTGCGAGCGCACACACACATGCACACGACTCAC GTTGTCACACAATTGAGAGTCGCAGCCTGACCGCATCACACATCAAG GCGTTACAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTCGTGTGA CCGCGTTGAGGGATCTAATGGATTCGGAACTTTGGTCGTTTGGTCTC TCATGCTGCCCAATCCCATGCGCTTTTCTCCGTGCCTCTCTGTCTCC CCTTCCGTTCTATTTGGACAACGATGTGTACTGTAATGCGTGCGCCA TCTGACAACGAATAGATCAGCAGCATTCGCACACTTGCACATACCCA GTGAAGCTTTTGTGTCTGTCGTATTGACAACACCGACTGCAACAAGG

SEQ ID NO.	Description	Sequence
		TGTAGATAGAAGTTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCT CCTGCTTTCCTTGCTGTGCCTTGCCACC
118	5UTR	AGTCGCAGCCTGACCGCATCACACATCAAGGCGTTACAGCCTCTCCG TCTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTTGAGGGATCTA ATGGATTCGGAACTTTGGTCGTTTGGTCTCTCATGCTGCCCAATCCC ATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCCGTTCTATTTGG ACAACGATGTGTACTGTAATGCGTGCGCCATCTGACAACGAATAGAT CAGCAGCATTCGCACACTTGCACATACCCAGTGAAGCTTTTGTGTCT GTCGTATTGACAACACCGACTGCAACAAGGTGTAGATAGAAGTTGGC CTTCTCGCTCGCTCGCACGCTCTTCACGCTCCTGCTTTCCTTGCTGT GCCTTGCCACC
119	PolA	GCGTGGGGATGGATCGCGAGGGACGCGGGGTTTGAGGGCCGTGGGTG GTGTGGAGAGTGTGGTTGATTATTGTATGGTGGTGAGGGTGGAAGGT GTGGCGGGGATGGTGGTGCGGTGGTGTCGGAAGGGGTGTGTGAGAGG GCGCGGGTCCTTGAGGGAGGGTGGGTGTGTTGTTGTTTTGCGGGTGT TATCCGGGGCTTGGGTGTTGGTGTGATTGGTGACTATGTAGGGGTGA AGGGTGAGTGGAGGGGGTCGCCAGAGGCGTTCCGTTCTACGAAGCTT CATTCCTATGTCCGACTCCGAAGCATGCCTGCAGTTCTGCTGGCTAT GTGGGCGTGTCTGGGCAACGACTGAATTGAGAAGGGGAGTCGAAACG GTGCGTGGATGCTGTGTTTGTGCTACACACAAGCAAAGGCAACAACA CAAGCGCATCGAGCCAGACGAACCAACCCAATATTCACACAACTGTA CGTGGCCGCGCGCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGC CACCACCACGTACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCT TTTGCGTTGTGCTTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCG TATCCCGGGACCTGCGGGCGGTGGGTGCCACACAACCCGTCACATTC AACATCACTCATACATCTCACCGATGTGTGCGTGTGCTTGCTGTGTG CGTGTGTTGTGTGGCGTCAAACCTGTTTGAAAACACACCCCTAGCAC TATTCGACCGCGAAAGCGCCCCCCCAAAGGGGCCGGTGTGCAATGCG AGCTACATGTATGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTG CTGAACATGTTTTGTGTGTGCTGCCGTGTCTACACGTTTGCAGCGGA AACTCGGTTGAACCAGAAACAGAACTTGATTGTTGCTGCATTTCGAG GAATTTCAGCCAAACAAGAGGTCAACAACCAAGCCGCGTGTACACAT ATACACACACCGCGTGTATGTATATATGCGTTTGTTTTGTTACCACA AATACTGAGTTGTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGG AAATACAACAAAATACAACACTTGATCATCAATGCGCAATGTGCGCG TGTTGTGTGTGTGTGTGCGAGCGCACACACACATGCACACGACTCAC GTTGTCACACAATTGAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCC TCTCTCCTCTCTCCAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCT CTCTCCTCTCTCCAGAGCTCGAGCCACC
120	UtrA	CTAGCCTCGGAGATCCACTAGTTCTAGTTCTAGGGGCCGAATTCAGA TCCTCGTGTGAGCGTTCGCGGAATCGGTCGCTCGTGTTTATGCCCGT CTTGGTGTTGTGCTCGCAAGGCGGTGCAGCAGGATACCGTCGCCCTC CTCTCTCCTTGCTTCTCTGTTCTTCAATTCGCGATCTCACAGAGGCC GGCTGTGCACGCCCTTCCTCACCCTCCTTTTCCCACCTCTCGGCCAC CGGTCGGCTCCGTTCCGTCTGCCGTCGAGAAGGGACGGGCATGTGCA GCTCCTCCCTTTCTCTCGCGCGCGCATCTTCTCTTGCTTGTGGCACT CACGCTCATGCGTCAAGGCGGCCCCACGCCGAGCCCCTGCGCTCCCT TCCCTCTTGCGCATCCGTAGCGCGGATGCCGTCGATGCGCAAGGCCG

SEQ ID NO.	Description	Sequence
		GCATGAAGGAGCGCGTGCCCTCAAGAGGGCACACTATCATGCCCTAC GTGGGCCACGCAGCGATGAGGCCGGCTTCGGCGGAGATGCGTCACGC ACGTGCCAGATGATGCGCTACGCCTTCCTTGACTTGCGCCCCCCTCT CTTCCTCCGTCTCTCACTCTCTCTCTCTCACACACACACACACACAC ACACACACACAA
121	IrLmA	TGAACTGCCTGTCGCAACGACCACGGCCCTCTCGCTTTCCCTTGGTT GGTTCGTCAAACGGCTGAACCGGCTTCTCTTCCTCTGTCGCTCCTTG TCCTCATTTCTGTTTCACACGACATACTTGTCTATTATGTCGCTGCC TGTATGTGTGTGTGTGTGTGCTGCAATGACGGGTAGGGGGCTGAGGC GGCAAGGTAAGCAGGGGCGCCGAGGCACGGGTAGAGGCCAAAGGCAG GCGTCGGCGATGATGGACCTTCCTCGACTTTCTTCGTTGTGGTCTTA TCTTTGCTCGTTTCAATTCTTGTTTTCATTTCTCGTCGTCTGAAAAG AAAGGCAAAAAAAAACAAAGAAGGGGCGCAGAAGAGCGGGATCGCGA CGTGCGTACACGTATCGAGGTCGCTTCCCTTTTTTGCGAAGTCTTTT CGACCTCTCGTACACATCTTTCGTGGGCTGTTGTGCACCATGTTCAG CGCGCGACGTCGAGCTGTGCTCGCTTCCTGCAATGACTTCCCGCCCT TCGTCTTTGTCTTCCACTGGAAGAGTGTGGCACTTCACTCGCCAGTG ATGAGGGGAAGGGGGAGCGGACCAACACCGTCTTTTTTATAGCGATA AGGAGGTGAGGAGGTGGTCTGTGTGGCGTTCCTCGTGATGATAGGCT TCATGGTCGACTTACTTACCGCGTGAGGAGCAGCATATCCATCCACC TCCAAGTTCCTCGAAGAGGTCAGGAAACGCCACTTCTCATGCCCCGC CAGTCTCTTGTGTAACCTTCGTCCCTCTTATTCTTCATCTCACTCAT CCGTGCCTCGTTGACCACTTCACCGTAACCCGCTCCCTCCCTTTCAA TCTCTCCTGCCCCCCCCCCCCCCACACACACACTATCGCTCACTCGC GCCCCTTTGTTCGTGTTTCCCTCCCTATCATATGCGTGCGCATTCCA TAAAGTGTTGCAATC
122	IrLmB	CGAGCGCGTTGCCTCTGCGCTGGTGAACGTGCCTGCGCACTTACATC TCAGCCGTGCTTTCTGGGAAGACCTTCTGCGACGCGGGGCGCTGTGC TGGTACAGATGGAAAGATGTGCGCCATCACGGATGCATCCTTGCATG GTGCGTGCTCACGTGCTCACCACAGTTTGTGTGTGTGTGTGTGAG TGTGAGTGTGAGTGAGAGAGAGAGTGTGTTTCGGCGCACCTCCCATC CAACAGTGGCGTGAACGGCTTTCTCTGTATGCGCCCTTTCGTTTTAA CTCTTTCTTTTTCCGCCTTTGTTTTTTGTGATTTTTGATGAACTCAA ACACAAAATGAACATCC
123	IrLmC	AGCGGCTTGCCGGATGCCGCGTGAGTAGGAGGGTGGCTGCCGCAAAC GCTGACCTCGGCGACTGCGGCGTGGCGCTCCCCTTCTCCTCCTTTTC CGGCGGTGTGTGTCATGCATCTGCGTGACTCCTCCCTCTCATAGATG CAAGTTTTTCTTTTTGACCCCTCCCTGTTTGACCTGCAGCCACACGG ATCGCTGTGCGACGTGGACGGTGCGTGCTGACCGCAGAGCAAAACAC AAGACACATTCTGCACCGCCGTTGGTGCCACCTGCGGCCTGCGACGC CGCCAGTGATGCCCATCTCGCCCCGTTGCCCTATACACCCTGTGAAG AGAGGCGCCGCGGTGCCGACGCCTTCTAGCATCTCTTCCTTTCCCGT GACCACTGCATGCTTCCTCGCTTTGCCTTCCTGCCACGCCGGCTTCC TCAACTTTCCCTTCCCTCGCCACCTGCTTTTTCTCCTCATGGGTTCT GCGGCAGCTTCCCAGCCCACCTTCGCTATCCAGCCACTCTCGCTCTT CTACATCTCCCACCCCCTCACACCGCC
124	IrLmD	GCGGCGGTGGCTGTGCCGCGGCACCCACTGCCGGCTCGAGCGAATGC CTGGGCGCGCTGTGCTGCCACGGCAGGCATGAGCGACCACCCGCTTG

SEQ ID NO.	Description	Sequence
		TGTGTGCCCGCACGCGCTGCCCCCTCCTCCGGCAATGTCCTTTCATC TTTTTCATTTGTGATTTCCCACTTCCCTGACGGAGAATGGCCGATCA TCTGCAGTGGGCGGCTCCTTCTGAGCGCGCGCCGCAAAGGGGGGCGG GGCGGGGCGGGGGGGGTCGTAGGGCTTTCGTTGCGGGTGGCAGCAGGC GTGAGAGCGCGCAGCGAGAAAGGGAGAAAGCGCCCCTGAAGCCCTCA CGCGCGTTGCTCGACCGACTAGCGGCCCTGTGCCGTGCTGGCGGCTG GGCTGCGTAAGTGGCGCGTCGTGCTGCAGCGCCTCCCCACCCGCTGT CGTGCGAGGCGTGTAAAGCGTCACTCTCCCCCTCCCC
125	IrLmE	TCAGCGTTCCGTAGCGCGCTGCACATCCGGTACTGCGTTCCAGCGCA TCACGCGACGCACAGCAACACAAATTTTCGTTTTGTTTCTCTTCCAT TCGAAAAAAAAAAAGATAACACCCACCCCACTTAACCTCCATAACAAG AGAGCGTGAGAGGAGAGTCTGCTCTTGGCCTTCACACCGCAAATGCA GCAAAACGCGGCTTGTACGCAACGCATCTCTTAGCACGTCAAGCTAA GCAGAATCTTTGCGTACGGCAACCAGGCTCTCATCGACCCGTCGTTC GCTCCTCGCTCCTCCGGCATTCTTGAGCCACGACGCGTATGCTTGGC TCCGTGCGTCTGCGAGCGTTTGTGCGTTTCTCAAATACAAGCCGAGG GGCCACCACGTTTATCTTTGCCGCTCGACGCACCTCCTTCAACTACA TGTACTTACGACCCCTCGATCTAAAAACCTCTGCCCATCGCATCACT TCTCATTCTGTCGTTGTGCCTCTTTCTACCTTCATCTTTCGCTTGTG CTTTCTTTCCTAATACCCTTCTCGTGTAATCCCTCATCACTTTTCCT CTACAGCTCGTTTCGTTCCCTTGCCGAAA
126	IrLmF	GCGTGCGGTGCTCCGCCGCCCGCGCCCCCTCCCTCCACCCCTTTCTT TTCGCTTGTATCCCTCCCCCACGCGTCCCGCGGGGCCTCTCCTCTTT TCCCCCAAACCCACGCACGCCCACGCCCCCCTCTCTCTCTCTTTCGA TATATATGCGTGTGCGCGTGCGTGTCTCGTAAACCACCCTGTAAGGC GCAGAGCCGAAGTATGTGTAAGCACAACGCCCGTGGCGCGCGCGGGG ACGTGCAGGCGTGCGTGCGGCTGTGCGCGTGTCTGTGCGTGCCCCCT GCGCGACGCCGCGGTGCGTGGAAGGAAAAGGTAAAGCAATGTCATTC CCCTGAGAAAATGAAGGTAGCGTGACTGGCCCGTGAAGCGACCCCCA GGCAAGTAAGCATGCGCGCGATGGTGCCCCCGAACGCGCGCCACTTA GGACTAAGCAGACGGACATGCAGGCGCACAGCCGTGAAACCGAGCGA CTTTGGCGGGCATGGGCGGGGCGGGCGCTGCTGCTGCCCCCCTCTCC TCCCCCCCCCTCCCCGCGACCCGTCCCCTTGATACCGCCAGCCTGCG TGCGGCTGGCGCGTGACTGCCCATGGCGCGCGCTGCCGTGCACCCTC TCTCTCTCTCTCTTCCCCCACCCCTCGCGCTCGCTTGGCCGAGCTGG CGGCTGCTGCGGTGGCCGTCGCGCCGCACCCCTCCTCTGCACCACCT CCGCCGCACTCTCCTCTCTCTCCTCTCTGTCCTCTCCCTCGGTCTCT CCTCCCACCACCGGCACACGCCGCCCCCGCTTGCCTGCCCGCCGCGC GCAGATAACCAGCTCGCTATCTAACATCACGCTCTCCGCTATTCACC
127	IrLmG	GCAGCCCCTACGATGATGAGCGAATACGTGGTCGGGGGAAGGCAGAG GGCAGTGGTGCTCTGCACGTGCTTGGGCACCGTGTCTTCTTAGACGA GTAGACGGTGCCGGGTGGGGGAAGGTGGAGGGGGGAAGAGAGTTTGG GCGATGAGGGAGTCGAGGCATAGCACACGCTTATGTGGCTGTCTGCA TGTAGGGTATGCCGATCTCGGTGAGCTCAGCTCTTGCAGGCGCATAC CCTACATTGACCCGCTGCCGCGTGTGTGTGCTGTCCATTCTCTCCAC CCCACCTCCACTCGTACTGTTGCCTCATCTCTGAGCGGGTCGCCTGC GCTCCTTCCTCCGCCCCTCTTCCTCGCCGTCTCCATCAGTCAAGTGC ATCGGGCCGCCGCGACGTCTGGCCGCTGTTCGTTGGTGCATTTCCGG

SEQ ID NO.	Description	Sequence
		CAGCGACGGCGTTGCGTCGGTGTGTGTGTGTTTGTGTGTCTCT CTCTCGGACACACGGCACGTATGCGAGAGCGCGATGGGGAATTCGCT GGACAGTGTGTGCGTGCATGCATGCGCACTCGAGAGCCTTTCGTCCC ACCACCCTCCGCGTGCACGCGTATCGATGCCTGCGTGCATGCGTGTG TGGTGGGTGGTGGGTGGGGGAGGGTGTTGCTTCTCTCTTACAATTTT TCTGTTGGTTTCCTCGTTTCTTCTT
128	IrLmH	GTCCTCCGGCTTGACAGCGCACACGCGCCGCTGTATGTGCGCGTGCG CGCGGGTCCCGACTGGGGCCGGCGATGAGGCGCATCATACCTCCATA GAGACCCTATTTTTTGTTTTATGGCTTCTCAGATGACCACTTGGTTT CTTCCTTCCTTCGTTTGGTTTGTTTATCTCCTCCCCTTCGTTGAGGG TACGAGTCAGGGTAGGCTCGGACAAAACTTACCGCACCCGCGATGGG CCACAGCTGTCTATCGCTCTCGCTCTCTCGGTCTCCTGACCGGGACA GGTTGTCGCCCCGTCACGCGTACCGGCGTGCGCGCCCGCTCTTGCGC CCTGCCCCACCATTCGTCGAATGATGCGCGACGCGCATGACAGGCGC TGCTGCAGCACTGCTCCCTGCGGTTGCTGAGTGCGTACATGGCGTTG CTACTGATGTGTTTGCACTGCATCTCACCTCGCTCTCTTCACGCATC CGCTCGCCCTTCTTCCCTCTTCACGAGACTGCGTCGGTCTTTTGGTG CTGCTGTGGCGCAGCCCGCCGCCTTCCACTCCCCCCAAACACACACG TTCATACGTCCACACAGCACTCGTGCGCACCGACACACCCACACCCC CTCCTCTCTCTCCTCTCCCCAACC
129	IrLmI	GCCTGTGTGCTGCCTCCTCATTTCCGGCGGCTCGCACGCGCTCGCAT GCTTCGCCACACAGACGTCCTCGTGTCTACTGAACAGCTAACGGATT TCCATGTCATTTCTCGTTTCCCATCTTCAAACACAAGAGCACCACTG CAACGTCAGCAGTGAACGCCCAACACTGCGGAGAGCGTGGTCACGCC CCTTCTGACTTGCACCATGAAAAACGATGTGAGGCAGCGGCGCGTCC TCTCTCCCGTTCGCTGACTTGCCCCACGCGAGTATCTGCGCGCCGGC ACCCCTCTCCGCAGCTCGGTTTGCCTGCAGGTGTGCGCTCTCGATAC CTCCCGCCTCTGTCATTCTGTTTGTCTCTTCCTCCCAGCTCCACTCT TCTTCTTTTCCTGCTTCTCCGTTTGTTTGTGCGGCGCAGTGCCGCGA CCAGCACATTTTGGCTCTCTCTCCGTTGCTAGCACCAGGGGTCGGGA TCGACGTGCGCGTTGCTCCTCCGCTCTCCCCATTTTCATCTCCTTAT TCTGCTTTGTTTTGCAAACTCGCCGGCGAACGCTGTCAAATCTTCAC GGGTTGTTTTTCTCTCTTCCTCTCTCGTGGAACGCCGGCGTGCCAAG ACGAGGCC
130	IrLmJ	TTCCTTTCACCTATACACGTGGTTCATATATTATCGGCTTTTTACCT GAGAGAGCAAAGAAAGCTTATTAGCACGGAAAAACGTAATGTGCTGA TAGGGGAAAGAAACAAAAACAACCGCAGCCGAGACATTTTGTTTGTG TTGGAGGAAGTAGAGGAGGCCCATCGGTGTCTAGAAGACAATACCGC AGTGTGAGACAGTGACAGAGGTGGCAGAGGAGAGGTAGGGGGAAGCT CAAATGAGTGCTGTATCATGTATGCATGTCTCTCTGGCTGCTTCTCA GCTTTTCGTTCCGGCTTCCACTGGACTGTGGCCCTGCTCCAAACCTT CGACGTGGGATGATTCGATGACTCTTTCTTTTATCAGTGACTGATAC CGATACTGTGCTGCAGAGAATCGAGAAAAAAAGCGGAAAAGGCGGCA GGGCCTCGATGGCAAATCGTTTAGTTGTGTGTGTCAGTGATGCCTCT CTAGGTGGCGGAGTGGGGCTGCACGTGATGGACGACGACGTAGCGCA ATACGCGCCTTCAGTCGACAGATCGAACAAGCACCGTGCTGGTTTCA GTATCCCTGCGCACTCTCCTGGTTATGGGCGCCTTGAATGCGAGCCT TTGTTTGAGCTCCACTTGCTGCTCATCAAATGGCCACACTTCCGACC

SEQ ID NO.	Description	Sequence
		TCCCTTGCTCTTTTTTTTTGCACTTTTGTGGCACCTGTGTCCTTGCT GTCGGTCCTTTCCAACTTCAGCACACGGAGAAACCACCCTGACTGTA GCAATCACGATCCAGTGGGGACAAAGGAGACGAGGTGTCGAGTGCCA TTTCGACGATCGGA
131	IrLmK	GGTAGACTCGTGCCGCGCGCTGATGATGTAGGTGCACGCGTGCGTGT GCTGCAGCGGAGCCGCCGCCACCGCGACTGTGTGTGTGTGCGCGCGT GACGACCGGCTCGAGGAAGGAGGAGCGCGCGTGTGCGTGCGATGCGC CTCCTCTTTTTTTTTCGCCCTCGTCGGTTTTTTTTTTTCTGAGAGGA CGGCGGCGGCGGATGGCGGGGCGGCGGCGCTGACGGAGCGGCCACGC TCTGCACCTCCCCGCCCTCCGCCGTCTCTCCGTTCGCCGTCCTCTCC TTCCTCGTGCGTGCGTCTGCCGCGCATGCACACGCGCGCGCGTTGCC GTAGCGCTGTGTATCTGTGGAGGAGGGCCTTGTCTCTCCCTCCCCGT CGCTGAGAGATGAAGGGGCAAAAAGAGAGAGCAGTGCGCATGTGTGC CTCCGCTCCCTGGAGCTCCCCACGAGCCCCCTGCGCCACGCACCTGC GAACCTGCACAGCGGCCCACCTGCCCGCACACGTGAGCAGAAATGGG TGTGTGGAGCGGGTGATGTCGGCGCGCACACGCGCGCGCGCTGACCA CTCCGACGTGAAAACACGGAAGAGCGAGGCTGGCAAGGCAGGGCAGG AACCTGATCACGTGCGCGCGCACAAACGGAATGAGCAGCTCCTGAAG AGGAGATGGGGCTCATGCACGCAGACACGCACGTGCACACTCCTCCG TCTTCACGGAGCGCGGCCCTGCTGCTGCTGCCATGTGCCGGACGTCT GCCACGCGTCTCTTCCCCACACCTTGCTCTTCCCCCCCCCCCTTCCC TCCCGGCGAACACAAAACACGCGCACGCCCACCGAAACAACAACGCG CAGCTCTTCGCTCTCGTTCTTCGAACAAACACCTTTAAACCGCCTTC CAACCCCTCTTTCTTCTTTTTCAGCC
132	IrLmK2	GTGCCTCCGCTCCCTGGAGCTCCCCACGAGCCCCCTGCGCCACGCAC CTGCGAACCTGCACAGCGGCCCACCTGCCCGCACACGTGAGCAGAAA TGGGTGTGTGGAGCGGGTGATGTCGGCGCGCACACGCGCGCGCGCTG ACCACTCCGACGTGAAAACACGGAAGAGCGAGGCTGGCAAGGCAGGG CAGGAACCTGATCACGTGCGCGCGCACAAACGGAATGAGCAGCTCCT GAAGAGGAGATGGGGCTCATGCACGCAGACACGCACGTGCACACTCC TCCGTCTTCACGGAGCGCGGCCCTGCTGCTGCTGCCATGTGCCGGAC GTCTGCCACGCGTCTCTTCCCCACACCTTGCTCTTCCCCCCCCCCT TCCCTCCCGGCGAACACAAAACACGCGCACGCCCACCGAAACAACAA CGCGCAGCTCTTCGCTCTCGTTCTTCGAACAAACACCTTTAAACCGC CTTCCAACCCCTCTTTCTTCTTTTTCAGCC
133	IrLmL	TCGTGCGCGTCTGTCCTCAGCGTCTCGGCGTTATGCGTGTGTTCGGT TTCGTTTTGAATCCGTTTCTCTTTCTCTCTTTTCTGTCGTTTTACGC TTGTTTTGTTTGGGTTTCAGCGAGGATGTGCTCTACAGGGGTGACAC CCCTGCGGTGTGTGTGTGTGTGTGTACGCTTATGCGAGGCGTGCACC TTGTTCAGTGAGCGTCTCTTACGATGTGTCCTCCCATTTGCCCATGC CGCACAGAGAGACACGCCTACACGGGTCCCTCATGAAGCTTCTGTAG GCACAACGTGCGCTGTTATTATGCTCTTCCCTTCCCTAAAGAAATAT TACAGGTCTGACACCCGCCAAGGCGGAGGGCGGGCGAGAGGGACCGC AGGTCAGCGCGAGCGCTTGCCCAGCCTTCCATCCTCCCTCCCCCATT TTCCCTGGTCGCTTCACCGAGAGGAGCGGATGCGCGCAGCAAGGGCA GCGACCAGCGAGGTCGGGGACCAAGAAGAGCGCGATGGCGCTTTCGT TGGCGGTTGCGTCCGTGTCGAGGGCGGATGAGACGAACCTCCTTCTC TTTTGCTCAGGCAGGAAGAGCCTCAGTGAACGAAGAAGCCTTTCGGG

SEQ ID NO.	Description	Sequence
		CCGCGTAGCCGCTTCCGCGAGCTGTTCGAGCTCCGCTGGTGTGTGCT ATGAAGACGTGCCGCTTAACCTGCAGAGCCCGTCTTCCACTGCGTCG CCATTGGCAATGATTGTTCGTCCCTCCCGCTCTACACTTATCCCCGG TCACCGTTTTCCCCTTAACCCTTCTTGTACGTGCCGCTGGCTTCATT GCTCCCTCTCTTGGTGGCTCGATGTGCACGCCTTTGGCGTTGGCGTG CTCAAACACATGCGCACGTACACATACACCCTCTCTTTCCCCACATG CACGAAACAACTCTTTTCCCCCAGCAGCATTGTGTGTGTGTGTGATT CAATC
134	IrLmM	ATGCTCCTGGCTGCCGGTTGCAAGCACGTGTTTCTTCCATCTTGCCA TGCGAAGCCCGCGCGGTATCTTCTCAGCGTGCCCTGTGTGTCGTGTT CGTAAGTTTTGTTTTCCTTTTCGATGGTTCTCATTTCCTTCTTTCTA ACGACGCTCTACCAAACCTGTACACGTACTGCAAGCGCTATCGTGGA GGCAGCAGGGGCAGGTGAGAGGGAGCCGCGGACGGCGTCGGCGGAAG CGTTAATCCTGCTTCCGTACTCGTCGGGCTCATCATCGTCGCGTATC CCGATGAGTCGTCCCAAACTCCCGCTCTGTGCCAGAGAGTGGACTGC CCTGCGCACCGGTGCATCGGTGCTCTGCGCGGCATTGGCATTCTTGA TTCGTGTGGCGGTGCTTGTCGACCACGCTCTCCGCACCTCTATCCTC TCCTTGGCGCTCTCCCGATGTGGCGCGAGCCGGCAGGTCTCAAGAGG CGCATGTGAATGTTTGCCTGCAGGGAGTACACTAAATTACTTTTCTC TGTCTCTCTCTTTCTCTGACTCCCTTTGGCCTCCCTTTTCGAAACTC CCCATGCTGCCATTGCGGCGACCCTCCTTGTGGGATGTACCGACACC ACAACCACACGACACTGCATCCTCCCTCGTCTACTCCTACCTCCTCA CTGATGCGTGTGCAGTTAACTGGAAA
135	IrLmN	GGGAAGGATAATGTGAACGGACAACTTCTCTGTCCTTTTTCGTTTTA ATTTGTGATTGTTTCCCGAAGAAGAAAAGCAACAAAACCGAAAGGGG AAGGAGCGATGTGCGCTCGGCAGAATAGCCTGTGCAAAGTTGGCGGC AGCGCACGTGCGCACCTGGAGATGGCAACAGCGGCGGCAGTATGCAC GCATGCACACACCTGGCAGCGCCAGAGATGGAAAGGGACGAGGATAG AGAGGGTAAAGTGTCGGAGGAGAACAAGCACATAAAGGGAGGGGCGA GGTCGTGACGGCGCGCGTGCTTGTTTTGCCCCCCCCCCTTTCCTGTG GTTTTGCTCCGACCTCTCTCTTCCTGTGTGTTCCCACCCTCTCTCTG GATGCATATCTGCGCGTGTTTTGCATAGGCACACACGCGACCCGCGC TGTTGCTGTCCGCTGCCATCATGTCACCTCCCGCCTTTTCTCTCCTC TGCACCCGCTGTGCTCGACAATCGCAGTGGAAAAAAAGGCGTGTGCT CCTTTTACATGCTTCATGCCCGACCCCTCTCCGTGGCGTGTTTACAC TTCAACGCTACCTCTTGCTCCTCCCCCACCCCCGCCTTTGCGTGATC TGCCAGAGTCGGCAGTACACCACCCTCTCGCTCTCGTCCTCCCTTGC TGCTCAACATCCGCGCGGAGACACGCACCCACACAGGCACACCAGAC GCCAAGAAGGTGAGAGGGCGAGTGAGAATCAGCAGGGGAAACCTCTT GCCGCGGTGTGCGTCCGTCTGTCTGTCTGCTCCTTGCCTCTCTCGAC GATTGGCGTTTGTTTGCTCTCTTAGTGCATATACGATGCTTTACAGG TTTTCCAA
136	IrLmO	TCGTGCGCGTCTTTTCACAGGCACCTGCAGTGATCTCCGCTGACGCT GCAGTTATTTGCTCGATCTTTTTCGTTTCGGTTACGTTTGGTTTTGT CATTTTTGAAAAAAAAAGCGAACACCGGCAAACTAACAGCGACACAC CCACACACATCAAAAAATCGCGAAGGGACGAAGGCGACGCCTCCTGC GCGGCGCCCCACTGCTCCGATGGGACTCTCTCTTCTTCGCACAGGCC ACATGTCCGAGTGCTGCGTAAAGCCCCGTGGCGCGTTACGCGAGTGA

SEQ ID NO.	Description	Sequence
		CAAGAGCCGAGGCGGAGAAGGGTGCTGCGGACTGCACTGTAGATGCT GTCAGCGAAGATGAAGGGGATGCCGTTGTGCCAGCGCAGGTGTTTCG GGCGTCGTTAGCCACTCGCCGCCATGCTGCTCTTTGCGCGTTGGCCC AGGGAGGAAGAAGAATTCAAGCCGCACGTACAAAGCGGTGGTGCCTC CGTCCTAAGGCACCGAGTTGCGGGCTGTGTCCGTCTCTCTCTCCCTC CCTTCCTCTCCGTTTTTTCCTATTCCCGCATGCCTTTTCATGTCGAA TACGCCTTTTTCTTGTGTTGCTATCCTCCATTACACTCACTTCCCCA CCATACGGTATGTGTCTCTTCTCTTGATACTCGGATGCGGACGCGCG TGCCGTCCTCAATGGCCGTGTGTGCATCTGCTTTCCTTCTCTGCCCC TCATTGGACACCTGCACTTGTTGGACCCTCGTGCTTTCTAGTGCACT TTTCCAGGAGCGTGTACCGTTTTAGCCTTGCTGCTATCCCACGTTCG AGTCGGCACCGTTCCTGCTAGTTCGAGGACACCCTTGCCCAC
137	IrLmP	CGGTGATTGCGGACACGCTTTGAGGACGTAGCTGTACCCCCAATGAA TTCTTCTCTGAAAACCACATCATAAGCCTCTTAAGAGGTTATTTTTC TTGATCGATGCCCGGTGGTGACCAGCACCATTCCTTTATCGGATTCA CTCACACTCCTAGCGAATCATGTAGTGCGGTGAGAGTGGGCTCTGGA GGAGACTGTTGTGTAGCCATGGCTTCAGGAGAGAAAACAAAATACAA GGAAAGGCAATATGTAACTATGGGGTTCCCTTTTTTACTATGCAAAG TTTTTATAACTCCTGATCGGCAAAAACAACAACAACCGCCATACACC AAGAGCAAATGCTTTCTTCTGCGGACTGTGCTTCTGTTTTTTTTTAT GAAGGAGTGACTCGCGCGATGAAAAGTGTGTGCGTGGGAGATGTATT TCCTTTTTTTGTTCATAGTGGCGACAGCTCACTGTTGACGATGACAG CACATAAACAGATGCTCATGGAAAGTGGCATTCATTCCTTGCCTGCT TCCATGGTGTTTCTATGCTTTTTTCTTGGGGTGTTGGACTCCTCGAA GGTCCGGTTTCATGGTGCACTGGTGAGGCGGTGCCTTGTAGTCTGCG CTCTGCTTTTCTCTCTCCTTTCTCACTCGAGTAACTGAGATGAAAGG CCCTTCAAAGGGCAAGGGGACAGTGACTGGGTCTCTTGTTGGATGCT TTGGCGCAGAAAAAAAAATCCTCCCTCCCGCTGTAGCTGGATGATCC AAGGTGCTCGGGACAGGGTCAAGCATACGCCATCTCTCACCAAGGTA CCGCAGACCACCACCGCTCACAGATCGACTCAAGTCGCACACACAAA TACACATACTGCCCACCAAGGAGTTTAACCACAGAAAAGCCGGTTAG AGGACACAAAGAAGCAGAACACGCATACACACACATAGAGATACAAG
138	IrLmQ	AACCCTTTTTCGCGTCATGGTCGAGATGGCTGGCACGGCTGCGCGTC TCTTTTCTGTGAATCGAGGGCATTGAACAGAGGGGTCTCTCATTTCC TTTTTCCCTTGCAAGCGCATCCTATGCAGTGCCATTTTCGTGTTGAC GGAGGCTCTCTCGGGCGGGTGCCCCGACTTTCGAGTTCGGATGTAAA GGGCTCAGACGTGCCTCTTATCTCACGCAGTGGCGACAGCCAACAGG CAGTCGAGTAAGTGGGAAGATGCGGGTGCGCGCGGCGTAACTTCTCT TTATCTTTGTGGACATTCCAAAGGACGCTGCACGGTTACCTTGGAGG GCGTCGTGCCCTACTCGGCATACTTCTCATCTCGCCGTTCTCCTGCC TTCCCTCCCTTCACAAACATCAAAAGAGAAGTAATGCGTATGCGACA GAAGCGAAGCGCACAACATGTATGGAGGACTCGTATCCCGGATGCAT ACATATGTATACATGTATGTCTACATATGCGCACATGGGGACACATT GATCGCTCCTGACATGGGCGACGAGGCACTTCATCTGCGCACTACTG GGTAGGTTGCATCGTGTTCTGTCAAGCAGCATCT
139	IrLmR	GACGTGCACGCAGTCCTGTCCCCACCCCCGACAGCAGGAGTGCGGGA CTGGGTGCTCTAACAAGCGCATGGTACGAGCTATGTGCTGGTGTGTA GCCAGCGGGGCTGTCATGCCATGTCGATCTCTCCCCGTGAGCAGCCC

SEQ ID NO.	Description	Sequence
		CCCAAAAAGACAACCTGATTTCTCCCTTTTTCCGATATTTCTCCCTT TGTGCTAAGGGGACCCTTCAGCAGCTCCCAGCGCCGCACATGCACAC ACTGGCGCGTGCTTCCGAGGTCCTCGGTGCACATATTTTCTATTATC TCACACACCCGGTTGCAGGGCGGCTCAATGTCACGGCGCGCGCACGC ACTGCCTTGAGTACGGAACGGCGAGCGATACGACCGAGACGGCGCTG CCAGTAGGGTGTAGGACGCTGCGCATCTCATGAATGTATGAAGCATG CAGCCAACCACACAAACATATGGGCGCACGAGTCTTCCCTCACAGAC AGCGCGGCTGGTGAGGCGGCAGAAGGTCGGCCGCGGAAGGGCACACA CTACGTTTCACGCGTACATGACCCCGTCCGCTTTCCGCGCTATTTTA GGCGCACACCCGTTCACCAGCCTCTCCGATCCTGCTTCCACTCCTCC TCCGCCTCCGCCCTCCCTCTCCCCGTCATGACGCCGCACGCACCGCG ATCGCACACAAGCTCTCTCTCTCTCTCAACACAACCGAACCAACATC CCTCACCCCCTCTCTTACCACAAA
140	IrLmS	GCTGCCCCTCCTCTCCGCGTGCAGTGGCGATGCGCTTGCGCTTTTGT CGTTGACGTGCCACAGCCGGCGCGTGTGCAGCGCGTCCCCCCGGTAT GCTCTGCCTGTTCTCCACCCACACCCCCGCCTCTACCCCGTGCGTGC GTGCGTGCGTGCGGTCGCCCTCCACCTGTGGCGCGGCAGCTGAACGG AAGGCAAACAACAGCGAAGAGAAAAGTAACAAGTACAGTCAAATGAA GAAAAAAAAAGAAAGCCAAATGCTGGCGCGGTGTGGTGGGACTGGTG TGCGTGCTCTGTCTGTGCTGATGGGCGCCAGGGAGACTGCTCCCCTG TCCCCCCGCCCCGCCGGGGCAGCTCCCATTATCTTTAGGCAGTTCCC AGTGGACCGGCGACGGTAAGCCGCCATCTCTTTTCCTGTGACCTCAG TTATAAGCCTGTAAGCCTGATGTACGCATAAACCAAACTCCCGCGCA CAAGCACACAGCCGACTTTCGTAGTGTCATCTGCAGAGGTGTCGGTG ACTGTGTGCGTGCGCGCTGCTGCGGCGTCGGTTCCGAGGCGCGTGCG GCTGCCTTCTCCCCGCAACCTGCTGCTGCGGTAGGGCGCTTGATGGC GCCGTGCCGTGAGCCCGCGGTTTTCGCGCTGTCGCGCGCGTGGAGGA CCGCTCCCCCTTCTTCGCTTGCCTCCGCGTGGCTGCCTCCTGTCTCT GTGCCTCACTTGCGCCTCCGCCTCCCTCTCCTTCGTCTTTGCCTCTC TCCCGCCCCGCGGCCTGCCCCGGCGTTGCGTGCGCACCACTGACGTG TGCGCGTGCTGCTCGCCCTCTCTCTCTGTGCGTGTGCCTGTGCGTGG TGCGACCCCGCCGCGCGCCGCACCCCCATTCTCCCTATTCCTCCCAC ACTTTTCTGTACCCCTGCTCCTCATGCCCCGACGACGTGTGCGCCGC GTGCAGTAAGCGCAATCGAGTTTCAACAGCTAACAAA
141	IrLmT	CCAGCGCGGCCTTCGCGCTTCCCATCCTCTCTGTTCGTCTTTCTTTC ACCCCTTCCCCCCAGTGACTTTGCTTGGAAAACCGGAGCGTCGCTGC CGTCCTCATGTGTGATGTTTTTCTCGGCTCATCCCATTCCGCGTGCG TGCGCGTGTGGCGCCTCCCCTCAGCCCATACGCGAGCTGGTTCCTGG GCAGCGGTCTACGCGGGCACTCCACACACGCACACGCGCACCCCCGC CCCACCGCCGCGTGAAACCTGTGTATCACCCATGTGCGCACGCCCTC TCTCTCTTTCCGTTCGTCCTCTTCTTTTGCTGCGGGGGTCGTGCTGT CGCCGCGCATACAGCCGGCAGCGCACACCGCCCTCCCTTCATGTGTA CAGCCCACTCGCAGTCCTATCTGCCCCTCCCCCCCCCACACGCACAA GCACGCATACCCTGACCGCCAACGTCACCCAGCTGCGCTGCAGACGC CGTTGCGTCACGCCCGCCATTCGCACCAGCCGCCCCCCCCCCGCGGT AGCCCCGCCGGCCGCTCTTCCAGCGGCGCACCGCCCCTGCATCTGCC TCCTATTGCACGACCTCTCTCCCCTGCCACTCCTCGTCCTCCCTCCC

SEQ ID NO.	Description	Sequence
		TCCCTCCCTCCCCCTCTGCGCCGCACCGCTGCACGCAGCAGCCCATT TGCCCTCGCACCGCACCCCCTCCAGCCCACCA
142	IrLmU	CATGCTTGGTTCACAGTCGTCTTCCGTTGAAAATGAAGACAATGTCT CTTGCTTCCTTCCTTGTAGGTCCTCGCATCAATTTTTTCTTCCTTTT CAGTTACAGGCGACATACGATTAGCTACCCTCTGTTTGAGGCGACAG AATTCTCAACGTGTTTCATGACCGACAAACGCGTGCTTCTATCGTCT GTATATGTAAATCGATTTTCGGTATGCTATACGAGAACACTTGACTT TTCTACTCTGTCAGCGGCGGTGTGCCTACCAAAAGAAAAACAGAAAC CAATCGAATCTGCTCTGCTGCTCGGGCTCTTTCACATGTTCTGCTAA GATGCATGGTTGACCTGCGATCTGGCGAAAGGTGCAGCTGACAAGCG CTGCTCGGGCAGCATACCAACTTTTCCAACGATTTAAAATGCTTTCT CGTTTTTCTCTTTGCGCAAACAACTGGAGCAGTGCCTCACGGGCTCC TTGCAGCCAAGAGTCATATGTGTCTGCAGTTTGTGCCGCTGCTGTTG CCACCCTCATCTTCCCACTCCTCGTCGTGCTTTACGACTTGCAGCAG CGAGGCGCCCTTTTTTATAGATACATAGAGAAGCCGCAACACCACCC ATACAGTTCACTTAGCAGCCCTGTCGGAGAGTACAATAGACTGGCTA TTCGTGCAGGCCGAAGAGCTGCATCAGAACGCGGTTAGACACCGTCA AACTGTGTTTCCTCCGCTTCCCTGTCGTTTTCTCATTGATTGCTTTC CTCTTGCATTCTTACAACATCGGCAGCCGAT
143	IrLmV	TATGGTCGTGTGTGAAATATTTCTAGAGAGCTAACAGAACTCGTTCT CTCCGCCTGTTTCTTTTCGCCCCCTTTTTCACTTCCATACACAAACG CCTTCGTTTCATTCGTTACTTTTCATGTAATTGCAAGTGATTTTATC AGTGCGGCCTCTTCTTTGAGGCTGAAGGTGTGAATACTTTGATCTAT TCAAACACAGCTCTATTGCTGGTGATTGTGTTCTTACCTTATTATCA AAAACCGAAAACTGTTCTCTTCCATCTATCACCATTGACCAAGCTCT TGCTTCTCACTAGTGTCCACTCAGCGGTCACAGCTCGATTTTCATCT CGCCGCGCGTCTCTTTTCTCATGGCTGTCACACAGTGCGCACTGAGA GACTTGCGCTATCGTGCGCGTTCTCTTCCCAGTCCTCAGGTGGAAAA GCAGCAAGTTTCCTGCATCGCAGCCCAACGTACTTGCGCTCGCCCTA CAACAGCGTCTTCTTTCACTTTGTCTACTTCATACTTTCTTTGCCTC ACTTTCCCTCACGTGGTTGACAGAAACTCATTGAAAGCGAAGCAGCC CCAAGTG
144	IrLmW	GTGGTGGAGGCAAACTATTTGTTGTTAAACCAGCACTATATTCTCGT GTCCAATCGGTAGTGCAGTCATCGAGTGAACGCTGTTCTTAGCACCT TGATTCCAAAGGGGAATAGTACATAAGATATGTGTCATGAGGCGTGT ACACAATTATTTCTCTTAGGATTTTTTTTTAGTTGAAATAGGTCCTT GTTGTGTCACCATTAGCGTTGTCCGAGTGAGGTCAGCAGAGGTACCG TGCGCGCGTGAAAGCACTTGCTGCCCCTGCTCTTTGGCGTTGGTGTA ATGCACTCAGATATCGTCTCACTTTTTCTTCTTTATTGCCCAAGGTG GGCAGTGAGGAGACGATAGTGAGCACCTATTTCGGACATGACGTTCT TCTGTGTGCCCTCATCTGGAGCACGAGGCGCTTTCTTGTGTCTATTA TTTTTCTACTTGTTCCCTGATAAGCAATGATACCACTGCCTCCGTGT TGAAACACACTGGATCGCTTGTAGCCTCACTGAGAGTAAACTTCTTC ATCAGAAAACAGACAGGAAT
145	IrLmY	TGCCCCGCCGCCGTTGCCGCCACACCGCCGTGGCCAATACCAAAGCG TGCATATTTCGGGCGCGTCTGCATTTTTAGTCCCCCTTCTTAGGCCT TGTATTGTTCACTTCATCTTCCCTTCTGTAGGACGTCTCTCTGTTCC ATTTCTTTTCTTGTATGCGCCCCCTCACTACCGCCTCCCACGCTCTC

SEQ ID NO.	Description	Sequence
		TCTCTCTCGCTCTGTGTGTATGTGTGTGTGTGTGTGCACACTTTC GCGTCTTCGACTTGTCCCTTTGTTTTTCTCACTCTCTCTGCCCCCTC CCCACCTCACCGCCTGTCTATGCGCTTCCCTCCCTGTTGTTCTGTAT GCGTAGGTGTATACGTGGTACACCTCGAGTGCCACGGCGTGGCGCAC ATAGCAGCGTTTTCGTTTTTTCGCTTGGTAGAAGATGCGCAAACGGC GTTCACGACCACTGAAACAGCGCGACATCGGCGCGCACGCAGTCCCC TTTGCCAATAGCGAAATCCGGCACCCGCACGTCAGTTCTGGCTCTCT TTCCTCCTCTTCCCATGACCCGATGGTGGAGCTGCAACCAGCTTCTC TTTTCGCCTTCTGGGAGGCGGGGGTCATGCCTACTCCCTCAGTCTTC ATGCTTTATCCTTCATTGCCTACCCCTTTGTTTGCTGCCGTCTACCT CACTTTCTTCCGACACACACACACACACACATACACACACACATACA CACACACATACACACACACATACACGTGCCGTTCATCTCTTCTTGCA CCTCACAATCTGCGCCTTCTTCTTTCAGCTGTTCACTGAACTAGAAG CATCTGGCGAATACCCTCCCCCCTCAACATACACACCGTACCACCCC CTTCTCTCCCCCTCCACCTCCAAAAAAAAAATATATATTTCTCCTCT GTGCCTTCGCCCATCTCATCATTTATC
146	IrLmZ	CTGCGTTACGCGCACACTCGCATGGGATAGAGGAGAGGAGTGTTTCG AATGTAAATAGTTTCTCCCCAGGAATGTGTCTAAGCGCGAACAAATA ATACGAACAGTGAACACGCCGCAGCCTTGCTGTGCATTCAGACTGCC TTTGACAAAGAGACATACGCATAGCCACGCAAAGATGCCGTTGACCC ACCGTCTTGCTCTCGTGTTGCGCAACATGTCCTTCCGTCATTTTTTC ACCTGTGTCCATGTCAACTTCCCTTCCTACCATTGATGCCGAGTCAT CATCTCCGCGGCTTTGGTTATGCGCACTTTTCCGAAACGCCGGCTAC TCTCAGCTTTTCCCTCCGCTTTTCACCTCTATTGACTTACATACCCT AAGCTGCAGGTGCTGAAGCTTCCCAGCTTGTGGTTGCAAAAGTAGCA GCTGCTGGTTCAAACACGCATCTACGAAAGCAAATAGAAAAAAACGC CGGAAACTCCGTGCACACGCAAACACGCGTACGGGCACAGCGCAGAC AAGGAACACGGAACAACATCACA
147	IrLmAA	TGGACTCTAACGGATCAGGTTTGCCTACCCCTTTCCTCTCTGCACTC TTCCTGTCTCTGAAGGGAGGGCAAGGGTGTGCATGGTGCCATCCTCT CTCTCCTTTTTTGTGTTTGCCAGCTTTTTGTGTGTGGATTTGGATGG TAGAGGGTCCCCTTCGTCTGTGTACAGTGGCCTTGCGTGTGTGACGA GGAGGAAGAGCGGAGAGCGAAAGAAAACCATCACAATACGAGAGCGA GTCAAGGAGGTGAAGTTGCGTTGTTTACCTTTTCATGACCTCTGGGT TTTGCATTTGAACGCAACGCAATACTGAAGAAGACAAAAAAAAACTA TTGAACTGTAGGCAGAAAGGAAATTGTTAGACTCGGGAGATCGGCCG GTATGACGCACTATGAACGGCTTTGGTCTCTCTTGGGGAGGACTCTT GGCATAATGTGCGCACGCTTTAGAGACGCCGCATAGGTGTTTTGGGG GCACTGCACGTGCGAAGGTCGGTCTCCGTGCTGCATTGGTGTCGCAC ACTTTTGTGCGACACGGCGTGTTGCGGACGCTGTCATGCGTACTTGT AAATAGAAAAAAATGCACACTGCGCCTCCTCTTACAGGCCGCATCTA TGCAGCATATGCGGGACTCATCTGATGAATCCCGCGCACTTTTCCAC AAACTTCA
148	IrLmAB	TCGCGCGGCTTCACAAAGAGAATGGATGCGGCTTTGACGCACATCGA CCAGCTGTGCTTTCTTTTACCCCCTACATCCTGTTGCGCTTGTTCAC TGACCCCTGCACGCTTCCGCGTGCCCAGCAGCGCACCACAGAAGGTC ACCGCTCGATCTGCGCAGTTGGAGCAATAGTAGCGCAGCGGAGAGCA TCAAGTAGGTAGCACTGTGTCACCTGCTGCCGCGACATGTGCGCCGC

SEQ ID NO.	Description	Sequence
		CTTCTCGATCTCCCACGGCACGCGCACCTCCCTTCTTAACGGCACCG CTGTATGTGTGAGTGCACGCATCGGGTGCGCGTTCATTCGCTTCCCT TCACTTCCCCAGCCGCTGCGGCCTTGTTGCCGCACGCTTTTTCCACA CGCTGTTTACTTGGTTTTATAGGATAGCACTTACTCCCACCACCCGT CACAAGCTTCTCACCCACACTCACACCCCCACACCCGCCAACTTAGC AGTGGCGCGATGAGGGACGAGCAAACCAAAGACAGGGCAGACAAAGT ACGCGAGACTGTCTCTCTTTTACCTCCTGCCTTCTTTCGCTGTCGCT GCCCCGCGATTATTGAAGGTGATTCACAGGTGTCAGTGGGTGCAGTG GGCCCTCCGAGCAGGCGTGCACACTTGTGCACGACACTCAACCTCGC TGCGCTCTCTTGCACATGGGCTCACCTTTTTGTTTCATTCCTTCTCC ATTCCTTCACCCTTTGCATGGGTGGTCACAGCATGTGCTCAGAGAGG TCGATGACGCTTCAGCAACGGAGCACCTACTCATGGCGCTCTCGTCG ACCGCGCCCCTCCTTGTGCCTCCGATGGGGCAGCATCCGCTACACTT TCCCCCTTTTCCATTCTACTCGTCCTTTTCCTTGTTTGTGCCCGAAA CATAAATCACTTCTCAACCCCTTTTCGGCCCTTCACTACTCGCAGTC TTTCCACTTT
149	IrLmAC	AACAGCGCGCGAGGCAGCAGAGACGTAAAAGTTGACCGAGAAGGGCG TAACGAGAGAGATGTAAGAGATATGGGCTACAGCAGTGGATGGCACA CACACAGACACACGCGAACACGCAGCGATGGTGTTGCACCTCTTGCT TCTACTTTGCGGCCTTTCCTGTGATAAACAAGTGCACCTGTATTCTT GTTGTATGTACACATGGGTGTATGGGTGTGCATTGTGCATCTCTCCC TCCTTCCTTCTCCCTCGCTCTCTGTCCTCTTTGCTATTTTTTTTTCT TTGGCTTGCTCTCCGTTGACTTGAGCACCCGTGGAAAGTCGAGCCGA CCACAAGACACGCGACACGGAGCAAGGCAGCCCCCTGGCGAACGATT CACGTTCGATGTGTATTTCCTCTTGTGCCTCCCTTTTTGTGAAGCAG CCAAGCGTTTGCGCGCATGGGATGGCGCCTAAGCGACCGCAAATGAT CACTCTCACAACACATGCTCTCACCTCTTCTCACCCCAACGCTGGTC TTTGCCTCTCATGCACACGCACACACACGCACACACATCTGCAGGTT GGAAGAATCACCGCAAGCATCCTCACTACTACTAGTCTTTTGTCTTT TAAGCCTTCTTCTCTTCAACCCAATTGCCACTCCACCGCCCGCCCTC GCTACCTCACCCCCAGAACTGTGTCGCCGCTCAACTCCCCGACATAA CGCAGGCACATACGCCCTCCTCTCCATCCCCGCTCTGCACCCCACCC CACCCCTCTCGCTCTTTGCCTGCTCTGTCAGCAACGGGAAAGCTGAG CAGACTCAAG
150	IrLmAD	GCGCGATTTTTTTATAGGCCACATGCGCTCAGTGCTTTTTGTGCTTT CGAATTCTCGGCTTGCTATGGTAGTCTACTGGAAAAAAACGCAAAGC TTTGCAAAGAAAAAAATATTGCTATTGGGCAGGCTCTCGACGGCTAG TTTTTTTTTTTAGTCTTGCGGATATGGATTGGTGACGCTTTATAGCC GTTTGCACCATCTACATCAGAACTGAAATGCATGGTGGCGATGTCGA AGACGGCCAGCATTTGCTGTGGGTTCGCTTTGTACTGAAATCCTCAG TGTAACCAAAACAACGAAAGAAAAAGCGGATATATAAATGCATCAAT ATGCTCAGCATCTTTCTCATTTCTTTTCCCCTTTTTGAGCTCCCTTC ATTTTATGCTGCTCTTGTGTATTCCTTCTGCTTTATGCTTACGATTT AGACTGCAGAACAGTACAAGCCAGT
151	IrLmAE	CGTCGTTGCTCGGTGGTCTTCACCAACGCCCAAAACGGCTCTTCGTT CATGAGGTCATAGATTTCAACCTTCGCCCTTTTCTTCTGTATAAAGA TCTGTAAGGTAAGTCGAAAAAAATCAAAACACCTCTGTGTGTGCGTG TGTGTATATGCATGTGTCAGCACCTGATCAGCATTGTGTGTCAACCA

SEQ ID NO.	Description	Sequence
		GAGCAGTAGTAGCGGCTGTTGGCCGAGCGGATTTGGTGCTCGGAGCG CCAAATTGATTGAACAGCTCTTTCAGTGGCACGGTCCGCCTACCCCA ATGCATAACGTATCCGCAATGCACGTCTGCTGAAATACTTCCACACT CTCGTTCTCTCTTTTTCTTCTTTCTTTCCCAAGCTAGTTCTCCTTGC GTCCCCAGATCGAGG
152	IrLmAF	TGTGCCGGCCAGGAGGCCCACTGCGCGCATGCGGCCGCCTGGTGTGC GTGATGCGCATCATACTCTCATTCTGCCTGTGACGAACTCGAGTGTT TGGTTTTGTATCTCTTCTTGTGCATTTTTCCCCCACCCCCGTTTCTC TTGAAAGGACGCGCTGTCCTCCTGCTTGGCGTGCCTGTTGTGGGCAG CGGAAGCCTTGCTGGCGGCCCAGTTGCACTACCGCTGTTGTACCGGT GTATGGCAACGCGTACGTGCACCGTGCTACCCGTGCGGCACACGCCG TCCCTCCCTCCATGTGTACAGCCCCTCTTTCGTCATCATGTGTTGAA GAAGCGACCACACGAAGAAAGCTGATGAGCCGCTCGCCGCCCACAGT CAAGGAGAGCGGTGCTTCGTGATGCGCAGTGCTGTGGCATACATTGT CAGCAATGAGTGTGCTTTTCGGTGCTGGAGGTATCCGTGAGGCCCTG TCCTGCTGCCCTGTGTTTCAGGCTTCCCCTCCCCCCACCCACCCGTC CACCTGGATAATCGTCCCCTGCTGCTGTGTGGCTGTTTTCCTGCCGG TGCACCATTCTTGTTCTTCAATATTCGCTCTTCTCCTGTCCTCTCAC CCACCTTCACGCAGTCGAGGACATCCTTTTCTCTTTCCCGCTTGCCA CCAGCGCCACCTCTTCTGGGCATAGCTTCCGTGCACTCGTCTCCTCC CCTCCGCATGCACTGCGCTCGTGTTTGGAA
153	IrLmAG	CGCAGTTTGCTTTTTAGCGTTACTTTGTTTCCTAATATGGGCTTGTG TATGGCTTTTCCCCTTCTGTTCTTGTTGGCATTTTACTGTGTGCTCT GCGTAAAATGATTGTTTTTGCTCTCCATCGAGATACGTGGTTGATTC ACGTCATCTGTTTTATGTGCTTTGAAAGTGTACGAAACGAAAAGCAG AGGGGGAAAGGAGGGGATTATAAATGTGTTTGCGACCTCTGTTATTG CCACTTTTTTTTACGATTGAATTCTCATTTTACACACACACACACAC ACACACACACACACACACACACACACACACGAAAAAAAAAAACAAAGAT TGACGACTTGTCCTTATCAGCATTTTTTTTCGCTGTCGTGACAAAAA AAAAGTGTCTCTACAAAGCTGTGATAGTGTATAAAATAGCCTAGGGC TTGCTGCCGTCACGAACACCCCCCTTATAGGTTTCGTACAGCTGTGT CATTTGGCATAAACGCCTGCTCTCTTAAAGCGATTTCCAGGCTCGAC AAATACATTTTTTGCTCTAGAGTATTTTCATTACCTCTCTGCTTCCT CCACTTCTCTCTCGAATACCTAACCTTGCAACTGATGATATATATAT ATATATATATATATATATACTTTTTGAAAGCACATCCCTTTGCATAT TATTATTTACCGCACAGTACAATATTCAACTTACACCTCTCAAAACA CGACACCTTTCAATCTAGTTTTGTACTAATCTGCAGACTGAGAAAAA
154	IrLmAH	AACGTGCTTTCCGAGATAGCATTTCCGCAGCTACTTTTGGATGCACA AAAATGTTTTCACCCCTTTTTTTAGCCCTCGTAATGATGCCACCTTT CCAATGCTACAAGATAACAGTTGAGTTTTAGAATCAACGAAGTTCTA GAGCTATCGCTCAGAAGTACGGCGGCGAGCCACCTGTGTTGATGCAG TCCGCGGATCAGAGCAGCATGGCTGCCGATGAAGCACCGCTCACTCT TGCCTTCCTTCACGTATACTGTCCCTCTGCTTTGCCGCCTTTTTTTT GTTTTCAAAAAAAACTCTACAGTTGCTCATCCTCATC
155	IrLmAI	TTGGCCGCAAATGCTACCAAATCGTCGACTTAGTCTTCTTGACTCTC TGACACATTCATCTTTATGTAGTGTTGACAAATTGCTAGGTCCCGGG GTTGAGTTTAGTGAATTATTTCCTCTCTTTGGCGAGAACATACTGGC TGCCTGCGAAGGTGTCAACTTCTGTTTACTTGTGGCAAGGGTCGACA

SEQ ID NO.	Description	Sequence
		GCTTCCAAAGCGGTAGATACCGTTGGAATGTTGCTACTGCAGCCCTT TTCAGTCGTCTCCCTCTCTTTCTCTTCTGCGATTCGGGCTCGCTTTC AGTTGAGAAAACTGAGGGATTGACGGAAAATGTGTATGCAGTGAAAG GCTTTCCTTTTCACGTTCGGAAAAGCTGTTGAGGAATTTTCCCTGTC TTTTTTTTTTTCTCTTGTCGTTGTTCTTTGGTCGTTTCGGCGAGTTT CCTTTGCTTCTCTCCAAAAAGAAACTTCCAGATTCACGCGTTGAGGA TCGGCAGCCACTGTCATGACACTACAGATTCGTATCCAAAGATAACT CAAGTAAGCGTGTCGAGTGCAGTGGAGGGGATCGCTGCACTGTCACC ATGTTTTCGAGTCCAAAGGCCTCGATTTTACGCCACAGGGGAGTTTC CAGTATAGTGAGAGGTGCTTCTTTTCTATGGGACAACCTTTTTGTCT GCATGAGGCAACAGCCACTGGTGAACTATAAGTTACAGGCGCAGCAT TTCCCTACTCGTCTTGAGCGGTTCGCACGCCGTCGTTCGAGCGTGCT GTTCGTGGCTTACTATTTTGCGCTCGCCTACTTTCTCCACTCGTCTC TATGCTTCTTTGCAACGAAATGCACTTTTGCGAATTTAACAAATGCC CCCACACAATGCTCACATGTAACGACCTCAAACTTAACACTGCCAAT CCCACAATCACAGTTCCTAGAAGTTTGACAAG
156	IrLmAJ	TGGCCACTGCCTGGAAGTAGGCCACACAAATGCACAGGCATTCATTA GTGAGCGTGCAAGAGCAGACGACCGCCTTCAACAGCGCTTCGCCCTC ACGCATGCAGAAGCGTTGCTTTTTTTGTCTACTCAGCTTCCTTCTTC CCAGCTCACTCGGTCGCGTTGGCTGGGGTCTTCAAAGAAGAGGGCCA AACACCAAACAAGAACGAGCCAGCGCCACTCAGCTACGGGCTAAAGC ACATGCGGACACGCTCACAGGCGCGTTCGCTGCGCAGAAGCACAGCT GAGCTGCAAAGATATAGATGCGCCCCCGCGAGGCGGCAGTGAGAGCG GTTCTCCTTCATTGACTGACACGTGAAGCTGGCCCCATCCACCCCTG CCCACGCAGCCCGTCGAAAGGGGGACACCGGCGCATGATAGGGTAAG GCGAGCGTGCGTGTGTATGTGCGTCTGATCGCTCCCTCACGGGCTCA TGCTGCATCTTCCTCGGCGTCCTCTGCACGCCCGCTCTCTGCGTCTC ACTCTCTTCCACCTGATGTATTTACCTCTCCGTATCTCTCCGTGTTC ATTTCTACGTTCTCGCCTTCGCGCCCAACGTCACACCTGCTGTCTTT TGTTTCTTGCACACACGCGGCGTCCCTTCCGCACTACCCACAGTCCC AGCGCTTTCCACTCACCCCACCACCTCACCTCTACA
157	IrLmAK	GGCCGAGACTAAAAACGCGAGGCAGCGGCCTCTCTTCCTTTTTTTCT ATATCTCCCTGCGTCTCTATTGCATCTTTGTTGCTTGTTTCCACTGT TCTCGTTCAGTTTTCTTTTCTTTCTTGTTGTGCTGCTACAAGGTGGA CGTCCTGTAGTTCTCTGCTTTTCGCTTTCCCGTCATCTTTTTCCACT GAAAACACCCTTTTAGCATGTCGCTGGTCTTCTGATTCGAAAAAAAA AAATACAGCACGGCAAAAGCAAAATGCCGCCGACATCTTGAGCAAAA GAGACACCTTGCTGCTCTCTCCCCTTGTCACCTCTTTGGGCTCCAAG TGACTTGCATCGGGTCGCTCATGGAGTGCATCCGACGTCGAGAACCC CGCGCGTACTCTACTGTCTGCATGCACAGCCTTGCGTCGCAGCCGAT CGCGGTCAGCAAACAGTGGCACTTTCTTATCCGTGAGCACTGATGCC TCCTACCTCTTTCTTCAGAAAACAATCCTCCTGTCGCTCGCTTTGCA GCGTGTTCTGTATCTCCTGTACATGAAAATGGCACGAGAAAGGCTGT AGAAGAAAATGTCGTGAAG
158	IrLmAL	TGCACTAAACGCATGTCATCCCTATTTATTTGACACACTGTGCTAAG CAATTTGGAGTGTGTGTGTGATAGGGAATGTCTGTCGGTTTATCGCA CTCACAGCTTGTGTCGCCGCTTTTCTTTCTTTTTTGTTGTTGTTTTC TAGCGGATGTGCCTGGAAAACAAATACAGCAAGGGCAAGTTTTGCTC

SEQ ID NO.	Description	Sequence
		CTTGTAATACATGGTTGTTGACAGTGGCAAAAGCAAAAAGCTGTGAA ACCGTTGACAATGGAAAAAAAGAACTGAAGCAGCGCGCCTGGCAAGC GTCTTCGTTTCTTTCCCTATCACGCTCTTCGTTCCCATACGAGGGAT GTTAGTGGGAACCACAACACAGGTAAAGGGTAGCATGTTATCTGTTT GTTTGGTGTTGCTACCAGTTTAAGGCGCGTTAACATCGTTGCTTTTG TCGTTGTTAATCTACAAAAAATATATATATATATAAGCATTTCACTA ACGTGGTAAAGGAAACAACAAAATAATGTTTGAAAAAGTAAACAGGG CTACGAGCATCTGGTCAACTGTGCTGGCATTCAACTCCTTTCCTTAC AGCTCCAGTGGTGAAACCATCAGCGTATTCGGTTAACGACTCTCGCA GGCTGTCATGCATACTCAGCAGCGCTGCACAGTATTTGCTCTCGCAT ATATTGTCACGCCCGTACCTCGTTCCGGCACAAGCAATTCAGAAAAA GATGCGCTCCCTTTTGCAAAATCCAGTGCTTTCACTTTTACTCTAAC GTTCCTCTCGCTTTTTCCCTAAAGGAGAAACTGCTCTTTGCTGTAGC CCGTGTACTTTTCTTTTCCATATTGAATACCAGCTCTGTGGTGTCAG TCAGCGAAAGAAAGCTTTGCGTTTTCA
159	IrLmAM	GACTTAATGGGGATAGTGAAAGGTGCCAAAAACCAAGGCGTGGCGTG TGTGAGTGTGAGAGCGAGAGGTGCACGCGCAAGGACTCTGTGAGCAT CCTATGTCCGGGCGTAGGTGTCGGTGAACAGCTGTTCTCTACCATCC CCCTCCCCCTCATTCGTCTACTGGATCGACTCCGCTTGGGTGGAGTG CGTGCATGTATGTACGTAGGTATATGGTATATACATATATATACCAT ATATATATATATATATCGATATGTGTGTGTGTGTGTGTGTAGAGGGCTT TTTCTTCTGTGCTGATTCTTCCTCAACTCAGCGATCAACGCGTGATG TGCCCGTGATCGGGATGGGATAAGACAACCCGTGCACGTAGAAACGA AGAGAAGCGCACATAAGCAGTGTGGGCAGCAGACATGAATACATATA CATATATATATATATATATGTGTGTGTGTGCGTCTGTTTTGCTTCCC GGTGTCGCTGCTTTGGTTGGCTCCCTTCACCTCACCTGGCCCGCTGA CTCCTCCGTGTTTCTAGTGCTGCCTGTACCTCGCTGCGCTCGCCTCC CTTCACCTCTTTCGCCTCGGCCCTCTCCCCCAAAACACAAGAGCACA CCATAAGCATCCACACCTCTCACCCTTTCACCAATCACCGTCTCTTC CCCCTCCCTCCCTGCTCGCTCACCGAGCCCCACAATCTCCCTATTCC CCTCATTAAGACCACGCACACGCAGCAGCAAGCGGTGCCCGTCGTCA TAGCCAAGATCCATTCTCGCTCCGTACGAATCATCC
160	IrLmAN	CTGTAATAGAAAGCTTCTCTTGCTTCTACCATCTCGAGGCACCCCTT CTCCTCGCTCAAAGCGGGAGGCACTCTGCGGCTGCTTCGTGTCTTCC ACGAAGAGCAGAAAGCTTGGCGTTCCTCGCCTATTGCTGCTCGTGAA AAGCGGATGCTGAAAAGTCGTGCTGTTTCGGGCACGACAGCACGCTA TACATCGAGGCTCTGTCGCGCGCCACACTTTTGTGTCTCTCTTCGTT TTGCTAGCACTTTCACTACATATGGCGACACATTGCCTCCCTTTTCT CTGCACTGAGTGTTTTCATCGTTCCTGACTCTGTGGGAATACATCTG AGCTTCTCGTAGTATCTTGTGACCAATGCCAGTCGATGGAGGCTCGA CTCTTCGCTCCTTTGCACCTTCAAAAGTGTGCTGCGTCGATCCTGAC AGGGGAGGCTACAGTGCTGCACTGATAAAAAAGCAATCTGTACTGAC TTCTCACTTCATGTATCTATTTCACTCCTCTACGCGTTTTGCTCGTC TTCACAGTGAGTTCTTTCACATTTCCAGTTTCAAACCCGATATGTGC AGCGTGCCAATCAGCTGCAGTAGCACTCATACCCACACGCCGCATTC ACTCATCGTC
161	IrLdA	ATTGCACGGCTCTTATTTGTCCTTTGAAGTATATATATATATATATA TATTCTGTTTTCGACTTCACTGAGAAGCGGAGAAATATCATTAAAAA

SEQ ID NO.	Description	Sequence
		ATTTCAGTGGGCTTGAATGTCGCTGACTAAATGTGATGCACATCTCG AAAGAGATGCGTAGGAGATCGAGTGGCTGACAGTTTTTGTGTTCAAC CACTTCCCCTCCGTTACAAATGTGCGGATAACTCCGTATTTTCCGGA TGTGGCACAATGAAAACGATATGTGGATATAGAGCTGTTTTCCTTGC CTGTGCTCGTTATGTTTGTTTTCTTGTCTCTCTTCTGTCTTCCTCTC GAGATTACTGTGAGGAGGAAAGCTATCATCTGTGATCTTACATACCT AGCCTCTTTTCGCGATTACAAAGGTACTGCAGGCTCAGCGCACATAG ATTTACTCTCTGAAGGGACTGTGCTCAGTCCATTTTTAGACTAACTG AGGAGCACTGACGACAACAAGGATACATAAAC
162	IrLdB	GTCCTCCGGCCTGACAGCGCGCGCGCCGCTGTATGTGCGCGTGTGCG CGGCTTCCCACTGGGGCCAGCGATGAGGCGCATCATACCTCCATAGA GACCCTATCTTTTGTTTTCTGGGCTTCCCAGATGACCACTTGATTCC TTCCTTCCTTTGATTTGTTTCTCTCCTCCCCTCCGCAGAGGGTACGA GTCAGGGTAGGCTCGGAGAAAGCTTGCCGCATCCACGATGAGCCACG GCTGTCTCTCTCTCTCTCTTGACCGGGACAGGCTGTTGCCCAGTCAC GCGTATCGGCGTGCACACCCGCTCTTGCGCCCTGCCCCACTATTCGT CGAATGATGCGCTACGCGCATGACAGGCGCTGCTGCAGCGCTGCTCC CTGCGGTTGCTGAGTGCGTACATGCCGTTGCTACTGATGTGTTTGCA CTGCATCTCACCTCGCTCTCTTTGCGCATGCGCTTGCCCTTCCTCCC TCCTCGCGACCGTGTCGGTCCTCTCGCGCCGCTGTGGCGCAGCTCGC CGCCTTCCACTCCCCCAAACACACACGCTCATACGCTCATATAGCAC TCGTGCGCACCGACACACCCACACCCCCTCCTCTCTCTCTTCTCCCC AACCTACCCATCGCAGCC
163	IrLdC	GTGACTATAAAGTGCTATTGAATTTTTTTTTCTTTTCCTTTCACGAA ACAAAAATCTGTGTGTGCGCATTTTCTTACTCTCCATTTGGTGCGCA CCCTTCTGGGGGTATGACCTTCAGCACACACAAAGAACGTGTGCTGC GCATATGTGTTCAATGCATGTGCTTTTCCTCTCTTTGTTTCTATCAA GGAGGTTCATATGAGAGGGCATGCTCACAGCAGCTTCCCTTATGCAT ATGTAGCCTTCTGAGTTCAGATGTGATACTGCTCCCTTGATCTCCCT TTTGTGTTTTTGTTCGAAACAACAATGACGCTCTTACATTCTCTCTA CCTATTATCGTTTCTTTCGCATCTGAAAGCGTGGTACTAGTTAGCTT TATCTTAGTAAAACAGTTACCATTCACTGCCACCAAAA
164	IrLdD	AGTCGTAGGCCGATGCTCATATCTTCCCCTTTTTTCACGGTGCCGTT CCTTTTCTTCTTTCATTTCTTCCCTTCCGAGACAACAAATAAACGCA ACACATAGAAGTATAGACAGGAACTGCGCCAAGCTGTGTATTGCCCT TCTCCCCCCTCCCACAACGACACAGTGTGTGCGCTGTTCATGGACGC TTCATGTGAGGAGGAACGCGACGAGAGACGGACAGGGATGGAGAGCC GCGCTGAACACGCAAAGCGCCCGCCCACAGGGACACAAACAGAGGCA CAGATGGCCCGCTACTGGCTTCCTTTTCGCCGCCAAGAGGGCGCTGT GCATGCGCACGTGTGGGGTGGCGGTGGCCCAATAGCACAAGCGTGCC GCTGTGTATCTGTGCATGACACAGACATGCAAGCATCTTGCTGCTCC GGCTCCTTTTCTCGTCTGAGTGTCGGTCGTTTTTTCTGTCTCTCGTA CGCCACCTTGATCTTTCTCCATCCTTCCCCCTCTTTATCTCTCGCCA TCTCTGTGCCCCCGCTTGTGCGAACTGCCGGTGTGCGAAACCCCCCT CCCCCAAGAAGGAGGTATTTGCGTTCTTTCTCGTCGTGTCTTCCCGG CCTGACGTTTCTCTCTAGTCTTCTCGGTTTTGCATTCTGAGTGCTTT CATCCCTGCTTTCCGTGAGTCCAGCGTGCGCTGCGCTTAGCTACCCG TGTGTGTCTCACACACCTACACCCCGCCTATACTAACCCTCCGCCCT

SEQ ID NO.	Description	Sequence
		GGCACCCCCTCTCTCCATCTCTTCTCTTCGTCGCACGCGTGCACGCC ATCCAATC
165	IrLdE	ACCTGTGCGCCGCTCCCTCATTTCCGGCGGCTCGCACGCGCTCGCAT ACTTTGCCACACAGACGTCCTCGTGTCTACTGAACAACTAACGGATT TCCATGTCATTTCTCGTTTATCATCTTCAAACACAAGAGCACAACTG CAACGTCAGCAGTGAACGCCCGACACAATCGGAGAGCGTGGTCACGC CCCTTCTGACTTGCGCCATGAAAAACGATGTGAGGCAGCGGCGCGTC CTCTCCTCCGCCAGCTTCAAAGCGCTCGTGCGGTTTCGCGTGCTTTG CTCGGTGTTCCTCTCCCGCTCGCTGACTTGCCCCACGCGCGTATCTG CGCGCCGGTACCCCTCTGCGCAGCTCGGCTCGCCTGCAGGCGCGCGC TCTCGACACCCCCCTCGTCTCTGTAACTCTGTCTCTTCCTCCCAGCC CCACCCTTCTTTTTTCCTGCTTTTCCGTTTGTTTGTACGGCGCAGTG CCGCGACCAGCCCGTTTTGGCTCTTTCTCCGCGTTGCCAGCACCAGG GGGTTGGGGTCACCGTGCGCGTTGCTCCTCCGCTCTCTCTATTTCCA TCTCCTTGCTTTGTTTTGCGATCTCGCCGACGGACGCTGTCAAACCC TCATAGGTTGCTTTTCTCCCTTTCTCGCGGAACGCCGGCGTGTCAAG ACGAGGCC
166	IrLdF	GGTCCTTGTGACCGCGCGTTTGGCGGACTGCTCAACAGAGCGGGCTA ACGCTGACGAAGATATGCTGGTTTCCCTGTGTTTGTGATTTGCCATC CTTTCGTGTCAAAAAGAAACAACAACAACAGCAACCCGTTTAGGCCA AGAAGCGGGCGCTCGGACTCTTTCCCTGCCTGCCCCATCCCCATGAA GCACGCCGGCTGTCGCACTGGGCACCTCATGACCCTGTTGATAGCGC TGGAGGCCTTCATTGCGTGCTGGTTGTGGGGGGGGGTGGAAGGGGGA GAGGCGTGTTGTATTCATGTGAGGTGGTGGTGGCATTGCGCAGCGGT GGGAAAAGCAGGGTCTTTTCCGTACTCCGTGACAGAGCTGCCGTGCT CATCTTTTCCCGGTTCACTGCTTGCACTGTTGGCTGCCTCGCCTTCT CCCCTCCCCCTGCCCCCACGAAACGCGGTTACCGCGTCTCCTTCGTG GGAGAAGTGGAGTGGCACAGTTAAGGCGACTACAAGGAGTTCCCCCT ACCCTGGAGGGAGACTTGCGGGCGCGGGACGCCTTGTCTACGTGAGC GTCTCTTCCCAAGTAGACGACTCCCTCGACTTTGTCCCCTCCGTCGC ATTCCGCCCCTCTCCGCCCTCCTTTCGTGTACGTCTCTGCATTGTAC ACTTCCTTTCGCCTGCTTTCCCACGCTCGCGCGCAACAACGTGGACG CACCACATCGCTCGCTGGAGAAGAGAGAAAAGTGGTGAGTACGTGTT CCGCTCTTTCCCTTCTCCCCTCCGCTCGCGTCGCACCTCTCCGCAGC TTTACCGCTCTCTTCCCTTCCATCATCCGCGTCGTGCACCACTTCCC TCATTTTCCGTGCGGCAGTAGAAA
167	IrLdG	TTCGCTTCGCGGTGCCGGCCATTGGCGTACTCTCGCTTTTTCTTATT TTGCCTTTCCTTTTCATTTCATGAAGAAACAAACTGCAAACGAATCG GACAGCGGCACGACCTGCACTCGCCGCTTACTAGACTATCAGCAGCA CAGCTCCGGGGAAGGATTCTCTCTGCCACAGAGAACAATCTCTTGGT TTTCTTCCCTTACCTCACCGCAACTTAACCGTTGGTGCCGTCTTCTC GCTTGTGTGTGCGTGTAAGTGTGCTCTTGCCACTGCTCCCGCACAGC CTGCCTGATTCTGCGCTGCGGGCGAAATGAAGCCGAGGGTCTTCGAC CCAGCCTCGTGCCACGTCCGTTGCATCTGCTCGCTTGTAAGATGGCT GTTGATCGCCTCCTCCTCCCCATTTCTTCATTTGATTGGCTTCTGGG GCACTGTTCAGCTCCCTTCACACATACCGGAACTCAACCAGGTATCC GTCGACACCGCTCGCCATCGTGCGCGTTCACCGGCCGCACGGCGCCT CAGTCAGCCTTCTTTGCCACTCACTCGATCACCACAGACAGAGTGCA

SEQ ID NO.	Description	Sequence
		GGGTGTCGTGTCGCACAGGACTACCTCGCGGATCGTGTCTTGCGACT TTGGTTGCGCTCACACCTTCTCGTCTTCTTCGTTCTCTCGCGAGGAG CTGCAAATCGTGGTTTCTACGCCTTTTTCTCTTTCCCGGTTTGACAG CGTCTCGGCGTGTGCTGCTGTTATCCCAGTCCAGGGCTCTCTTCCAC ACCTCTTCGGAAGAGTCTTGTCAACGTTGACGGTGCCACGTAGGAAG TAGGCTTGAGGCTTTTCGCGCTTCTTTTTGTCCTAGCCAGAAGAAGC CGCA
168	IrLdH	CGAGCGAGTTGCCTCTGCGCTGGTGAACGTGCCTGCGCACTTACGTA TCAGCCGTGCTTTCTGGGAAGACCTTCTGCGACGCGGGGCGTTGCGC CGGTACAGATGCATCTTTTGCATGGTGCGTGCTCACCACAGTTTGTG TGTGTGTGTGTGTGTTTGCGCGCACCTCCCATCCAACAATGGCGCGA ACGGCTTTCTGTGCATGCGCCCTTTCATTTTAACTTTCTTTTTTTCG CCCTTGTTTTTGTGATTTTCGATGAGCTCAAACACAAAATGAACATC CACATGCACTCTTAGGCGCACTTGCTTTGCGTGTGCGTGTGTGCGTT GCGGTGCTGCCGTCAGCCCTACGCCCCGGTGCCTCCGTCTCTCTCCC ATCGCATCA
169	IrLdI	GGATGTGAGTGGACGAGGCACGTCCCTAGCTTGTCTTCCGACGTGGT GCGCCGTTTCTTTCTGTCGTGTGTGATCTTATTTCTCCTCTTCTACT TTAGTTTTTACATGAATCAGCCAACGTTTGCGTGAGGCCCTCTCCTT TCCTCCCCTCTTCTGCCGCGTGCTTAGTGGATGGGTGGGTGGGGGCA GGGGGAGAGGGAGGGGACGACGAGTTGTCGAGCGATGTCATGCCGCC TTTGCAAAGGCGCGCGTGAGCGGCGACGGGGGCACCCGACCGCCCCT CTGCCGCATACCATCTCGGTAGTCTTTTTTGGCTGCCGATGCTGATA GATCTGAAGTGCTATTCATTCCGATATAAACGAGACTCTATCCCGTT GAGGAGCAGGCGCACGTGTGTGCGTGCATGTAGGGTACCCTCCATTG AATTCGCGCGCACCTTTCTCTCTCTTCTCCCCACCCTTTCTCTTTGT TGGTCATGCCGCTTTCCCAGATGCGCGCCCACTCACGTACACATACG CACGTATTCTCACCTTTTCGTACGCATGCAGCTGCGTGCGCTCACAA ACTGCTGTGTGTGTGTGTGTGCAAAAAAGGTGTAACCGCTCGTATAG TTTCAATTCTCCGGTGACATCCACGCGCCGCGCATCACTCACGA
170	IrLdJ	AGGAAGGATAATGTGAACGGACAGCTTCTCTGTTCTTTTTCGTTTTA ATTTGCGATTGTTTCCCGAAGAAGAAAAACAACAATACCGAAAAGGG ACGGAAAAATGTGCGCTTGACAGAATGGCATGTGCGAAGTTGGCGGC AGCGCACGTGCACACCTGGTGATGGCAGCAGCGGCGACAGTATGCAC GCATGCGCACACCTGGCAACGCCAGGGACGGAAAGGGAAGAGGATAG AGAGGGTCAAGTGTCGGAGGAGGACAAGCACAGAAGGGGAGGGGCGA GGTCGTGACGGCGCGCGTGCTTGTTTTGCTCCGACCTCTCTCTCCCT GTGTGTTCCCACCCTCTCTCTTGATGCTTATCTGCGCGTGTTTTGCA TAGGCACACACGCGACCCGCGCTGTTGCTGTCCGCTGCCGTCATGCC ACCTCCCGCATTTCCTCTCCTCTGCACCCGTAGTGCTCGACAATCGC AGTAACAAAAAAGCGTGCGCTTCTTTTACATGCTTCATGTCCGACCC CTCTCCGTGGTGCGTTCACACTTCAGCGCGACCTCTTGCTCCTCCCC CACCCCCGCCCTTGCCTGATCTGCCAGAGTCGGCAGTACACCACCCT CTCGCTCTCGTCCTCCCTTGCTGCTCAATATCCACGCTGAGACACAC ACCCACGCAGACGCACCAAAAGCCAAGAAGGGGAGAGGGTGGGTGAA AGTGGGCGGAGGAAACCTCTTGCCGCGGTGTGCATCCGTCTGTCTGT CTGCTCCTTGCCTCTCTCGACGATTGGTGCTCGTTTGCTCTCTTAGT GCATATTCGATGCTTTACATATTTCTAA

SEQ ID NO.	Description	Sequence
171	IrLdK	GCGAGTGCGACGTCTTCCTGGCTCTTTCTTTTCCTTTTAGTTTCATT TTCGTGAACGCAAGCATATCACACAAACACCCGCGATGTCGACAAGC GTGTATACGCATACACACATGTCGGTGTACGCCTCATGTGCCCCCAT GGACGTCAGTCCGGGCCATGCCTTCCCCCTCCCCCTCCATCCCAACG CGTGTGCGATGAGGTTTGAAGGGCACCTCGGAGTGCGGAATGCGAGC GCATCGGCCAAGCCAGGTGATGCACCCCCTACCCTGTGCGAGACGCA TGGCTGCAGGTGTCTATGCTCTTTTCCAGTTGCGCACAGCGGCAGCT GTCGCTGTAGGCTGGAGGAGAGTTCCTCTCCATTAGCGGCGCGGCCG CAGGTGCACTGTCGCAGCAACCAGCACAATCTCCTCTTATTCATTGA TCGTTTTCCCATCTTTGCGCGTTTGTCTCGCTCCTTTCCCTCCTTCC TCCCTCCGCGTGCGGTCCTCGCACGCCTTTGTGTGCCACGCGCTCCT CCGTCACTCGCTGCCCATTCCCTAACAACGCAGCCCGTCGCGTAGCT TGCCCGTGCTCAGGGAAGCGGACAAGGCTCACCGCATACCTGCCGCG CGTTACATGGAACCTATACGCTGCGCACCCGCAGGTGACACGAACGC ATCAATCGAAGGCAACACGCACGCACACAG
172	IrLdL	TCGTGCACGTCTTTTCATAGGCGCCTGCAGTGATCTCCGCTAACGTC GCAGTGATTTGCTCGATCTTTTTTTGTTCGGTTACGTTCTTTTTCGT CATTTTTGAAAACAAAAAACAAGCAAATAACGACAAACTAACAGCGG CACACCCACACTCAACAAATAAATCGCGAAGGAGCGAAGGCGACGCC TCCTGCGAGGCGCCACACTTCCCCGATGGGACCCTCTCTACTTCGTA CGAGTCACATGCCGAGGCGCTGCGTAAAGGACCATGGCGCGTGACGC GAGTGGCAAGAGCCGAGGCGGAGAAGGGCGCTGGGGACGGCACTCTC GATGATGTCAGCAAAGATGAAGGCGATGCCATTGCGCCAGCGCAGGT GTTTCGGCCGTCGTTAGCCACTCGCCGCCATGGCGCTCTTTGCGCGT TGGCTCAGGGAAGAAGAAGAGTGCAAGCCGCACATTCAAAGCGGTAG AGCCTCAGTCATAAGGCTCCGAGTTTCGGGCTGTGTCCGTCTCTCTC CTTCCCCTCCCCTCCCCTCTCCTCTCCGTTTCTTCCTGGTCCCGTAT TCTTCTTCTTGTCGAATATGCCTTTTTCTTGTGTTGCCATCCTCCAT TACACTCACCTCACTACTATACGGTGTGTGTCTCTTTCTTGCTATTC GCATGTGGACGCGTGTGCCGTCCTCAATGACCGTGCACTCATCTGCT TTCCTTCTCTGCCTCTCATTGGACACCTACACTCGTTTGGCCCTCGT GCTTTCTAGTGCACTTTGCCAGGAACTTGTACCGTTTTAGCCTTGCT GCTATCTCACATTCGAATCGGCACCGTTCCTGCTAGTTCGAGGACAC CCTTGCCCAC
173	IrLdM	GATGGAAGAAGCACGCCCTTGTGCCGCACCGGCGTGGGGACGCATTG TGCAGGCTGAAGGCGTTTGCCTCTCATACGATCGGCGCTTCGAGTAC CTTTGGGCTCCCTGCGTCGCACGTGTAGAGAGCGGCCCGACCCCCCC CCCTCGCGTCCGTCTTGTACGCGGCACTGACTGGGCACGTATACGAC GTTGTGAAAACGCCCCGATCGTTTCGTTTTGCTTTTTTTTTTGCTTT CCTCTATGATCATCATTTCACCGCCCAAATCCCTACACAAAGCATGC GCATCCACGCATCCACCATGGCAGGAGTTGTCGCTGGGGGTTTTCTC AGCGAGGACGTCATCTCCGTATTTGCCCGTACCGTCTCGCGTTTCTT TCGTCCGAGTTCTCGGACGGCGCGAATCTGCCTCCACGTGCCACTGA CTATCCGCCGCTAAGTTTGCTTGTGTGGTTGACTTTCAACAGCGAGC GGCGACAGTTGGTGTGGCAGGCGCGGCGGAAAAGCAGACGCGGATAT CAACACTATGGATGCTGAGTCGTTGCCAGCTCCATGGGCGGCAGCAT TACGTTTCGCAGCTTGCCATCCAGAAGAGCGTCCCTCCCCCAACCAG GTATCGCGCTGTAAATGTGTGTATGCTCCGCGCGACCTCAGAGGACT

SEQ ID NO.	Description	Sequence
		GTAGCGCGAGCGGCCCTATCACCCACCGCACATGGGCTGCTCTGCGC CTCTGCGTTCTATGTGCGTTTCCACTCTCCGCTTCACTGCATCACCG ACACGCCCCTCACCCCCTTCCCTCACACACACAAACACACACCACGG CAACGTCCTACACAATGCGCGCCTCCCGCGCGACTCCACAGTAAACT AGGTTTCTCAAGCTCGAAGTCAATCCACCACTATCTCATACTATACA CACCCCATATCCTCTACCCCTTTGACCATTCAAAACATCCGCC
174	IrLdN	GACCACGGCCTGCGGGGTGGGCTCGATGTGTACGTGCTGGAGGTGCG TGTGAGCCTTTGCGAGGCTCACGCCCACTCATGCGCACACCCGCAAC GCGCCACTGCGCATGGAAAGCTACAGGCACACGCTCGCTCTCGTTCA CTTCTTTGTATTGATTTCTGTCTTGCTCTTTCTGTCATTTCTGTGGC GGTATATGACGGTCACCGAGGACGAGACGGGTGGGGGGGGGGCGAAG GAGGGCCAATCTCTGATCCCACGCATCTTCCTCATCCCCACACCCTC CCCGACTCGCGTGGCCGAGCATCTCTACCGACGAAAAACAAATATAT GAAAAAATAAAACTCAAACACGAAAGTAGCGCCCCACCCCCAGAAAA GAGGGATGGCGAGCTAGCAGCTCGTGCGATGCTTATCGAAGCGCACA ATGCTACGAGCGCAACACGTGTGTGGTGTGCACGTCTCTTCGTGAGC AAAGGCGCTGCTCTAAGAGGAGGAAAGGGGTAAGGCGAGGAAGGGTG AGGAAAGTGCTCATGTCGGCCACTTCCCTTTTTAGCGTTTATCGACC TCAAGAGCAGCTTCGCAAAGAATACAAAAACGGAGTGTGGTGTTCAG CCACTACCACTGTCCACACATATTGCGTTGCGAGCGAGCAGTGCGCT TCCTCTCGCTACGTAGATGCTCAGCTGTGGTGCATCGCCGTGAAACC CCTCTCCCCTCTTCATCTTCGTTCGGTACCCCTCTCCATATGCTGGC ATTCTAGGGGCTCTAAGGAAGTCACGTTGTGAGCTCTATGTAGTGCT GTGCAGCCTCCTCTGCGCATACTCTGTTGTCTCGTCATCTCCCTCTC CATGACTGCATGTCTGTGAGTGTAAGCCACATTCATCGCTTCGCATT ATTTGGCA
175	IrLdO	GGAGCGCAAATGTGTGGAACTGATACGCGACTGCAACGGGTGACCTG TTTGACAGCTGGTCTGCCTTCGCTCCCATTTTTGTTTTCTGCCAGCC GCTGCTGTAAGCTTTGTAGTAACAAACAGTCTCATGCAGGGCGGGTC GCGCCTACGTCGTTTTGTTTTCGTCCCTCTTCCTTTAGGAACTAAGT AGGAAATACTTCACGCCTGTCGTGTGTAGTGAAAAAGGCCGAAAAAG CGCAGAGAAAGAGAGCAAGAAGCGCGTTGCTGTGCGGAACCACGCAG AGCAGCGGCGGCAGGTTTGCGAGATGGCTCAGGGTAAGACTCATGTG CGCCGCTGTGTGTTGCATTCTGATCGCACGCATGCCTGTGTGGGTGG TGGGCCAGTGCTTTGTATGAGTATTCTCTTGTTCAAGAGGTGCCGGA TGGCGTTGCTGATGAAAGGCGGCTTCGTGCTGCTGTGCGTCCTGCTC CTCTCCGCGGCTGTCGTCGCCTGTGTTATGTCAATTGAATGTGCTTG CTTCCTGTGCTGGCCTTACAACCCTTTGATTGCTTCCTTTTTACTTC CCTGTGTAGAGCATATCTGTACGTGTGGTAGTTGCTCAAGCGCGTGC GCTTTGGTTAGGAGCC
176	IrLdP	TCGACACAACTTTTACGAAAAGGAAAGGAGAACAAAAATACTAACTT GCTTGTTTCCGTCTTTTTTGTTGTTTGTTTCAAGTTGGGAAATCTTA GCACTTAGGATATTACAAAGAGCTTCCCTTTTTTTGTTCGCCGTGTT TGGGCAAAGTGGGAAAATGAGGCGTTATATTGAATCAGGGTCTCAGC GCTTTGTGATCCTTTTTTCCGCAGCCCTAAGCACGCCTTCTTTTCTG ATTTCCTTTTATTTTGCTGGTCAGCTCTTCAGATTAGTGTAGTCAAG CAAACAAAAGAGTTCTTGGGAAATCTTTAAGAAAAGAGTGAAACCTT GGTGAACTGTGGCTGGGGCAGCAGCCACCACAGTTTTCTGTCGATAC

SEQ ID NO.	Description	Sequence
		ATTCTGGAGTTCATCGAAGCACGTGGCGGCGCAAGTCGCCCCTACCG CAGCAGAGGCTCGGTAAAGAGAGCCAGCATACCTCTGATGAGCACGC CTTGCCTTTTTTTTTTTGCAGGGTCGCAGTGATCTCTTTCACGTACT GAAGCCCAACTTCATGTAATGATTCTAACGTATACATTCCCCTCTAT TCTACTCAAGATTTTCTTGCGAGGCCATCATTTCATTTTCGTTGATA TCTGTTATCAAAAATGCGCTTTGCCTTGTGAGCTACCAGCGTCTTTC CATTCACATGAAGCGGCGCTGATA
177	IrLdQ	AGAGGGAGGAGAGATGAAGAAGAACGCCTCAGCCCTTCCACCTAGCC GTGATGCACGGGTATCACAGACCAGCAGGCATGCAGAGATGGAAAGG GGAAGAGGTCAGCAGGCAGTGACGTCTGATCTCCTTCAGCGTCGGTC GCTTCGGCCGCTTCCTCTCCGACCTCCCCCCCCACCACCACTGCCAC CACTCCTCCTCTCCGCATAACCTATCAGCAGTCGCGCACGCCTCATC AATACGCACGCACACCCGCCGGTGGCGGGGCGCAGGATGGAGAAGGG CAGCGGATGGAGCTTCCCTTCTCCCACGCCCTTTTCACCCCACCACG CCGTGCGGGTTTTGTGGTTTGTGCGTGTGTTTGTGCTTTCTAGTGGG GAGAAAGGCCTCTCCGCATCGTTCAACTATTTCGCTCTGCGTGTGAG CACGCGTGCGCACTTGCGCGTTCGCGTGCTCGTTCCTTTCTTGCCTT CTTTCGCCCTCCGCGTGCGTGCGTGCGTGCTCTCCCATATATATTAT TCTGGTTTCCGTTCCGTGTACTCTTGTGTTCTTAGGAAGCTGCGCAG ACCCGACTTCTCCCATCGTTGTGCCCTCCCCCTCCTGCTGCTGCTGC TGCTGCGCTGCCCGTGGGTGTGCACCCCAGGGGGGGGGTGTCTACGT GGTGTGTTCCTGTGCGTGACGGCGAGGGCGACGGCCGTTGGAAGCGC ACATTTTTTCCGTACCGTCGAGAGCCGCTCCTCCTCCCACCGTGCCC CTCCTCCGCCCCCGCTACATGTGCACCCCCCCCCCTTCACTCTCTCC GCATGCACATCTTCCTTCTCGTCTTCGCCTTGCCTCGCCTACCCACC CGTATAGCAGTGCACCAGCACACACGCACGTTCTTTCCTTTCATCCC TCTTGCTCTCTCGCTCTGCTGTCCTCCTTAGCAGGCTCCCCCTGCAG CGCTACAGCAGCCGC
178	IrLdR	GCTTCATGTACAATCATCGCGCACCTTTCTTTTTCATTGATTAGGGC CAACTCCCCACCGATGTAAAAAAAATCCTGAAAGTGGGATGACACAA TTCAGTGACAATGGAAAAAAAAGAAGCGTGATTGGTATTCAAGCTTC ACACACGTATTTCCCCCCATACACAAGGATGTGTTATTGTTTTCTAC TTGATTCGGGTACGCTCACCACAGCGCACCTCGTCTGAAAAGCACTT GATACTGTTCCTTCTTTCGCGTATGTTCATCTATGAAAGAGCAACAT TATTCGGCCACCTGTTTCGCGTGGGCACACGCACACTAGGGCTATGA TGTTTTGCTTCATCGGCAATCTGTGCTCTGCTGAGGCAGCCGCTGTT TTGCTTGGTGCTCTTTTTCCCTCTTCTTTGGTGCAATGCATTCCGCT TGTCGCAGCAACCATTCTCCCACTCTGTTTCTTTCAACTGTCGTCGC TTCTATTCCCTCGATCTTTTATCTGGATGCATGACAATATGCAGAAC AAAAGCAAGACCAGTGAGTTTGGTTTCGTTTCCACCTGAAAA
179	IrLdS	GCACAGATGTAGTTGATATGGGGAATGCGTTTGTTTTACCATTTCCT CCTTCGCTATGAAGATAAAAATCAAAAGGAGGTTCAACGCCGTTTGA TAGCGTGGCTTTTATTGAAAGCTCTAAGCCAGCAGACGCAGTTTTGC AGTTTGTTCTCTATGTAGTCTCAGAAATTTCCGTTCATGTATACTAG TTTTTTGTGTGTGTTGTGCGAAACAGAGTAAATACAGCAAAAAAGTG ACCGCGTGAGCAGTGCGCCTTAGCTGCAGGTCAAGGATGATGTATGC AGTACGTATGCTGCCTAGTTTGCATGCAAATAGCATTTTTTCTTTCT CCAGCACTTGGAACGCCAAGAAAAATATACAGATGATACGTTGCCCA

SEQ ID NO.	Description	Sequence
		ATCTCCTGTTGTTGGTGATTGCCGCATCTCTTATGCTTCGTCGCTAA AAGCTGCGTTCGCGATGCGCTTGTTGCGGAAGTAATGCAGAAGCCTG GCAAAGAATGTGCATTGTTGTCTCAGCTGTACTCTTTTCCCTACACC TCGTGTCTCTACTGCTTTGCGTAGTGTGCTCGCTTAGTTGATGGTTT GAATATCACTCTCAAGGGATCTTTCCCCTCTGTAGCA
180	IrLdT	TACAAACTCAACGTCTTCATGGCATGCGCCTGGTTCCTAACCGTTTC TCACACCTGTGCTTGCCACAGCACCAATGTGCGTGCATGCACGTGTG TGCGTGTTCGTTTGCATGTTAACCTCTTGATGTACGTATGCATGCTC ATCTCTTTTTCTTCCTGCGTGCGCGAGTGTACGTGCCGGACGCCTCT TTCCTCCAAGGCGGCGCTTGCTCGAAGCACAAGCGTAAAAGAGGGAC GAAACGAAACGAGAAAAACAAAAAGATGGGCACGCCTAAAAAGAAAT GGCCCCAAAGGGAGGTGAGTAGCCGAGGAGCTGTGCATCAAGGCAGC GGCTTCCGAACTGCTGCTTACGCCACTTGCGAATACCGCCGCTCATG CGCGTCTGGTTTGAGCACAACTGCGGTATCTGCTGCTCTCCCACGCC TCATTACTGCCCTCATTGGCGCGCCTATAAGCGCAAAATCACACGCA TCCCCTCACCCACGGCGGTGTCTTGTCGGGTGTGTTATCTCGAGCTT GAGGGTTTGGGGCGGGTATAGTCAGGTGCGCTCAAAACCTTCAACGA CATTTGCAAGGCTGCTTCTTTGTCGGTTACGGAGTCATTTAGGGCAT TACACGCGGCGTCTGGCGTCTTTTTGTTATCCTGGTCTGCGTGGGTG CAAGTCCAGACACACACACGCATACACACACACACACACACATATAC AACATTATCCTTCC
181	IrLdU	AGAAGGGGCTTTCAGGCACTTTCCGGAAGGTTTAGCTCTTTCTCAAT TAGGTCTTTTTTCCCTTTTCCCTCAGCGCGATATGCAGCACTGTTTT ATCTAGTTTTCCCTGATGTCTAGCGCGAGATGGGCTCTCGTGACTAG TCTTTTTTTCCACGACTCTATAACCGAGAAAACACACACTGTACATA GCAAGCAAGCGACATCATTCTGTAGCCTGCCCAAAGTTTCAAAAGGC TGTCTAGGTACTCTTCCGCGGCTCCAACTTCTTTGCTGTCCTTTGCT TTTAGCCGCTCACATTACTTCTCCGCTACACCGAGCTGTCCAGGTGG CTCTCATCTCTCCTTGACTACGACAATGCGGAAACTCTCTTCCCCCT TCAACTTCGACAGTTCACCGCTTCTTCCCTGCGCCCTACACGGCTTT ACTCTGCACACTATCCGGAAAGCTGTATGCTGAACGCCAGCCACTGA CGATCAGAAGTCTGTTTCGTTCCCCTAACTACTCCTTTTCCTTTCTT TTTTGTGTTCGTCTTCTCCCTTTACAGACAGGACACGCAAACACACA CACACACACACACACA
182	IrLdV	GACTGCAAGGGATGTGGCGTTTATAGGCTGCCCTGCCATCCCTTGCT GTTTCTATCAAGGATTAGACTTGTTCGTTATATGGGGGGAGGACAAG AGAGTGCTAGCGCTTCTTCTTTTTTCCCTTTCTTTTTGCTTTGCTTT CTTCGTGTTGGCGTCCATGCAAGCGTTCTGTCGACAGCTCTTTGCCA ACCTGCGCCCTATCTAGCAACATCGATGTGAAAAGAGTAGAGAAAGC TAACGATGCGTGCGCTGACTGCCGTTTTCATGGGCACAATTTTGAGA AGGAAAAATTGGAGAATGGACAGGATAGTGAAATTAGCGCTACGACA AGGACGTGCGTCTTTTCTCTGTCGGTCATTAAATTTTTGGGCTTTGT AACAATGAAGGAAATCGCACAGAAAGGGAAAGTATTCATCGATGGTC AATGCCGGAACGGTACATCGAGCGTGCTTTCTGTATGCAATCTGAGG ATATACGGTACTTGTGTGGCGCTGCTGTGTTATCGGGACGAGGGGTT GTAGCGGTCGACATTATGTGTTCCCGGCGCTTATCGCGCGCCTTCAG CGTAAGTGCGGTTACTCTTAACTGCGCGAGAAGGAACTGGTGGCCCA TGAGAATGACATCGGTCTTCTCTGCAATGCCTCCGCTGTTTGTTGCC

SEQ ID NO.	Description	Sequence
		ATGCTTTCTGTGCTATTCGTCTACTTTCCCTTTTCTCTTACTCTGTT TTGCTCTTATTGGTTTTCCTTTGCGTGTACACGGTGGGCGCGATGAT AGCCGTGCAACGTGACTCTGCGAGCATGTGCACCAGGTGGCATTGAA AA
183	IrLmxA	GGTTTATCAGCTCCAGGAACGAATGTACTTTTATTATTATTGTTTCG TGTCATGTAATTGACTCTATTTAAAACCAAGCAAAGCAACTCTTTAC CAGGGAAGCCGACAAGGCTTTCTATTCCCGAAGAACCTTTGCGGCTT TCCAACTCATAGGAGAGCCGTCTCTTCCCCACTTCGGCTTCAATAAA GGAAAATGGCGTCTTTCGAGTAGAAAAGGGCAGATGCGGCGCATTGC GTGCTTTGCACCTATATCCGCCACAGCTCGCATTTCGACTGCGTAGA AAGTAGTGGAAATATGTTCTTCACCAAGACCGTGCCTGTTTGCTCTC TCAATTCTCGTTTCGCTATAACATCCCTTCCTCTTTAAAAAAAAATC TGTTGTGTCTCTGCAGCATTTCTGGTACCCGAGCTGTTTCCTCTCGC TAGGGAAGCAACAACAGCTACTGCTTGTTGTTATTAGTGCGAAATAG AGCATCTGAAACGGAAA
184	IrLmxB (40S ribosomal protein S19-like protein)	ACCCGTGACGGCATGTTTGCCTCTTTTGCATTTTATTTTATTTTTAT TTGCTAGTGAGAGATTCTCATGCGCGTTTATAAAAAAAGAGAAAGAC AGGCGATGAGGGGGCACATCTGTGATCCTTGTGCACCGTGAATGGCG CCTGCCTGCGCCTACCTGAGAAGCAGTGGGGATGTCACGCCTCTCAG ACACACGTTCGAGACAGGACGTTGTGAATGCTGTTTCTCCTTCTCCG TCTTCCTCGCGCCTGCTGGACAACTGGTAGCCAATCGTGTTGTCCTT TTCACCTCCGCTTGATAGGGTCACAAGCGGCAAGGAACGCGGAGGGG GAGGGGCCGTAAAGGTAAAGGAGCCCGTTTCTACAGGGGCACCGTGC GTCATGTTGGCAAGATGATGTAGAATTTTTTAAGGGGCCGGCCCTAT CCCCTTCTCTGTGCTCCGCACGGGTCGCCTTTTTTTCTGTCGCTGTT GTTGTCGCTACTCACGTTCTTACCCTCCCTTTCTCTCTCTTTGGAGC TGTCGTCGTCACACAAGCGCTCAACCTCTTGCCAGTGAGTCTGTTGG ACAACGTTCACCGAGTAAAAGACGTCTTTGCGAGCCTTTCTATGACG GAAGCTCGGAGTC
185	IrLmxC	AGTGTGCGGGGCAACCACACGCGAGGGACGAAGACAAGGATAACAGA AGGCAACGCGGCAAAACGGAGGACGGCCGCATACAAAAACAAACAAA CAAACAGGTGAGCGGACGCACACCTGCCTGAGAAGTGCGCTGCCGCA GCGTGTGTGTGTGTGTCGCCGCGTTGCGGTCTGTACCCTCCCCCCAC TTCCCCTGTCTGCGTCTCTCTCTCTCTGTGTGTGCGTGGGCTCATTT TCTCCGTTTCTTTTTTTCGTTTTGTTTTGTTTTATTTCTCTTCGAAA ATGAGAAAAACGACCCGAAAATGGTCTCCGCCGGCGTTGTATCTCTG CCCCCCCCCCGCTGTCCCAGAGCGTAGGGTGCACCGTCTGCTGCTTC CCCAGACGGCGCGCAGGATGGGGCGGCAGTCTCGGAGGCTGCGACGT GTGTCATGATAGCTGTGACGGCGGGTGCGTACGGCTGCTTCTATCTC TGCGGCGATGCACCGCCTCGTGTTGCGTTGGATTTCCATCCAACTCC TCTCCCCACCCCCACCCGAGGCGTGCGTGTGCGGCGGTGTGCGGTGG CTCGCACACGACACCTTGTGTTTCCATCGCATGTTGCGTCGCTCGCT GCAGTTGGTGCTCTGAGCGTTTTCTTCCCCCTTCTCGCAGTCTTTTT ACCCCTTGCTTTCATACTCCACAGAGAAAAACCGCTCCCGTCTTGCA GCCGGGGCGTGCCTGCGCTGCCCACCCCGCACCCATTTCCTTTCCTG CCGTTGTGCGTTCTGCACATCGTTACTC
186	IrLmxD	ATGTGTCTTTCTGTGCGTTCGTGAGGGGAGAGAAGGATTGCCTGCTT TTTCACGCGCGCGCTCTCTCGTACACCAAAACACCTCTTCCCGCGTT

SEQ ID NO.	Description	Sequence
		CACTGCGCCACCGCCACACGGCATCTCTTCCCCCTCCCCTTCGCTTT CGCGGTGATGGTTGGAGTGCGGCGGCGGCGGAGCTTTGAGCTCGTGT TTTCTTCGCTTTCTTTATTTCGTTCTCTTGTGATTTGACTTACCAAA CACACCTTTCCTTCCCCGAAAAAAGGTAAGAGGCCACACAACGCAGC ACAGCACACAGGGATGGAGGGAGGGAGGATTGGGGGCGAACGGGGCA GCGGATAGGGCTGCGCGCGCACCGGCGGCTGAGGCGTCGTGTGCATT CAAGCTCTCTCTCTCTCTGTGCGTGTGTTTGCGGAGAGTCGCGCTCG AAGCCCCTTTTCCTTTCATCTCCTTGTTTTACACAAGCGGGGGTTCG GGCAAGAGAGAAGGAGAGGGAGATGGAGGGGGGGACGGGTTGCTCAG CGGCCGCCAGTCTTCCCGCCCCCTGTCCTCTCCTTCTGTCCAAGTCC ACGCTGGAACAGCGGTGCTGCTGTTGTGCCCTCTGCCATGTACATTG GCAGGGAAGCAGCGCACAGCGCAAAACGTGCGCATACACGCACGAAA GCAAGAACCG
187	IrLmxE	TCCGCGTGCCGTAGCTCGCTGCGTATGAGGTACTCGGTTCCAGTGCA TCACGCGGCGCAGGGCAACACAAACTTTCTTTTTGTTTCTCTTCAAG TCAAAAAAGAAAAAGAAAACAGCCATACCGCACACCATCCATAACAA GGGGCGTGTGAGGGGCGGCGGCTCTCGGGCTTTACCCCGCCAATGCA GCAACACGCGGCTTGTACGCAACGCTTCTTTTGGCATGTCACGCTGA ACAGAATCTCTGCGTACAGCAACCACGTTGCCATCGGCCCGTCACTC GCTCCTCTCTCCTCCAGCATTCTTGAGTGACTACAGGTATGTTTGGT TCAGTGCGTATGCGAGCGTTAGTGCATCCCCTATACAAGCACGTGCC GCCAGGGCGCGTATCTTCGCAGTGAGACGCACTTGCTTTACCGACTA CCTGTGCTTAAGTCCCCCCCACTGACCTAAACAAACTCTGACCATCG CATCACCTCTCGTTTCGTCGTCGTGCCTCTCTCCCTTTCTCTGCCGA TTGTGATTCCTCTCCTCATGCCATTCTCCTGAAATCCCTCATCACTC TTCCGCAACAGCTCCTTTTTTCCCCACCAAGG
188	IrLmxF	CGTATTCGGCAGCTGTCATCACTTTTTTTTCTACTTTGGCAAAAGAT CAAGCGAGAAAATCAAAAAACAACAACAAAAACAATATAATGGTTAA AAAGTTGTGCGATCACAGTGCCTAACTGCACCTTTTCCACGCGAGCT ACTCCTGTGCTCTGGTGCCTTCTCTTTTGTGACAATCTCTGTGATAT CGCTTGATGCTCTACTATTCCTTCTGTGCTATCATCTCTGTTCTCTC TTGAACCCCTGCACTATTCATCTGTGTGACGTGAAGCCAGATTGCTC TTTATCCTCTCGCCAGCTCAAGCTCGACAAGAAA
189	IrLmxG	GTGCGGCACGCATGAATTTACAGGCCAACATTCTGTTCTGATTTTGG TTTTATGGGAGCGAAAAAAAAAGCAACGTTAAAGATGACAAGCGCAG TTGCGCTGCAGGGGTAGGTATGCTTTCTGATGGGGAGATGCACCGAG AAAGCTGAGCGTCGTCGTCTCACACGCTGAAGCGAAAGCAAGCCTGA TCGTCCGCGCGCTGCTTCCGCGTTACAATGAACTCGTGAGTTAGCAG ATTTGCCTTTTCGGCTGTTCTCCCCCCCCCTCTTCCCCGAGTGCTGC TCAACTTCCTCATGTCTTCTTGTTTTCTTTTTTACTTTTGCCTGTTG ACACGGCATCTTTACGCTTCGCATTGCGTTTCTGGTGGCATTCACTG TTTGTCGCGAAGTATCCAAAGAGTTTAGCGGCACGTTCTGTCACAGA GCCGATTGCTGCTTTCTAAAAGTAGGCGAGGATGCGCTTAGA
190	IrLmxH	AGATCTCGCCCAACGAGATGGTGTGAAAGGGATACGTATGTGAGAGG TGACGTAACACCCCCACACACACCCCACATCCCACACTCACACACGT CGTGGGTGTTCGCCTGGAGACGTCTGCGCGGCTCTTCTCTTTCTGAT TTCACTCATTTCAACTCAAACGCGAACAATCAAAAGTCGACTCGTCT CACCAGCGTGTGTGCGCGGCGTTCCCATCCTCTCTGCCGCCCCCCCC

SEQ ID NO.	Description	Sequence
		CTCCCCCTCCCCCTCACACTCACACACACCCTCTGCGTGCGTGTAAG CTTCTCAGTGGTGGAGGGGCGAAGGAGTGCCTTACAGGCGGCGCCGT AGTTGGCGGTGTTGTCCGGATTAGTGTGATGCGAGTGACCGCCCCTC ACCCCCCATTCGTCCATCCCCTCGATTCGTTGCTCAAGATGCGAGCT TGTGCGTTCGTCTTGCCCCCATTCTCTCTCTCTCTCCTCACTTGCTG CTCTGCATACTCGACTGTGACGGTGGTGCATCCACCCACTCACCCGC TTCGCGGCGGCTCATGCGCACCCCTCGCCCCAGTGGGCAGTGTGAGG GCCGGCGGAGCCGCGCTCGAGTCACGTCGACACACTGCCTGGTCATG TGGGCGGCGCACAGGCGTGCTCGCCGTCGCAGGTCGCTCCGACGCAG CGCCCGTCCAGGACCTGGCCGCCGGCATTAGTGGTGGTGCGTCGCTC TGACCTCCCCTACCTTGTAGGTGCTTGGCCCTGTCACCACGCGACGT GGCTTGGCATTGGCAGGGTTAGGTGGGGGCTGCTTGGCGTCCGCCCA CTGAGTGGGGGCGCCGTGCCCTGAGATGCCATGCGCTGTATGAGGTG TACCCCGGTGATCAGGGCCACGAAAACACTGCTGTGAACAGGACAGA GGGACATCATAGTGAGCCTCCTCAGTGCCCTCTGTCATCGCCTGCCA TCCCTCGGTGCAAGGAACCTCGAGCGTCGTCACCGACACACCG
191	IrLmxI	AGGAAGGAAAATGTGAACCGACAACTTCTCTGTCTTTTTTCGCTTTA ATTTGTGATTATTTCCCCAAAAAAGAAACGCAACAACCGAAAAGGGA AGGAAAGATGTGCGCTCGACAGAAAGGCGTGTGAGAAGTTGGCGGTA GCGCACGTGCGCACCCGGAGATGGCAGCGGCGGCAGCGGTATGTACG CATGTCCACACCTGGAAACGCCAGAGATGGAGAGAGAAGAGGGCAGA GAGGCTCAAGTGTGGGAGGAGGACAAGGACAGAAGGGGAGGGGGCGA GGTAGTGACGGCGCGCGGGCTTGTTTTGCGCTTCCCCTGTCGTTTAA CTCCGATCTCTCTCTCCCTGTGGGCTCCCACCCTCTCTCTCTCGATG CATATCTGCGCGTGTGTTGCATAGGCCCACACGCAGCTCGTGCTGTT AGTGTCCGCTGCCATCAATGCCACCTCCCGCATTTTCTCTCCTCTGC ACCCGGTGTGTTCGATAATCGCACTGGAAAGAAAGGCGTGCACTTCT TTCACATGCTTCATGTCCGACCCCTCTCCGTGGTGTCTCTACACTTC AGCGCTACCTCTTGCTCTTCCCCCACCCCCGCCCTTGTCTGAGCTGC CAGAGTCGGCAGTACACCACCCTCTCGCTCTCGTGTCCTCCCTTGCT GCTCAACATCTACGTTGAGACACACATCTACACAGAAGCGCACCAAA AGCCAAGAAGGTGAGAGGGTGGGTGAGAATCGACAGGGGAAGCCTCT TGCCGCGGTGTGCATTCGTCTGTCTGCTTGCTCCTTGCCTCTCTCAA CGATTGGCGTCCGTTTGCTCTCTCAGTGTTTGCTCGATGCTTTACAG GTTTTCAAA
192	IrLmxJ	GTCGGAGGCATGCACCACTCTCCAAACCGGCAACTCTCTTCCCTCTA CGTGTAGGAGTGCTGGCGACGTGCGCAATGCCCCGTGCACTCTGCTG CGTTGGCGGAACGGAGGAGCGACGTTGGGAGGTGACGCCCTCGTGCG TCTCTTCTTGTGCGCTCTTTTTTTTTTCGGTCTCTGACTTTTTTCTT TTTTCCTTTGAATGGCTCATTTCAGTACCTTTTCCCTTCACAACGTC CAGCGAACATATGCGCGACAGCGGCACGGTGCTGGTGGGCAGCCACT CTTCTCGAAGGGGACTGCCGTTATGCGGAGAGCAGGGCGGCCCTCTT GAGGTTTCCTGCAGGTGAGACAGCGAGCGTTTAGAAGGGGAGCTGAG ACACCCAGCCACCTTGCTACCTCGCACAGCTTCTTACGCAACACCAC TCGCGTCTCT
193	IrLmxK	GTCAGCTGCTGCGTCTGAGGACTCTCGCTGGCTTGTCTGGACGCACA AGGGCTGGATGCCTGTGCCTCTGTTTCTGTTTCGATCACGCCTTTCT TTCTTTTTTATTAAAATGGTGTTGGTCCGTGTCCTCGAATGGTTCTG

SEQ ID NO.	Description	Sequence
		GTGTCTTAACAAGTGACTAAGCAGCCGCACGAACAGTGAAGGGCGCA CCCACGAAGCATGGGAAAAACAATGCAGCAGCAGACAATGCACACGC ACACGCACACGCATGCACAGGAACGAAAAAGATGGACACCCCAAAAC AGGCGAACCAGCGCACGAGGGAGCGGGGGGAGCTTAGGCGGGGAAAG AGGTGGTGGTGGTGAGGGAGAGGGGCGCGAGGGAGCGGTGAACAACA CCAGCAACACAACATCGCGCTCTTCCCGGCATTGTCCTGCTTGCTTC TGTCGTGCGCTCAACTATCCTGCTGCTTCTATCGCTGACTGCTGACC CTCCACTTCTTCTGTTGAACAACCCTATGCGTTGCGGTGATGGCACT GCGCAAACCACATCCACAACGGCATGATTCCCATGCGCATGTTGGCA AATTGGGTGCGCGCGATCGTCACAAAGAAACCCGCGAAACACTCGCC CACGCACTCGAG
194	IrLmxL	TCGTGCGCATCCTTTCACACGCGCCTACAGTGATCTCCGCCAACGCC GCAGTGATTTGCTCGCTCTTTTTCTTCCCTTTTTGGTTACGTTATTT TTCGTCATTTTTGAAAAAAAAACCACGACACATAGACACGAAAGTAG CGAAGGAGTGAAGGCGACGTCTCCTGCGAGGCGTCCCACTGTCCCCG CTGAACCCTCTCTACTTTGTACGGGCCACGTGTCGAAGTGCTGCGTG AAGCACTATGGCGTGTTACGCAAGTGACAAACGACGAGGCGGAGGAA GGTGCTGGGGACTGCACTCTCGATGATGTCAGCGAAGAGGAAGGCGG TGTCGCTGGACCAGCGCAGGTTTTTCAGATGCTGTTAACCACTCGCC GCCATGGTGCTGTTCGCGCGTTGGCCCAGGGAGGAAGATGAGGAGTT CAAGGCGCACATACAAAGCAGTGGCGCATCAATCATAAGGCTCGGAG TTCGGGGCTGTGCCCGTCTCTCTCCCTCTCCCTCTCCTCTCCTCTCC GTTTCCTCCTCGTCCCACATGCCTCTCCTTGTCGAATGCGCCTCTCT CTGGCGTTGCCATTCTCCATTACCCTCTCTCCCCTACTCTGCGGTGT GTGCGTCTCTGTCTTTGATATTCGCATGCGGACCCACGCCCATGTGT CGTCCTCAATGACCGTGTGCTCATCTGCGCTCCTTCTCTCCGTCTCA TTGGACACCTGCACTCGTTTGGCCGTCGTGCTTTCTAGTGCACTTTG CCAGGAACTTGTACCGTTTTAGCCCTGCTGCTATCTGACGCTCGAAT CGGCACCGTTCCTGCTAGTTCGAGGACACCCTTGCCCAC
195	IrLmxM	ACCGGCTTGCCGGATGCCGTGTGAGTAAAGGAGGGGGGGGGCGTGTG TGGTTGCCGCAGACGCTGTCCTCGGCGCCTGCGGTGTGGCGCTTCCC TTCTCCTTCTCCTCCGGCGGTGTGTGTCATGCATCTGCTTGACTCCG CCCCCTCATAGATGCAACTTTTGTTTTCTCTCGACATTTTATTTTTC ACCTCCCCCTCCCTCAATGTGAAGTGTATGTGACAGCGTACTGGACA TGAAGTAGAACAAGAAATGCCCCTTTGCTGCGGAGCCGCAGATGAGG GTGGTCGATCGCGTCTTGCGGCGGGTGCTGCCGTCTCAGCAGGGGTG TTGGAGTGTGACGGCGACACGCGTGAGGAGCATCCTCTTGCTCTCAC CTACGCGCAGCTGTTCTAGCCTCTTGTCGCACTTTCTGTTTCACACC GATTCCCCGTATTGATCTCTGGGTCTCGCCAGGGAGCTGGCCCGTTC GAGCTGCAAGCAACTCAGCTCGTTTCCCTACCACCTCCAATCTCTCT CCCTTCCCGTCACCCACCCCTCTTCATGCCTCTGCCACGGTGTGCAC ACACGCATGCACACACCCGCACGCGGAAACCATGCAGCTATTGAACA CACGCGATTTTTATTTGTTTTTCTCTAACCCCCTCCGTCTTTGTAAG AAGCGATACCACCCGACGTTGGACCAGAGAGCTCCAAAAAAAGTCAA GAGCGAAAAGGTGCTAATTTTCTTTTGAAA
196	IrLmxN	ATGCGCCTGGCTGCTGCTTTCAAGCACGTATTTCTTCCGTCGTGCTA TGCGAAGCCCGTGAGATGTCTTCTTGCCTTGCGCTGTGGGCTGTGCT CGTAAGTTTTGTTTTCCTTTTCTACGATTCTCATTTCCTTGTTTCTA

SEQ ID NO.	Description	Sequence
		ACGACGTTCTACCAAACAAGTACACATACCCCAAACGTTATCGTGGA GTCAGCAGGGGCAGGTGAGAGGGAACCGGGCACTGCGCCGGGAAAAC GCCAATCCTGCTTCCGTGCTTGTCGGGCTTATCATCGTTGCGTGTCC CGATGAGTCTACGCAACTCCCGCTCTGCGCCCGAACAGTGGACTGCC CTGCGCTTCTGTGCATCTTTGCTCTCTACAGCCTTGGCATTGTTGCT CGTGTGGCAGTGCGTATCGATCGCCTTTTTGCGCACCTATACCCCAT CCTAGGCACTCTCCTGATGCGGCGTGAGACGGAAGGTCTCAGAGGCA TATGGAAATGTGCGCCCACCGGGGGTACCTTGAATTATTGTTCTCCG TCTCTTTTTCTCTCTGATTCCCTTTGGCCCTTTTTTTTTGGTACCTC CCCATGCCGCCGTTGCTGTCACCCCACTTGTGGGATGTACCCACAAC CCAAACCACACAACACTGAACCCTCTCTCCTCTACTCCTACCTCCAC ACTGATGTGTGTGCAGTTAACTGGAAA
197	IrLmxO	GGAGCGCAAATGTGTGGGGCCGATACGTGACTGCAACGGGTCACCTG TTTGACAGCTGTTCTGCCTTCGCTTCCATTTGTGCTTTCTGCCAGCC GCTGCTGTAAACTTGGCAGTAACAAACAGTCTCGAGCAGGGCGAGTC GCGCCTACCTCGTTTCGTTTTCGCCCCTCTTCATTTAGGAACTAAAT AGGAAATACTTTACACCTGTCGCGTGTAGTGAGAAAAAAAAAGACGC AGGGGAAGGAAACGGGAAAGTACAGAGAGAAAGAGAGCAAGAAGCGC GTTGCCGTGCGGAACCACACAGAGCAGCAGCGGTAGTTTTGCGAGAT GGCTCACGTTAAGACTCGTGTGCGCCGCTGTGTGCTGCATTCCGATC GCACGCATGCCTGTGTGGGCTGTGGGCGAGTGCTTCGTGTGGGTATT CTCTTCTCCCTCAGGAGGTGTAGGACTGAGTTGCGGATGAAGGGCGG CTTCGTGCATCCGTGCGTCCTGTTCCTCTCCGTGGTTCTCGTCACCT GTGCTATGTCAATTGAATGTGCTTGCTTCCTGCGCTGGTCTTACAAC CCTCTCATTGCTTCCTTTTTACTTTCCTTTGTAGAGCATGTCTGTAC GTGTGTTAGTTGCCCAAGCACGTGCAGTTTAGTTTGGAGCCATGCGT GCACCGCTCGCTTTGCTGCTGCTGGCCATTGTTGTGTGCCTGTACAT TGCAGCGGGTAATGCCGCCGATCTTGTCCCATCACCCGTCATACTTC CCAGGGGCAGAAGCAACACCAAGGTCACACTCTACGTGCGCACCGGA CGGGTTTCCATCCCGCTCGAGCGGACCGATGGGGAAGAGGTTTTCTT TGAGTACACAGGACGCTTGTATGAAGAGGGTAACAGCGGACCC
198	IrLmxP	TCGGCGCGACTTTCATGAAACGAAAAAAGAAAACAACAAAAACACTA AACTCGCTTGTTTCCATTTTTTTGTGTGTTTGTCAAAGTGGAGAAAT CTTAGCACTTAGGATACTACAAAGGGCTTCTCTCTTTTTTGTTTGTT TGTTTGTTTTTGGTTTCCCGTTGTTAGGCAAAGTCAGAAAATAGGGC GTTATATTGAATCAGGGCTGCAGTGTTTTGTGATCCCTTTTTTTTAT GAAACCCTAAGCGCGCCTTATTTTCTGATTTCCTTGTATTTTGCTAG CCAGCTCTTCAGATTAGTGTAGTCAAACAAACAAAAAAGTATGGGAA ATCTTTAAGGAAAGAGTGAAACCGCGGTGAACTGGAACTGTGGCAGC AGCCACCACAGTTTCCTGTCGATGCATTCTAGAGCGCATCGAAGCAC GCGGCGGTGCAAGTTGCCCCTACTGCAGCAGAAGCTTGGTAAAGAGA GCCAGCATGCCTCTGATGAGCACGCCTTGACTTTTTTTTTGCAGGTT CACAGTGATCCCTTTCACGTACTGAAGCCCAACTTCATGTACTGATT CGAACATATGCCTCACCTTCTATTCTCCCCAACACTTTCTTACCAAG TCACCATTTCATTGTCGTCGATTTCTCTTCTCAAAAATGCGCTTTGT CTTGTGGGCTACCAGCGTCTTTCCATTCACATGAAGCGGCGCTGATA
199	IrLmxQ	AGAGGGAGAGGAGATGAGGAAGAACGCCTCTGCCCTTCCGCCCAGCC GTGATGCACCGGTATCACACACTAGCAGGCAGGCAGAGATAGAAATG

SEQ ID NO.	Description	Sequence
		GGAAGAAGGTCACCCGGCAGCGACGTCTGATCTCCTTCAGCGTCAGT CGCCTCGGCCGCTTCCTCCCTAGACCCCCCCCGCCCTCCCCCCTCCT CCTCCACCTCCCACTACCACCACCACCACTCCTCCTCTCTGGATAGC TTATAAACGGTCACGCGCGCCTCATCAATACGCACGCGCAGCTGCCG GTGGCGGGGCGCAGGATGGAGCAAGGAAGCTTCATCCGCTACCCCTC CTCCCACTCCCCTTTTCACCCCACCGCGCCGTTCGGGTTTTGTGCTC TGTGTCTGCATCTGTGTGTGTGTGTGTGTGTGCTTTCTATTGGGG ATAAAGGCCTCTGCACATTGTTCAACTATTGGGCTCTGCGTGTGAGC ACGTGTGCGCACGTTCCTTTCTTGCCTGCCTCTCCCTCCCTCCCTGC CCTTCGCGTGTGTGCGTGCTCTCTCATACATATTATTCTGGTTTCCC TTCTGTGTACCTCTCCTGTGTTCTTACGAAGCTGCGCAGACCTGACG TCTCCCATCGTTGCGCTCCACCCCTTCTCCTCCTGCTGCTGCGCGGC CCGTTGGCGTGCACACAAGTGGTGGTGGGAGGGGGGGGTCTGTGTGG GGTGCTCATGTGCGTGACAGCGAGGGCGACGGCCGTTAAAAGCGCAC GTGGTTTCCGCAACATCGGGAGCCGCTCCTCCTCCTCCCACCGCCTC CACAACATGTGCCCCTGACCCGTCTCTCCTCTCACTCTTCCCGCCTG CACGTCTGCCTCGTCCTGCCTCGCCTACCCACCCCACCTGTATAGCA GTGCACCAACACACACGCACGTTTCTTCCCTCCCTGCCTCTCGCCCT GCTGTCTTACTTAGCAGATTCCCCTGCAGCGCTACAGCGCAGTCCCC
200	IrLmxR	GAGGGGTGTCACGCTGTTTCCCGCTGCTGCAGTACGCAAAGCGTGTG ATGAGCCGACACGTGACTTCTCACGTTCATCGTTGTCGCTCATCTCT GTCATTGCCGGTTCACCAGTTCTTCGCGTTTACTGATAGCAGCGGTG TCTCTCTCATTCCCTTCTTTCTTTCGGTTCTCGAGATTCTCCTCGCG TAGCGTCTTTACAAAGCTTAGGAAGTGCCGGGGAAGGGGGCACGTGT GTGTGTACGTGTGGAGGTGAGTGGAGTGGTGCCACGTATATATATAT ATATATATACATGCCCGCACCATCTAAGGCACAGCGAACAGAAGAAG GGTGACTTCCCTCGCTTTTCTTCTCTGATTCGGTCCTTCTCTCTTTT TTTTCGAGTTAGTACAAAGGCATTACTTTTCATATGAAGTTCATTAA CACGCGTAGCACCGGCAAAAAAGAACAGCAACAACAAACGGCTAGAC GCGTGCAACACACGCGCGGGCACGCAATACTTTTGTGGCAATCCAAA AGCGATTGTATTAGTGCCGGAGGCACCACGGGTGCGATACTGGATGA AGTGTAGCGAAACAACAGTGTACACCGTGTGAGATCACCGACTGTGC GTGCGAAGGCGGTGCCTTCGGATAAGCAGCACCGGTGGAGTCGCAGG AAACCACCTTTCTCCGCAGGTGTCTTTTTGTTTTCGTATGAGAATGC GCAAAGGCCTGCTGGCGCTCTTCTCAAATATCATGTCTTTCATTGCG CGCTCGCTTTCCCTTTCCTCTCCTTTCCCTCTCTTCCGTGGCGCCGT GTATGTTCCTGACACCCGCTACGTCACTTTGCTGGTTTGAACAGAAC CACTGTGAACACCCACGAGCAATCACACCCATACGCATTCCTCACAC ACACACACACAGCAACATCTATCCAACATACAGCTGAAAAAAGTCTA CGAACAAAATTTTTACAGTGCGTTGCCGCACATTTCTCCGTA
201	IrLmxS	AGCACACCTACCCCTCTCTTTCTCTCGCTGATAGGGGGAGGGGTGTA CGTTGTTGTGTGGGAGCGAGACGCACACGCGCACACACGTGTTCCCC TCTCTCCCTCTCCATAGATCCAGTCCTTTTGTTTCTCGTGTTCGTTC TTCGGTGTCATCTGTGTCTAGCTCTCACCAGGGGGTTAGTAAAGGTT GCCGTTTGAAAACTTATTTTTGTGTCCAAGAACGAAACCCCTCCCGT GCGAGCTCATGTTGCCTGTAGTGGGAGTGTGTGCGGGTTTGATGAAG TTCCCTGGAGCTGCACAATCTGTGTTCATCTTTCCACACACACACAC ACACGCACACGCAGAGCCTCCTCTCCTCCTCCTGCAGTTTTCCTTGA

SEQ ID NO.	Description	Sequence
		TGCTATTTGCGTGTGTGTGTGCGTGTATGGCGGGGGTGCACGTGACG TGATACACGAAGCTTTCCACCGGTTGACATAGTTGTTCTTCGCTTCT TGACAGCTGTGATCATTCTGACTCGTGTAACCAGCTATCACAGCTCC TTGGTGACCTGGTCGTGTAAGCCGCGTCATCTCTACTCCCTTCTCCC TTCTCCCTTCGCCCACCCCGGTCCCACCCCCTCCTTGCTCTCTGATT CCACTATGCCCTTCAGTTGGGCTCTTGCTGCTTACGCAGACGTTGCA CGAATACGCACACTGTGTGGCTGGTCAGCGGCAGTGCTTGCTGCATT AGACGTTCACATCTCTTCCTCTCTTCCACCCTTCCTGTCCTGCGGCG CCGTGTGTGTGTGTGTGTGCTCGGGGTGTACACCCTTCTGTGAAACG GCGCTCACCGGCAAAGTGCATCACGTGCGTACTTCTTCGCTCTTTCA CGCGCCGCTGTC
202	IrLmxT	AGGAGCTAGGCGGACTCTAGCTCTACCCCTCCCCCCTCCCCCTCTAT CTCTATGTGTCTCTTAGATTTCTGTCGGAGGCAGTGGAGGTTATGAA CCCCCCCCCGGCTCATCTCCTCCGGGAGAGGGAGAAGCACGGGGCCT CTGCACAGGACAGCAGCGCGCACACGCGCAGATGTCTGCATGTGTAT TGGGTGCGTGTGGCAGGCAGCGCGTGTGCGTCCATGCTGCCGCGCAC GCCGTATCATAGATCCACCTCTGTCTTTATATATATATATATATATA CCATGGAAAGAGGAGAGAGGAATAGGTTCGGCGTAATCTGTGTGTGT GTGTGTGCGCGCGCGTCCTCGATCTCTGTGGCCTGGCGATGGCGTGC TTGAGGGGGCCGTCCCTGGGTGCGATGGACGGCGTCCTCCTCACGCT GCATCCTCGCCGGAGGCTGAGGAGAAAACACAGATGACGCAAAGGTA GCGAGCAAGGAGCGGAACGTCCCACGCAGTGCGCGCGCGTATAGGTG GATGCCTGTCTGCACGATTCGTGCATGTGCGTGTGCCGCGCAGGTAG GAAATGGCGCACCGGCGGTGCTGCCGCTGCCTTCCGCCCACCTCATC GAAGCGACCCCGTCGCCAGCACGCAGGGACGTCTGTGCTGCCCTGAC CTCAACATCCTTTTTAACCGCTCAGCAGCAACATCAGGGTGACGCGG TGGATGTGCACGCCGCCAGTCTCCATCACTTCCTCGCCCCCTCCCCT CCCCCGCTCCAACCCACTCACCCACCCCTACCCCCTCTCCCTCTCCT TCCCGTAACATTCGAATGCGCGCATGTGCGCAGTGCATCCTCAGCGC AGTCCACACGCCATCTTTCTCCCCCACCGTCCTCACCCCCTTTCCAT CCAGACCAGAGAAGGAGTCTTAGCCACGTCGGCCACCGTACCCGAGC ACAAGCAGGCCTGCAACACGACCACCGCTTGTCATC
203	IrLmxU	CGGACGGAGTGCGCTCACGGAAAAGAGACCCATTCATACTTTTTTTT TACATCGTTTCTTTGATTATACATTTTGCTTCAGCTTTTGGAACTCA TTGTTGGTACCGGTTGCACGCTGGAGTTGTAGTTTTATTGCTTGTGC TTGCCTGCGCCCAATCAAGGTGGTGCAATCAGCTGTCTCACTTTAGT TTTTCTTTTTACGTGTTTTTTCTCTTCTCTCTTCTCCCCTCATATTT CTTCCTCTTTTTTGCCCCTCTGTGAAAACCCACTCTTCATATATTAC GAGGTTAGTGCCACCTACACTATTTTTTTAGACTGTCTCCGTCTCCT TTTTTGCCCATCTGCATGCATGCGTGATGGTTCTTCGTATGTTATGC AAAGGTGAGTACCATTCGGTCTTTCTATGCAATTCATGTGATGAGCT ACATAGGTCACCTCGCCGGCGGTCATTAAGTGCAAAAGAACAGGGAT GACCTGTACTGTATGCGCGAAGCAGTACATTCTCGGAGCTGCTGAGG GCTGTAGCAGGTAATCGTTGCGTGCTGAGCGTTTTTTTTTTCATCGT TGGCATGAATATATATCTATATATAGGTAGATATATATATATACTTC TTTTGCCCTCTTCTCCTTTTTACGCGGTCTACCTCCTTTTGGTTGTA AAAAAAACTATGTGTGTATCTCTTGAGAGAAAAAAGATATGGCAATA GAAGTATGACAAAACTGCATGTTATGGTCATCAGTGATGCCCGCAGC

SEQ ID NO.	Description	Sequence
		CTCCACCCCTAGTGAGGAACTGTGCTGGTGGGCGAACTCGTGGCGGT TCATTGACAGCAGCCATGCAAAACTGGTCCAAAGGCCGCAGCGATGC TGAAACTCATGTGATTCTGGCTTATATATTGACTTCTCTCCGCCCAT CCTGTCATTTACCTTGTTCATATCATTTGCTTTTCTGCTGTCACTTA GAGTAGATCTAGTAGTTTTCCCGTCTTGTGCG
204	IrLmxV	CCAGCGCGGCATTCGCGCTTTCCCTCCTCCCTGTTTGTTTTTCGCTC ACTCCTCCCCCTCCCCACTGACTTCGTTCTGCTGGGTAAACCGCAGC ACCGCTGCCATTCTCATGTGTGCTGTTTCCTTGGCTTATCTCATTCC GCGTGCGTGTGCGTGTGCGTGTGCGTGTGCGTGTGGCGCCTCCCCTC AGCCCATACGGGAGCTGGTTCCTGGGCCGCGGTCTACGCGGGGACCC CACACACGCACGCGCGCACCCCCGCCCCGCCGCCGCATGAAGCCTGT GCACCACCCATGTGAGCACGCTTTCTCTGTTTCCGTTCTTCCTCTTC TTTTGCTGCGGGGGCCGTGCTGTCGCTGCGCATACAGCCGGCAGCGC GCACCGCCCTCCCTCCAATGTGTACAGCCCATTCGCAGTCCTAGCCG CCCCTCCCCCCACTCGCACAAGCACGCATATCTTGACCGCCAACGTC CTCCCCCCCCCCCTCCCCTCCCGCTGCGCTGCGCTGCAGACGCGGTC GCGTCACACCCGCCCGTCGCACTCCCCTCCCTGCATCTGCCTACTAT TGCACGGCCCCTCTCCTCCCTCTCCCCTGCCACTCCTCGCCCCGCCT CCCTGTCCCCTTCCTCCTCTGCGCCGCACCGCTCCACGCAGCAGCCC ATTTGCCCCCGCACCGCACCCCCTCCAGACCACCA
205	IrLmxW	GTCGCTGAGGGCTGCTTTGTGTGCGCGTTGCACCGTCAGGTCAAGCG ACACGGTGGGAGGGAGGAAGGGGGGTGACGGAGAAGCTGGAGAGAGG CCTCGGAGCAGGAGCGGGTGTGGTTCCATCACCCACCAGCGCTTGGC GCTTCTCTTCACCTTGTGACGTGTGCGTGTGACACGTCGGACTTCGC CAATTTCCTGTGTCTTATGTACCGCTACTGTGGGGAGTGGGGTACAC CGGTGGTGGCCCCCCTTCACTGCCTCCCTCCCTGGCACTCAAGGCCA CTCAGACGAACACCCCACACCGAGCGGTGTCGGTAAACATGGAAGTG AGGGGGGTGCCGTGCATATACCTGGCATGCGTCCGTGTCCGCTCTAC TCTCGCCTCCCCTTTCCTGTCGCACGGATGAGCCTTTTGCGCGACGT TGTGGGATGGGGGAGCGCGCAGGGAATGGCTGGCATACGCGTGCACA CGCATGCATGTCCTGCCGCGGAGTGACGTACACAGGCGCAGGCGGAG GCAGACATCCGGTAGCCCCAAAGGCAAAGCCACTGCATTCTGTCGTG TGTTCTCCTTCTGTGAACTTGCGGTCCGTGCCCAGCAGCCCGTCATC GCCCTCCGCCACCCCCTCAAAGTCGCCACCCCTTCTCCTTCACCTCT CCCTCTCTAGGTATAAATATATATATATATATATATGCGTATACACG TATGTGTGGACAGGCCTCTCTGTGCCCCGCCTCCACCCCCTACCGAC CCCACCCACCCACCCCCATCCCTCCCCTCTCCAAACCTCTTCGACTC CCCCCTCTCTCTCCCCCCCAAAGTAACATGAGCGCCTGAGCATAAGAG TGCAAAGCTCTCGCTGCCGCCCCGTCCCCCACGCTGCGGCTCGTGTC AGTGCTCACGAGTCTCCGTAGTAGCGGGTGGTG
206	IrLmxX	TGCTTTCTGGTTTGGCTTTCGTCAAGCATTGAGGCCGTCGTGCTGTT GGTTCGATCGGTTAGTGCGATGACATGTATTTGAAAGCACTTCTTCG TTGAAGCGGTGTGTGTGTCACTCTATTGTTTCTTGCCTCTTCCCTCC TTTGGTCGGAAATGCAATTGTTCGTTGCTGTGCATCTCTTGGTCTCG AGGGAGTGTTTTCATGAAAACGGCTGAAGCTCTTACTCGAGTTCGAG CTTTTGTCCGTGTACAAGGTGTTTTGCCAGAGGGGCGGCGCATCATG TTTTATTGTTCCCTTGGTTTCATTTCCTTCCGGGACTGGACGTAAGA TACATGCGCGAACTAGCGGCTACAGGATGACAAACAAAGAAACCGAG

SEQ ID NO.	Description	Sequence
		TAAGTGTTCTTTCTCATAAAATGATGAAAGGGGGGGGGTCTTGTTG CGACTGGCGCCTGCCGCTCACCTTTTCCTCTCATCGGTCTTTTTTCG TGACTCTGGGTTTTCATGAGACCGAGTTCGCGGAGCGTATGGCGGCT GTTTCTCCGTGCGACTGCATGAGCCGCAACATCTCGAAGCGTGCCCA ATCTTTGTTACTGCTCTCACCTCCTTTTTTTCCTAACATCAACACTG ACGCTTTCTTTTAGATTTCGCCTGATAGA
207	IrLmxY	GGTGCCCGGGCGCTCTTTATTTTCAAGGGATTCAATTGTGCTTTTTG AACTTATTTCACATCTAAAAAACCAACAAAAAAGAACGTGCATGGGA GCAGCATGTGGTTTTAAGCAATCGTAGACGTAGGTGCAGCGACACTC TAGCTCTGGGTGTCATCGCACTTCTACTATAAGCGCCGGTGTCTCTG TGTGAGTGTTGCCTCCGAAGCAGATCTTCGCACCGACTCTTTTCCAC CCGAATGCCCTTCAATTTGTTTGGTGGAAGATGTGGCCAGGCTCGCG CGTAATGCAAATTTCACCGCTCCTCCTAGTGCCCATTCTCAACAAAT TTTCCTCGCGTCTCTGAAACCTAAATTGATGTGCTCTTCCTTTCTAC TGCATTATCCCATAACGACGCCGAAAAAGGAAACACGAAGATACACG TTGTCTGGGAGAAAATCAGAGGCGACGACAAAGAGCCTGAGGATCCA AGTGAGCGGCGACGCTGTGTTTTCACGAAGTAGGGGTGAGCCTACCG AGTAGTTGTATTTAGTTCAAAGGGAGAAAGCAAGTAAACGCATAATT AAATCCGTGACACACACTCGCAAGCACACGCAGTCGCTGCACGGCAC GAAAAACGGATATATCAGTGTAGCTGTGGGGACTGTGTGTGTTGGCG AAA
208	IrLmxZ	GCAGCCGCCGCACTGGGCCGCGTCACCCGCCTCTTGCCGCAGACTTC CATGCGGACCTGTTCTCATTGTTGTGCCGCGTCGCTTCTTTCTTTGC TTGTCTCTTTGTTTTTTCGTTTTATTTGGACCGGAAAGAGTCTGCAA ATCGGACACACGATGCGGGGTGAGTGGATAGAAGGGGGTGGGAGGAT GTGAGGTGGCTGCTTATGAGGCTGTCATCAGAAAAAGAAATAGAGGC GCCCTCCCTCCTCCGTTTCTTCTCTCCTCGTAGATGAGAGAGCCGAA AAGTGCCAAGGACACTGCACCAGCGTCACTAGCGGTGCCATGAAGAG AGGAAACTGCGCTTTTCTGCCGTGACCCCCTGCCTTAGATGAGCGAG AGAAGGTCTCATCTCACAATGCCGTCATGACGCCATGCTTTTCTCTT ATTCCTCCCTGGTCTTCTTGCTTCCTTCTCGTTTTTTTCCTTTCCAT GCACTTTCTCCCGTAATGTTTTTGCCTCTTCTCGTACAAGAGGTGTA GTCAAG
209	IrLmxAA	GCGGCGATGGCTGTGCGGACACGGCACGCATGCGCGGCCACCCGCTT GTGTGTGCCCGCACGCGCCGCACCCTCCTCTGGCAATGTCCTTTCGT TTTTCTCATTTATGGTTTAGCACTTCCCTAACGGAGAATGCACGATT AGCTGCACTGGGCCGCTCCTTCTGAGCGCGCAGCGAGAAAAGGAAGG CGCCACCGAAGCGTTCGCGCACTTTGCGCTACCCACTAACGACTCTG CGCCGTGCTGGCGACTCGGCTGCGTAAGTGGCGAGTCGAGCCGCAGC GCCCCCCCCCCCACCCGCTGTCGTGTGAGGTGTGCAAGGCCACATTC TCTCCCCGCATCTCCACCGCGCATCCGCCCATCTCTCGCTCTCTGCC TCCGCCTGCGCCCTGTTCTCTTGCACCTGCTCCGAGCGCCACAGACG CTGACCACACAAGCCCACCCCCTCCCCTCTCCACCCGCACGGACACA TTCTTTCGTCTTTCCTCTCGTCTATCGCCTATCGACCGCCATCGCGC GTTGCCATCCTCCGCTCCGCACAGACGCTCTCTCTCCCTCTGTGTGC TCCCGCTGTCTCTTCTTGCTGAACCCTCGCCACC
210	IrLmxAB	GCGCGGGATCCCTTCGGCCTTTGCGGAGGTTGCTGCTCTGGCAGACA TGTGTGCCTCTCTTCAGTGATTTGTTTTTGATGGGGCAGTGGTGTGC

SEQ ID NO.	Description	Sequence
		AGGGCCTGCGAGAATCCGAGCTGAACAACGATGGTGACTGACCACAC CCACTGTTTGTGTCGCCGTCGCGCCATCGGAGCGTGTAGTGCACAGG GGAGGGTGGAATGCGAGTGCTTGTGCCTCTGTTGGTGCCCACCATTG ATCAGCTACATATGTACGGTAGGGTGTGGGCGAAGGGACGGCGGCCG CTACAGCGGTTTGTCTTGTCTTTTTTTGTTCTGCGTGCCGTTTTCTC GCACTGTTGCCGTTTATTTCTCTGTGATGTGACGTCTTCTTCTGGCA GCGCCAGCGAGGAGGGGGTGATGATGAAATGGGTGGCACAGCAGACA ACGAAATGAAGTGGAATCGCGCAGGCTCTTCAACGTGCAATGGCGAC ACCGCTCCGCCGTCTCTCTCGCTTTTCACCCCTTTCCTTCTGTGGGC TTTCATTGGTTTTCTTCTGTCAAACGACAACGAGGGAGCTGGATAGA CAGATAGCAGTGACAAGCGCCACCCATCGTGCCGCACAGGAGACCGG CATGCGTGCCTCCTCGGTTTCTGATGCAAAGCAGGCATGCCGGCATG GGGAAAGGGCTTGTGATGTGAATCTCCTTCGTTACTGGATGCCTAGG ACTGACACGATCATGCTGGTTTCTATCTCTCTTTCCGCTTCCGTCTT GGTCCGTGATTTTGGCGTCCTTCTCTCCCACATACTGTGCGCCTGAC GCCAACCGCTACTTGCCATTCTTAGAATTGCACGTCGTCGACGAAGA CGTTGCAGAGCCTGCGCTGGCAGAGGACACCTGCTCGCTTTCTAGCC TCGCCACTACAGCGGTGGTGGTGGTGTTCCG
211	IrLmxAC	GCACCGGATACCCGTACGCGCTCTCGCAGCACGTACTCGTGTTGTAG CCTCGCTACCTCTACAGCCTCTCTGGTGAGGCGCGTGCCGACGTGTT TCTCGGTTCTCCCGCAGGCGTGGGCGTCTTTTCTATTTTTTGGTTTC TTCGCTTTCCTTTAAAAAAAAATCACCCGCAAAGAACGCAACAAGTG AACATGTCCGCGCATGCGCAACCAGATGCGATCCTCGCTCTCATGCA GCCCATCACTCGCGAGTCATGGGGCGTATGTATTCGTTGCTTTAGTC GGGTCTTCCACGTGTGCAGCTGTGGACTCGCACACGGTAGCTGCATG GCCGGTGCGGGCCCTTTGGTGCCTGATTACGCCCCCCCCCCCAACCC CAGCACGCGGGCGCGGGCGTGGACTTTGCAAACGCCTGCAAGGCTGC TGTGGTGGTGGGCAGGTAGAGGTGCTGTGATGGCGGCTAATGCGTGC CATTGCAGGCACGTCTCTTTTCCATTTTTTTCTTCTGTTGCGCTGCC ATCCCTCCTCCCTCGTCTCTCTGCGCTTTGCGTGCGTGTTTCCGTGA CCGTGCCTGCGTGGTGCGAGCTGATTCGCGCTTGTTTCTTGTGTCTC GGTGATGGCAACGACGCCGCACACGCGCCGGAAAGCTTACTCGTGCA TCTGCTCGCACACACACACGCACACACGCGCAAGTGGATGTCCCCCC TCCCCATTCACACAAGCAAAACGGAAGTCGATTATTC
212	IrLmxAD	GCATGCCAGCGCACGCACGTCTTGTTGTGTGCGTCTGCCTCTCTGCG TGACCTTCTCGTGTCTGCCAGGGTCGCAGCGCGTCCGCCTCTTCCTA CGGCCGTGCTTGTTCTCTTCGTCTCCGCGTCTATGTCGCTCGTGTGC TTGCCAGCGGAGGCAGCGGTGCGGAGTGTGTGGATGTGGATGGCTCT AGTGATGACGGAACACTCTGCTTCGATAGCGGTGCCAATTTCTGCGC GTCCCTTGACGAGTGGGGCCTCGGGTGCTAATGTGAAGCTCATTTCC TGATTTCTTTAACGTATTTTCGATTTTCTTTCCCAGCACAAAGAGAA AACGGAAGAGAAGGATGGGTGCGGAGAGGCATCGGAACTGACGTGTT GTGTGTGCTCGGGCAGATCCGCGGCATGGGCTAGTTTCACGGCCGGC GATGTCAGCGTCCAGCCAGCACATGCCACAGAAACGCAGTTTCAGTG CTGAATGGCTCGTTACGGTGTCGAGCACCCTTCCTTTGCTCCTCGTC GTTTTGCGTGGAGACAACAGCTCGTGTTAACGTATGTCACTGGGGTC TCTCACGGTTCCCCCTCAACCACCACTGCCTGTAGACGATGAACATG CAGCCCAAAATTACGCGCACAGCAGGTCTTCTAGCTGTGTGGCGAGC

SEQ ID NO.	Description	Sequence
		TCCATGAACCGTATCCACGTTACGTTTTTTTTTCTCGTGGGTGGCGG TAAACTGCGTGGCTGCCTCAATCACGACTTCCACTTCCTTCCCTCCC TTTCTCCCTCTCAACCGTCTGCTGTGGTGTTTTTGTTTCTTCTCCTC ACACATCATTCCTGCGGACACTGTGTTGTCTATCCTTAGCATTCAAC GGTCTCTCTCTCCATCGGCAGCC
213	IrLmxAE	TAGAACAACCCAAACTTCTTTACGGCATGCGCCCGATTCCGAACCTT TTCTCACAGCTGTGACCTGCCACAGCACCAACGAGCCGCAACCGCGA CAACGACAACAAGAAGACGTGACGGGCTGCTGAACCCTGTCTTCACC CCGGTACATACATGTGTGTGTGTGCGTATGCGTGTATTCGTTCGCAT GTGAATTTCTTTATGTATGTATGCATGTTCATCTCTTCTTGTTTTCG TGCGCCTGTGTGTGTGTGTGTGCACGTGTCTGACACCTCTTCCCCCC CCCCCCAAGGCGTTGCTCGCTCGAAGCGCAAACGTAAACGGGGGGGG GGAACGAAACGCAAAAAAAAGAAAAGAAAAAAAACGGTCCAGGAAGA GAGGTGAATAGTGGAGGAGCTGTAATGTCGAGGCAGTGACTGCCGAA AACTCTACGTGCGCCACTAGGGAATACCGCCGCTCATGCGGGTCTGC CGTGGGCACAACTATGGTATCTGCTTCTCTCCCACGCCTCGTTGCTG TCTTTCACGTGCTCGTCGATAAGCGTAAAAAAGAAAAGCACGCACCT CCTCACCCACTGCGGTGTCTTGTCGGGTGTGTTATCTTTGAGCTTGA GGGGCTGGGAAAGGGTTTAGTCAGGTGCGATCAAAACCTGCAAGGGC GTTTGCACAGGCTCCATCTTTGTTGGTTACGGAGTTGTTCAGAGTAT CACACGCGGCGTCTCGCGTCTTGTTCTACTCGTCTGCCCGTGTGCAA GCACACACACACACACACACACAGAAACACACGGTGGCACATACAAC ATTTTCCTTCC
214	IrLmxAF	GCGAAGGCAGCCGCTGATGGGATGGGCGGAGGATGTCGTGAAGCCTT TCCGCGCGTCGTTTCGCCCGCGACAGGAAAAAGGCCACATCGGTCCA CACAGTGATCGGAGCCGATGCGTTTCTCTTTCCGGTTGTTGTTTTTC ATTTTTCTCCGTTACGAGCCAAAGACATACAAAGCGCAGCAGTAGCA CCCGTGTCTCGCTGAGCACCAGAGAAGGGGACTGCGGAGGCGGTCTC TGTGAGGACTCTGAGCACCTTTGTGCGCGTGGCTGCCGACGTACACT GCGCACGTGAGAGATGACGCGAGTCTTCAGAAGGTTCGCGGACAGGC TGCCCTCGCCGTCACTCACGTGACGCCGGAAATAGGGGACAGGTGAA GAAGACGGCGATCTCCTCAGCGGTGCGGTGTCGACGGCACCAGCTGG CGCGCCCATCTTCGCCTCGTTCCCGGTTTGTTATCAGCGTGTCTGCC GTGTCCACGCTCATTCACTTTGGGGAGCTGCTATCTCGACGCCAAAA CGCCGTGCGTCTTGCGCACCCTGCATGCCAAGTTCCCTGTTGCCCCC TCCCTCTCGCCCCCTCTCTCCCTTTCCTGACCTTCGTCCGTTTCTGT GTGCCATGTTCGTGGCTTTCTCTCTACATTGGTGCGCACATGAGTGC GCACGCATGCCGCACTACTCGCCCACCTATGTGACGTGGCGTCACTC TCCACCACATTCCGACTCGCCTCCGCTGCTTGTCTCACCACTCTCAC CCTCCTGAGAAGCGCAGCCACTTCGGCGCGTAGTACTCTCGCCAAAC AGTGTTCTGTCCTTCCGCTCATCCCGTAACACGCACACAGGCAGGCA CTTTGGGCCGTCAGAGGGGGTCGTCGCTCATAGACGTGGATTCCGGA AAGCAGCAGCGGATCCCCTCTTGGC
215	IrLmxAG	ATGGAACAGGCACATTACAATGGAAATGCACTCTCTGCCATAAGTGA CCTACTTCCTCCTTTTTTTTGGCTTCCGTTTTTATTCTTACTCCGTC TCTCGTCGTTTTTGTCTGTGTTATTCATGTACCGTTCCATGTCTCGT GTGCGCAATGTTGGCGTTGGGGTTGGCAGCTTTTTTTTCTCGTTTTC GCTAACAGAATGCAAACAGAGAGACATCAGAACTGCTGAAGAAGGCA

SEQ ID NO.	Description	Sequence
		GCAATGAGGATGAACAGACGTGATGTAGACGGTGCGCAGTCGCGATC ATGTGATCTTTCGGACGGACAGAAGATTGGTAGCATCGAAGCAGCTG CCTCTTCCCCTCTAAAAGACACACACACACACACACAAAGATGCGCG GTCTATGCAGCTCAAGCTACATGCTCCCTTGTGTAAAGCCTCCACTG AAGGCAGGCTATGCGCGCACATTCAGGCAATCATAGCGAGCTTTGTA CGCAGTGGATTGGAGGCCATTGCACTTCTGTCTCTTGGATTATGTGT GCTTGAGCTTCTCTGTGCCCGATCACCGGGGCCCGTGTGCCCGCACC TCTTCTGTTCTTTCTGTAAACCTCTTCCTCTTTTCTTTTCGTCGTTA CTATTTTTTTTTTGATATTTCGCTGCTTTCCATATCGCTCTACTGTG CTCTCACCACGACGGTGTTCATGCGTGAAGGCAAGCAGTGTCCGTGG CGCGACTTCAGGCATCCTCTGAAGCCTTCCGCGCGTTAATCGAGGAA CCACCTTCCGCTGCGTTTTCATCCACCTACGCGGTGCCCATCGCAGG CAACTAGAGAACGTTCGCCTCTAGCCAAGGCTCAACACCGCGCTCGC ACACAAAGGCACACCTACATAAAGAAACCTAGATAGATTTGTTCACA GGTACGGGCAGCTACACTGTAGTCTTGACGCC
216	IrLmxAH	GCTGCGGACTAACGGGTTTACTTGCTCTGTCATCTGGCAGGCGGCCT GAACATGTTTAAGTATGCCCCGTAATGTTAATATGCTTTCTTCTGAG GGGTTTTCTGTGTGTGCTTGTTTTCCGTTTGTTTTGAGGGGCCTTTT GGTCGACTTTTCATCTTGACGCGGGGTGCTTCTCCGCTCTTCTGGAG TTTTTGTGTTCCTCTGGCGCTGGATAAAAAAAGAGCTGTGGTGCGTC GCGTATCGACGGTGAGGTGTATTGATGCGGGATCTTTGTGTGGAGTT GCTTATACTGTTTAGCACCGATCTCTGCCCTTTCTTAGGCGCAGTGA CATGCCAGGTACGCGTTCTGGTTTTTTTTTGCCTGTCACCTCTGGTG AGAAATCTATTGGGCTGTACCTGACATCTGCCTCCATGTCTTGCTCT TACACTGCTCGTGTTCGTGTGTCTTCTTGTTTTTTTTGTTCTTGAGC TGGTGCATCGCTCCTCCTCCCGGCGCTTGGTTAGTTGCGCAAGTGAC GGGACGCGGGGGGTACTGAAGTTCTCCATTTTGTGCTGCTTTCTGTA CTTTTGCGTATCGAAAGTGTGCAGAGGCACTCGAATGAATCGAG
217	IrLmxAI	AGCTCCGCCGGTGTTCGTCCTTCTCGATGCATAGTCCAATGACCGTC CACTGACGCTGCCATCCGTGTGCGATGTTTCGAGTGTACTCTACCTG CCCTTCGTTGTGTTTCTTTTTGTTTTCGTTTTTGAGTAACGTTTTCA TGCAAAGAAAAAAAACAAAAGGAGAAGAGCCACGCTCTCGTGTCGAA CTTGTGGAGAATGGGGGAGAGGCTGACCACTGTCTGTGCCGTGTGTG CATCATGTACTTCATGATGGGCACCGTTGATCATATATGAGCGTTGT TTCGCGCGTCGCATGGGCGGTTGGTGCGCTATCCCGCACGACGTCAC GCACCATGTAGTGTTTTTTTTTGGTGTTCGCCTGGTGTTTGTTGCAA TGCTCCAACGTTTGCGGATGCCCGTCTCTGTGACGCTGAGCCGTGCT CCATCTCGAAAAGCGAAGCCTGCGCTGGCCGCCAACCACCTTGCCCT ACGTCGTGTATGCATCTCACGTTTTCTTCTCACTGACATTCCATCGA TACCCCTCCCCCTCCCTTCTTTGCTTCTGCTGATGGCCGCGCTTTCT CATCTAGAGTGCTGTCGTTGCTGCCTGAACAGCTCGACAGCTGCTTG ACACTACCAGATTAGAAAGAAAAACACTTTTATGCAGAGCATAGAGA GAGTGCGTGTCGTCGCACTGTGTCATGAGCTTCAGCTCAGGACTCTT CGCTGACATCATTACCGCTGATTTGCAAAAGTGTGGTGGCTTCCGCG GATGAG
218	IrLmxAJ	TGCCGTTAAGCAGGAGCGGTGTATCTGCTGCTCATTACATTAATGGC GCCCCCCCTCCCCCAGGACTGCACCCGTTGGTATGTCATTGCTTTCG TGATTTGTCTTGCTTCTATTTCAAAAATAAAAAAATAAAAACTAAGC

SEQ ID NO.	Description	Sequence
		CGAACGCAACAGAGCGAATCGTCCTCTCTCCTCCCCGATGAACGCAG GACGGTGCTGCATTGGTGCCATGCGCGGCGACGGCGTCCGAGATATG GGAGGGTGGGTGAGCGGAGCCGCCTCAAAAAGAAGGCAGCACTGTGG GAGACGTGATGAGAGGAAAGAGGTACGTGATGGTGTAGGAGACACAT ACGAGTGTCTCGGCATCGCCTCACCTTCTTCTCTTCCTCCTTTCCCA TCAATCTATTGAGAAAAAGGGGGTGGTTGGGGGCGTCGATAGTGGCG GAGTATCCACTGCTACCTAATGCGCGTGTGCCACCTCGCCCTCCCTT CAACCTGCTCGTCTCTCCTTTCTTTGACTGCCGGCCGAACGCGCTGC TAAACCTCGTCTCCTCTTTCTTCCCACCATGTGCACTTTCCTTTTTT TTTCTGTCTGACGTGCCACCGCATTTCTCCGCCCCGCACACGAAATT CCGCGCACGGCTAAACCAATAAAACGCACAAAAAACGTCAGTAGGCT TTTCGAGCTTCTGTGTGAGCACCACC
219	IrLmxAK	GACTGCAATGGATGTGGCGTTTATAGGCTGCCCTGCCATCCCTTGTT GTTACTATCAAGGTTTAGTCTTTCTATATATATGTATATATGTATAT ATATACATATATATATATATGTGGAGGATGACAACAGCGGGCGAGCA CTTCCTTCTTTATTCACTCTCTCTTTTGCTTTCCTCGTCTTGACGTC TGTACATGCGCTCTGTCGACGTTTTTTTTTGTGCGCCTTGCGCTCTA TCCAGCAACATTCATCGGAAAAGAGTAGTGAAAGCAGACAATGGGTG CGCTGACTGCCGTTGGATTGGCACAGTTTTGAAAAGAAAAAAATCGG AGAACGGACAGAATAGGGAAATCAGCACTACGACGAGGACGTGCGTC TTTACTCTGTCGGTTATTAAATTCTTGGGCTTTGTAACACTGAAGGA AATCGCACACGAATGAAAAGTATGTTCGACTGCCAATGCCAATACGG TGTATCGAGCGTGCTTTCTGTATTGCAGACTGGGAAGCTACGGCACT TGCGTGGTGCTGCTGTGTGATTGGGACGACGGGCTGTGGCAGTCAAC ATTATCTGCCCCTGGCGCTCATCGTATGCCTTCAGCCAAAGCGCGGT TACTCTCAACTGCGCGAGATGGAACTGCTGATCCATGAGAACGACAC CCGTCTTCTCTGCAATGCCCCCCCCCCTCCCTCTCCCCGATGTTTGT TGCCATGCTTTCTGTGCCATTCTTCTACTTTCCCATTTCTCTTCCGT TGTTTTGTTCTTTCTGGTTTTCCTTTGCCTGTACACGGGCGCGCTGA TGATTGGGTAACACGGTTCTGCGAGCGTGTGCACTAGGCGGCTGCAA AA
220	IrLiA	GCGGTCATTACGATGATGAGAGAATACGTGGTCGGGGGAAGGAAGAG GACAGTGGTACTCTGCATGTGCTTGGGCACCGTGTCTTTTGGACGAG TAGACGGTGCCAGGTGGGGGAAGGGGGAAGGGAGTTTGGGCGATGAG GTAGTCGAGGCACAGCACACGTTCATGTGGCTGTCTGCATGTAGAAT ATGCCGATGTCGGTGAGCTCAGCTCTCGCAGGCGCATACCCTACATT GGCCCGCTGCCGCGCGTGTGCTGCCCATTCTCTCCACCTCACCTCCA CTCGTATCGTTGCCTCATCTCTGAGCGGGTCGCCTGCGCTCCTTCTT CCGCCCCTCCCCTTCGCCGTCTCCATCAGTCAAGTCCATCGGACCGC CGCGAAGTCTGGCTGCTGTTCGTTGGTGCATTTCGGGCAGCGACGGT GTGGCGTGGGTGTGTGTCTCTCGGGCACACGGCACGCATACGAGAGC GTGATGGAGAGTTCGCTGGATAGTGTGCATACATGCATGCATACTGG AGTACTTTTCGTCCCACCACCCTCCGCGTACACGCGTATCGATGCCT GCGCGTGCGTGTGTGGGGGCTTCTCTCTTACACGTTTTCTTTGTTTT TTTTTTGGTTTCCTCGTTTCTTCTTTCAACGGTACACCGCCATGAAA AGAAACAACACCAGACGCGAGAGCATCCCGCCGCTGCATTGGCGACC CGATGCTAACGAGGATGATGATGCGGATGGAAAGGGAGGGGGAGGAG GAAGAGGAGATGATCGTTCATGACGGCCGACATGGAAGTTGGGCGAA

SEQ ID NO.	Description	Sequence
		GGAAGGAAGAAAGGCGGGACGCGCGTAAACGCACACGTCCATCCTTC TCTTTCTCTGTGTATGTATGTGTGTGTGTGTGTGCCCAACGCGTAGA ACCCCATCATCACCTCCAACTTCCCCCCCCCCACCCACCCACCCACCC GCCTCTTCTTTCCATTTTGATGCTGCG
221	IrLiB	GCTCTCGCAGCAGCGTGAAACGCGTGGGGAAACGGGTGCGTGCGTCT GTGTGTGCGTGTTCAAATGGCATCCGCAGCGTGCCGCGCGCACCCGT GCCCGAGCACCTCTGGGATGAACGACCTCTCTCGTCGATTGAACGCG ATGTCACCAATGGCAGTCATCTTTTTTCCCCCTTTTTTCACGGGCGC TCTGTGGCGTGCGCCTTTCATTTCTTGTTTTGACCCCTCGGCAAAGA ACCAAAAGAAGCAGGGGTCGGCCGTGTAGCAGGCACCCACCCGCTCC GCCTCCGTCCCCTCTCGCACGCACCGCCTCAAGACGCGGTGCATCGC CTGCGCGCCGTCTTGCGCACACAACTGCGTTCTGTTGTCACGGCTGT TCCTTGCGCGCGCGCGCGTGCGTCGTTGACGACTCTCTCCGACGCAC CACCGATGAGCACCCTCTGGATGAGGGCACGCACGTATGTATACACG CATGTTGTGTGCCTATGCACGTATGTATGCTCCTGCGCAGTCTCTCT CGCCTCGCCTCTTACGTCATTGCTTCGCCCTCGCCATACCTGCAGCG GTGCGTGCGTGTATTGTGTAAGTTTTCGCACGCGAGCGGAGAGCTGC TACGCAGCAGCGACGCAGTCGAGTGCGTGACTACGCTGGCACACCGG CGCTAACTAGCGTGTTTGCCCCACCAACACCAACAACACCCTAAGCC TTGGCGCACCCTTCTCCATAGACACACGCACAGGCCACATAAGCCGT TGCGCGCATCTTCTCCGGAGGCCGGTGAGCGCCTCTTGTTGTTGTGT CTTCCGATCTCCCTCTCTCATCCATTCAACAGATCCGCAAACCTCGC ATACTGCGCGCGCACGCTCATCACGGTACTGGCAGCAACAGCAACGG TGACCGCGAGCGAGGCC
222	IrLiC	GGAGGTGGTCATTCCATGATTATCTTGGTTTCCTTCATTTTTTTTAT GCGTGTGCTTACTTTAAAAAAGAAGCAAAGAAGTAGTCAGTAGAATC AGTACGACCACGTCGGGAACTGACACGCGCCGTGACGGATTTCGGCT ATGTTTGTGGAGCACACCTGTAGGGGAAAAAAGGACATCTCTCCGCA GGCACACCGGCGATTTCCCTCGACAGCGTTCAGTGAACCCCCTGGCG AGTCTCGTTGAAACCACAGGCACGTCCTAGACGCGTTGGGTCCCTTC GACGAGAAGCTCTCTCTCTCATTCCCTGCAACTCATCCTCTGTGACT TCTCTTACTTGTTTTTTATTCTCACCGGGCCGCCCCCCCCCCCTCAC ACTCCCCCTTCCCTCTCTCCCTGAGGATGGCAAAAGCGCTTAACAAG CAAACGGCATCCAAGCCTCTCCTCCGCACGGCAGTTATCCTGGAAGG AACGGGGCCGTACCTTGACCTAAGACACTCATACACGGTGCAGGGCG TTGCGTAGAAGGGCTGTTGAACAAGGCGGGTTCAACCCGGTCACACC GTTGTGTCGCCGCTGTAGACGCCCTGGTAGAGGCG
223	IrLiD	GGTACACTCGTGCCGCGCGCTGATGTTGTAGGTGCACGCGCGCGTGT GCTGCAGCGGGGCCGCCGCCACTGCGACTGTGTGTGTGCGCGTGACG GCCGGCACGAGGAAGGAGGAGCGCGCGTGTGCGTGCGATGCGCCTCC TCTTTTTTTTTTCGCCCTCGTCGGTGTTTTTTTTTTCTGAGAGGACG GCGGGGCGGATGGCGGGCGGCGGTGCTGACGGAGCGGCCACACTTTG CACCTCCCCGCCCTCCGCCGTCTCTCCGTTCGCCGTCCTCTCCTTCC TCGTGCGTGCGTCTGCCGCGCATGCACACGCGCGCGCGTTGCCGTAG CGCTGTGTATCTGTGGAGGGGGGCCTTGTCTCTCCCTCCCCGTGGTT GATAGATGAAGAGAAAGAAAAGGAGAGAGCAGTGCGCATGTGCGCGC GTGTGTGCCTCCGCTCCCTGGAGCTCCCCACGAGTCCCCTCCGCCAC GCACCTGCGAGCCTGCACAGCGGCCCACCCGCCCGCACACATGAGCA

SEQ ID NO.	Description	Sequence
		GAGGTGGGTGGGTGGAGCGGGTGATGTCGGCGCGCACACGCGCGCGC GCTGACCACTCCGACGTGAAAACACGGACGAGCGAGGCTGGCAAGGC AAGGCAGGAATCTGATCACGTGCGCGCGCACACAAACGGAATGAGCA GCTCCTGAAGAGACGATGGGGCTCATGCACACAGACACGCACGCGCA CACTCCTCCGTCTTCACGGAGCGCGGCCCTGCTGCTGCTGCTGCTGC CGCCATGTGCCGGACGTCTGCCACGCGTGTCTTCCCCACACCTTGCT CTTTCCCTCCCCCCTCCCCTCCCCTCCTGGCGAACACAAAACATGCG CGATGCACACACGCGCACGCCCACCGAAAAAAAAACGCGCAGCTCTT CGCTCTCGTTCTTCGAACAAACACCTTTAAACCGCCTTCTAACCCCT CTTTCTTCTTTTTCAGCC
224	IrLiE	GCAGAATTTGGATGATGCGATTACTTGAGATAATTTCATTTTCATCA GCAAAAACGAAGTGCAACGGTATCTTTGGTTCACCAGAGGCCGGCAA AGCTCTTAGGGTGGTGTAATGGGCTGTTAGCGCTACGGTACACTGAA GCGATCAGCTGCGGTATCTGTGTGAGCGTCAAGGGTGCGCTGGTTTC TGCATCTCCGAGTTTTTGATTCGCTCTGAGGATGTATCGCAAAAAGC ACGCTGCGGTGCTGCTTTACTACTCCTGCGCTGCTGCTCCTTCAAAT GCGTCGACATGTCCGATTTTCTGCAGCTACTCGCCTCCACTTTCATC TCTCCCTCTTCCTTGTTGTTTTCTGTGTGTCCATGCGCCTTGTGTGC GTCTCAACTTGCGACAACTTTTCTTTCGCGTCTCTGTGGAATAACAT CTGAACAGCTTTAGGGCTTCATTCGCAACGGATC
225	IrLiF	GCTGCCTTCCACTGAAGCGCGCACACAGACCGACGGACACAACCACC CCTCTCTTTTTTCTTCCCTTTTTTACTTTTCATTTCCTCTGAAGCAA ACAAGCAAACAAACAACAGCAAGCGCAACGCTGAGAGTCACAGCGGG GCATCGACCTCTCACAGTCGCGGCAGCGGTGTGAAGTGCGCAGACGT GCACGACGATGCTCTCAAATGGACGGAGGATTGCTTCGTGTGTGTGT TTCGCACCTCGAAGGTGAGACAGAATGCAGAGAAAGGATAGGCGAGG GGCCAGGGACGGCGCTGGAGAGGGTGGTCCTGTGCGGGTGGGAGGGA CGAAACAGACGCGAGTTGTCGCTTTACCTCTTTTCTTTTCGCTCTCT TTCCACTCACTTCTGCCATGCCGTACCTTGCCGTTGGTAGCTTACAC ACATACACACATCAGTGTGCACCCCGGTCCAACGCATCCCCCTTCTC TGTTTTTGAAGACATGGATAGCTGAGAAAACGAACAAGCAACACACC TCTCTCAAGGTTGCTCCTTGGCTGCACCGCCCATGCACCCACTTCTC CCCTCTCTGCACTTTCTCTTCCCTCTTTCATCACCATTCAGAACTCT CTCCGACGCTATTGTCGATGGGATAAACAAACCACAAAAAATACGTT CCCTCTCTGCCTTCCCTTCCGTGACGGTTGCCTTCATTCTGCATGGG CCCGCACTCAACCTCCTCCAACTCCACTCCTACGCCCTCCTTCGCCT CTACCCCCTTTCCTTCTCACACAGAGAGCAGCTCTCTGATCTCGTGG CTTCCCTTCATTCCCCTCTTTCCCTACTCTCCTTTCGTGTAAAAACT TCCACGGTTGCTCCGCATCTGTCGGCTGCTTTTTGATCTTGCAAAGA AATCAACTCCTTCAGCC
226	IrLiG	GGCCATACCCTCACTTCGCTTGTTTCGTGATTTTTCGTGGGAGTCGG TGGCCCTACCACCGGTCTTTCATTGGCTTATTTCTATCCGGTCTGAA AGAGGTACAAAGGCGAACGCATTGTAGTGAGTAATGGTGTCGCAAAG GGTGATATGAGTGGGGCCTATGTACATCCCTCAGAATCCACGAGGGC GGGCGTATGTGGAAGTTGTTTGCGGCATCTGTGAGTGCTCGCGTGTG CCGCGGTGCGTCGGTGGCACTTGTTCGATTCCCCAGGCACGCACGCG GGAGCTGTCGATGTGGAGCGATGAAACGCCTACGAGAATCGTCGTGT GTCTCCCCCTTGACTTTTGCCTGTGGAGTCTTCGTGCGCACGTTGCA

SEQ ID NO.	Description	Sequence
		GTTGTGACCGGATGATGCAAACCGCAGCAAGTTTGACAGTCATTTGT GGGTGGCTTCTTCAAGGACCCTCTCGCTTTCTCTCTTCCTCGCTTAT CTTCTTTCGCATTGCACAGTCGTTTCCACGTGGAGGGGTAGTGCTTT CACTGCTTCTTGGGGAGAGTCACAGGCGTACATATGTACACATACGC ACTCTGTCGTTGTGTTTGAGAAGGAAGTGGCAGAGGAAAA
227	IrLiH	ACTTTTGATGGCACTGTTTTTCTTTACTTTTATTTCTCTCAAAACAT CAGAAGCAGTAATGTAAATATTCATTTTGTTTCAGCGCTCGTGCCAA ACATCACGCGCTTGTTCAAGAGGCTATGCGAAGTGATCATTGCCGTT TTTTTTTTCCTCAGCGTAAGCGGTGCATATGCTCAAAATGCATGTGC TTGTGGAAAATCAAGGCAACTTTGCATCTCCTGTTGAGAGTTCTAGT CCAGCAATCTATCCATGGCCTTTTCTTCTTTGGGATACTTTTATCGC GATGCTTTGCGCTTCGTCTCTACCCCTTCTGTATCCTACAAAAATAT CATAACGCCGATTATGTGCTCGATGCGCTGCTTCGAATAGCTCTGTT TTCTTCATTTAACACG
228	IrLiI	AGAGGGCGTGCCTGGGGAGAGGGAGACATTGGCGGCCCAGGTGGTGC GTGTGCGCGGATCTGCGTGCAGAGGTGCGCAGGGCGCGCGCTCTCGT CTTTTGGTCTCTTTCTGTTTTCGCTTTATTTCTGTTTTTTTCTCCTT TTCAACAGCAAGAACAGCCACCACGCGCACCAAGCGAAGGTAACGTG AGACTCGGCTTGTGGGATTGCTTCGGTGCGCGGGGGGGGAACGGCGA GGAGGTGGGGTGGTGGGTGGGGACCTCCCCTCATCTGCCTCCTGCGC AGCACCCCATCACTCACGCGCACACAGATGAGCAAGTCCGCCGACGC ACTGCAGGCCACCCAACTGTGCTTCGTGTTGCTCGTGCATCGATCTC CCTCTGTGCAAGCGAATAGGCTCTCCTCAGATCAGATGTGATTTTCG TTCCCCTCCACATCACTTCCTCGAGCAGCTGACCTTTACCATGTCTT CGCAGGCGATGACGGCGCCCACTAGGCCTCGCCCCCTCCACCGCTGT TGCCAACATTGCAACTGCTTCTCTGTACTTCTCTGTGTTTCTCGAAC TCTCTTCCCCCTCCCCCACCGTTTCCATCTCCGCGCGTGTGCGCGTC GCTGTACACTCTTCGCTGGATGCCGGATCCCACGCAAACACACACGC ACACACACACACACACATCAGACGTGCCTCACAAACCCGTTCGTGCT CGAACATCGACAGCGCACCCAGACGTGTGGTCTTGCTCTTCTTCCTT TCGCTCGTTCTCAGCTCTTCTTCCTCCTTACCCAGTACGACGAGCTC TGACCTCTTGTCGTGTGCCCGCCTGTGTGCCATACACCTGGCACCCA CTCCTAAACACGCACTTATCACACCTCCATCGCAACACC
229	IrLiJ	ACCCGTGCCAGCATGTTTGTATCCTTTGCATTTTATTTTATATATAT ATATTTTTTTTTCATTTGCTAGTGAGGGATTCTCATGCGCGTATACA TATAAAAAGAAAAAGCCAGACGGTGAGAGGGCACATCTGTGATCCTT GTGCACCGTTTGTGGTGCGTGCCTGTGCTTCTCTGCGAAGCCATGTC TACGGCACGCTTCTCAGACACACGCAGTGCAGACAGCAGACGGCGAA TGCTTTTTCTTCCTCTCCGTCTTCCTCGCGCCTGCTGGATAGCGGGT GGCGCATCGTGTTGTCATTCTCACCTCTGCTTGATAGGGTCACAGGC GGCCAGGAAGGCGAAGGGGGGGGGGAGGGGCATGGAAGGTGAAGAAG CCTGCTTAACGGAGGCGCCGTGCGTCATGTTGATGAGATGGTGGAAT TTTCATTGGGCCGGTTCTATCCCGTAGTCGGTGTCCCGAACGGCTCA CCTTTTTTTTTGCTGTCATTGTTGCGCTGCTCACGTTCTCCCCCTCC GTTTCTCTCACTTTGAAGGTGTCCTCGTCACACATCCACTTCACTCT TGCCGGGGAGTCTGTTGGGCAACGTTCGCCGAGTAAAACGTTTTTTC GAGCCTTTCCATGAGGAAACCAAGGAGTA

SEQ ID NO.	Description	Sequence
230	IrLiK	AGAGCAATTGAGCGCGTGCGTGTCGGTGTTCGGGTGTGTTTATGGTC ACTGAGGAGGGAGGAGAGAAATGCAGGGCTTCCTCCTCGTGTGTTGC TCTCTGTTTCGTTCTCCCTTCCCCGTAGCCTGCTGCCGCACTCTGCT CGTCCCGTGCGTCCAGACCTCTGTAGCCTTTCGATTCCTTTATCTTT TTTGTTTTAATTTTCTTTTTTGTCCGTATGCTTCCCAGAAACGAAAA AAAGAACAAGAAAGGACGAAGTACAAGTGGATGTGCGCCGAGAGCAC GTCTGCCCCCCTGTGAAGGAGCGCAGCGGATGCGTGCTCCGCTCCAC TCGGTCATCTCTGCCGTCCCTCAGGCACGGCAGGCCCAGGAGAGTTC AAGGAGCTTGATGCTGCATTGCAAGGCGAATGCGTTTTTTTTTTCGT TCGCCCTCCGCCAGCGGTGCTCATGAACTGCGATGCACTCGAGTTCC CGAAAGAGCAGCGAGCCACTGTTTCTTCGTCGAGAGTATCGCTGAGG CACGGCGTGCTTGCGATTGCTCGCTCTGCAAGTGCGCGTGCATGGCG GCTCTCTTTGCAGTGCTCCTCTACTTTTCTCCCTCTGTTCTGCGCTG CCATGCCTCCTTGTATGCCTCGGCCCACGATCACTCACGCCTGCGCA CAAACGCATACTTTCTTTTTCCACTCGTTCTCCACGGTGCGCCTTGA TTCGCACTCGTCCAATGACTAGGGCGTGTGGAGAGAAGAGAAGGTAC AGATAGCGCCAGGAGGCGGCTGAGCAGGGAGACACACGCTGGCACAC GTCAACGTATAGCGCACACCCACGTCCCACTTCTGTACGGCTGCTCT CTTCCTACTAGTTGGCCATATTCAGCCCTTCGTTCTGCCCATAGTCC CAGTTATCGAAGTGACGCTGCATGATATAGCTGCGAGCACACA
231	IrLiL	GTCGAACGCTCACTTTTGAGCACACGACTCTCTACTTGTCTCCCGCT CTGATGTCTCTTTCCTTATTTCTGCGCCTGCAGGTAAAAGAAGTGCA TCCGCATGGCTGTCTTTTAACGGGGACAGCGAGGCGTGCTGGCGGCA ACTGTGTGCGCTTGTGTGCGCGCACGTTACGCTGAGAGAACCTCACA TTTCCTTTTTGTTTTTACTGTTAATTTTCTGTATGTCCTTTTCTCGG CCTCTTGTCGCGTCTGCTCCCCCCCCCGATGGGGCGCTGGCGAGGCGG AGAGGTCATAGGTTCCTCGTTATAAGCCAGTAGCGGTGCTGCACGGG CATGCCCTATGGAGGGAGAAGGGGTGCTGCGTGGAAAAGGGAGCGCA GTGCGCCAGAACACAAGCGTGCGCGCTTGTAGGTGCGCACATGTTTG CTACTTTTTTTTCTCTCCGTTCCGCTCTGGCTAGTGATCTTCGCCAC TGCCGAGTGGGTGTTGGCCTGCTGCAGAGACTGCAACATTGCTCCCG GTGCGGGCTGTGTGCGGTCATCGCGTGTGCGCAGCTGCAGTGTGCGG AGGGGCCGTCCAGGCACGGTCTTACTTCAATCTCCGCTGCTATGGGT GCGTCCTGATGAAGGCCCTGCCTACGGATCGCCTTTCTGTAGGCGCT CTTGTCCATCTCTGCTGTAGCTCAACTTTCTGCGCTTGTTTTTCCTC TTTTTGTTCTTCGGCATCTCCGCCTTTGTTGGTGACTGGTACTGCCT TGCGTCTCCATGAACTAAAACAACGGCTGCATATCTTCCCCTTCCCT TGCGGATATAAAACTCGTACCTGTGCGACTTTCTCACGTTCGCCGCA CGCTCACGGACGTTCGACGTCCAATCGATGCGCGCATGCGCACCATG ACGCTTTTTCGAAGTTTCTACGCCTCGCCATCGTACAGACACTTAAG CTAACAACTCGCTCACACACTCGAG
232	IrLiM	TCAGCGCTCCGTAGCTCGCTGCACATGCGGTACTGCGTTCCAGAGCA TCACGCGACGCACAGCAACACAAACTTTCTTTATCTTTCTCTTCCAT TCGAAAAAAAAAAAAGATAACACCCACCTCACATAACGTCCATAACAA GAGAGCGTGAGAGGAGAGTCTGCTCTTCGACTTCACACCGCGAATGC GGCAACACGTGGCTTATGCGCAACGCTTCTTTTGGCACGTCATGCTA AACAGAATCTCTGCGTAGGGCAACCAGGCTTTCATCGACCCGTCGTT CGATCCTCGCTCCTCCGGCATTCTTGAGTCACGACACGAATGCTTGG

SEQ ID NO.	Description	Sequence
		CTCCGTGCGTCTGCGAGCGTTTGTGCGTTCCTCTAAAGCAAGAACGC GGGGACACGACGTTTATCTCCGCCTCGCGACGCACTTTCTTTACCAA CTACGTGCACTTACAACCCCCCGATCTCAAAACCTCTGCTCATCGCA TCACTTCTCATTCCGTCGTTGTGCCTCTCTCTACCTTCATCTCCCGC TTGTGCTTGGTTTCCTAATACCGTTCTCGTGTAATGCCTCATCCCTT TTCCACTACAGCTCTTTTTTTCCCCTCGCCGAAG
233	IrLiN	GCCCACACCCTCCCTCCTCTCTGTCTCTCTTAGATCTCTTTCAAAGG TCGTGGTGGAGATGAACATCTCGGCTCATCTCCTCCCGGAGAGGGAG AAGCACTGGGCCTCTGCACGCGGCAGCGGCACGCACACGCGCACATG TCTGCGTGTGTAAGGGGCGTGGCAGGCAGCGTGTGTGCCTCCACGCT GCCGCGCACGCCGTATCATAGATGCACTTCTGTTTTTTATTATTTTA AATGCGCCATGCAAAGGGGGGAGGGGAATATGTTCTGCGTAATGTGC GCGCACTCGATCTCTGTGACCCGGCGATGGCGTGCGTGAGAGAGGGC CGTGCGTGGGTGCGATGGACGGCGTCGTCCTCGCACTCCGTGCTGGC CGGCAGCTGAGGAGAGAGCGCAGAGGACGCAAAGGTAGCGAGCAAGG AGCGGCACGCCCACGCAGTGCGCGCGCGTATAGGTGGATGCCTCTCT GCGCGATGCGTGCGTGTGCCTGTGCCGCGCAAGTAACGAATGACGCG CCAGCGGTGCTGCTGCCGCTGCTTTCCGCCCACCTCATCGAAGCGGC CCCGTCGTCGGCACACAGGGACGTCTGCGCTGCCGGCCCTGCGCTGA TCCGCTTGTACGTGCGGCGCTTCAGCCCTCTACGCAGCAGCGGGGTG GGAGGGGGGTCAAAGCATACCTGACCCCAACCTCCTTTATAACCGCT CAACAGCAACCTCAGGATGACGCGGCAGATGTGCGCGCCGCTGGTCT CCTTCACTTTCGCGCCCCCTGCCCCAACTCACCCACCCACCCCCCCC TCCTCCTCTCCTCCGCCTTCCCGTTAACATTCGGATGCGCGCATGTG CGCAGTGCATCCTCAGCGCAGTCCACACCGCCATCGTTCTCCCCGCC ACGCCCCTTCCACCCAGACCAGAGAAAGAGCCGTAGCCACGTAGGCC ACCGCACCCGAGCACGACCATCGCGTGTCACC
234	IrLiO	GCTCTTCGGATCGCAGCGAGAGAGTGTACGCACGTGCGTGCGGGTGT GTCGCGGGCTTCGCCCTTTACTTTTAGTTTGTGTGCATCGCTTCTTC ATTTTTTAATGGCCCGCTTCGAACGAAAGCGAAACAAGACGAGATGG CGTCACGACGAGAGACAGACGGACGGACAGAGAGAAGGACCGCGGAG GGAAGGCACAGATGTAGCCGCACCTCGAATCGCCATTCCTTTCGAGC CTTCATCTCGCGCTCTCTCGCCTATCATGAGCGGCGTCAATGCACTT GCCGCCTATTTGTCAGTGCCGTGCCTGACGTCTGTGTGTGTGTGTGT ACCACACTCGTCTTCCGTGTGCTCGACAGCGGGTGAGGTTGGGTAAG GGCCCGATTTGGTAGTATCAGGCAATGTCCACGTTGCTCGGCAACGT AGGGCCGAGATAGGATATGGTAGAAACGGCATGTTGCTTGAAGGAGG TGCTCTCCGCCCTCCCCTGCCCCCGCTTCCAGTCCCGACTCCGCTCA GTCACTGCACCGCAACTCTCGCATCATTGACGCAAACATCTCACTTC CCTCGGTCTCGGTCTCTTTTCTTGCTAACGCACTTCTGCGTGGCGCA TCACGCACGCATTCATCTTCGCACGCGTGGCCGCGTGTGTATTTGTG TGTTCGCGCGTCGCCCCCCCCCTCCGCCCATCTCCCTACCGGTGTCT TACTGCTCCTGTGAAAGCATACGTATCCACGCCCCTCTGTGTGTGTG TCTGTGATCGCA
235	IrLiP	GGCACGCAGTGTGTGTCTCGTTTGCTCCGAATTCTTTTTCCTTTTTC GTTTTTCGTGTTTCGCGTGCCTCTCTTTTCGGCGCATGCGAAAAACA GCACAGCAATCCAGCAAACGAACAAAGAAAATCATCGATGGCGCACG CTACGCCAAGGTTGGGGGTGGAGCGGGGGTGGCGGCAACGCCGTGTG

SEQ ID NO.	Description	Sequence
		CAGCAGAGCAGACACCCATCGCAGAAGCCCCCGGTATCTGCGTGCAT GTGTGTTCGGTGCACGACCGGGTCGTGCTGCTTGTATGTTTGGGGAG GGAGGGGCTGCGTTGCCTTCCTCACGCCTCCCATCCCTCCATCCCTG TCGCCTTCTAGGGGTCGCCGAGGCGCGTGCAGAGACGGACTCTACAG GCCCAGGCGAGATGGCAACGGGCGCACGCACACACGCACGCGGAGGG AGGAATGTTTGGGATGAATCACACTGCACTGAAACCTCTCTTCTACC CTCATCAGCCTTCATCTTCACTCGACACACAGACGCGCCGCTGTCGC CACCGCCTCAGAAAAGGCAGCAAGCACACGTGAAACCCTAAA
236	IrLiQ	ATCACACCTACCCCTCTCTTTCTCTCGCTGATAGGGGACAGGGTGTG TGTGCGTTGCTGTGTGGGAGCGAGAGGTGCACGGGTCTGCGCGCGTG CACTACGTAACTGGCGCATGACGTCGTCGTCTGCCTCTCGCTCCCTG TGACACACACACACGCATACGTATCCCCCTCTCTCCCCCTCCATAGA TCCAGTCTTTTTCTTTCTCTTATGTTATTTCTTCGATGTCATCTGTG TCTCGCTCTCACCCAGGGGCTAGTAAAGGTTGCCGTTTGAAACCAAT TTCGTCTCAAAAAAAATCCCTTCCGGGCGAGGTGATGTTGCCTGTGG TGTGTGCGTGTGTGTGAAGTTCACTAAGGCTGAACAATCTGTGTTCG TCTTTCCACACACACACACACACAAACAGCTTCCTCTCCTCCTGCTG CATTTCTCCTTGATGTTATTTGCGTGTGCGTGTGAATAGGGGCGGAG GTGCACGTGGCGCGATACACGAAGCTTTCCACTCGTCGACATAGTTG CCCTTCTCTACTTGACAGCTGTGAGCATTCTGGTTCTTGTGACCTCC TATCATATCGCCTTGGTGACCTGGTAGTCTGTGCTGTTCCTCTCTAC TCCCTTCTCCCATCCCCACCTCACCCCTCCTTCCTCTCCGACCGCAC GTTGCCTTTCTGTTGGGCTCTTGATGCTTACGCAGACGTGGCACGAA TACGCACATTGTATGGATGGGCAGCGGTAGTGTTTGTTGCATTAGAC GTTCACATATCCTATTCTTTCTCCCACCCCTGGGAGTCCTGCGGCGC GGCGTGTATGTGTGTGATGGGAGGGGGGACCCCTTCCGTGAAACGGT GCACACAGGCGAAGTGCATCACGTGCGTTCTTTGCTCTTTTAGGCAC CGCTGTC
237	IrLiR	GTGCAACAGGCACCTTAGAACGGAAATGCGCTGTCTGCCGTAAGTGA CCTCCCTCCTCTTTTGTTGGTTTCAGTTTTTCTTCTCACTCCATCCC TCGTCGTTTTTGCCTGTGCTATACATGTACCGTTCCGTGTCTCGTGT GCGCAATGTTAGCGTTGGGTTTGGCAGCTTTTTTTTCTCGTTTTCGC TAAGAGAATGCAAGCAGCGAAATGTCAGAGCTGCTGAAGAAGGCAGG AATGAGGATGAACAGACGTGATGCAGACGGTACGCAGTCACGATCAT GTGATCTTCCGGACGGACTGAAGATTGGCCGCATCGAAGGAGCTGCC TCTTCCCCTCTAAAACACACACACACACACACACACACACATGCACA TACAACGATGCGCGGTCGATGCAGTTCAAGCTAAACGCTCCCTTGTG TAACGCCTTCACTGAAGACAGGCTATGCGCGCACATTCAGGCAGTGA GAGCGACCTTTGTACGGAGTTCATTGGAGGCCATTGCACTTCTTCCT CACGGCTTACGTGTGCTGGAGCTTCTCTCCGCCGATCACCGGGTCCC GTGCGCCCGCGCGTCTTCTGTCCTCTCCGTAAACCTCTTCCTCTTTC CTTTGAACCATTTCTGTGTTTTTTTTTCTTTGGAAATTTCAACTCTT TCCATATCTCTCTACTGCGCACTCATCACGACGGTGCTCATGCACGA AGACAAGCAGTGTGCGCGGCGCGACTTCACGAATCCGCTGAAGCCTT CCGCGCGTCAATCGAGGAAACACCGTACTCTGCGTTTTCATCCACCC ACGCGGTGCCCATTCCGGGCAACTAGAGAACTTTTGCCTCTTACCAG GGCTCAACACCGCACTCGCACACAGACGCACACCCACCCAAAAAAAA

SEQ ID NO.	Description	Sequence
		AACCTAGATAGATTCGCTCACAGGTACGGGCAGCTGCGCTGCAGTCT TGGCGCC
238	IrLiS	GCTACGGGGGAACGGTTGCCCTTGCTGTGGCAGCTGACGTGTGGAGT TTGCGTGTTGAAACTCATTAAGGCTTTCGATCCTGTTCTTTTTTTTT TGGTGTGCGGTGGTTTATGTGCTTGTTATGATGGTAGCTTTGCGGAC TGTTTTCCTTGCCGTCTGTAGGTGTTTCTTTTGTTTTTTTTTTATAG TATTTGTGTTCCACTTTCGCTTGATGGAAAAGAATTTGTTGGTGCGC TGCGCATCGTGGTTATGTTTTTTGAGTCTGGAGCCGTGGATGCTGCT GATTCTACTCGTTTGTACCTTGCTGTTTTCGGTGCCGTGGTGTGCCA GGTACGCGTTCTATGGTTTCTTGCGTCTCACCGCTTGAGAGAGACCT AGCGGGTTTTCCTGACATCCTCTATCATGTCCTGCTCTTCTCCTGCA CGTGCTGGTGTGTCTTTTTCTTGTTTTTTTTTTTTTTTGTGTGGAGC TTGTGCATCGCTCCTAATCCTGGCGCTTGGATAGCTGCGCGTCTCCC GGTCGCGGGGGGTGTAGAGATTCTCTGTTTTGCGCTGCTTTCTTTGCT TTTGCATATGCAAATCGTGCAGAGGCACACGAATGAGTCGAG
239	IrLiT	AGCTGTGCCGATGCTCGTCCTTTTGATGCATATTGCAATGGCCGCCC GCTGTCGCTAGCATGCGGGCGCGGACTTTGCGGTGTGCTGCAACTGC CCTTGGTTGTGTTTCGTTTTGTTTTTGTCTTTGAGTAGCATTTGCAA GCAAGCAAAGAAAAAAAAAGGAGCCACGCTGCCGTGATGAACTTGTG GCAAATGAGGGAGCAGCTGGCCGCCTTCTGCGCCGTGTGTGTGCTTC ACGTACTCCACTATGGGCACCGCTGGTCATGTCCGTGTTGTTGCGCG CGTCGCATGTGCGGCTGGTACGTTATACCGAACGACGCCACGCAACA TACATGTATTTGGGTTTTCTGCTGTTTGCTGGAATGCTTGAACGTTT GCGGATGCCTTTCAGTGTGAAGCTGGGCAGTGTTTCGTCTCGCACAG CGAGGCCTGCGCTGTGCGCCACCACCTTGCCCTATGTCGCATATGTG TGTTTTGTTTTCTTTGCACAGACATTGAATCGACATCCGCTTCTCTG CTTCTTCTGATGGTCGTGCTTTCCCAGCTGCAGTGCTGCCGCTGCTG CCTGAGCAGCTCGACGGCTGCTTGTCACTGCTAGATTTTAAAAGAAA CACTTTTATGCAGAGCACATAAAGAGTGCGTACCGTCGCACTGTGTC ATGAGCTTCGGCTCAGGAATCTTCGCTGGCATCGTTATCGCTGGCTA GCCAAGGTGTGGAGGCTTCGGTGGATGAG
240	PacBio raw subread	TGTATGTGTTTGGGATGTTGACGCTGTCATTTTCTCCGCCCCCACTT GCATAGATGCGGAAGAAAGGCGTCCGAAAGGTGAGGGAGAGACACGC CGGATCAACCACATCACGACACCCACACACAAACACACACCGAGAGC GGGGGGGGGGGGGGGGGGGGCCTCACTCGATAAAGCTAACTGTTTGT TGGACATAATTCCCTTTTGGTTTCATAGTTTTCCTCGTAAAGGAGCA CGATAAGCTTTTGGATTCCACAGCACTCTAAAACAAGGAAAATGAGG CACGTTATCCTCTGCGAGTCTCTCTCTCTCTATTTTCACACCCACAG GCACAAATTTTGCAGTGTCCTCCTCCTCTTCGTGTGCCGCGTGGTTT GTGGTGTATGTGTGTGGGTCCTTCCGACAAGAAAAAACATGAACGCT CAAGAAACGGAATGTCAGCGGTGTCATAGGTACCGTTGTAGTCACAC AGGCGAGCGGCTCCGCGAATCTGACCGAACTGGTGGCTGAGGAACAC CACAAGGTACAAGAAAGCTAAACTGAACCAGAAATGCGGCTCCGAGT ACCGATCCACTTCTTTTGCCTCCCTCCTCTCCCTCTACACTATACCA CTCTGTCGGCTGAAAGGGAAATATTATGCTCCACTGTGCCCCCTTCT TCATCGCGCGCCTGGTCTTTACTCGGCCTCCGTTAAAACGGAACTGC TGTCTCAGCATCAGCACTCAAGCGTAGAGAGTTTAGGCGCGACTGCG GCACTGCTTGCCGCAACCTCAGCGCACTACTCGAAATCCCTGAACTT

SEQ ID NO.	Description	Sequence
		GGAACTAAGCGCGTCGCTGTGTCTCGTGACCCCCTCCATCTGTGCCT AAATTCGCTGTTTCGGGATTTTGGTTGTTCACTACGCATCACCAGTA AAGGCTTACAAAGGTGTATCGCATTAGCGTTAACCTCTGACGCTTTA TACATCTTCGGCTTTTCAGTCACCTCATACACCCATAGAAGCCACCT TTAATCGACCGGCGGGGCCTCTTCCACTTTTTGTATCCTTCCACGGC CCCTCCCCGCACCCCCCACCCCCGCCCACCAAGCACCGGCCCCCTTT GGCTCTTGGGCAGTACGGACACTGGCCCCGTTTGAAGCTCTCGCGCA GTGTATCGTCCTAATTAAATGCTCAGCCGCTCATCATGTCGCCTCCA GACAATCGTTTCTTCTATGTGGCCCAGCACCCTTGGCTGAAGGCAAG CCGGTTTTGTGGAGATGTCGCTACAGCCCCTTGTCTTGGACGCGCCT CGACATGGCCTCTTCAGACGTTCTTTCACACCAAGTGGTACTTACGC CTCCTTTCTTTGAGTGCAAGACCATCGAGCGCGCTCTTGCTCGAGCA TTCGGTTTTGGGTTTTTGTCTCTCATCGAAAAACGTGTTGGATCACC GCGAGCTGTTCGGCTCGCGAGGACGGGTGTAAAGAAGCTGCGGTTGC TCGCGCACACACTGTTCCTCTCCGTTGTCCACGCATGCACCCGCATT ACCAATGAACGCCGCGAGACACTCGCAGGCGAAACCCCAACAGCGTT CATTTGAGCACACTCTCCATTGACATGAAACCCTATCCGTGACAGAC GAGGAGCGAGATGCGCCCGCTCTCCCCTCCCGCCGCGGTCTCCACCA CTATTGCACGTCACCGTGAAGTTCTTGACAGGGTCATGCTGACTGGG CAAGCCGCACCCGCCTCTCCACAAAATGTCTATGCCACTAGGGACGT AAGCGGAGAGACTGAAGAGTGCTTGAGCATCGAGATTTCAGCTTTTC TCTCTACTTGTCGCCGTAACGACTACTCTCTGGATAGTGCTTCGGTG CGCCGTAACCAACAGGAGGCCCGCGCCTGCCTTGTTGCAGAGGCTCA TCAGCGCAAGAAAGCCGTTCCCTGCCAGATGGCGTGCCGATGTGGTC AAACGCCGGTGGCGTACCAGATCATTCAGCGCCTCCCAGGATAGTGG TCGGACGGGTTTTCTCTACCCTCGTCCCTGGTCTTTCCCTTCTCGGC AGACGGTGCGGAAGCTCGTCGCCTACTGTCTGCCGGAACACGCAACT CCTCCTCTCGGCTCCGACCACTCCCGGTGATGCTAACGTGGTATAAT GTCGCTCATGACAACCAACCCTGAACGTTATTTCGACAAACCATCTT GTGGCAATCCCAAAGGGGTTGTTGTCTCTACTTACCCTCCCCGCCGT TGCCTGAAGAACTGAACTTTTTCATCTCACTGTTTCGACGAGTGTCA TCCGTGTGCGGCACGCGCGCCGATACGGCGTCACACCGTGCTGAAGC TTCCACTGCACGGCCACTACTCTTCTACAGCCACCCCACCCCCGCCG TACACACACCCCAAAAAATGAGTGACACCGGCTACTTTGGCGCATCG CGTACCGCTAGCTTACCTTCGTGAGGGTATCAACGACTGCTACGTGA CCTCCTTCTGCGTCCGCGTCGTCCTGGTCGGCAGCCCTCTCGCGCAC ATGAATCCCTACATTTTCGAAGCGATGCGCATGGTGGGACCAGATGC TCGTCCTTTTGGCCGCGACATTGGCCCTGCGGTGAAGATGTACAAGA TTTGATAGCGGGACACCCCCAGTGACGTCGCAGCCTACTCCGTACCA TGGCTCACTCGCGTAGGGGCAGCGCAGCCGTGGCGAACGCCCTAACC GTCCCTTCACAACGCGAAGCGTGCGTTCCTCTTGAATGTGCGCCCTT GTTTCAGGAAGTGTGGAGACCGGACCTGACGCCGTTTTTTTTGCTGG CTTCCACTTAACAGCTCGCGCTACATCATTTTCGAGCATCTTCCGCC GCTGAATAGACTAGATGGAAAGCCGCCATCGTTCGTCTTCCTGCCAG CCGTCTATGAGTGCAAGTTACCCGCGGACCACCCGATAACCTACAAA GCTGTTTTCCACTCTCCTCCCTTTCACTGATGCTCTCATGGACGAGT ACCCGACGCTCTTTGAGTCACATTATCGACCCTCAGAAGAAGTCGTA TGACATTGGGAACTTCGTCGCTTTCGCTCACTCAGGCCTGACGTCAA

SEQ ID NO.	Description	Sequence
		GAAACTCCAACGATCGTTCTGCCGGCCATTCGGCGTGGTGTCTCTAA CTTCCACCCGCACCCGGAACCGCCTGGCAACCGTGCCTGCGCGTTCC GCGTGGACGAGCAGCTTTGAGAGATGAAGCGCATCGTGACGAATGCA AACCGATATCCCAAGACAAACACGCTGGGTGGTCGTTGGAACACAAT GCGATGAACATGTTCCTAACATAAGTGCGCCGCGGCTACAAGTGTAC GAGCGCGGAGAGCCACCTACCTCCGTGCAAACCAGCTTCGCGACCTT GACAGCCTCCCCGCGTTGGAGCAATACGTCGTGCACGGGCCGTACCC ACCCGTGGAAGAGTGCCTGAGACACTTGAACGCCACTTGCGCGTTGC ACAAGAGGGTTTCCCGCCCCTTGACGTACCCAAGGGCGGCTACTCGG CCTAGACGCGAAAAAAAAAAACCGGGGGGGGGGGTTTGGAGCGGCTGC GGGGTGTCTCATGCCCGTCTCAGGTCGGACAGTCTACCCCAAATAGG CCTCTCACCAGAGAAGCAGCGACCTGGACCGCCGTCGTGCGCCGTAC AAGCGGCGATGGCGGGAAGCGCGGACACCTCTGGTCGATTTGTGAAG AACGATGTAACCATGATCACCAGAATGACAGAAATTCAAGAAGCTGT TTGAAGGCTGACTATGTAGAAGCGTTCACACGTACATCGAGGTGGCA TTTTCCCCGGGTACCCGCACAAGCACGCCCACTAATGGAAACCTAAC AACCTGCGCAAGGCCTGTGTCCGCCGCGTCGACCCCACCAGGCCTCA ACCGGAAAAAAAAGTGGAAGCGTCTTAAGGCAGGCGGTGCCAGCTCGG CGACGAAGGAAGCCACTTTCATTGCGCATCTGGCATCTGCCGAACAT CGTTTCTGTTCGACTGGAAATCGCACCCTCCAGTAAAGACCATGTGC GCGCGTCGCGAAGAAAACGCGCCGTGAGGGTGCTCCCGGCGCGAACA CGGCCTAGCCGCTTGGCGGATTTCATGAGAATGTACTTTATCGACCA CGCCACATACTACCATCCAATCCGACCGCAACACCCAACCTTTTGTT CCTCGCCAAGTGTGACCTGCACGGAAAGGGCATCCCTCCCTTGCGAC CGCTGCAGCTCTTGTTGTCCTGCTCCCTGCAAAAGCTGAATGACCCA CCCCCATCTCCATCCTTCGGCGCGCTCTCCTCCTGGCTATCCAGCGT TCCCTGACTTTCCACTAACTATCACTTTCTTCTGGTTGGTAGAAACG CATTCCTGCGTCTTCACCGTGCTTTCTTTCTGCACGCATAGGCCCGG AAGGACGTCGCAGACTGACTATGGGGGGGCAACTTTGTTAGGAAAGG GTCGACGGGGCGTGTGAACCTCAGTCGCGCTGTACGCCTTTAAACCA GACGCTGCAAAAGGATCCCTGCGGGAGCGCACCTACTGGGAGGAAAA CAAGGCACCCCCCCATCCACCGCTGGCCTTAACCGCCCTTGAAGTAG CGGAATCGAGGGCTGTCCATGTTCTAGGAACAACGAGCAAGGTGCCG GGTGGATCAAATTCAAAATCAAGAAGCTGCCTCACCGTGGCCAACGT GGTCCGTCATCGGTCATCGTCCTTGGTGGTGTACTTCCAACATTTTG CTACTTCCGGTATCCCTACCGCTGGTGGGGAATTTACGCCAATTGAT GGCACTAGACGCCACGCCCGCAGCATCCAAAGCAACCTCCACGGCCA CCCGGGGGTAACTAGCCTACCGGAAAAACTACACATCTCACCGCTCGC CGCTTGCGCCACATGATGTCCCTGGCGTTCCCCGATGCAAACGAAAA CGGGTCACTTCATCAACACAATCGCTCACTTTCAAGTGCCACGTGAG AGGTCAGCCAATGAGCAGCGCCCTCAGGTTCTCGCGCATCTACGCAC GCCGCCTGCGCGTTTGGTGGCCTACTGCCCTCTTACTCGCAGTATAC GCACCTGACGGAAAAGCGGTCGCTGGTGAGATCATTTGCCTTTTCCT CGGTCTTCTTATCCCGGCAGAACAACCCTCGCTGCGCTCCTCTTCTT TCGTCACTTCTCTTCAATCCCCTCTTCTATCTTCTTTTTTTTTTCG ATGGGAGGCGCTCTCACCAGTGAGTGGCCCGCTCTTCGCTCTCTGCC TTTGGGTGTGGCGCTGTTCTTTGCTGTCCACTACACCGATTCTTTGC TCCATCCAACAGTTCTTTTTGCGTGGTGAGGCAGGTTGGGCACGTCG

SEQ ID NO.	Description	Sequence
		CCCGGTATCAACCCCCGTCTTATCCCCCTTCCCCTCCCGCCCACTTT TTTCTCAATGGCGGCCTCCGATTCTCATGCGCCCCTCGTGTCCGCGG CACTGCCATGAACTCCTACGTCCACTCTTCCTCAAGTGTAAACGCGG CTTTTCCCAGCAAGCCATATCTCTAGACGCGCCCTACCGGCACCATC CGCCCGCGAAACATCGAGTTTTTTCTCCTCTTCCGCTCCCTTCTGAC CTTAGCGTAGAAGGGCGGTCTTCGTTTTTTCGGCATGTCAACCACAG GCAGCCCATGGGCTGATCGAGTTCGAGTTGTTCGGACGACAACCGCC CCCGCCGTCTAACAGCGAGTAGCTTTTCCCGGTGAGCTGTGCCCGGG GAACGTAGCAGCTGTCCCCAGACGGGCAAGCCGCTCACCTACAAGGT CTGCGTCTTATTCATCGAATTAAAAATCGCATATTTTTATGATTCAA GGTGGAGACAATCACGAGTGCAACGGCACCGGTGGCTGTTCCACTAC GGATGTTGCGCTTCAAGGACGTCCCTCGACGGCAAGGGCCGGCAAGC ACAAGGGCCTGGTATGCTCTCCATGGACAACGCCGGGCGCAACACCC CGGCTTCGCAATCCCTTCATCCTGCACCATATCGTGCCCTGTTTGGA CATGGGAAGCCCGGTTGTGCTTTGGTCATGTGCTTCCACGGGTAACG AGCAGTGCAAACTTTGGAGCTAACGGTACACCGCACGGTAAGCCCAC CGTGACGGCTCATTCATGACTGTGGGTTGTGAAGGAGATGGAACCCT AGCACTACTCTTGTCTCGATCGTTTTTTTCGTCTTGTGTGCTGGTCA CTGTTGATAAGGTGTTGGCCACGCTACGCGAGGCGTGCAGCTGCGGG AGCTCTCATTAGGATCACACAGACGTAATGCAACGATTATCTGCATC TCTTGGGTGTCGCTCTACGCGCGGCGCACACAGCTCACTATACGGTG CACAGCCCCCTGCACGGGGGACGCCCCAGCGATGCCCCCCCTCCCCT CCCTCCCCACCTCTTTGCCGTTTTCTGCGGTACATTTGGGAACTGGT CCTCTCAGGCCTCACTTGCTTGGTAAACTACTTTGGTCAAACTGCGC TGCTCGCCTGCGTCACGGTCACCCCTTCCCGAACTCTTTCGTTCACC ACCCCACCGCTGTGTTTCTCCTTTCCCTTCCCTCACAATAACGGGCA CTCCTTGCGCACGAATGAATTCGTGCCGTTACCGCTACCGTGTGCAC GACAAGCCCTTGCTTACGAAGGCCCCACCACAGAGTCAGTCGGCAAA GCCTCCCCACCGTAATGCGCTCCCCCCGTGCCTCGTCCACGTTCCTT TCTCCCTATAGACGTCCTATCTTTCTAGCCTCACACGCGACACCCCT GCCTGTTCGAGCATGTTTTCCCCGACAGTCGCCGAGGGGGGCAGCGG TTGAGAAAGTTACCAGCGAAAACGAGTAAGAGAGCCCACGGCCACCT CGAGCGACAATGGCGACGCAGCCCCAAATTCGTGGGTGAGCAGCTAC TGGAAGCATGATGACACGAAGAGATGTACATAGCCATGTCCCGATTT TCCTTCATGTCTCATCGTCTCTTGCCCTGCTGACGAGCACAATTAAC TCAAAATGACTATCTGATGGGCTCCGTTTGCCACGACGAACTTACTC CCTCGTGGACGACGGCGGCAGCAGAAAGCAATTCTACTCCTTTGCTA CCAACATGCTATAGCCTGGGCCCGCTCATTTGTCTTATGTCGAACCT AATTCGCATTGCGCGCGAGCGCTTTTTTTTTTTGTACGCCCCGGTCAT CCTTATTTCCTGCGTCATCAACGCTCTATTGTGTGCTTTGTGTGCTT TTCGACCAAGAATATGCGGAGCGACTTACAGCACTACATTCCTCGTT TCTGGCCTGATCATGCATGTGCAACCGATGTTCCTCTTACATGCCCA TGAATGCCGTAGGGTCAACTACGGAAACCAACCCGCCTGGTTGATCT TCACACGAAATTCGGCTCGCATCGAGGACTCATGTCACCTGCGATTG GTGGCGCACAGCGGGATCTCTGGTGCAGCACTGTTTTTTTTTTTGGG TTTTTTTTTGTTTTGATTCAGTTTTGCTTATGAAAAATGTGGCGTTA CCCCATGAAGCCAACTTCAACTACCGCTGGTTGTCTAATTGCTGTTA TCTTCTTGCTGCCTTCTACATGCCTACAGGTTCTCTTCTCACGGAAG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		TTCCCTATTATCCCCGTCGCATGGTGCCCCTTCTTTCACCCAGCGTC CATTTTTCCCTGCAGTCGGGGGGGACTATGTCGTCCGTGACTCTGCA CACTCCTTTCCAACACCGTCCTTCCTTTTTTTTTTCCTATTACCTCC CTGTCTATTCTTTTTTTCGCAGGATTCCATCAAGCGCCACTGCACCT CCCCGACTGTACATCCCACCAGAGCCCACGCCAGCTCTCCTACATCA CGATGCCCCGCATAAATGTACGGCTCCCTCGCAAATACGATGTCGAG GCTCAGTTTCTAATGAATCAAAAAAGAGGCCCCGGACGAGGTTGCCA CTGGAGTTCACATGAATGAGGAATATCCGCAGAGAATGGAGCAATGG AACTGGATTCACAGAGCAATGGCCTCTACGCGTTCATGGCAGTTACG CGAGTTACTTCAGCGATTTCTTTGGAACGTTTTTTCCTGTTGCCTTC GCACCGGCGTGTGGCGACACTTGTTCAACGCTGGTGCCACCTGGCGC CGGCCAGAAAGTCGAACCCGAAGCTCAACCTGTCATCAACACTTTGT CTGGGGTTTGGCGGACCATCAGCCCTTTTTCTCCTGACCAGTTGTGT GTCCGGTGGTCACTTGAACCCGCTGTGACCTGTGCAAACTGCGTGTT TGCCGGGTTCCCTTGGAAGAAGCTCCCAGGCTATTTTCCTCGCTCAG TTTCTGGGAGCTTTTGTTGGTGCCGCCATATACTTCGGTCTTGTGTG TGTTGTTGTTTGTGTGTGTGTGAGAGAGAGAGAGTGAGCGACGGAGA AGAGATGTGCGCAAGTCAAGGCAGCGTAGCGCCTCACTGCACGTGCG TGACGCACTCCGCCGAGCCGGCCTCATCGCTGCGTGGCGCCACGTAA GGGCATGATAGTGTGCCCTCTTGAGGGCACTGCGCTCCTTCATGCCG GCCTTGCGCATCGACGGCATCGCGCTACGGTGCGCAAGAGGGAAGGG AGGGCGCAGGGGGCTTTCGGCGTGGGGCCGCCTTGACGCATGAGCGT GAGTGCACAAGCAAGCTAAATGCGCGGCGAGAGAAGGAGGAGCTGCA TGCCCGTCCCGTCTCGCGGCAGACGGAACGGAGCCACCGGTGGCCGA GAAGTTGGAAAAAGGAGGGTGAGGAGGGCGGCACAGCCGGCCTTGTC TATCGCGAATTGAAGAACAGAGAAGCAGTGAGAGGGAGACCAAAACG ACGGTACCTGCTGCACCGCCTTGCGAGCACAACCAAGCGTCATAAAC CGAGCGACCGATTCCGCGAACGCTCACAGCTAGGATCTTAATTCGGC CCCTACAACTAGAAATATGGATCTCTCGAGGCTGCTATTCCTTTGCC CTCGACGAGTGCTGGGGCTGTCGGTTTCCACTATCGGCGATTACTTC TACACAGCCCTCGGTCAGACCGGCCGCGCCTTTGTGCGGCGATTTGT GTACGCCCACAGTCCCGGCCTCCCGATCGGCGATTGCGTCGCAATCG ACCCCTGCGCCCACCTGCCTCATCGAATTGCCGCAACAGCTCTGATA AAGTTGGTCAAGACCAATGCGGAGCATATACCACGCCCGGGATCCGC GGCGATCCCTCAAGTCCGGAAGCCTCCGCGCGAAGTATCGCGTCGCT GGCCCATACAAGCAACCACGGCCCCAGAAAAAATTGGCGACCTCGTA TTGGAATCCCCCGAACATCGCCTCGCATAAAAAGTCCAATGACGCGC TGTTAGGCGGCCATTGCCGTCATGAGACATGTTGGAGCCGAAATTCG CGTGTCACGAGGTGCCGGACGTCGGGCAGTCCTCGGCCTAAGCATCA GCTCATCGTAGAGCCTGCGCGTACGGACGCCGGCGGTGTCGTCCATC ACCTTTTTGCCAGTGATACACATGGGGAGCCGCAATCCCGCGCATAT AATCACGCATGTAGTGTATTGACCGTCCTTGCGGTCCGAATGGGCCG AACCCGCTCGTCTGGCTAAGATCGTCCGCAAGCGCTCGCATCATCGC CGTCCGCGACCGGCTGCAGAACAGCGGCCGTTTCGGGTTTCAGGCAG GTCTTGCACGTGACACCCTGTGCCCGGCGGGAGATGCAATAGGTCAG GCTCTCGCTGAATTCCCCAATGTCAAGCACTTCCGGAATCTGGAGCG CGGGCCGATGCAAGTGCCGATAAACATAACGATCTTTGTAGAAACAT CGCGCAGCTATTTACCCCGCAGGACATACCCCGCCCTCCCTACATCG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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241	pLMTB6681	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG

SEQ ID NO.	Description	Sequence
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242	pLMTB6683	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCCGACCAAGGCTTTGAACTATCTACCAGAAGTGTGAGCCCC TACCGGAAGGATTACATCTCGGATGATGACTCTGATGAAGACTCTGC TTGCTATGGCGCATTCATCGACCAAGAGCTTGTCGGGAAGATTGAAC TCAACTCAACATGGAACGATCTAGCCTCTATCGAACACATTGTTGTG TCGCACACGCACCGAGGCAAAGGAGTCGCGCACAGTCTCATCGAATT TGCGAAAAAGTGGGCACTAAGCAGACAGCTCCTTGGCATACGATTAG

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SEQ ID NO.	Description	Sequence
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243	pLMTB6737	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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245	pLMTB8223	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT CCACACAATACCACCGTGCACACGCACAGCTTCTCTCTCCCCCCCCC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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246	pLMTB8254	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT ATGCGCCTGCGTGAGCCTCTTTTGTCAGGATCGGCGGCTATGCCCGG AGCCAGTCTCCAGCGGGCCTGCCGGTTGCTCGTTGCCGTCTGCGCGT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		CCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAG GGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTT TTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTA AACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACT GCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGC CGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGAT GGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAA TACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAG AAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTT ATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGT CATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGC GCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACA AACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAA CAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCT GTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGT ACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCC AGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCT TTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAA TCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATT TATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTA GAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCA ATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACA TATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACA TTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCAT GACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
247	pLMTB8281	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTAGACTCGTGCCGCGCGCTGATGATGTAGGTGCACGCGTGCGTGT GCTGCAGCGGAGCCGCCGCCACCGCGACTGTGTGTGTGTGCGCGCGT GACGACCGGCTCGAGGAAGGAGGAGCGCGCGTGTGCGTGCGATGCGC CTCCTCTTTTTTTTTCGCCCTCGTCGGTTTTTTTTTTTCTGAGAGGA CGGCGGCGGCGGATGGCGGGGCGGCGGCGCTGACGGAGCGGCCACGC TCTGCACCTCCCCGCCCTCCGCCGTCTCTCCGTTCGCCGTCCTCTCC TTCCTCGTGCGTGCGTCTGCCGCGCATGCACACGCGCGCGCGTTGCC GTAGCGCTGTGTATCTGTGGAGGAGGGCCTTGTCTCTCCCTCCCCGT CGCTGAGAGATGAAGGGGCAAAAAGAGAGAGCAGTGCGCATGTGTGC CTCCGCTCCCTGGAGCTCCCCACGAGCCCCCTGCGCCACGCACCTGC GAACCTGCACAGCGGCCCACCTGCCCGCACACGTGAGCAGAAATGGG TGTGTGGAGCGGGTGATGTCGGCGCGCACACGCGCGCGCGCTGACCA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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248	pLMTB8333	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GCAGAATTTGGATGATGCGATTACTTGAGATAATTTCATTTTCATCA GCAAAAACGAAGTGCAACGGTATCTTTGGTTCACCAGAGGCCGGCAA AGCTCTTAGGGTGGTGTAATGGGCTGTTAGCGCTACGGTACACTGAA GCGATCAGCTGCGGTATCTGTGTGAGCGTCAAGGGTGCGCTGGTTTC TGCATCTCCGAGTTTTTGATTCGCTCTGAGGATGTATCGCAAAAAGC ACGCTGCGGTGCTGCTTTACTACTCCTGCGCTGCTGCTCCTTCAAAT GCGTCGACATGTCCGATTTTCTGCAGCTACTCGCCTCCACTTTCATC TCTCCCTCTTCCTTGTTGTTTTCTGTGTGTCCATGCGCCTTGTGTGC GTCTCAACTTGCGACAACTTTTCTTTCGCGTCTCTGTGGAATAACAT CTGAACAGCTTTAGGGCTTCATTCGCAACGGATCATGACCGAGTACA AGCCGACCGTGCGCCTGGCGACACGCGACGACGTGCCACGCGCAGTG CGCACACTGGCGGCAGCGTTTGCGGACTACCCGGCGACACGCCACAC AGTGGACCCGGACCGCCACATCGAGCGCGTGACAGAGCTGCAGGAGC TGTTCCTGACGCGCGTGGGCCTGGACATCGGCAAGGTCTGGGTGGCA GACGACGGCGCAGCGGTGGCAGTGTGGACGACACCAGAGAGCGTCGA GGCAGGCGCGGTGTTCGCAGAGATTGGCCCACGCATGGCGGAGCTGA GCGGCAGCCGCCTGGCAGCACAGCAGCAGATGGAGGGCCTGCTGGCA CCGCACCGCCCAAAGGAGCCAGCCTGGTTTCTGGCGACAGTGGGCGT GTCCCCGGACCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCG AGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAA TTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCC CGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCG GCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT TCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGC

SEQ ID NO.	Description	Sequence
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249	pLMTB8381	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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253	pLMTB8461	GACGTGCACGCAGTCCTGTCCCCACCCCCGACAGCAGGAGTGCGGGA CTGGGTGCTCTAACAAGCGCATGGTACGAGCTATGTGCTGGTGTGTA GCCAGCGGGGCTGTCATGCCATGTCGATCTCTCCCCGTGAGCAGCCC CCCAAAAAGACAACCTGATTTCTCCCTTTTTCCGATATTTCTCCCTT TGTGCTAAGGGGACCCTTCAGCAGCTCCCAGCGCCGCACATGCACAC ACTGGCGCGTGCTTCCGAGGTCCTCGGTGCACATATTTTCTATTATC TCACACACCCGGTTGCAGGGCGGCTCAATGTCACGGCGCGCGCACGC ACTGCCTTGAGTACGGAACGGCGAGCGATACGACCGAGACGGCGCTG CCAGTAGGGTGTAGGACGCTGCGCATCTCATGAATGTATGAAGCATG CAGCCAACCACACAAACATATGGGCGCACGAGTCTTCCCTCACAGAC AGCGCGGCTGGTGAGGCGGCAGAAGGTCGGCCGCGGAAGGGCACACA CTACGTTTCACGCGTACATGACCCCGTCCGCTTTCCGCGCTATTTTA GGCGCACACCCGTTCACCAGCCTCTCCGATCCTGCTTCCACTCCTCC TCCGCCTCCGCCCTCCCTCTCCCCGTCATGACGCCGCACGCACCGCG ATCGCACACAAGCTCTCTCTCTCTCTCAACACAACCGAACCAACATC CCTCACCCCCTCTCTTACCACAAAATGAAAAAGCCTGAACTCACCGC GACGTCTGTCGAGAAGTTTCTGATCGAAAAGTTCGACAGCGTCTCCG ACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGTGCTTTCAGCTTC GATGTAGGAGGGCGTGGATATGTCCTGCGGGTAAATAGCTGCGCCGA TGGTTTCTACAAAGATCGTTATGTTTATCGGCACTTTGCATCGGCCG CGCTCCCGATTCCGGAAGTGCTTGACATTGGGGAATTCAGCGAGAGC CTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCACGTTGCAAGA CCTGCCTGAAACCGAACTGCCCGCTGTTCTGCAGCCGGTCGCGGAGG CGATGGATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGCGGGTTC GGCCCATTCGGACCGCAAGGAATCGGTCAATACACTACATGGCGTGA TTTCATATGCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACTG TGATGGACGACACCGTCAGTGCGTCCGTCGCGCAGGCTCTCGATGAG CTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCA CGCGGATTTCGGCTCCAACAATGTCCATTTAAATATCCCAATGGCGC GCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATT

SEQ ID NO.	Description	Sequence
		GTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAG TGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGC GTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGC TGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATT GGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGT TCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGT TATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAA GGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTT TTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCT CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCC GCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT CGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCG CTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGAC ACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGA GCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA CAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGAT TACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTA CGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTG GTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTA AAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGT CTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTA TTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTG TAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGAT CCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCT ATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACC ATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTT CTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAA TCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGC GAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAA TCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTT TCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCC AGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAA AATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGT CTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATG TTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGA TTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCA TATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGA CGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATT GAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAA TGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCG AAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAA CCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTC GGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGT CACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGG

SEQ ID NO.	Description	Sequence
		GCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCG GCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAAT ACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGC CATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCT TCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATT AAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGA CGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT
254	pLMTB8488	CCCTTCTTTTCGAGAAGAATATGGTCAAGCACCTCAACGAGGGTACG GATGAGGACATTTACCTGTTTGGGAAGGCAACACTCTCCGGATTTCG TAACAACCGTTGCGCAGGAGCATACCCCTACGACGTGCCAGATTACG CCTACCCTTACGATGTACCGGACTACGCTTACCCGTACGACGTGCCG GACTACGCGTAGGCTGCCCCTCCTCTCCGCGTGCAGTGGCGATGCGC TTGCGCTTTTGTCGTTGACGTGCCACAGCCGGCGCGTGTGCAGCGCG TCCCCCCGGTATGCTCTGCCTGTTCTCCACCCACACCCCCGCCTCTA CCCCGTGCGTGCGTGCGTGCGTGCGGTCGCCCTCCACCTGTGGCGCG GCAGCTGAACGGAAGGCAAACAACAGCGAAGAGAAAAGTAACAAGTA CAGTCAAATGAAGAAAAAAAAAGAAAGCCAAATGCTGGCGCGGTGTG GTGGGACTGGTGTGCGTGCTCTGTCTGTGCTGATGGGCGCCAGGGAG ACTGCTCCCCTGTCCCCCCGCCCCGCCGGGGCAGCTCCCATTATCTT TAGGCAGTTCCCAGTGGACCGGCGACGGTAAGCCGCCATCTCTTTTC CTGTGACCTCAGTTATAAGCCTGTAAGCCTGATGTACGCATAAACCA AACTCCCGCGCACAAGCACACAGCCGACTTTCGTAGTGTCATCTGCA GAGGTGTCGGTGACTGTGTGCGTGCGCGCTGCTGCGGCGTCGGTTCC GAGGCGCGTGCGGCTGCCTTCTCCCCGCAACCTGCTGCTGCGGTAGG GCGCTTGATGGCGCCGTGCCGTGAGCCCGCGGTTTTCGCGCTGTCGC GCGCGTGGAGGACCGCTCCCCCTTCTTCGCTTGCCTCCGCGTGGCTG CCTCCTGTCTCTGTGCCTCACTTGCGCCTCCGCCTCCCTCTCCTTCG TCTTTGCCTCTCTCCCGCCCCGCGGCCTGCCCCGGCGTTGCGTGCGC ACCACTGACGTGTGCGCGTGCTGCTCGCCCTCTCTCTCTGTGCGTGT GCCTGTGCGTGGTGCGACCCCGCCGCGCGCCGCACCCCCATTCTCCC TATTCCTCCCACACTTTTCTGTACCCCTGCTCCTCATGCCCCGACGA CGTGTGCGCCGCGTGCAGTAAGCGCAATCGAGTTTCAACAGCTAACA AAATGTGGTCTCACCCGCAGTTCGAAAAAGGCGGATCAGGAGGGGAC AGTGTAGAAAAGGGCGCGGCCACAAGTGTCAGTAATCCGCGCGGCCG CCCCTCGCGCGGGCGCCCCCCAAAGCTCCAGCGCAATTCGCGGGGCG GTCAAGGCCGCGGCGTGGAGAAACCCCCACACCTGGCCGCACTCATT CTGGCGCGGGGTGGATTTAAATATCCCAATGGCGCGCCGAGCTTGGC TCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCA CAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGG GGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACT GCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAA TCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCC GCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCG AGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAAT CAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAG GCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT CCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGA

SEQ ID NO.	Description	Sequence
		AGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATA CCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCT CACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTG GGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATC CGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGC CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTA GGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC TAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCT TCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCT GGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAA AAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG CTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTA TCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTT TAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGA AAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGA TTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGA AAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGT CTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCC TCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC TGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTT GTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCA ACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATAC GCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACC GGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCA GGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGT GGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGG TCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCA TCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAA CTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTG ATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCA TCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTG AATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATC AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAA AATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACC TGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATA GGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGT GAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCT GTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGG GTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAG ATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATG CGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGC GCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGC CAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAAC GCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAAT TGACGCGTATTGGGATATTTAAAT
255	pLMTB8490	CGTACCTGGGCAACGAAGTTTCCGATGAGGAGTGTCTGAAGCGTGTG GGACTCAGCGGCGCACCTGCGGACGCGTGCTCCACAGCCCAGAAAGC AGTGGGCTACATCTGTAAGTGCAACGGTGGACGAGGCGCGATCCGCG

SEQ ID NO.	Description	Sequence
		AGTTTGCGGAACATATATGCCTCCTGATGGAAAAGGTCAACAACAGT TGCCAGAAGTAGCCAGCGCGGCCTTCGCGCTTCCCATCCTCTCTGTT CGTCTTTCTTTCACCCCTTCCCCCCAGTGACTTTGCTTGGAAAACCG GAGCGTCGCTGCCGTCCTCATGTGTGATGTTTTTCTCGGCTCATCCC ATTCCGCGTGCGTGCGCGTGTGGCGCCTCCCCTCAGCCCATACGCGA GCTGGTTCCTGGGCAGCGGTCTACGCGGGCACTCCACACACGCACAC GCGCACCCCCGCCCCACCGCCGCGTGAAACCTGTGTATCACCCATGT GCGCACGCCCTCTCTCTCTTTCCGTTCGTCCTCTTCTTTTGCTGCGG GGGTCGTGCTGTCGCCGCGCATACAGCCGGCAGCGCACACCGCCCTC CCTTCATGTGTACAGCCCACTCGCAGTCCTATCTGCCCCTCCCCCCC CCACACGCACAAGCACGCATACCCTGACCGCCAACGTCACCCAGCTG CGCTGCAGACGCCGTTGCGTCACGCCCGCCATTCGCACCAGCCGCCC CCCCCCCGCGGTAGCCCCGCCGGCCGCTCTTCCAGCGGCGCACCGCC CCTGCATCTGCCTCCTATTGCACGACCTCTCTCCCCTGCCACTCCTC GTCCTCCCTCCCTCCCTCCCTCCCCCTCTGCGCCGCACCGCTGCACG CAGCAGCCCATTTGCCCTCGCACCGCACCCCCTCCAGCCCACCAATG GCCGCGCCACGCGATAACGTCACCCTGCTTTTCAAGTTGTACTGCCT GGCGGTGATGACTCTGATGGCAGCGGTGTACACCATTGCCCTGCGCT ATACGCGTACCTCGGACAAGGAGCTGTATTTCAGCACAACGGCCGTG TGCATTACAGAGGTGATTAAGCTTTTGCTGTCAGTCGGGATCTTGGC AAAGGAGACATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAG CATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGC CTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCG CTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGC CAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTC CTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGG TATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGG GATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAG GAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCC CCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGA AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTC CCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGT CCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGC TGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTG TGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTG GCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGG TGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAA GAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAG CGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAG GATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAG TGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAA AAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAAT CAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAAC TCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATC AATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACT

SEQ ID NO.	Description	Sequence
		CACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCG ATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTC AAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAAT CCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCA ACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAA ACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGAT CGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGC AGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATA TTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGA GTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGA AGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGT AACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTG GCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGC CCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCAT GTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATAT GGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGT TATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAA ACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACG TCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGT ATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAA CCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAG CGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTT GGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGT ACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAA GGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAAC TGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCT GGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAG GGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGACG CGTATTGGGATATTTAAAT
256	pLMTB8564	AACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTGTGT GCGAGCGCACACACACATGCACACGACTCACGTTGTCACACAATTGA GAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAG AGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGA GCTCGAGCCACCATGCGCCTGAATGTTAAGAAGGCGCTTATATTTGT TGGATGCGTCGTGTTCCTCTGGGTCCTTCTGAGCTACGCGAGCGTCA TTGAAGTGCCTCGTGCAGTCCCCCAGAAAGACCCGGCCGTCGAAATC GAAAAGAAGATCATCAAGCTTCAAAAGCAGGTCGATGCACAAATGGC GGAGTCCAAGAGCTTGCTCGCCAAGGTGAAGAAACTGAAGAAGATCA GTGAGGGAGAGAACGTTGGCGGCGAGGAGGACTCGCTGAAGGACAGT GAGGTTATGCAGCACCTGTCTCAGCCGATCCTCCCCGTTCTGGTGAT TGCCTGCGACCGCGTCACTGTGCAGCGTTGTTTGGACAACCTGGTGA AGTTCCGCCCCTCGAAGGAAACGTTCCCCATCATTGTTTCGCAAGAT TGTGGCCACAACGCGACCTATGAAGTCATTACGTCATACACGGCCTC CGACCCGACTATCTCTGTGGTGCGTCAGCCTGATTTGAGCGAAATCG TCCTCCCCCGCGTGAAGGTGAAGTTCCGCGGCTATTACAAGATTGCT CGGCACTACAAATTTGCCCTTAACCACGTTTTTGAGACCCTTGGCCA CGAGGCGGTGATCATCGTGGAAGACGACCTGGATATCAGTCCAGATT TCTTTGAGTACTTCCTGGGGACGTACCCGCTGCTTTTGAAAGACCCG

SEQ ID NO.	Description	Sequence
		TCCTTGTGGTGCATCTCGGCGTGGAACGACAACGGTAAGATGGAGGT CATCGACATGTCGCGCCCGGACCTGCTGCACCGCACCGACTTCTTTC CGGGCCTTGGCTGGGTCCTGCGCCGCGAAATGTGGCGTAAGCTTGCT CCAAAATGGCCCACCGCGTTTTTTGACGACTGGCTGCGAAACCCGGT TAACATCGACGGCAAGGCCTGCATCCGCCCAGAGATATCTCGTACCT ATAGTTTCGGGAAGGTGGGTGTGTCTAAGGGACTGTTCTTCGATCTT CACCTCCGCAACATTCAGCTCAATATGGAATACGTCGAATTTACGAA ACTGAACCTCACATACCTGCTTAAGGAACACTACGACGATGCCCTCG TCTCCACCGTTTACAATCTGCCGGAGATGAGTGCATCCGAGGTGGTT GCAGGCAGCGATCTCAGCGCAGACCCGGTGCGTGTTATGTACTCCAA TGCCAAGACATATCAGCGCGCCGCGAAAAAGCTCGGCCTGATGGACG ACTTCCGCTCCGGGGGTACCGCGCACGGCCTACCGCGGCATCGTGACG TGTTTCATTCGGGGCCGACGAGTATACCTTGCCCCGTCGTTTGAGTG GAACAAGTACGACCCGACCTGGGGATAGATTTAAATATCCCAATGGC GCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAA TTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATT GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTA TTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTC GTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACG GTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACG CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTG CCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCG TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCT GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCA AACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAG ATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC TACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTT TGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAAT TAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTG GTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATT TATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTC TGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAG ATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAAC CTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCA CCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCAT TTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAA AATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGA GCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGG

SEQ ID NO.	Description	Sequence
		AATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATAT TTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTC CCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGAT AAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTA GTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCA TGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATA GATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACC CATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAA GACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTA TTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTG AATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCC CGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATT AACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTT TCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACG GTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCA GGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATG CGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAA ATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTC GCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCT CTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGA TTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAAC GACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT
257	pLMTB8567	GCGCAGACCCGGTGCGTGTTATGTACTCCAATGCCAAGACATATCAG CGCGCCGCGAAAAAGCTCGGCCTGATGGACGACTTCCGCTCCGGGGT ACCGCGCACGGCCTACCGCGGCATCGTGACGTGTTTCATTCGGGGCC GACGAGTATACCTTGCCCCGTCGTTTGAGTGGAACAAGTACGACCCG ACCTGGGGATAGTGCCCCGCCGCCGTTGCCGCCACACCGCCGTGGCC AATACCAAAGCGTGCATATTTCGGGCGCGTCTGCATTTTTAGTCCCC CTTCTTAGGCCTTGTATTGTTCACTTCATCTTCCCTTCTGTAGGACG TCTCTCTGTTCCATTTCTTTTCTTGTATGCGCCCCCTCACTACCGCC TCCCACGCTCTCTCTCTCTCGCTCTGTGTGTATGTGTGTGTGTGTGT GTGCACACTTTCGCGTCTTCGACTTGTCCCTTTGTTTTTCTCACTCT CTCTGCCCCCTCCCCACCTCACCGCCTGTCTATGCGCTTCCCTCCCT GTTGTTCTGTATGCGTAGGTGTATACGTGGTACACCTCGAGTGCCAC GGCGTGGCGCACATAGCAGCGTTTTCGTTTTTTCGCTTGGTAGAAGA TGCGCAAACGGCGTTCACGACCACTGAAACAGCGCGACATCGGCGCG CACGCAGTCCCCTTTGCCAATAGCGAAATCCGGCACCCGCACGTCAG TTCTGGCTCTCTTTCCTCCTCTTCCCATGACCCGATGGTGGAGCTGC AACCAGCTTCTCTTTTCGCCTTCTGGGAGGCGGGGGTCATGCCTACT CCCTCAGTCTTCATGCTTTATCCTTCATTGCCTACCCCTTTGTTTGC TGCCGTCTACCTCACTTTCTTCCGACACACACACACACACACATACA CACACACATACACACACACATACACACACACATACACGTGCCGTTCA TCTCTTCTTGCACCTCACAATCTGCGCCTTCTTCTTTCAGCTGTTCA CTGAACTAGAAGCATCTGGCGAATACCCTCCCCCCTCAACATACACA CCGTACCACCCCCTTCTCTCCCCCTCCACCTCCAAAAAAAAAATATA TATTTCTCCTCTGTGCCTTCGCCCATCTCATCATTTATCATGGTGCG GAAGAAAGGGAGCCTGATCCTTTGCGGCGCGTTCCTCTTTGTGGCAT GGAATGCCTTGCTGCTGTTGTTCCTTTGGGGCCGCCCCCCGATCGGG

SEQ ID NO.	Description	Sequence
		CGCCTCGGTGAGGGCGGGGGCGCCGAACCGGGCGCCGGAGAAGAGTG GGGCGCTGGAAAATCAAAGGTGGGCGGCGCCAATGGTCTGGCAGGGG AAGTATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGG TCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACA CAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAAT GAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC CAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGC TCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAA CGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACC GTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCT GACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCC GACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCG TGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC TTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAG GTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGC ACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGC AGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTA CAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG GTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCT CAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAA CGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGA TCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATC TAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATC GAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATAC CATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCG AGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCC GACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAA TAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGT GAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGG CCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGT TATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTG TTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAA CACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTT CTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAAC CATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGG CATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACAT CATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCA TCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGG AATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTC ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTG TCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAA TAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAA

SEQ ID NO.	Description	Sequence
		GAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCAC GAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCT GACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGG GTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGA GAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGA AAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTG GGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGA AAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTT TCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGACGCGTAT TGGGATATTTAAAT
258	pLMTB8568	ATGGTGCGGAAGAAAGGGAGCCTGATCCTTTGCGGCGCGTTCCTCTT TGTGGCATGGAATGCCTTGCTGCTGTTGTTCCTTTGGGGCCGCCCCC CGATCGGGCGCCTCGGTGAGGGCGGGGGCGCCGAACCGGGCGCCGGA GAAGAGTGGGGCGCTGGAAAATCAAAGGTGGGCGGCGCCAATGGTCT GGCAGGGGAAGTCATCCGGCTGGCGGAAGAAGTGGAGAGTGAACTCG AAACGCAGAAGAAGCTGCTGAAGCAGATTCAGTCGCATCGCGAGTTG TGGGAGCAGCGCAAAGAGCTGGAGAAGCGCGAGAGCGAGGACACAAA AGACGAAAAGATTGACGTTGAGCCAAAAAAGCCCCGTCAAATCCCCG CGGTACACTTGTCCCACAAGGTCGTGGAGGATGCCCAGACAGTGACG AAGAAGATGCAGACGTTGATGGTAACCCCGCCCCAACTTGTCATGAA GGAACAGGAGACGGACCAGAAGAATAAGCAAATGATGGAGGACCAGT TGGGCTTGACCACCCCAAGTCCGCAAATAATCATTCCGATCTTGGTG ATCGCGTGTGACCGCGTGACTGTCAAGCGAAGCCTGGATCGCCTCAT CCAGTACCGCCCAAGCGCTGAGCTCTACCCGATCATCGTGTCCCAGG ACTGCGGTCACGCAGACACCGCTCGCGTGATCGGCAGTTATGGCTCA CAGATCACACACATCTCCCAGCCGGACCTCGCCGATATCCCCGTTCG ACCGGATCACCGCAAGTTCCAGGGGTATTACAAAATTGCACGCCACT ATCGCTGGGCACTCAACCAGGTGTTTAATGTGTTTGCGTACAGTACC GTGGTGATCGTCGAGGACGACCTTGAGGTGGCCCCGGATTTCTTCGA GTACTTTCGCGCGCTGTACCCCATCCTGCGTTCAGACCCCACACTCT GGTGTATCTCAGCGTGGAACGATAACGGCCGGGACGGTCTGGTGGAC CCGGGTAAAGCGGAGCTTTTGTACCGTACGGATTTCTTCCCTGGCTT GGGCTGGATGCTGCTCAAGGAGGTGTGGGCGGAGCTTGAGCCCAAGT GGCCAAAGGCTTTCTGGGACGACTGGATGCGCCACCCAGAGCAACGC AAAAACCGCAGTTGCATCCGCCCGGAGATCAGCCGCACGATCACATT TGGCCGTAAGGGTGTATCGCTCGGTCAGTTCTTTGATCAGTACTTGC GCTACATTAAACTCAACACAGAGTTCGTCCCTTTCACAAAACATGAC CTGAGTTACCTGGTCCGCGAGAAGTACGACGTGTCGTTCGAGAAAGA CGTCTACTCTGCCCCTCTTGTGAAGGTGGAGGAGCTCCAGCACGGTG GGAGTCTGAAGGGTAGCGGGCCTTTCCGCGTCCAGTACTCCTCTCGT GATTCGTTCAAGGTGCTTGCACGGAACCTGGGGGTCATGGACGACCT GAAATCAGGCGTTCCACGCGCCGGATACCGCGGGGTCGTGAGTTTTA TCTCGCGAGGCCGGCGCATTTACCTGGCACCCCCGGAGGGCTGGACG AAGTACGACGTTAGCTGGTCTTGAATTTAAATATCCCAATGGCGCGC CGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGT TATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGT

SEQ ID NO.	Description	Sequence
		TGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTG CATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGG GCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTC GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTA TCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGG CCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTT TCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCA AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTT TCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCG CTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCT GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGC GAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACT ACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAG CCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACA AACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTA CGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACG GGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGT CATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAA AATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCT GACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATT CATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTA ATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCC TGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTAT TAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCAT GAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCT TTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATC ACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGA GACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATC GAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTC ACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAG GGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAA TGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCT GACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTT TCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATT GTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATA TAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACG TTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGA AGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATG TATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAA AAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACC TATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGG TGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCA CAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGC GCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGC ATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATAC

SEQ ID NO.	Description	Sequence
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259	pLMTB8599	ATGCGTTTCCGCATTTACAAGCGCAAGGTCCTCATTCTGACGCTCGT CGTGGCCGCCTGCGGCTTTGTGCTGTGGTCCAGCAACGGTCGCCAGC GTAAAAACGACGCCCTGGCACCACCGCTGCTGGATTCGGAGCCCCTG CGAGGTGCTGGGCACTTTGCGGCGTCAGTGGGGATCCGCCGGGTGTC GAATGACTCGGCCGCTCCCCTCGTACCGGCTGTCCCCCGCCCCGAGG TGGACAACCTCACCCTGCGGTATCGCTCGTTGGTTTACCAGCTGAAT TTCGACCAAATGCTGCGAAACGTGGACAAGGACGGAACATGGAGTCC GGGTGAACTCGTGCTTGTGGTGCAGGTTCATAACCGGCCAGAGTACC TTCGCCTCTTGATCGACTCGCTCCGCAAGGCTCAAGGAATTCGGGAG GTGCTTGTGATCTTTAGCCATGACTTCTGGTCTGCGGAAATCAACTC ACTCATTTCCAGCGTTGATTTCTGCCCAGTTCTCCAGGTGTTCTTTC CGTTCAGCATCCAGCTCTACCCAAGCGAGTTTCCGGGCAGTGACCCA CGTGACTGCCCTCGCGACCTTAAGAAGAACGCAGCCCTGAAGCTCGG GTGCATAAATGCAGAGTACCCTGATTCCTTCGGGCACTACCGGGAAG CTAAATTCAGCCAGACGAAGCACCACTGGTGGTGGAAGCTTCACTTC GTGTGGGAGCGCGTGAAGGTACTCCAGGACTACACCGGCCTCATCCT GTTCCTCGAGGAGGATCACTACCTGGCACCCGACTTTTACCACGTGT TTAAGAAAATGTGGAAACTGAAACAGCAGGAGTGCCCAGGCTGTGAC GTGCTGTCTCTTGGCACGTACACCACCATCCGTAGCTTCTACGGCAT CGCCGATAAAGTAGACGTCAAGACTTGGAAAAGTACAGAGCACAACA TGGGGTTGGCCCTGACACGCGACGCATACCAGAAGCTTATTGAGTGT ACAGACACATTTTGCACGTACGACGACTACAATTGGGACTGGACTCT GCAATACCTCACTCTGGCCTGCCTGCCGAAGGTCTGGAAGGTGCTGG TGCCACAGGCCCCCCGAATTTTTCATGCCGGTGACTGCGGAATGCAT CATAAGAAGACGTGTCGACCCTCTACCCAGAGCGCCCAGATTGAGAG CTTGTTGAATAACAACAAGCAGTACCTGTTTCCGGAGACTCTGGTGA TTGGCGAGAAGTTTCCTATGGCCGCTATTTCCCCCCCGCGGAAGAAC GGCGGGTGGGGGGACATCCGTGACCATGAGCTTTGTAAGAGCTACCG CCGCCTTCAGTAGTTAGCGCTCCGTAGCTCGCTGCGTATGAGAGGTA CTGAGCTCCAATGCATCACACGGCGTACGGCAACACACACTATCTTT TCAGTTTATTTTTTTAATTATCCCTCCAAAAAGAAGCAACTGACACT TCAAAATATTCCCAACAAGGAGCGTGAGGTCAGTGACCAGTCTCGGA CTTCACACCGCGCATGTAGAAGCACATTTAAATATCCCAATGGCGCG CCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTG TTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGT GTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCG TTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCT GCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTG GGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTT CGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAG GCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTC

SEQ ID NO.	Description	Sequence
		AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT TTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCG CTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCT TTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTC GCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGC TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACA CGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAG CGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC GGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAA AAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTC TGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTAT TCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGT AATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATC CTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTA TTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCA TGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTC TTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAAT CACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCG AGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAAT CGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTT CACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCA GGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAA ATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTC TGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGT TTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGAT TGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCAT ATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGAC GTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTG AAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAAT GTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGA AAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAAC CTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCG GTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTC ACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGG CGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGG CATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATA CCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCC ATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTT CGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTA AGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGAC GGCCAGTGAATTGACGCGTATTGGGATATTTAAAT
260	pLMTB8629	CTGCATGCCGAGCGGCCAGAAGACAAAGATTGAGAACGTGCTCCAGA ATAGCGGTAATCAGCTCTTCCCTAAGCAGCTCTTGATCACGAAGCGA

SEQ ID NO.	Description	Sequence
		CTGCCCGCGTCGGGGGCGAAGGGCGTAGCCCCCCATGTGAAGAACGG CGGTTGGGGCGACATCCGGGACCACGAACTGTGCAAGTCTTACCTGC GCCTTCAGTAGCGAGCGCGTTGCCTCTGCGCTGGTGAACGTGCCTGC GCACTTACATCTCAGCCGTGCTTTCTGGGAAGACCTTCTGCGACGCG GGGCGCTGTGCTGGTACAGATGGAAAGATGTGCGCCATCACGGATGC ATCCTTGCATGGTGCGTGCTCACGTGCTCACCACAGTTTGTGTGTGT GTGTGTGTGAGTGTGAGTGTGAGTGAGAGAGAGAGTGTGTTTCGGCG CACCTCCCATCCAACAGTGGCGTGAACGGCTTTCTCTGTATGCGCCC TTTCGTTTTAACTCTTTCTTTTTCCGCCTTTGTTTTTTGTGATTTTT GATGAACTCAAACACAAAATGAACATCCATGCTGAAGAAGAGCTCGC TCGTGCTGTGGGGTGTGGTACTGTTCGTGGCATGGAACGCCCTTATC TTGTTCTTCCTGTGGACTCGACCGCAAAGCCTCTCCGATCACAGCCA TCTCACGGAGGAGGTGATTCGGCTTGCGCAGGATGCCGAGTCTGAAT TGGAGCGTCAGAAGGACCTGTTGCAGCAGATCTACCGTTAATTTAAA TATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTT TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG CCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAA CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAA CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAG GCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAA GGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCA CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT AAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCT GTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC GGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT CGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCC TTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCAC GTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAG ATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATA TGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAAT GAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGA AAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCA TAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAA CATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCA AGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAA AAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTAC GCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGT GATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACA

SEQ ID NO.	Description	Sequence
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261	pLMTB8636	CAGACGACGGCGCAGCGGTGGCAGTGTGGACGACACCAGAGAGCGTC GAGGCAGGCGCGGTGTTCGCAGAGATTGGCCCACGCATGGCGGAGCT GAGCGGCAGCCGCCTGGCAGCACAGCAGCAGATGGAGGGCCTGCTGG CACCGCACCGCCCAAAGGAGCCAGCCTGGTTTCTGGCGACAGTGGGC GTGTCCCCGGACCACCAGGGCAAGGGCCTGGGCAGCGCAGTGGTGCT CCCAGGCGTCGAGGCTGCAGAGCGCGCAGGCGTGCCGGCATTCCTGG AGACAAGCGCGCCACGCAACCTGCCGTTCTACGAGCGCCTGGGCTTC ACCGTGACGGCGGACGTCGAGGTGCCAGAGGGCCCACGCACATGGTG CATGACACGCAAGCCAGGCGCGTAGGTGGTGGAGGCAAACTATTTGT TGTTAAACCAGCACTATATTCTCGTGTCCAATCGGTAGTGCAGTCAT CGAGTGAACGCTGTTCTTAGCACCTTGATTCCAAAGGGGAATAGTAC ATAAGATATGTGTCATGAGGCGTGTACACAATTATTTCTCTTAGGAT TTTTTTTTAGTTGAAATAGGTCCTTGTTGTGTCACCATTAGCGTTGT CCGAGTGAGGTCAGCAGAGGTACCGTGCGCGCGTGAAAGCACTTGCT GCCCCTGCTCTTTGGCGTTGGTGTAATGCACTCAGATATCGTCTCAC TTTTTCTTCTTTATTGCCCAAGGTGGGCAGTGAGGAGACGATAGTGA GCACCTATTTCGGACATGACGTTCTTCTGTGTGCCCTCATCTGGAGC ACGAGGCGCTTTCTTGTGTCTATTATTTTTCTACTTGTTCCCTGATA AGCAATGATACCACTGCCTCCGTGTTGAAACACACTGGATCGCTTGT AGCCTCACTGAGAGTAAACTTCTTCATCAGAAAACAGACAGGAATAT GCGGTTTCGGATCTACAAGCGCAAGGTATTGATTCTTACTCTCGTGG TGGCGGCGTGCGGCTTTGTGCTGTGGTCTAGCAATGGCCGGCAGCGT AAGAATGACGCGTTGGCTCCGCCGCTGTTGGACAGCGAGCCGCTTCG CGGGGCGGGCCATTTTGCCGCTTCGGTGGGCATCCGTCGTGTGTCTA ACGATTCAGCCGCGCCGCTCGTGCCGGCCGTCCCTCGTCCGGAGGTG

SEQ ID NO.	Description	Sequence
		GACAACCTCACCTTGCGATACCGCAGCCTGGTCTACCAACTCAATTT CGACCAGATGCTGCGCAACGTAGATAAGGACGGGACATGGTCGCCCG GCGAGCTGGTACTGGTCGTGCAGGTGCACAATCGTCCAGAGTACCTG CGGCTCCTGATCGACTCACTGCGCAAGGCTCAGGGCATCCGGGAGGT GCTGGTGATCTTTTCTCACGACTTCTGGTCCGCTGAGATTAACAGCC TGATAAGCTCTGTGGACTTTTGCCCAGTACTTCAGGTATTCTTTCCA TTCAGCATTCAGCTGTACCCCTCCGAGTTTCCGGGTAGTGACCCGCG CGATTGCCCGCGCGATCTCAAAAAGAATGCCGCATTGAAGTTGGGCT GCATCAATGCGGAGTATCCAGACAGCTTCGGCCACTACCGTGAGGCC AAGTTCTCTCAGACGAAACACCATTGGTGGTGGAAGTTGCATTTCGT CTGGGAGCGCGTGAAGGTCCTGCAGGATTACACAGGCCTGATTCTGT TCCTTGAGGAGGATCACTACCTGGCGCCCGACTTCTACCATGTGTTC AAGAAGATGTGGAAGCTGAAACAACAAGAGTGCCCTGGTTGTGATGT GCTCAGTCTCGGGACCTACACCACCATTCGTAGTTTCTACGGCATCG CTGACAAGGTGGACGTGAAGACATGGAAATCGACAGAGCACAACATG GGTCTGGCATTGACACGGGATGCGTATCAGAAGCTGATTGAGTGCAC CGACACATTCTGCACGTACGACGATTATAACTGGGACTGGACGCTGC AGTACCTTACGCTGGCGTGCCTTCCGAAGGTATGGAAGGTCCTGGTG CCGCAGGCCCCGCGAATCTTCCACGCGGGTGATTGCGGCATGCACCA CAAGAAGACGTGCCGCCCTTCCACTCAGTCAGCCCAGATCGAAAGCC TGCTCAATAACAACAAACAGTACCTCTTCCCAGAAACCCTCGTGATC GGCGAGAAGTTCCCTATGGCGGCGATCTCCCCGCCCCGTAAGAACGG GGGGTGGGGCGACATACGTGATCATGAGCTCTGTAAGTCGTATCGCC GCCTCCAATAGATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCG AGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAA TTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGT GCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCC CGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCG GCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT TCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGC GGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAG GGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCC AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCG CCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGC GAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGC TCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCT GTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAC GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGC TGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGG TAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC GGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAG AAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGT AGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAA AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTC AGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCA AAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAA

SEQ ID NO.	Description	Sequence
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262	pLMTB8698	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT GGTACCCGGGGGCAGCGGTGTTGGCGGAACGGCCAACGCCCTGCCCC CTCCCCGCCCTGCGACGTTTCTGCGCACCCGTTCTCTCCTTCCTGCG TGCGTGTCTGCGCGCATGCACATCTGTCCGCGTGTGCCGCAGCGCTG GTATTTTTGTGAGGGCAGAGCCCTGCCTCCCCGCCTCTCTGCCGTTG GCAGGTGAAGCGAAAACGAAGCGAGAGGGCAGTCTGCATGTGTGTGC GAGGGCATGCGGAGCCCCCCTCCCCCCGCCCCCTGCCGTGCTGCACC GCTATTGTGGCGTCTTCTCTCGTTGTGCGCAAGTGTGGCTGCACCAC

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SEQ ID NO.	Description	Sequence
		TGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAG CCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGA TGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCA ATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGA GAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTT TATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCG TCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTG CGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTAC AAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCA ACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGC TGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAG TACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGC CAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACC TTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACA ATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCAT TTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCT AGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTC AATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATAC ATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCAC ATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCA TGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
263	pLMTB8821	GCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATA TCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTG CTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGA AATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGT GCTTCTCGATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTG ATGGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGT TATGTGTGGGAGGGCTAACTAGCCTCGGAGATCCACTAGTTCTAGTT CTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGCGGAATCGGTC GCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAG CAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAATT CGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTT TTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAG AAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCT TCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGCCCCACGC CGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGATGC CGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAGGG CACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTC GGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCT TGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTC ACACACACACACACACACACACACACACACAAATGATGTCCCCTGAAGA TGCGACCGGGCTGGAGGCTGCACGCAAGCAGAAGATCCATAACCTGA AGCTGAAGACGGCGTGCCTAGAGAATGAGGAGCTTGTGCAGGAGCTG CACATCTCTGACTGGTCAGAGACGCAGCGACAGAAGCTGCGCGGCGC CCATGAGAAGGGCGAGGAGCTGCTTGCGTCCGTGGAGGTTGGGACGA AGTGGAACCTGATGGAGGCGTACGACCTGGCGAAGCTGATGCGCGTG TGCGGGCTGGAGATGAGTCAGCGCGAGCTGTACCGCCCGGAGGACAA GCCGCAGTTCATGGACATCATTGGCGTGAAGAAGGTGCTACAGGACC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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264	pLMTB8822	CAGACGACGGCGCAGCGGTGGCAGTGTGGACGACACCAGAGAGCGTC GAGGCAGGCGCGGTGTTCGCAGAGATTGGCCCACGCATGGCGGAGCT GAGCGGCAGCCGCCTGGCAGCACAGCAGCAGATGGAGGGCCTGCTGG CACCGCACCGCCCAAAGGAGCCAGCCTGGTTTCTGGCGACAGTGGGC GTGTCCCCGGACCACCAGGGCAAGGGCCTGGGCAGCGCAGTGGTGCT CCCAGGCGTCGAGGCTGCAGAGCGCGCAGGCGTGCCGGCATTCCTGG AGACAAGCGCGCCACGCAACCTGCCGTTCTACGAGCGCCTGGGCTTC ACCGTGACGGCGGACGTCGAGGTGCCAGAGGGCCCACGCACATGGTG CATGACACGCAAGCCAGGCGCGTAGCTAGCCTCGGAGATCCACTAGT TCTAGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGCGGA ATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGC GGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTC TTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCAC CCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGC CGTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCG CGCATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGC CCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCG CGGATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTC AAGAGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGC CGGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACG CCTTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCT CTCTCTCACACACACACACACACACACACACACACAAATGATGTCCC CTGAAGATGCGACCGGGCTGGAGGCTGCACGCAAGCAGAAGATCCAT AACCTGAAGCTGAAGACGGCGTGCCTAGAGAATGAGGAGCTTGTGCA GGAGCTGCACATCTCTGACTGGTCAGAGACGCAGCGACAGAAGCTGC GCGGCGCCCATGAGAAGGGCGAGGAGCTGCTTGCGTCCGTGGAGGTT GGGACGAAGTGGAACCTGATGGAGGCGTACGACCTGGCGAAGCTGAT GCGCGTGTGCGGGCTGGAGATGAGTCAGCGCGAGCTGTACCGCCCGG AGGACAAGCCGCAGTTCATGGACATCATTGGCGTGAAGAAGGTGCTA CAGGACCTTCGACAGAACCGGAACAAGACGCGCGTTGTGAGCTTCAC GCAGCTGATCGACAACAGCATCGCGAAGATGGAGAAGGTGGAGGAGG AGCTGCGGCGGTCGCAGCTGGACGCGACGCAGCTCGCGCAGGTGCCG TCTCGGACGGTGAAGATGATATTTAAATATCCCAATGGCGCGCCGAG CTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATC CGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAA GCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCG

SEQ ID NO.	Description	Sequence
		CTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATT AATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGC TCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCT GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAG CAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCA TAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTC AGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC CCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTC ATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC AAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGC CTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACT TATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG TATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGG CTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAG TTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACC ACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCG CAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGT CTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATG AGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATG AAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACA GTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATA TCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGA AGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGT ATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAAT TTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGT GACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCC AGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTC GCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACG AAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAAT GCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCT GAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGAT CGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCT TGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACC ATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAG AAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCG CACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAA TCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTC CCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCA TTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATT TAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGT GCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATA AAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGAT GACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGC TTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGT CAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCA GAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCA

SEQ ID NO.	Description	Sequence
		CAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCA GGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTA TTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTG GGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCA GTGAATTGACGCGTATTGGGATATTTAAAT
265	pLMTB8823	GTAGCGGGCCTTTCCGCGTCCAGTACTCCTCTCGTGATTCGTTCAAG GTGCTTGCACGGAACCTGGGGGTCATGGACGACCTGAAATCAGGCGT TCCACGCGCCGGATACCGCGGGGTCGTGAGTTTTATCTCGCGAGGCC GGCGCATTTACCTGGCACCCCCGGAGGGCTGGACGAAGTACGACGTT AGCTGGTCTTGACTGCGTTACGCGCACACTCGCATGGGATAGAGGAG AGGAGTGTTTCGAATGTAAATAGTTTCTCCCCAGGAATGTGTCTAAG CGCGAACAAATAATACGAACAGTGAACACGCCGCAGCCTTGCTGTGC ATTCAGACTGCCTTTGACAAAGAGACATACGCATAGCCACGCAAAGA TGCCGTTGACCCACCGTCTTGCTCTCGTGTTGCGCAACATGTCCTTC CGTCATTTTTTCACCTGTGTCCATGTCAACTTCCCTTCCTACCATTG ATGCCGAGTCATCATCTCCGCGGCTTTGGTTATGCGCACTTTTCCGA AACGCCGGCTACTCTCAGCTTTTCCCTCCGCTTTTCACCTCTATTGA CTTACATACCCTAAGCTGCAGGTGCTGAAGCTTCCCAGCTTGTGGTT GCAAAAGTAGCAGCTGCTGGTTCAAACACGCATCTACGAAAGCAAAT AGAAAAAAACGCCGGAAACTCCGTGCACACGCAAACACGCGTACGGG CACAGCGCAGACAAGGAACACGGAACAACATCACAATGCGTTTCCGC ATTTACAAGCGCAAGGTCCTCATTCTGACGCTCGTCGTGGCCGCCTG CGGCTTTGTGCTGTGGTCCAGCAACGGTCGCCAGCGTAAAAACGACG CCCTGGCACCACCGCTGCTGGATTCGGAGCCCCTGCGAGGTGCTGGG CACTTTGCGGCGTCAGTGGGGATCCGCCGGGTGTCGAATGACTCGGC ATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCAT AGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT GAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGT CGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCG GGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCAC TGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTC ACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCA GGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAA AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACG AGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACA GGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCG CTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTC TCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTAT CTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGA ACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTC TTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGA GTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTT GGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTT TTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAG AAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAA

SEQ ID NO.	Description	Sequence
		AACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTT CACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAA GTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGC ATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATA TTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGC AGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACT CGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAG GTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGA ATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAG CCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATT CATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAA AAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACT GCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAA TACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATG CATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATA AATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATT GGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGG GCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTA TCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATT TAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAC TCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTC ATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGG GGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAA CCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGG CCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACA CATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCG GGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGT CGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGT GCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAAT ACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAA GGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCC AGTCACGACGTTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGG ATATTTAAAT
266	pLMTB8994	CGCAAGGAATCGGTCAATACACTACATGGCGTGATTTCATATGCGCG ATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACAC CGTCAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTTGGG CCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGC TCCAACAATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTGA CTGGAGCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACA TCTTCTTCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGC TACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCG GGCGTATATGCTCCGCATTGGTCTTGACCAACTCTATCAGAGCTTGG TTGACGGCAATTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGAC GCAATCGTCCGATCCGGAGCCGGGACTGTCGGGCGTACACAAATCGC CCGCAGAAGCGCGGCCGTCTGGACCGATGGCTGTGTAGAAGTACTCG CCGATAGTGGAAACCGACGCCCCAGCACTCGTCCGAGGGCAAAGGAA TAGCTAGCCTCGGAGATCCACTAGTTCTAGTTCTAGGGGCCGAATTC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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267	pLMTB9070	GCGCAGACCCGGTGCGTGTTATGTACTCCAATGCCAAGACATATCAG CGCGCCGCGAAAAAGCTCGGCCTGATGGACGACTTCCGCTCCGGGGT ACCGCGCACGGCCTACCGCGGCATCGTGACGTGTTTCATTCGGGGCC GACGAGTATACCTTGCCCCGTCGTTTGAGTGGAACAAGTACGACCCG ACCTGGGGATAGACTTTTGATGGCACTGTTTTTCTTTACTTTTATTT CTCTCAAAACATCAGAAGCAGTAATGTAAATATTCATTTTGTTTCAG CGCTCGTGCCAAACATCACGCGCTTGTTCAAGAGGCTATGCGAAGTG ATCATTGCCGTTTTTTTTTTCCTCAGCGTAAGCGGTGCATATGCTCA AAATGCATGTGCTTGTGGAAAATCAAGGCAACTTTGCATCTCCTGTT GAGAGTTCTAGTCCAGCAATCTATCCATGGCCTTTTCTTCTTTGGGA TACTTTTATCGCGATGCTTTGCGCTTCGTCTCTACCCCTTCTGTATC CTACAAAAATATCATAACGCCGATTATGTGCTCGATGCGCTGCTTCG AATAGCTCTGTTTTCTTCATTTAACACGATGGTGCGGAAGAAAGGGA GCCTGATCCTTTGCGGCGCGTTCCTCTTTGTGGCATGGAATGCCTTG CTGCTGTTGTTCCTTTGGGGCCGCCCCCCGATCGGGCGCCTCGGTGA GGGCGGGGGCGCCGAACCGGGCGCCGGAGAAGAGTGGGGCGCTGGAA AATCAAAGGTGGGCGGCGCCAATGGTCTGGCAGGGGAAGTATTTAAA TATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTT TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAG CCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAA CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAA

SEQ ID NO.	Description	Sequence
		CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAG GCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAA GGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGA ACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCA CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTAT AAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCT GTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC GGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTT CGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCT CTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTT TGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCC TTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCAC GTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAG ATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATA TGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAAT GAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGA AAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCA TAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAA CATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCA AGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAA AAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTAC GCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGT GATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACA ATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCG CATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGG AATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATC AGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCG TCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACG CTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCC ATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAG CCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGC GGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCT TTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCG GATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCG CGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTAT TATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTC GTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAG CTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAG ACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCT GGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCAT ATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCAT

SEQ ID NO.	Description	Sequence
		CAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGAT CGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGT GCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACG ACGTTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTA AAT
268	pLMTB9072	GTAGCGGGCCTTTCCGCGTCCAGTACTCCTCTCGTGATTCGTTCAAG GTGCTTGCACGGAACCTGGGGGTCATGGACGACCTGAAATCAGGCGT TCCACGCGCCGGATACCGCGGGGTCGTGAGTTTTATCTCGCGAGGCC GGCGCATTTACCTGGCACCCCCGGAGGGCTGGACGAAGTACGACGTT AGCTGGTCTTGAAGAGGGCGTGCCTGGGGAGAGGGAGACATTGGCGG CCCAGGTGGTGCGTGTGCGCGGATCTGCGTGCAGAGGTGCGCAGGGC GCGCGCTCTCGTCTTTTGGTCTCTTTCTGTTTTCGCTTTATTTCTGT TTTTTTCTCCTTTTCAACAGCAAGAACAGCCACCACGCGCACCAAGC GAAGGTAACGTGAGACTCGGCTTGTGGGATTGCTTCGGTGCGCGGGG GGGGAACGGCGAGGAGGTGGGGTGGTGGGTGGGGACCTCCCCTCATC TGCCTCCTGCGCAGCACCCCATCACTCACGCGCACACAGATGAGCAA GTCCGCCGACGCACTGCAGGCCACCCAACTGTGCTTCGTGTTGCTCG TGCATCGATCTCCCTCTGTGCAAGCGAATAGGCTCTCCTCAGATCAG ATGTGATTTTCGTTCCCCTCCACATCACTTCCTCGAGCAGCTGACCT TTACCATGTCTTCGCAGGCGATGACGGCGCCCACTAGGCCTCGCCCC CTCCACCGCTGTTGCCAACATTGCAACTGCTTCTCTGTACTTCTCTG TGTTTCTCGAACTCTCTTCCCCCTCCCCCACCGTTTCCATCTCCGCG CGTGTGCGCGTCGCTGTACACTCTTCGCTGGATGCCGGATCCCACGC AAACACACACGCACACACACACACACACATCAGACGTGCCTCACAAA CCCGTTCGTGCTCGAACATCGACAGCGCACCCAGACGTGTGGTCTTG CTCTTCTTCCTTTCGCTCGTTCTCAGCTCTTCTTCCTCCTTACCCAG TACGACGAGCTCTGACCTCTTGTCGTGTGCCCGCCTGTGTGCCATAC ACCTGGCACCCACTCCTAAACACGCACTTATCACACCTCCATCGCAA CACCATGCGTTTCCGCATTTACAAGCGCAAGGTCCTCATTCTGACGC TCGTCGTGGCCGCCTGCGGCTTTGTGCTGTGGTCCAGCAACGGTCGC CAGCGTAAAAACGACGCCCTGGCACCACCGCTGCTGGATTCGGAGCC CCTGCGAGGTGCTGGGCACTTTGCGGCGTCAGTGGGGATCCGCCGGG TGTCGAATGACTCGGCATTTAAATATCCCAATGGCGCGCCGAGCTTG GCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCT CACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCT GGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCA CTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATG AATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTT CCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGG CGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGA ATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGG CTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG GAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGA TACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAG CTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTA

SEQ ID NO.	Description	Sequence
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269	pLMTB9080	ATGCGTTTCCGCATTTACAAGCGCAAGGTCCTCATTCTGACGCTCGT CGTGGCCGCCTGCGGCTTTGTGCTGTGGTCCAGCAACGGTCGCCAGC GTAAAAACGACGCCCTGGCACCACCGCTGCTGGATTCGGAGCCCCTG CGAGGTGCTGGGCACTTTGCGGCGTCAGTGGGGATCCGCCGGGTGTC GAATGACTCGGCCGCTCCCCTCGTACCGGCTGTCCCCCGCCCCGAGG TGGACAACCTCACCCTGCGGTATCGCTCGTTGGTTTACCAGCTGAAT TTCGACCAAATGCTGCGAAACGTGGACAAGGACGGAACATGGAGTCC

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270	pLMTB9082	ATAAGAAGACGTGTCGACCCTCTACCCAGAGCGCCCAGATTGAGAGC TTGTTGAATAACAACAAGCAGTACCTGTTTCCGGAGACTCTGGTGAT TGGCGAGAAGTTTCCTATGGCCGCTATTTCCCCCCCGCGGAAGAACG GCGGGTGGGGGGACATCCGTGACCATGAGCTTTGTAAGAGCTACCGC CGCCTTCAGTAGGGCACGCAGTGTGTGTCTCGTTTGCTCCGAATTCT TTTTCCTTTTTCGTTTTTCGTGTTTCGCGTGCCTCTCTTTTCGGCGC ATGCGAAAAACAGCACAGCAATCCAGCAAACGAACAAAGAAAATCAT CGATGGCGCACGCTACGCCAAGGTTGGGGGTGGAGCGGGGGTGGCGG CAACGCCGTGTGCAGCAGAGCAGACACCCATCGCAGAAGCCCCCGGT ATCTGCGTGCATGTGTGTTCGGTGCACGACCGGGTCGTGCTGCTTGT ATGTTTGGGGAGGGAGGGGCTGCGTTGCCTTCCTCACGCCTCCCATC CCTCCATCCCTGTCGCCTTCTAGGGGTCGCCGAGGCGCGTGCAGAGA CGGACTCTACAGGCCCAGGCGAGATGGCAACGGGCGCACGCACACAC GCACGCGGAGGGAGGAATGTTTGGGATGAATCACACTGCACTGAAAC CTCTCTTCTACCCTCATCAGCCTTCATCTTCACTCGACACACAGACG CGCCGCTGTCGCCACCGCCTCAGAAAAGGCAGCAAGCACACGTGAAA CCCTAAAATGCGGTTTCGTATTTACAAGCGGAAGGTGCTTATTCTGA CACTGGTGGTGGCTGCCTGCGGGTTCGTTCTGTGGTCATCGAACGGC

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271	pLMTB9083	ATGCGGTTTCGTATTTACAAGCGGAAGGTGCTTATTCTGACACTGGT GGTGGCTGCCTGCGGGTTCGTTCTGTGGTCATCGAACGGCCGGCAGC GGAAGAACGACGCGCTGGCTCCACCACTGCTGGACTCGGAGCCGCTC CGGGGTGCCGGCCACTTCGCAGCTAGCGTCGGAATCCGTCGCGTTAG CAACGACTCCGCTGCCCCGTTGGTACCTGCAGTCCCGCGCCCTGAGG TAGACAACCTGACCCTGCGCTATCGCAGCCTTGTTTACCAGTTGAAC TTCGATCAGATGTTGCGCAACGTTGACAAGGACGGGACTTGGTCGCC CGGTGAGCTTGTGCTCGTGGTGCAAGTGCACAACCGCCCCGAGTACC TGCGCCTGCTGATCGACAGCCTCCGGAAGGCCCAGGGTATCCGCGAA GTTTTGGTCATTTTCTCGCACGACTTCTGGTCGGCGGAGATTAACTC GCTGATAAGCAGTGTCGACTTTTGCCCGGTCTTGCAGGTATTCTTCC CTTTTAGCATCCAACTTTACCCATCCGAGTTCCCGGGAAGCGATCCT CGGGACTGCCCACGCGACCTTAAGAAGAACGCCGCGCTCAAGCTGGG TTGCATCAATGCGGAGTACCCCGACTCGTTCGGTCACTACCGGGAAG CGAAGTTCAGTCAGACTAAGCATCACTGGTGGTGGAAACTGCACTTC GTATGGGAGCGGGTAAAGGTGCTGCAAGACTACACCGGTCTGATCCT GTTTCTGGAGGAGGACCACTACCTGGCCCCGGATTTCTACCACGTGT TCAAAAAGATGTGGAAGCTGAAACAGCAGGAGTGTCCCGGCTGCGAC GTCCTGAGTCTGGGGACGTACACGACAATACGCTCTTTCTACGGTAT CGCAGATAAAGTGGATGTTAAGACTTGGAAATCAACTGAGCACAATA TGGGCCTGGCACTCACTCGGGATGCTTACCAAAAGCTCATCGAGTGC ACAGATACTTTCTGTACCTACGATGACTACAACTGGGACTGGACTCT TCAGTACCTGACTCTCGCATGCCTGCCTAAGGTCTGGAAAGTGCTCG TGCCGCAGGCACCGCGAATTTTTCACGCCGGTGATTGCGGCATGCAC CACAAGAAGACTTGCCGCCCGAGTACACAAAGCGCGCAGATAGAGTC CCTCCTGAACAACAACAAGCAGTACCTGTTCCCCGAGACTCTGGTGA TTGGGGAGAAGTTTCCTATGGCCGCCATCTCTCCACCTCGCAAAAAC GGTGGATGGGGCGACATCCGTGACCATGAGCTCTGTAAGTCGTACCG GCGACTCCAGTGAGACGTGCACGCAGTCCTGTCCCCACCCCCGACAG CAGGAGTGCGGGACTGGGTGCTCTAACAAGCGCATGGTACGAGCTAT GTGCTGGTGTGTAGCCAGCGGGGCTGTCATGCCATGTCGATCTCTCC CCGTGAGCAGCCCCCCAAAAAGACAACCTGATTTCTCCCTTTTTCCG ATATTTCTCCCTTTGTGCTAAGGGGATTTAAATATCCCAATGGCGCG CCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTG TTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGT GTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCG TTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCT

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SEQ ID NO.	Description	Sequence
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272	pLMTB9131	GGAACGGTGATTTCTCCGTGAACGAATACGAGACTCTGTTTGGCAAA GTCGCCGCATGTAACATTCGTAAAGGCGCGCAGATCAAGAAAACTGA TATCGAGGGTGGTTCGGGCGGTTATCCTTACGACGTCCCGGATTACG CGTACCCTTACGACGTCCCGGACTACGCATACCCTTACGACGTCCCT GATTACGCCTAAGACGTGCACGCAGTCCTGTCCCCACCCCCGACAGC AGGAGTGCGGGACTGGGTGCTCTAACAAGCGCATGGTACGAGCTATG TGCTGGTGTGTAGCCAGCGGGGCTGTCATGCCATGTCGATCTCTCCC CGTGAGCAGCCCCCCAAAAAGACAACCTGATTTCTCCCTTTTTCCGA TATTTCTCCCTTTGTGCTAAGGGGACCCTTCAGCAGCTCCCAGCGCC GCACATGCACACACTGGCGCGTGCTTCCGAGGTCCTCGGTGCACATA TTTTCTATTATCTCACACACCCGGTTGCAGGGCGGCTCAATGTCACG GCGCGCGCACGCACTGCCTTGAGTACGGAACGGCGAGCGATACGACC GAGACGGCGCTGCCAGTAGGGTGTAGGACGCTGCGCATCTCATGAAT GTATGAAGCATGCAGCCAACCACACAAACATATGGGCGCACGAGTCT TCCCTCACAGACAGCGCGGCTGGTGAGGCGGCAGAAGGTCGGCCGCG GAAGGGCACACACTACGTTTCACGCGTACATGACCCCGTCCGCTTTC CGCGCTATTTTAGGCGCACACCCGTTCACCAGCCTCTCCGATCCTGC TTCCACTCCTCCTCCGCCTCCGCCCTCCCTCTCCCCGTCATGACGCC GCACGCACCGCGATCGCACACAAGCTCTCTCTCTCTCTCAACACAAC CGAACCAACATCCCTCACCCCCTCTCTTACCACAAAATGATTGCATC AAGTGTCCGTCACGCAGTCATCTTGCTGTTGGTCGCCGTAGCGATGA TGGTCAACAACGTGATCGCCCCCGAGGCTAGCTTTCAGGTCTGGAAT AAAGACAGTTCATCGAAAAATCTCATCCCCCGACTTCAGAAGATCTG GAAGAACTACCTGAGCATGAATAAGTACAAGGTTAGCTACAAGGGAC CGGGCCCGGGTATCAAATTCTCTGCCGAGGCCCTTCGCTGCCATCTG CGCGACCATGTGAATGTGAGCATGGTGGAGGTGACCGACTTCCCTTT TAACACGTCCGAGTGGGAGGGGTATCTGCCAAAGGATTTAAATATCC CAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTG TGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGA AGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCAC ATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGT CGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGT TTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCG CTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGG TAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATG TGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTT GCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAA ATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCC GACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAA GCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTG TAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCA GCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACC CGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGG

SEQ ID NO.	Description	Sequence
		ATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCG CTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGA TCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAA GCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA TCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAA GGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCT TTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGT AAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAAC TGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAG CCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGA TGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCA ATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGA GAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTT TATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCG TCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTG CGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTAC AAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCA ACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGC TGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAG TACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGC CAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACC TTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACA ATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCAT TTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCT AGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTC AATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATAC ATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCAC ATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCA TGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTC GCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCC GGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTT AACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCG GTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGC GCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTG CGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGC AAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTT GTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT
273	pLMTB9132	CCCGAGGCTAGCTTTCAGGTCTGGAATAAAGACAGTTCATCGAAAAA TCTCATCCCCCGACTTCAGAAGATCTGGAAGAACTACCTGAGCATGA ATAAGTACAAGGTTAGCTACAAGGGACCGGGCCCGGGTATCAAATTC TCTGCCGAGGCCCTTCGCTGCCATCTGCGCGACCATGTGAATGTGAG CATGGTGGAGGTGACCGACTTCCCTTTTAACACGTCCGAGTGGGAGG GGTATCTGCCAAAGGAGTCGATCCGAACCAAGGCAGGGCCGTGGGGC CGCTGCGCGGTGGTGAGTTCCGCCGGCTCGCTCAAGAGTTCACAGCT CGGTCGTGAGATCGATGACCACGACGCAGTACTGCGGTTTAATGGCG CCCCGACCGCGAATTTCCAGCAGGACGTGGGTACGAAGACAACAATC

SEQ ID NO.	Description	Sequence
		CGTCTTATGAATTCGCAGCTCGTGACGACTGAGAAGCGTTTTCTTAA AGACTCGTTGTACAATGAAGGTATCCTTATCGTGTGGGACCCAAGCG TGTATCATTCCGATATTCCTAAATGGTACCAGAACCCGGACTATAAC TTCTTCAACAACTACAAGACGTACCGCAAGCTCCACCCGAACCAGCC CTTCTACATCCTTAAGCCACAGATGCCTTGGGAGCTGTGGGATATTC TCCAGGAGATATCCCCGGAGGAAATCCAGCCAAATCCCCCATCTTCC GGCATGCTCGGTATTATCATTATGATGACGCTGTGCGACCAGGTGGA CATATACGAGTTCCTGCCATCCAAGCGCAAGACCGACGTCTGCTACT ACTACCAGAAGTTCTTCGATAGCGCCTGTACAATGGGCGCATACCAC CCCCTGCTCTATGAAAAGAACCTGGTAAAACACCTCAACCAGGGCAC TGACGAGGACATCTATCTGCTGGGCAAGGCTACACTGCCGGGCTTTC GCACTATACACTGCTAGAGAGCAATTGAGCGCGTGCGTGTCGGTGTT CGGGTGTGTTTATGGTCACTGAGGAGGGAGGAGAGAAATGCAGGGCT TCCTCCTCGTGTGTTGCTCTCTGTTTCGTTCTCCCTTCCCCGTAGCC TGCTGCCGCACTCTGCTCGTCCCGTGCGTCCAGACCTCTGTAGCCTT TCGATTCCTTTATCTTTTTTGTTTTAATTTTCTTTTTTGTCCGTATG CTTCCCAGAAACGAAAAAAAGAACAAGAAAGGACGAAGTACAAGTGG ATGTGCGCCGAGAGCACGTCTGCCCCCCTGTGAAGGAGCGCAGCGGA TGCGTGCTCCGCTCCACTCGGTCATCTCTGCCGTCCCTCAGGCACGG CAGGCCCAGGAGAGTTCAAGGAGCTTGATGCTGCATTGCAAGGCGAA TGCGTTTTTTTTTTCGTTCGCCCTCCGCCAGCGGTGCTCATGAACTG CGATGCACTCGAGTTCCCGAAAGAGCAGCGAGCCACTGTTTCTTCGT CGAGAGTATCGCTGAGGCACGGCGTGCTTGCGATTGCTCGCTCTGCA AGTGCGCGTGCATGGCGGCTCTCTTTGCAGTGCTCCTCTACTTTTCT CCCTCTGTTCTGCGCTGCCATGCCTCCTTGTATGCCTCGGCCCACGA TCACTCACGCCTGCGCACAAACGCATACTTTCTTTTTCCACTCGTTC TCCACGGTGCGCCTTGATTCGCACTCGTCCAATGACTAGGGCGTGTG GAGAGAAGAGAAGGTACAGATAGCGCCAGGAGGCGGCTGAGCAGGGA GACACACGCTGGCACACGTCAACGTATAGCGCACACCCACGTCCCAC TTCTGTACGGCTGCTCTCTTCCTACTAGTTGGCCATATTCAGCCCTT CGTTCTGCCCATAGTCCCAGTTATCGAAGTGACGCTGCATGATATAG CTGCGAGCACACAATGGAGAAACAGAACATCGCGGTCATCCTCGCGC GGCAGAACTCCAAGGGGCTGCCACTCAAGAACCTGCGTAAGATGAAC GGAATCAGTCTCCTCGGCCACACGATCAATGCGGCGATCTCGTCTAA GTGCTTCGACCGCATCATTGTGTCTACGGACGGAGGGCTTATTGCGG AGGAGGCTAAGAACTTCGGGGTTGAATTTAAATATCCCAATGGCGCG CCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTG TTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGT GTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCG TTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCT GCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTG GGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTT CGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAG GCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTC AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT TTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCG

SEQ ID NO.	Description	Sequence
		CTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCT TTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTC GCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGC TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACA CGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAG CGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAAC TACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC GGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGG TCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAA AAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTC TGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTAT TCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGT AATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATC CTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTA TTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCA TGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTC TTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAAT CACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCG AGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAAT CGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTT CACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCA GGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAA ATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTC TGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGT TTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGAT TGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCAT ATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGAC GTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTG AAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAAT GTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGA AAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAAC CTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCG GTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTC ACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGG CGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGG CATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATA CCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCC ATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTT CGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTA AGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGAC GGCCAGTGAATTGACGCGTATTGGGATATTTAAAT
274	pLMTB9205	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		CACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTCGG CGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCTTG ACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCAC ACACACACACACACACACACACACACACAAAGCTCCGGTTCGTCCGGCC GTAACGCCTTTTCAACTCACGGCCTCTAGGAATGAAGGAGGGTAGTT CGGGGGAGAACGTACTGGGGCGTCAGAGGTGAAATTCTTAGACCGCA CCAAGACGAACTACAGCGAAGGCATTCTTCAAGGATACCTTCCTCAA TCAAGAACCAAAGTGTGGAGATCGAAGATGATTAGAGACCATTGTAG TCCACACTGCAAACGATGACACCCATGAATTGGGGATCTTATGGGCC GGCCTGCGGCAGGGTTTACCCTGTGTCAGCACCGCGCCCGCTTTTAC CAACTTACGTATCTTTTCTATTCGGCCTTTACCGGCCACCCACGGGA ATATCCTCAGCACGTTTTCTGTTTTTTCACGCGAAAGCTTTGAGGTT ACAGTCTCAGGGGGGAGTACGTTCGCAAGAGTGAAACTTAAAGAAAT TGACGGAATGGCACCACAAGACGTGGAGCGTGCGGTTTAATTTGACT CAACACGGGGAACTTTACCAGATCCGGACAGGATGAGGATTGACAGA TTGAGTGTTCTTTCTCGATTCCCTGAATGGTGGTGCATGGCCGCTTT TGGTCGGTGGAGTGATTTGTTTGGTTGATTCCGTCAACGGACGAGAT CCAAGCTGCCCAGTAGAATTCAGAATTGCCCATAGAATAGCAAACTC ATCGGCGGGTTTTACCCAACGGTGGGCCGCATTCGGTCGAATTCTTC TCTGCGGGATTCCTTTGTAATTGCACAAGGTGAAATTTTGGGCAACA GCAGGTCTGTGATGCTCCTCAATGTTCTGGGCGACACGCGCACTACA ATGTCAGTGAGAACAAGAAAAACGACTTTTGTCGAACCTACTTGATC AAAAGAGTGGGGAAACCCCGGAATCACATAGACCCACTTGGGACCGA GGATTGCAATTATTGGTCGCGCAACGAGGAATGTCTCGTAGGCGCAG CTCATCAAACTGTGCCGATTACGTCCCTGCCATTTGTACACACCGCC CGTCGTTGTTTCCGATGATGGTGCAATACAGGTGATCGGACAGGCGG TGTTTTATCCGCCCGAAAGTTCACCGATATTTAAATATCCCAATGGC GCGCCGAGCTTGGCGTAATCATGGTCATAGCTGTTTCCTGTGTGAAA TTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATT GCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTA TTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTC GTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACG GTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACG CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTG CCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGC GCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCG TTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGAC CGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCT GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCA AACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAG

SEQ ID NO.	Description	Sequence
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275	pLMTB9220	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACA AGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGC TTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATG CGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAG GCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGG TGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCT GCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT TTAGCGCTCCGTAGCTCGCTGCGTATGAGAGGTACTGAGCTCCAATG CATCACACGGCGTACGGCAACACACACTATCTTTTCAGTTTATTTTT TTAATTATCCCTCCAAAAAGAAGCAACTGACACTTCAAAATATTCCC AACAAGGAGCGTGAGGTCAGTGACCAGTCTCGGACTTCACACCGCGC ATGTAGAAGCACGCGGCTTGCGCGCCAGGCTTCTTTTGGCAAACCAC GCTGCACAGAATGTCTGTGTACAGCAGCCAGGCTGTGATCGATCTAT TATGCTCGCCCCTCGCTCCTCCGGCATTCTCGAGTCCATGTCGAGCT TGTCTGGCTCCGTGCACATGCAAGCGTTTGTGCGCGCCTCTAATGTA ACCACACGTCAAAACATTGTGTGTCTTCCGAAGTGGGAGACACCGGG GCCACCAACTCCGGTGGTTTACAGCCTCCTCCCTCAACCAACGCTGC CGATTGTACCACCTTTCATTGCGTCTTTGTGCCCCTCCCTATCTTCA TGTTTCCACTGCGCTTCGTTTCCGAATACTATTTTCGTGTACTGTTT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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276	pLMTB9299	TGGATAACTTGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTG TTCTCCACTCCAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCG AATGAATGACAGTAAAACCAATGCCTTCACTGGCAGTAACACCCAGC AGTGTTGACTCAATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGT CTTTTGACGAACAACTGCCCTATCAGCTGGTGATGGCCGTGTAGTGG ACTGCCATGCATGGCGTTGACGGGAGCGGGGGATTAGGGTTCGATTC CGGAGAGGGAGCCTGAGAAATAGCTACCACTTCTACGGAGGGCAGCA GGCGCGCAAATTGCCCAATGTCAAAACAAAACGATGAGGCAGCGAAA AGAAATAGAGTTGTCAGTCCATTTGGATTGTCATTTCAATGGGGGAT ATTTAAACCCATCCAATATCGAGTAACAATTGGAGGACAAGTCTGGT GCCAGCACCCGCGGTAATTCCAGCTCCAAAAGTCGCAGCCTGACCGC ATCACACATCAAGGCGTTACAGCCTCTCCGTCTTTGCTGCACCCAAG TGTATTCGTGTGACCGCGTTGAGGGATCTAATGGATTCGGAACTTTG GTCGTTTGGTCTCTCATGCTGCCCAATCCCATGCGCTTTTCTCCGTG CCTCTCTGTCTCCCCTTCCGTTCTATTTGGACAACGATGTGTACTGT AATGCGTGCGCCATCTGACAACGAATAGATCAGCAGCATTCGCACAC TTGCACATACCCAGTGAAGCTTTTGTGTCTGTCGTATTGACAACACC GACTGCAACAAGGTGTAGATAGAAGTTGGCCTTCTCGCTCGCTCGCA CGCTCTTCACGCTCCTGCTTTCCTTGCTGTGCCTTGCCACCATGGTC CGCAAGAAGGGATCTCTGATCCTGTGTGGGGCGTTTCTGTTCGTGGC CTGGAACGCGCTCTTGCTCCTTTTTTTGTGGGGCCGCCCGCCCATTG

SEQ ID NO.	Description	Sequence
		GTCGACTCGGCGAGGGTGGGGGGGCGGAGCCGGGCGCGGGCGAGGAG TGGGGTGCGGGGAAGAGCAAAGTGGGTGGCGCTAACGGCCTGGCGGG TGAGGTTATCCGCCTGGCGGAGGAGGTCGAGAGTGAGCTGGAGACGC AGAAGAAGCTTCTGAAACAGATACAGTCGCACCGCGAGCTTTGGGAA CAGCGTAAGGAACTGGAGAAGCGTGAAAGCGAGGATACCAAGGACGA GAAGATTGACGTTGAGCCTAAGAAGCCCCGCCAGATCCCGGCCGTGC ACCTGTCCCACAAGGTGGTGGAAGACGCCCAGACAGTAACCAAGAAA ATGCAAACGCTGATGGTGACACCGCCTCAGCTGGTGATGAAGGAGCA GGAGACAGATCAGAAGAATAAGCAGATGATGGAGGACCAGCTGGGGC TCACCACGCCATCTCCGCAAATCATCATCCCGATTCTCGTGATCGCG TGCGATCGCGTGACCGTGAAGCGGTCCCTCGACCGTCTGATCCAGTA CCGGCCAAGCGCAGAGTTGTACCCAATTATCGTCAGCCAGGATTGTG GCCACGCTGACACAGCCCGCGTGATCGGGTCCTATGGCAGCCAGATC ACGCACATAAGCCAGCCTGACCTTGCAGATATACCGGTGCGGCCAGA TCATCGCAAGTTTCAGGGGTACTACAAGATCGCCCGCCATTACCGTT GGGCGCTCAACCAGGTGTTCAACGTGTTTGCCTACTCAACGGTGGTG ATAGTCGAGGACGACCTGGAGGTGGCGCCTGACTTCTTCGAGTACTT TCGAGCTCTCTATCCGATCTTGCGCTCAGATCCTACCTTGTGGTGCA TTTCGGCTTGGAACGATAACGGGCGTGATGGTCTCGTGGATCCCGGG AAGGCCGAGCTCCTCTACCGCACGGACTTCTTTCCTGGACTGGGTTG GATGTTGCTTAAGGAGGTGTGGGCGGAACTCGAACCCAAGTGGCCAA AGGCGTTCTGGGACGACTGGATGCGACACCCGGAGCAGCGTAAAAAT CGCTCTTGCATCCGACCGGAAATTAGTCGGACGATCACATTCGGTCG TAAAGGTGTGTCCTTGGGGCAGTTCTTCGACCAGTATCTCCGTTACA TTAAGCTCAACACTGAATTCGTCCCTTTCACGAAGCACGACCTCAGC TATCTTGTGCGAGAGAAGTACGATGTTAGCTTTGAAAAAGATGTATA CTCGGCTCCCCTCGTAAAGGTAGAGGAGCTGCAGCACGGCGGCAGCC TTAAGGGCAGCGGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGT TTCAAGGTCCTTGCCCGCAACCTCGGGGTGATGGATGACCTGAAGTC AGGCGTGCCACGCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTC GCGGCCGGCGCATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATAC GACGTGAGCTGGAGCTAAATTTAAATATCCCAATGGCGCGCCGAGCT TGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCG CTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGC CTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCT CACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAA TGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTC TTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGC GGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACA GAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCA AAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAG AGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCC TGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCG GATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAT AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCT TATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTA

SEQ ID NO.	Description	Sequence
		TCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA TGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT ACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCAC CGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCA GAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCT GACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAG ATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAA GTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGT TAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATC AGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAG GAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTAT CGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTT CCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGA CGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAG ACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGC ATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAA ATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGC AACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGA ATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCG CAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTG ATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCAT CTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAA ACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCA CCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATC AGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCC GTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATT TATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTA GAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGC CACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAA AATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGA CGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTT GTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCA GCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGA GCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACA GATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGG CTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT ACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGG TAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGT GAATTGACGCGTATTGGGATATTTAAAT
277	pLMTB9301	TGGATAACTTGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTG TTCTCCACTCCAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCG AATGAATGACAGTAAAACCAATGCCTTCACTGGCAGTAACACCCAGC AGTGTTGACTCAATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGT CTTTTGACGAACAACTGCCCTATCAGCTGGTGATGGCCGTGTAGTGG ACTGCCATGCATGGCGTTGACGGGAGCGGGGGATTAGGGTTCGATTC CGGAGAGGGAGCCTGAGAAATAGCTACCACTTCTACGGAGGGCAGCA GGCGCGCAAATTGCCCAATGTCAAAACAAAACGATGAGGCAGCGAAA

SEQ ID NO.	Description	Sequence
		AGAAATAGAGTTGTCAGTCCATTTGGATTGTCATTTCAATGGGGGAT ATTTAAACCCATCCAATATCGAGTAACAATTGGAGGACAAGTCTGGT GCCAGCACCCGCGGTAATTCCAGCTCCAAAAGTCGCAGCCTGACCGC ATCACACATCAAGGCGTTACAGCCTCTCCGTCTTTGCTGCACCCAAG TGTATTCGTGTGACCGCGTTGAGGGATCTAATGGATTCGGAACTTTG GTCGTTTGGTCTCTCATGCTGCCCAATCCCATGCGCTTTTCTCCGTG CCTCTCTGTCTCCCCTTCCGTTCTATTTGGACAACGATGTGTACTGT AATGCGTGCGCCATCTGACAACGAATAGATCAGCAGCATTCGCACAC TTGCACATACCCAGTGAAGCTTTTGTGTCTGTCGTATTGACAACACC GACTGCAACAAGGTGTAGATAGAAGTTGGCCTTCTCGCTCGCTCGCA CGCTCTTCACGCTCCTGCTTTCCTTGCTGTGCCTTGCCACCATGCGC CTGAATGTTAAGAAGGCGCTTATATTTGTTGGATGCGTCGTGTTCCT CTGGGTCCTTCTGAGCTACGCGAGCGTCATTGAAGTGCCTCGTGCAG TCCCCCAGAAAGACCCGGCCGTCGAAATCGAAAAGAAGATCATCAAG CTTCAAAAGCAGGTCGATGCACAAATGGCGGAGTCCAAGAGCTTGCT CGCCAAGGTGAAGAAACTGAAGAAGATCAGTGAGGGAGAGAACGTTG GCGGCGAGGAGGACTCGCTGAAGGACAGTGAGGTTATGCAGCACCTG TCTCAGCCGATCCTCCCCGTTCTGGTGATTGCCTGCGACCGCGTCAC TGTGCAGCGTTGTTTGGACAACCTGGTGAAGTTCCGCCCCTCGAAGG AAACGTTCCCCATCATTGTTTCGCAAGATTGTGGCCACAACGCGACC TATGAAGTCATTACGTCATACACGGCCTCCGACCCGACTATCTCTGT GGTGCGTCAGCCTGATTTGAGCGAAATCGTCCTCCCCCGCGTGAAGG TGAAGTTCCGCGGCTATTACAAGATTGCTCGGCACTACAAATTTGCC CTTAACCACGTTTTTGAGACCCTTGGCCACGAGGCGGTGATCATCGT GGAAGACGACCTGGATATCAGTCCAGATTTCTTTGAGTACTTCCTGG GGACGTACCCGCTGCTTTTGAAAGACCCGTCCTTGTGGTGCATCTCG GCGTGGAACGACAACGGTAAGATGGAGGTCATCGACATGTCGCGCCC GGACCTGCTGCACCGCACCGACTTCTTTCCGGGCCTTGGCTGGGTCC TGCGCCGCGAAATGTGGCGTAAGCTTGCTCCAAAATGGCCCACCGCG TTTTTTGACGACTGGCTGCGAAACCCGGTTAACATCGACGGCAAGGC CTGCATCCGCCCAGAGATATCTCGTACCTATAGTTTCGGGAAGGTGG GTGTGTCTAAGGGACTGTTCTTCGATCTTCACCTCCGCAACATTCAG CTCAATATGGAATACGTCGAATTTACGAAACTGAACCTCACATACCT GCTTAAGGAACACTACGACGATGCCCTCGTCTCCACCGTTTACAATC TGCCGGAGATGAGTGCATCCGAGGTGGTTGCAGGCAGCGATCTCAGC GCAGACCCGGTGCGTGTTATGTACTCCAATGCCAAGACATATCAGCG CGCCGCGAAAAAGCTCGGCCTGATGGACGACTTCCGCTCCGGGGTAC CGCGCACGGCCTACCGCGGCATCGTGACGTGTTTCATTCGGGGCCGA CGAGTATACCTTGCCCCGTCGTTTGAGTGGAACAAGTACGACCCGAC CTGGGGATAGATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGA GCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAT TCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTG CCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCC GCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGG CCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTT CCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCG GTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGG GGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA

SEQ ID NO.	Description	Sequence
		GGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCG AAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCT CCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTG TCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACG CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCT GTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGT AACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACT GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGA AGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGG AAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTA GCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAA GGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCA GTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAA AAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAA TCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAA CTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTAT CAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAAC TCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGC GATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGT CAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAA TCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTC AACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCA AACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGA TCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCG CAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGAT ATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTG AGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGG AAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTG TAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCT GGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTG CCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCA TGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATA TGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGG TTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATA AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGAC GTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCG TATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAA ACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAA GCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGT TGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTG TACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTA AGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAA CTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGC TGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCA GGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGAC GCGTATTGGGATATTTAAAT

SEQ ID NO.	Description	Sequence
278	pLMTB9304	GCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATA TCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTG CTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGA AATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGT GCTTCTCGATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTG ATGGACAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGT TATGTGTGGGAGGGCTAACTAGCCTCGGAGATCCACTAGTTCTAGTT CTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGCGGAATCGGTC GCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAG CAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAATT CGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTT TTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAG AAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCT TCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGCCCCACGC CGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGATGC CGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAGGG CACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTC GGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCT TGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTC ACACACACACACACACACACACACACACACAAAGCTCCGGTTCGTCCGG CCGTAACGCCTTTTCAACTCACGGCCTCTAGGAATGAAGGAGGGTAG TTCGGGGGGAGAACGTACTGGGGCGTCAGAGGTGAAATTCTTAGACCG CACCAAGACGAACTACAGCGAAGGCATTCTTCAAGGATACCTTCCTC AATCAAGAACCAAAGTGTGGAGATCGAAGATGATTAGAGACCATTGT AGTCCACACTGCAAACGATGACACCCATGAATTGGGGATCTTATGGG CCGGCCTGCGGCAGGGTTTACCCTGTGTCAGCACCGCGCCCGCTTTT ACCAACTTACGTATCTTTTCTATTCGGCCTTTACCGGCCACCCACGG GAATATCCTCAGCACGTTTTCTGTTTTTTCACGCGAAAGCTCTGAGG TTACAGTCTCAGGGGGGAGTACGTTCGCAAGAGTGAAACTTAAAGAA ATTGACGGAATGGCACCACAAGACGTGGAGCGTGCGGTTTAATTTGA CTCAACACGGGGAATTTAAATATCCCAATGGCGCGCCGAGCTTGGCT CGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGG GTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTG CCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAAT CGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCG CTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGA GCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATC AGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGG CCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTC CGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAA GCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATAC CTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTC ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCC GGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCC ACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG

SEQ ID NO.	Description	Sequence
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279	pLMTB9320	ATGCGCCTCCGAGAACCCCTGCTGAGCGGATCAGCCGCGATGCCGGG TGCCTCCCTCCAACGCGCCTGTCGCCTCCTTGTGGCGGTATGCGCAC TGCACCTTGGTGTAACACTGGTCTACTACCTGGCCGGGCGGGACCTT AGCCGGCTCCCGCAATTGGTCGGTGTGTCGACCCCACTGCAGGGTGG CTCCAATTCAGCGGCCGCTATAGGCCAGTCGTCTGGCGAGTTGCGAA CAGGTGGCGCGCGCCCCCCGCCACCGTTGGGCGCCAGCTCTCAGCCG CGCCCCGGTGGCGATTCAAGCCCAGTGGTTGACAGCGGCCCGGGCCC AGCTAGCAACCTGACATCGGTCCCGGTGCCTCACACGACCGCGCTGT CCCTCCCCGCATGCCCGGAGGAGAGCCCACTCCTTGTGGGCCCCATG

SEQ ID NO.	Description	Sequence
		CTCATCGAGTTCAACATGCCCGTAGATCTCGAGCTCGTGGCTAAGCA GAACCCCAACGTCAAGATGGGTGGACGCTATGCACCGCGAGACTGTG TTAGCCCACACAAGGTGGCTATCATCATTCCGTTCCGCAACCGCCAG GAGCATCTGAAGTACTGGCTGTACTACCTGCACCCCGTGCTCCAGCG GCAGCAGCTGGACTACGGTATCTACGTAATCAACCAGGCGGGCGACA CCATCTTCAATCGCGCAAAGCTTCTTAACGTCGGTTTTCAGGAGGCT CTCAAGGACTATGACTACACCTGCTTCGTGTTCTCGGACGTCGACCT CATTCCAATGAACGACCACAACGCGTACCGCTGCTTTTCCCAGCCCC GCCACATCTCAGTTGCAATGGATAAGTTCGGGTTCTCGCTCCCCTAC GTTCAGTACTTTGGTGGTGTGTCCGCCCTCAGCAAGCAACAGTTTCT GACAATCAATGGCTTTCCGAACAACTACTGGGGCTGGGGCGGCGAGG ACGACGACATTTTCAACCGATTGGTGTTCCGCGGAATGTCTATCTCT CGTCCCAACGCGGTCGTAGGGCGATGCCGAATGATACGACATTCGCG GGATAAGAAGAATGAGCCGAATCCGCAGCGCTTTGACCGGATCGCCC ATACCAAGGAGACGATGCTGAGCGACGGACTGAATAGTCTCACCTAC CAGGTACTCGACGTGCAGCGCTACCCACTGTATACGCAGATCACGGT AGACATCGGAACGCCGAGCTGACTAGCCTCGGAGATCCACTAGTTCT AGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGCGGAATC GGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGT GCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTC AATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCACCCT CCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGT CGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGC ATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGCCCC ACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGG ATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAG AGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCCGG CTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGCCT TCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTC TCTCACACACACACACACACACACACACACACACAAATGATGTCCCCTG AAGATGCGACCGGGCTGGAGGCTGCACGCAAGCAGAAGATCCATAAC CTGAAGCTGAAGACGGCGTGCCTAGAGAATGAGGAGCTTGTGCAGGA GCTGCACATCTCTGACTGGTCAGAGACGCAGCGACAGAAGCTGCGCG GCGCCCATGAGAAGGGCGAGGAGCTGCTTGCGTCCGTGGAGGTTGGG ACGAAGTGGAACCTGATGGAGGCGTACGACCTGGCGAAGCTGATGCG CGTGTGCGGGCTGGAGATGAGTCAGCGCGAGCTGTACCGCCCGGAGG ACAAGCCGCAGTTCATGGACATCATTGGCGTGAAGAAGGTGCTACAG GACCTTCGACAGAACCGGAACAAGACGCGCGTTGTGAGCTTCACGCA GCTGATCGACAACAGCATCGCGAAGATGGAGAAGGTGGAGGAGGAGC TGCGGCGGTCGCAGCTGGACGCGACGCAGCTCGCGCAGGTGCCGTCT CGGACGGTGAAGATGATATTTAAATATCCCAATGGCGCGCCGAGCTT GGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGC TCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCC TGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTC ACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAAT GAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCT TCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAG

SEQ ID NO.	Description	Sequence
		AATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAA AAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAG GCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGA GGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCT GGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGG ATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATA GCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAG CTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTT ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTAT CGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTA CACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACC GCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAG AAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTG ACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGA TTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAG TTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTT AGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCA GGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGG AGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATC GGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTC CCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGAC GACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGA CTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCA TCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAA TACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCA ACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAA TCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGC AGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGA TGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATC TCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAA CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCAC CTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCA GCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCG TTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTT ATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAG AAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCC ACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAA ATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGAC GGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTG TCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAG CGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAG CAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAG ATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGC TGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTA CGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGT

SEQ ID NO.	Description	Sequence
		AACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTG AATTGACGCGTATTGGGATATTTAAAT
280	pLMTB9339	CTCCCACGAAACTCTACATCATGTCCCATCAAGATTCGATTGATATC GACACGGAGTTGGATCTGCAGCAGGCGGAGAACATACTGAATCACAA GGAGTCCGGAGGGAGTGGCGGTTACCCGTACGACGTGCCCGACTACG CCTACCCGTACGATGTGCCGGATTACGCGTATCCATATGACGTGCCA GACTATGCGTAGGTCGAACGCTCACTTTTGAGCACACGACTCTCTAC TTGTCTCCCGCTCTGATGTCTCTTTCCTTATTTCTGCGCCTGCAGGT AAAAGAAGTGCATCCGCATGGCTGTCTTTTAACGGGGACAGCGAGGC GTGCTGGCGGCAACTGTGTGCGCTTGTGTGCGCGCACGTTACGCTGA GAGAACCTCACATTTCCTTTTTGTTTTTACTGTTAATTTTCTGTATG TCCTTTTCTCGGCCTCTTGTCGCGTCTGCTCCCCCCCCGATGGGGCG CTGGCGAGGCGGAGAGGTCATAGGTTCCTCGTTATAAGCCAGTAGCG GTGCTGCACGGGCATGCCCTATGGAGGGAGAAGGGGTGCTGCGTGGA AAAGGGAGCGCAGTGCGCCAGAACACAAGCGTGCGCGCTTGTAGGTG CGCACATGTTTGCTACTTTTTTTTCTCTCCGTTCCGCTCTGGCTAGT GATCTTCGCCACTGCCGAGTGGGTGTTGGCCTGCTGCAGAGACTGCA ACATTGCTCCCGGTGCGGGCTGTGTGCGGTCATCGCGTGTGCGCAGC TGCAGTGTGCGGAGGGGCCGTCCAGGCACGGTCTTACTTCAATCTCC GCTGCTATGGGTGCGTCCTGATGAAGGCCCTGCCTACGGATCGCCTT TCTGTAGGCGCTCTTGTCCATCTCTGCTGTAGCTCAACTTTCTGCGC TTGTTTTTCCTCTTTTTGTTCTTCGGCATCTCCGCCTTTGTTGGTGA CTGGTACTGCCTTGCGTCTCCATGAACTAAAACAACGGCTGCATATC TTCCCCTTCCCTTGCGGATATAAAACTCGTACCTGTGCGACTTTCTC ACGTTCGCCGCACGCTCACGGACGTTCGACGTCCAATCGATGCGCGC ATGCGCACCATGACGCTTTTTCGAAGTTTCTACGCCTCGCCATCGTA CAGACACTTAAGCTAACAACTCGCTCACACACTCGAGATGATTGCAA GCAGTGTCCGCCATGCGGTAATCTTGCTTCTTGTAGCGGTCGCGATG ATGGTTAACAACGTCATTGCTCCTGAAGCTTCATTCCAAGTGTGGAA CAAAGATTCAAGTAGCAAGAACCTTATACCACGGCTTCAAAAAATCT GGAAAAACTACCTTTCGATGAATAAATATAAGGTTAGTTATAAGGGA CCCGGCCCTGGGATTAAGTTCTCTGCGGAAGCACTCCGGTGTCACTT GCGCGATCATGTGAACGTTAGCATGGTTGAGGTTACAGATTTTCCAT TTAACACTTCCGAGTGGGAGGGGTACCTTCCGAAAGAGTCGATTCGT ACCAAAGCAGGACCCTGGGGTCGCTGCGCAGTGGTTAGTAGCGCAGG ATCGCTGAAATCATCACAGCTCGGACGCGAAATCGACGATCATGACG CAGTACTTCGATTCAATGGCGCTCCTACAGCCAATTTTCAACAGGAC GTTGGAACCAAGACTACGATACGGCTTATGAACAGCCAATTGGTTAC GACAGAAAAACGATTTCTTAAGGACAGCCTTTATAACGAAGGCATTC TGATAGTTTGGGACCCTAGTGTTTATCATAGCGACATACCGAAATGG TATCAGAACCCTGATTATAACTTCTTCAATAATTACAAGACATACCG AAAGCTTCACCCCAACCAGCCTTTCTACATACTTAAGCCGCAGATGC CTTGGGAGTTGTGGGACATTCTGCAAGAGATCTCGCCCGAGGAAATC CAGCCCAACCCTCCATCATCGGGTATGCTCGGGATTATTATAATGAT GACTCTCTGTGATCAAGTCGACATATACGAGTTTCTCCCCAGCAAGC GTAAAACAGATGTTTGCTATTACTACCAGAAGTTCTTTGACTCGGCA TGCACAATGGGTGCCTACCATCCCCTTCTCTATGAGAAGAATCTGGT TAAACACCTTAATCAGGGAACCGACGAGGATATCTACCTTCTCGGGA

SEQ ID NO.	Description	Sequence
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WHAT IS CLAIMED:

1. A method of recombinantly engineering a *Leishmania* cell comprising
(a) introducing two or more DNA fragments into the *Leishmania* cell, and
(b) incubating the *Leishmania* cell to allow homologous recombination of the DNA fragments,
wherein a first DNA fragment of the two or more DNA fragments comprises a 5' homologous region and/or a 3' homologous region; wherein the 5' homologous region is homologous to a 3' homologous region of a second DNA fragment of the two or more DNA fragments or the 3' homologous region of the first DNA fragment is homologous to a 5' homologous region of the second DNA fragment; and
wherein the nucleotide sequences of the first and the second DNA fragments outside the homologous region(s) are not homologous to each other; are not homologous to a sequence in the *Leishmania* cell's genome; and/or have no homologies within the respective DNA fragment.

2. The method of claim 1, wherein each of the two or more DNA fragments comprises a 5' homologous region and/or a 3' homologous region; wherein the 5' homologous region of the each of the two or more DNA fragments is homologous to a 3' homologous region of another one of the two or more DNA fragments or the 3' homologous region of the each of the two or more DNA fragments is homologous to a 5' homologous region of another one of the two or more DNA fragments; and wherein the nucleotide sequences outside the homologous regions in each DNA fragment are not homologous to each other; are not homologous to a sequence in the *Leishmania* cell's genome; and/or have no homologies within the respective DNA fragment.

3. The method of any one of claims 1 to 2, wherein the two or more DNA fragments, optionally after the two or more DNA fragments are recombined with each other, are suitable for integration into a chromosome of the *Leishmania* cell.

4. The method of claim 3, wherein the two or more DNA fragments, optionally after the two or more DNA fragments are recombined with each other, are integrated into the chromosome of the *Leishmania* cell.

5. The method of claim 4, wherein the two or more DNA fragments are integrated in tandem into the paraflagellar rod protein (Pfr) locus.

6. The method of claim 4, wherein the two or more DNA fragments are integrated at the start of the 18S coding region (Ssu-PolI).

7. The method of any one of claims 1 to 2, the two or more DNA fragments, before and/or after recombination with each other, are not integrated in a chromosome of the *Leishmania* cell.

8. The method of claim 7, wherein the homologous recombination of the two or more DNA fragments results in a circular plasmid.

9. The method of any one of claims 1 to 8, wherein the nucleotide sequence of the first DNA fragment outside the homologous region is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length.

10. The method of any one of claims 1 to 9, wherein the nucleotide sequence of the second DNA fragment outside the homologous region is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length.

11. The method of any one of claims 1 to 10, wherein the nucleotide sequences of all of the two or more DNA fragments outside the homologous region are at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 200 nucleotides, 300 nucleotides, 400 nucleotides, 500 nucleotides, 600 nucleotides, 700 nucleotides, 800 nucleotides, 900 nucleotides, 1000 nucleotides, 2000 nucleotides, 5000 nucleotides, 10000 nucleotides, 15000 nucleotides, or 20000 nucleotides, 25000 nucleotides, 30000 nucleotides, 35000 nucleotides, 40000 nucleotides, 45000 nucleotides, or at least 50000 nucleotides in length.

12. The method of any one of claims 1 to 11, wherein the homologous recombination of the DNA fragments results in a nucleotide sequence that is 50 nucleotides to 100 nucleotides, 100 nucleotides to 500 nucleotides, 500 nucleotides to 1000 nucleotides, 1000 nucleotides to 5000 nucleotides, 5000 nucleotides to 10000 nucleotides, 10000 nucleotides to 15000 nucleotides, 15000 nucleotides to 20000 nucleotides, 20000 nucleotides to 25000 nucleotides, 25000 nucleotides to 30000 nucleotides, 30000 nucleotides to 35000 nucleotides, 35000 nucleotides to 40000 nucleotides, 40000 nucleotides to 45000 nucleotides, 45000 nucleotides to 50000 nucleotides, 50000 nucleotides to 55000 nucleotides, 55000 nucleotides to 60000 nucleotides, 60000 nucleotides to 65000 nucleotides, 65000 nucleotides to 70000 nucleotides, 70000 nucleotides to 75000 nucleotides, or 75000 nucleotides to 80000 nucleotides in length.

13. The method of any one of claims 1 to 12, wherein the 5' homologous region and/or the 3' homologous region of the first DNA fragment is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length.

14. The method of any one of claims 1 to 13, wherein the 5' homologous region and/or the 3' homologous region of the second DNA fragment is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length.

15. The method of any one of claims 1 to 14, wherein the 5' homologous region and/or the 3' homologous region of all of the two or more DNA fragments is at least 10 nucleotides, 20 nucleotides, 30 nucleotides, 40 nucleotides, 50 nucleotides, 100 nucleotides, 150 nucleotides, 200 nucleotides, 250 nucleotides, 300 nucleotides, 350 nucleotides, 400 nucleotides, 450 nucleotides, or at least 500 nucleotides in length.

16. The method of any one of claims 1 to 15, wherein the 5' homologous region and/or the 3' homologous region of the first DNA fragment is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400

nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length.

17. The method of any one of claims 1 to 16, wherein the 5' homologous region and/or the 3' homologous region of the second DNA fragment is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length.

18. The method of any one of claims 1 to 17, wherein the 5' homologous region and/or the 3' homologous region of all of the two or more DNA fragments is at most 500 nucleotides, 550 nucleotides, 600 nucleotides, 650 nucleotides, 700 nucleotides, 750 nucleotides, 800 nucleotides, 850 nucleotides, 900 nucleotides, 950 nucleotides, 1000 nucleotides, 1200 nucleotides, 1400 nucleotides, 1600 nucleotides, 1800 nucleotides, 2000 nucleotides, 2200 nucleotides, 2400 nucleotides, 2600 nucleotides, 2800 nucleotides, 3000 nucleotides, 3200 nucleotides, 3400 nucleotides, 3600 nucleotides, 3800 nucleotides, 4000 nucleotides, 4200 nucleotides, 4400 nucleotides, 4600 nucleotides, 4800 nucleotides, or at most 5000 nucleotides in length.

19. The method of any one of claims 1 to 18, wherein the 5' homologous region of the first DNA fragment and the 3' homologous region of the second DNA fragment have at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity.

20. The method of any one of claims 1 to 18, wherein the 3' homologous region of the first DNA fragment and the 5' homologous region of the second DNA fragment have at least 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% sequence identity.

21. The method of any one of claims 1 to 20, wherein the two or more DNA fragments are introduced by transfection.

22. The method of any one of claims 1 to 20, wherein the two or more DNA fragments are introduced concurrently.

23. The method of any one of claims 1 to 22, wherein the number of DNA fragments is 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 37, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50.

24. The method of any one of claims 1 to 23, wherein the nucleotide sequences of the two or more DNA fragments outside the homologous region are selected from a group consisting of intergenic regions (IRs), untranslated regions (UTRs), and open reading frames (ORFs) encoding polypeptides.

25. The method of claim 24, wherein the IRs, UTRs and ORFs are devoid of homologous sequences within itself, and/or homologous sequences to one another.

26. The method of any one of claims 1 to 25, wherein the nucleotide sequences of the two or more DNA fragments outside the homologous region encode the same polypeptide.

27. The method of claim 26, wherein the *Leishmania* cell is capable of expressing multiple copies of the same polypeptide.

28. The method of any one of claims 26 and 27, wherein the method increases the expression level of the polypeptide.

29. The method of any one of claims 1 to 26, wherein the homologous recombination of the DNA fragments results in a nucleotide sequence comprising at least 50%, 60%, 70%, 80%, 90% or 100% of genetic information encoded by the two or more DNA fragments.

30. The method of any one of claims 1 to 29, wherein undesired crossing out and/or crossing over occurs in at most 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or at most 10% of the *Leishmania* cells over a period of at least 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, or at least 10 days.

31. The method of any one of claims 1 to 29, wherein undesired crossing out and/or crossing over occurs in at most 0.01%, 0.05%, 0.1%, 0.5%, 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9% or at most 10% of the *Leishmania* cells over at least 1, 2, 3, 4, 5, 6, 7, 8, 9, or at least 10 cell divisions.

32. The method of any one of claims 1 to 31, wherein the *Leishmania* cell is *Leishmania tarentolae*.

33. A *Leishmania* cell recombinantly engineered using the method of any one of claims 1 to 32.

34. The *Leishmania* cell of claim 33, wherein the *Leishmania* cell is recombinantly engineered using the method repeatedly.

35. The *Leishmania* cell of any one of claims 33 to 34, wherein the *Leishmania* cell is *Leishmania tarentolae*.

36. A kit comprising one or more containers and instructions for use, wherein said one or more containers comprise the *Leishmania* cell of any one of claims 33 to 35.

37. A method of making a polypeptide comprising (a) culturing the *Leishmania* cell of any one of claims 33 to 35 under suitable conditions for polypeptide production; and (b) isolating the polypeptide.

38. The method of claim 37, wherein the method further comprises introducing a nucleotide sequence encoding the polypeptide.

39. A polypeptide produced by the method of any one of claims 37 to 38.

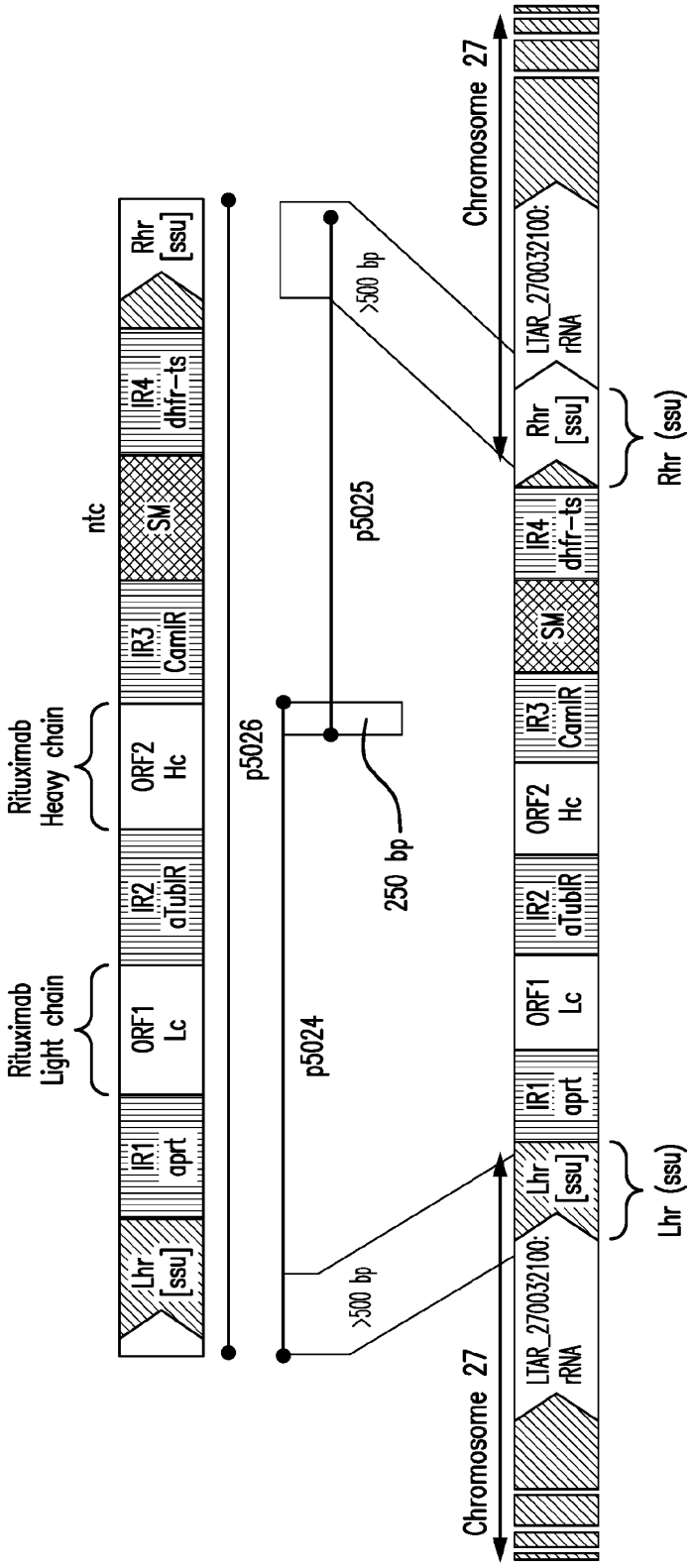
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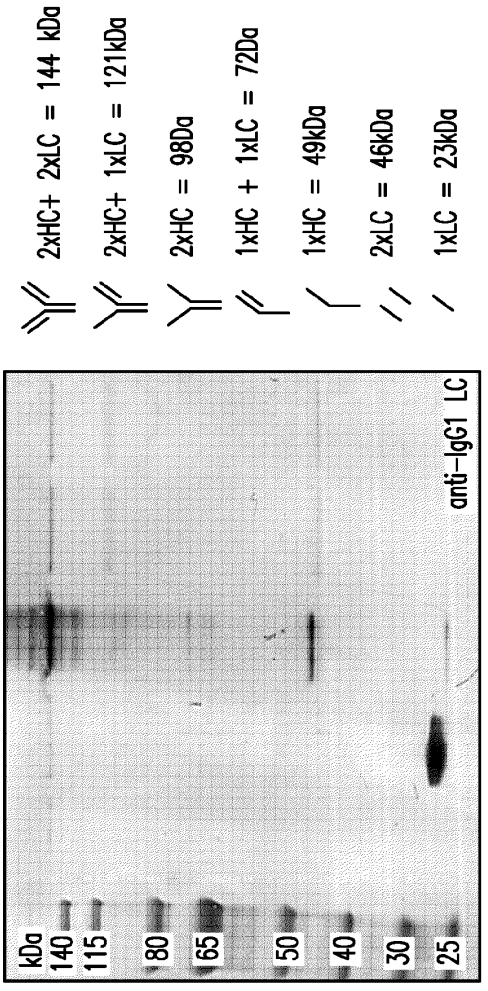
FIG. 1A



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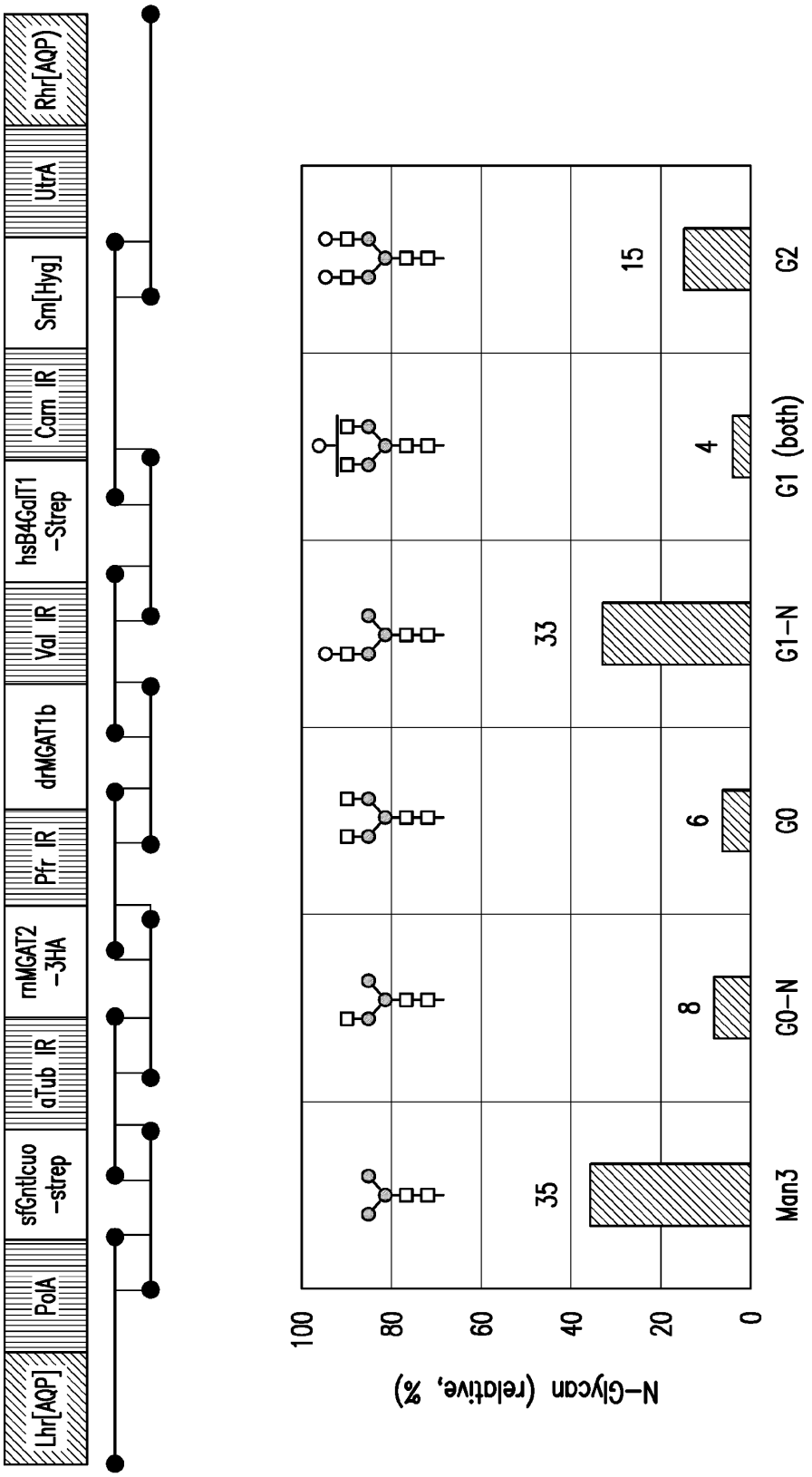
condition	reducing	reducing	non-reducing	non-reducing	

FIG. 1B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Cam IR
Sm[Hyg]
UtrA
Rhr[AQP]
N-Glycan (relative, %)
100
80
60
40
20
0
35
8
6
33
15
4
Man3
G0-N
G0
G1-N
G1 (both)
G2
St15257

FIG. 2

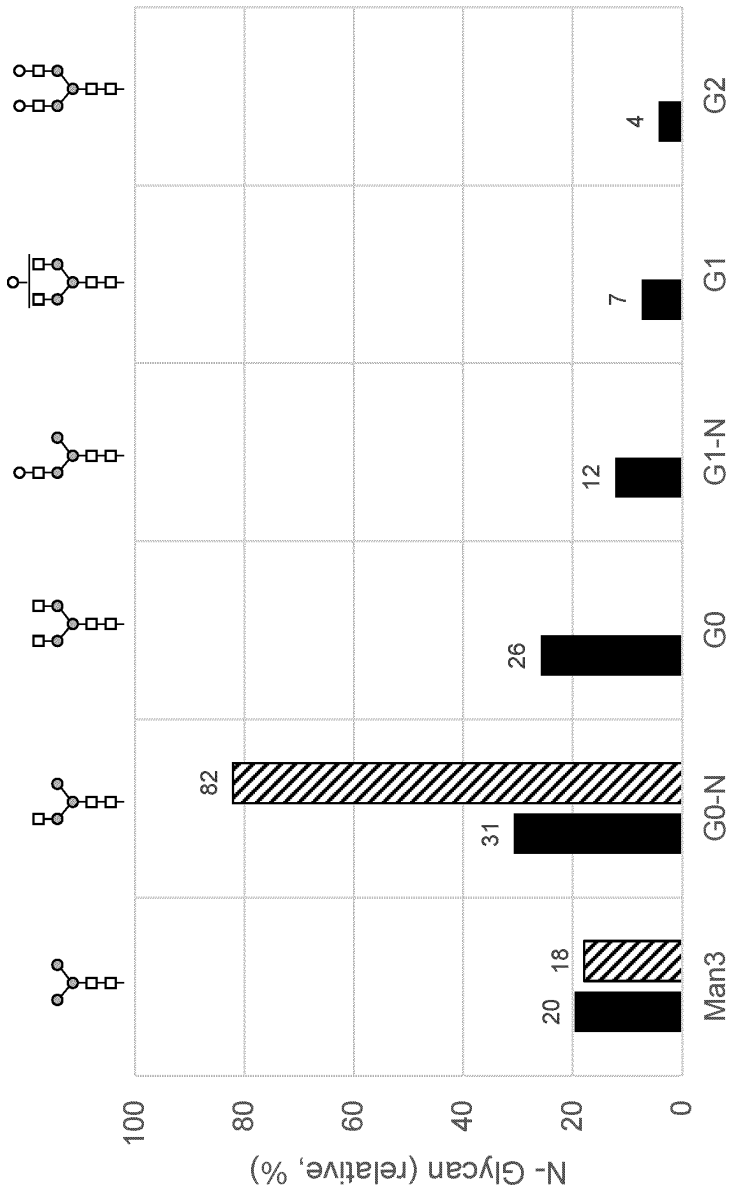
N- Glycan (relative, %)
100
80
60
40
20
0
Man3
G0-N
G0
G1-N
G1
G2
20
18
31
82
26
12
7
4
St15368
St15448

FIG. 3A

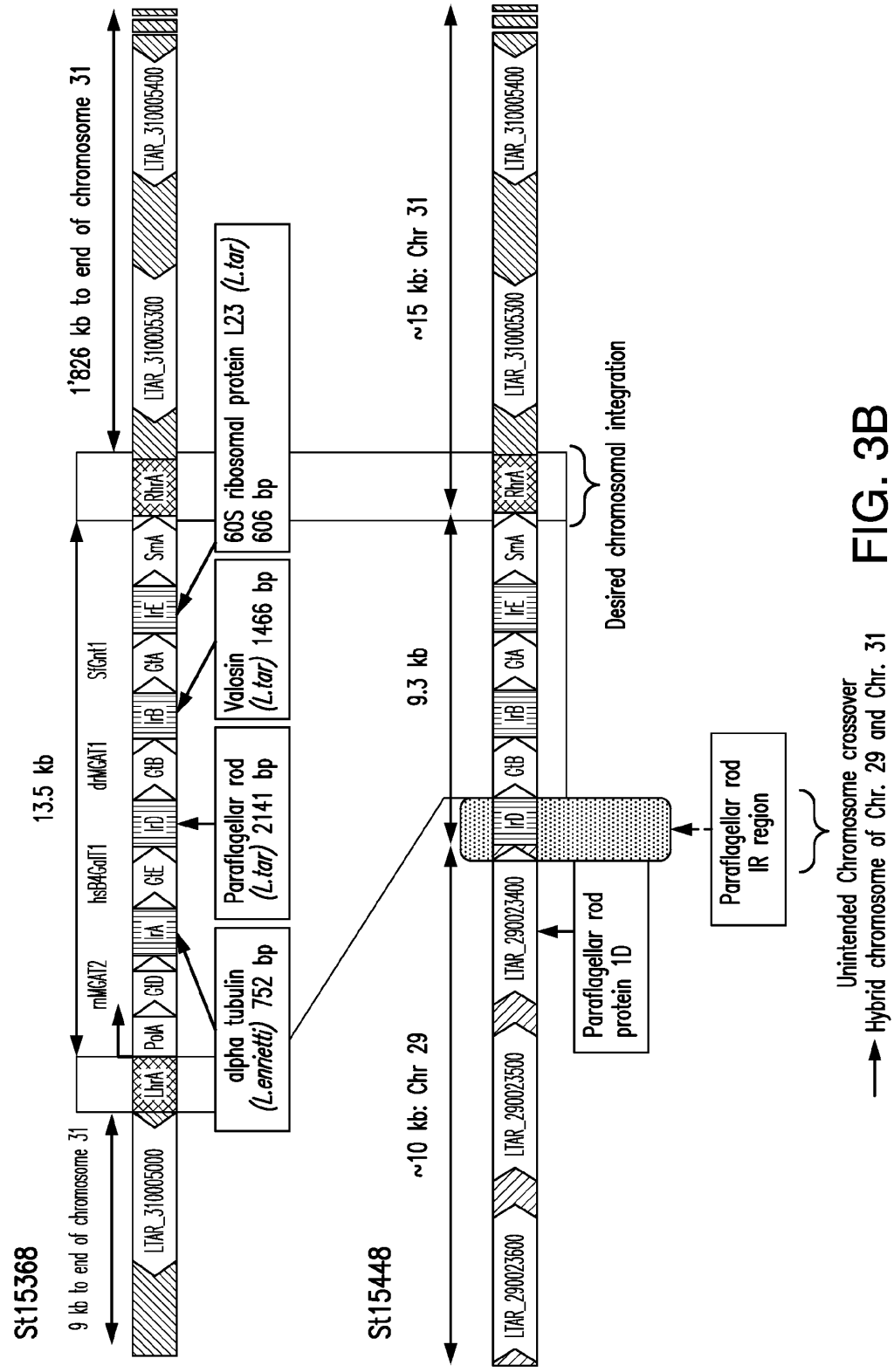
St15368
9 kb to end of chromosome 31
13.5 kb
1'826 kb to end of chromosome 31
LTAR_310005000
LhrA
PolA
GtD
mMCAT2
IrA
GtE
hsB4GalT1
IrD
GtB
dhMCAT1
IrB
GtA
StGnt1
IrE
SmA
RhrA
LTAR_310005300
LTAR_310005400
alpha tubulin (L.enrietti) 752 bp
Paraflagellar rod (L.tar) 2141 bp
Valosin (L.tar) 1466 bp
60S ribosomal protein L23 (L.tar) 606 bp
St15448
~10 kb: Chr 29
9.3 kb
~15 kb: Chr 31
LTAR_290023600
LTAR_290023500
LTAR_290023400
Paraflagellar rod protein 1D
Paraflagellar rod IR region
Desired chromosomal integration
Unintended Chromosome crossover
Hybrid chromosome of Chr. 29 and Chr. 31

FIG. 3B

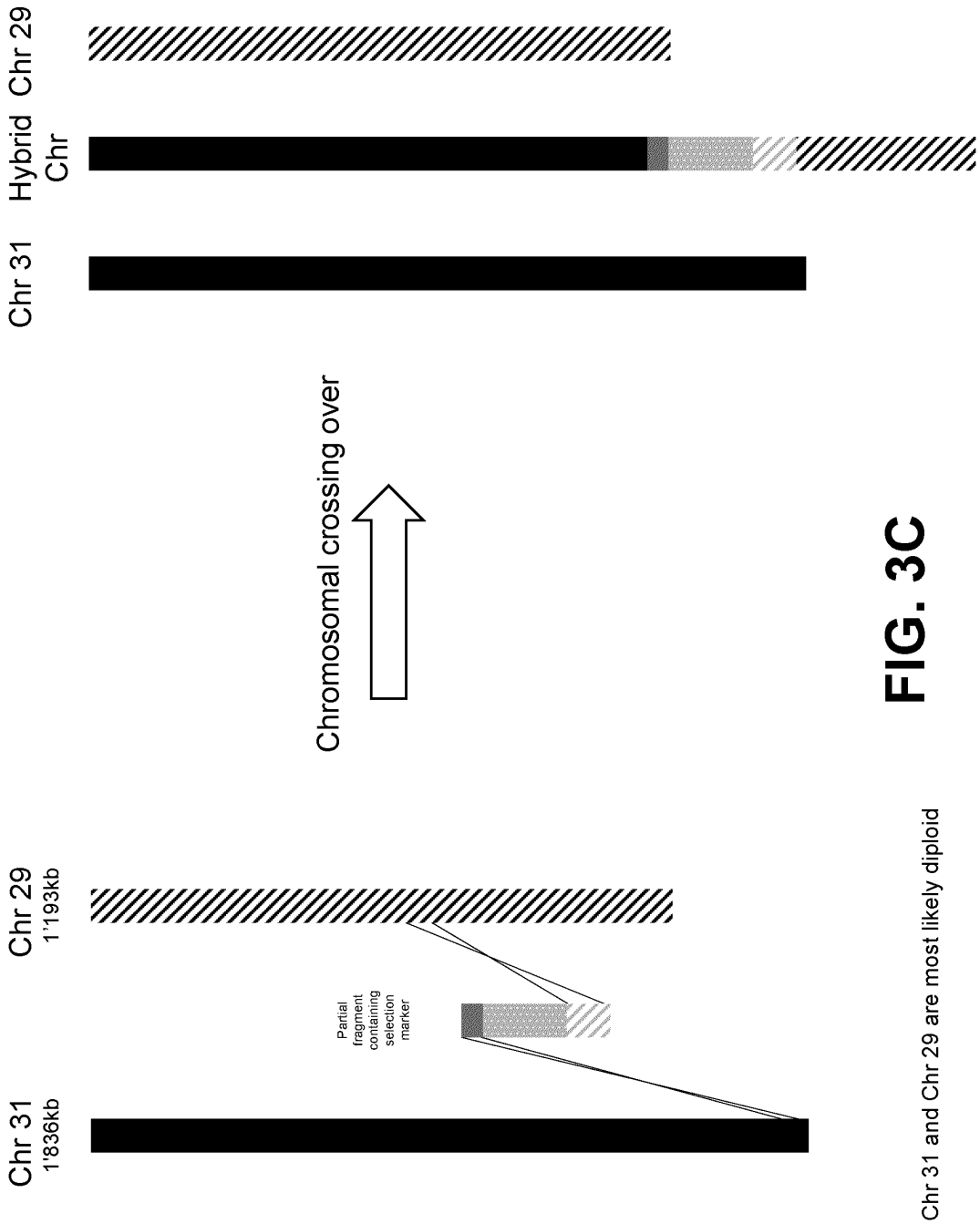
Chr 31
Hybrid Chr
Chr 29
Chromosomal crossing over
Chr 31
1'836kb
Partial fragment containing selection marker
Chr 29
1'193kb
Chr 31 and Chr 29 are most likely diploid

FIG. 3C

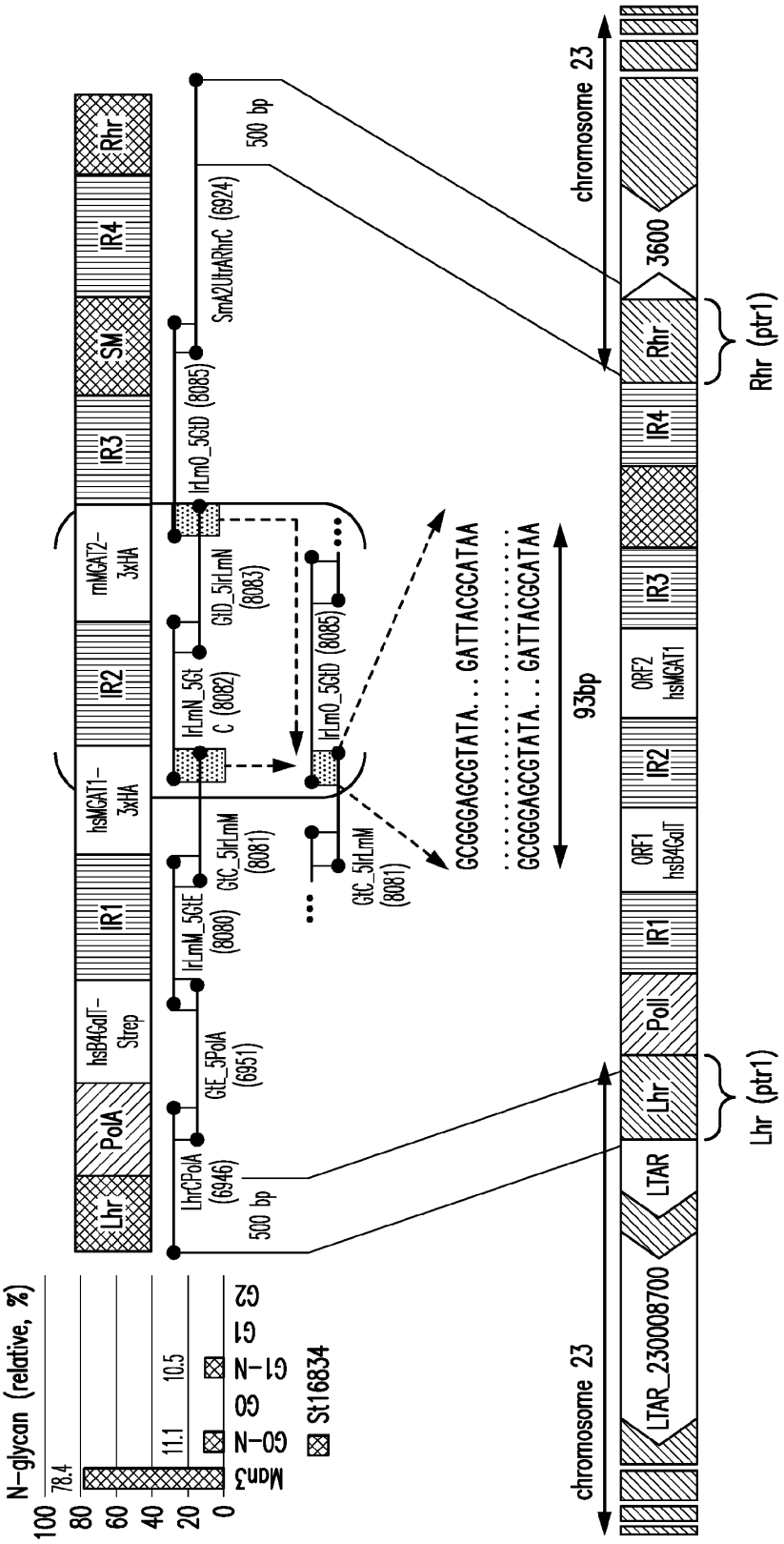
N-glycan (relative, %)
100
80
60
40
20
0
78.4
11.1
10.5
Man3
G0-N
G1-N
G0
G1
G2
St16834
LTAR_230008700
chromosome 23
LTAR
Lhr
PolA
hsB4GalT-Strep
IR1
hsMGAT1-3xHA
IR2
mMGAT2-3xHA
IR3
SM
IR4
Rhr
LhrCPolA (6946)
500 bp
GtE_5PolA (6951)
lrLmM_5GtE (8080)
GtC_5lrLmM (8081)
lrLmN_5Gt C (8082)
GtD_5lrLmN (8083)
lrLmO_5GtD (8085)
SmA2UtrARhrC (6924)
500 bp
chromosome 23
Lhr (ptr1)
ORF1 hsB4GalT
IR1
PolI
Lhr
LTAR
IR2
ORF2 hsMGAT1
IR3
3600
Rhr
IR4
Rhr (ptr1)
93bp
GCGGGAGCGTATA...GATTACGCATAA
GCGGGAGCGTATA...GATTACGCATAA
GtC_5lrLmM (8081)
lrLmO_5GtD (8085)

FIG. 4

Counterclockwise Disruption
• PolI regulated
• Disruption of homrec gene
• Target loci:
• AQP
• MT
• PTR1
PolI
Tandem Insertion
• Insertion in IR region; PolII regulated (endogenous from chromosomal locus)
• Use native IR region upstream of cassette
• Target loci:
• GP63
• Alpha tubulin

FIG. 5

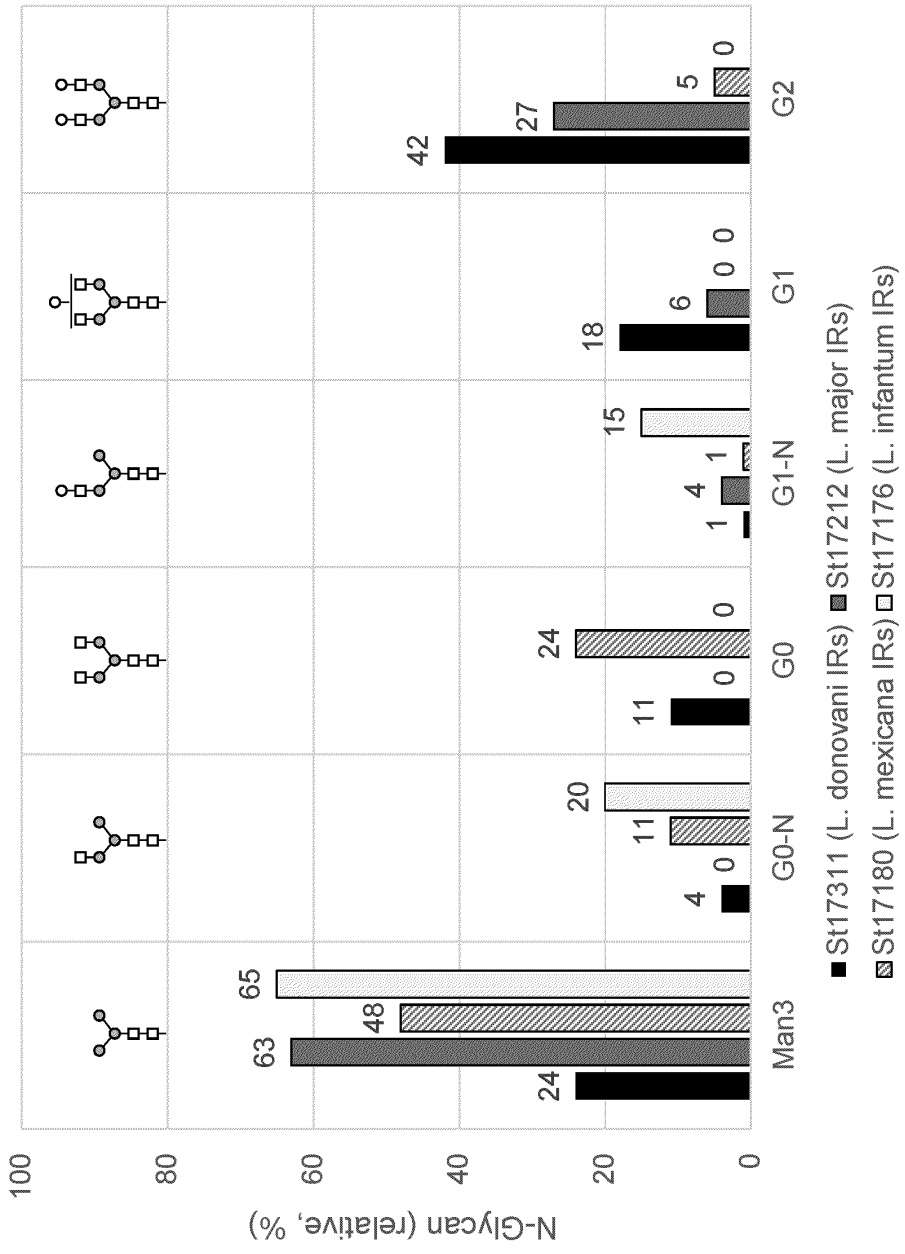
N-Glycan (relative, %)
100
80
60
40
20
0
Man3
G0-N
G0
G1-N
G1
G2
24
63
48
65
4
0
11
20
0
11
24
1
4
1
15
18
6
0
0
42
27
5
0
St17311 (L. donovani IRs)
St17212 (L. major IRs)
St17180 (L. mexicana IRs)
St17176 (L. infantum IRs)

FIG. 6A

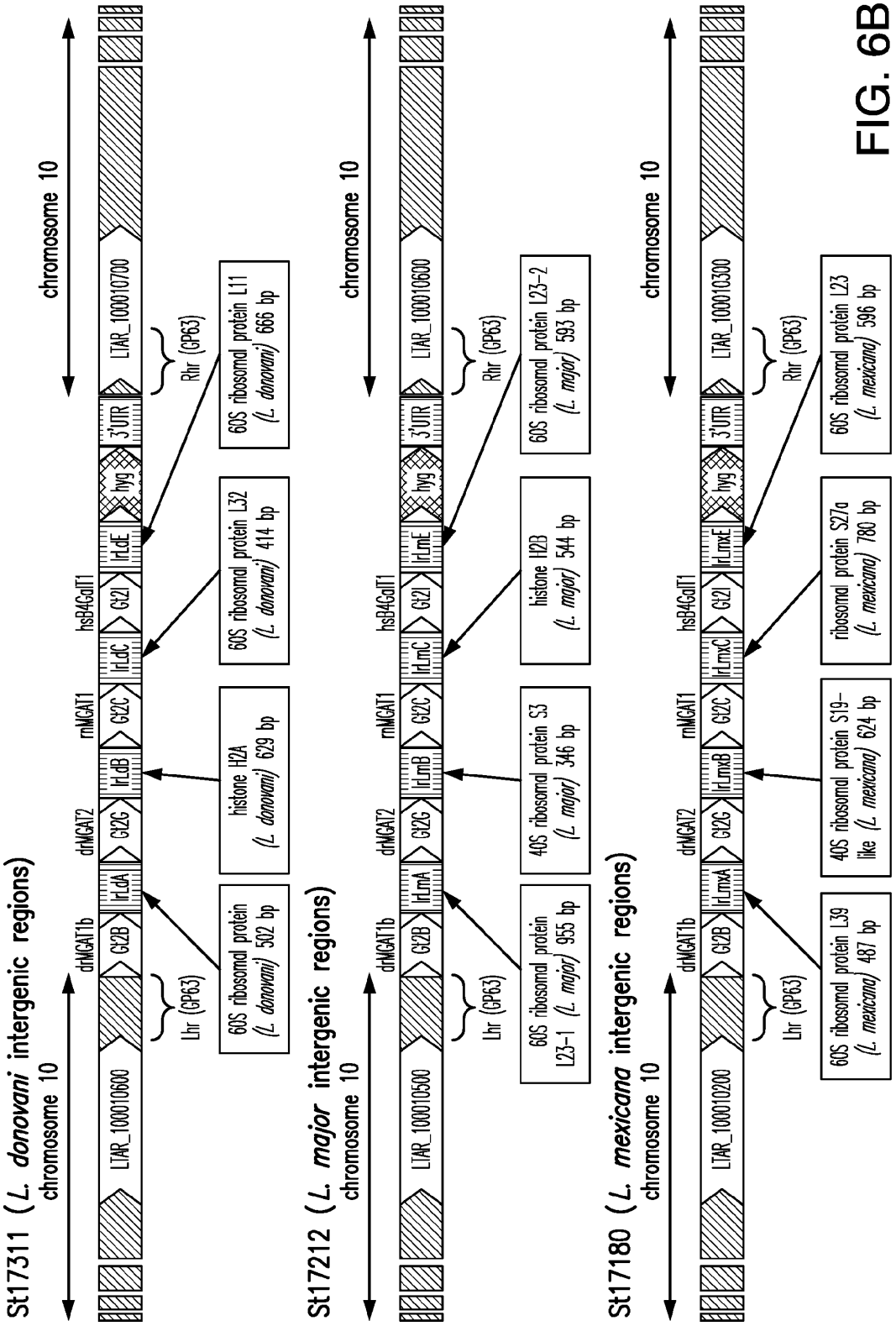
St17311 (L. donovani intergenic regions)
chromosome 10
chromosome 10
LTAR_100010600
dnMGAT1b
GI2B
lrLdA
dnMGAT2
GI2G
lrLdB
rnMGAT1
GI2C
lrLdC
hsB4GalT1
GI2I
lrLdE
hyg
3'UTR
LTAR_100010700
Lhr (GP63)
Rhr (GP63)
60S ribosomal protein (L. donovani) 502 bp
histone H2A (L. donovani) 629 bp
60S ribosomal protein L32 (L. donovani) 414 bp
60S ribosomal protein L11 (L. donovani) 666 bp
St17212 (L. major intergenic regions)
chromosome 10
chromosome 10
LTAR_100010500
dnMGAT1b
GI2B
lrLmA
dnMGAT2
GI2G
lrLmB
rnMGAT1
GI2C
lrLmC
hsB4GalT1
GI2I
lrLmE
hyg
3'UTR
LTAR_100010600
Lhr (GP63)
Rhr (GP63)
60S ribosomal protein L23-1 (L. major) 955 bp
40S ribosomal protein S3 (L. major) 346 bp
histone H2B (L. major) 544 bp
60S ribosomal protein L23-2 (L. major) 593 bp
St17180 (L. mexicana intergenic regions)
chromosome 10
chromosome 10
LTAR_100010200
dnMGAT1b
GI2B
lrLmxA
dnMGAT2
GI2G
lrLmxB
rnMGAT1
GI2C
lrLmxC
hsB4GalT1
GI2I
lrLmxE
hyg
3'UTR
LTAR_100010300
Lhr (GP63)
Rhr (GP63)
60S ribosomal protein L39 (L. mexicana) 487 bp
40S ribosomal protein S19-like (L. mexicana) 624 bp
ribosomal protein S27a (L. mexicana) 780 bp
60S ribosomal protein L23 (L. mexicana) 596 bp

FIG. 6B

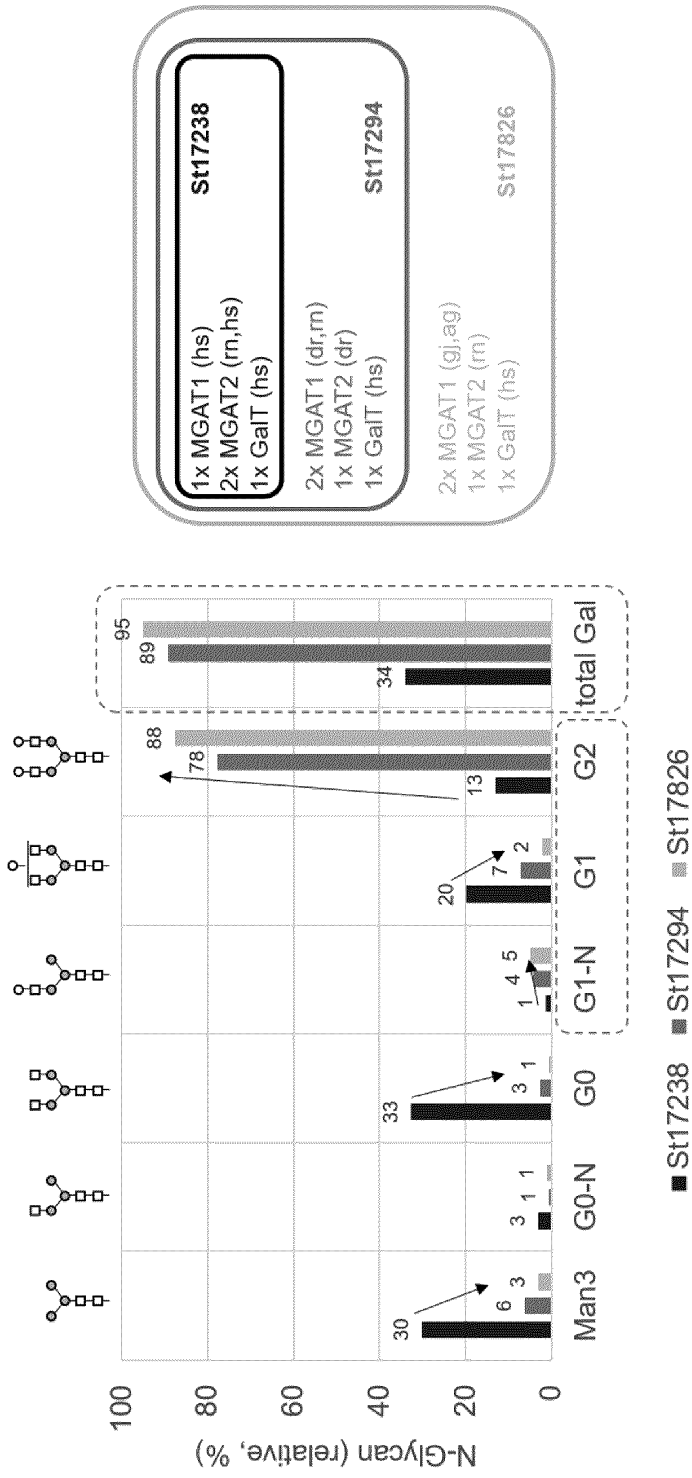
St17238
1x MGAT1 (hs)
2x MGAT2 (rn,hs)
1x GalT (hs)
St17294
2x MGAT1 (dr,rn)
1x MGAT2 (dr)
1x GalT (hs)
St17826
2x MGAT1 (gj,ag)
1x MGAT2 (rn)
1x GalT (hs)
N-Glycan (relative, %)
0
20
40
60
80
100
Man3
G0-N
G0
G1-N
G1
G2
total Gal
St17238
St17294
St17826

FIG. 7

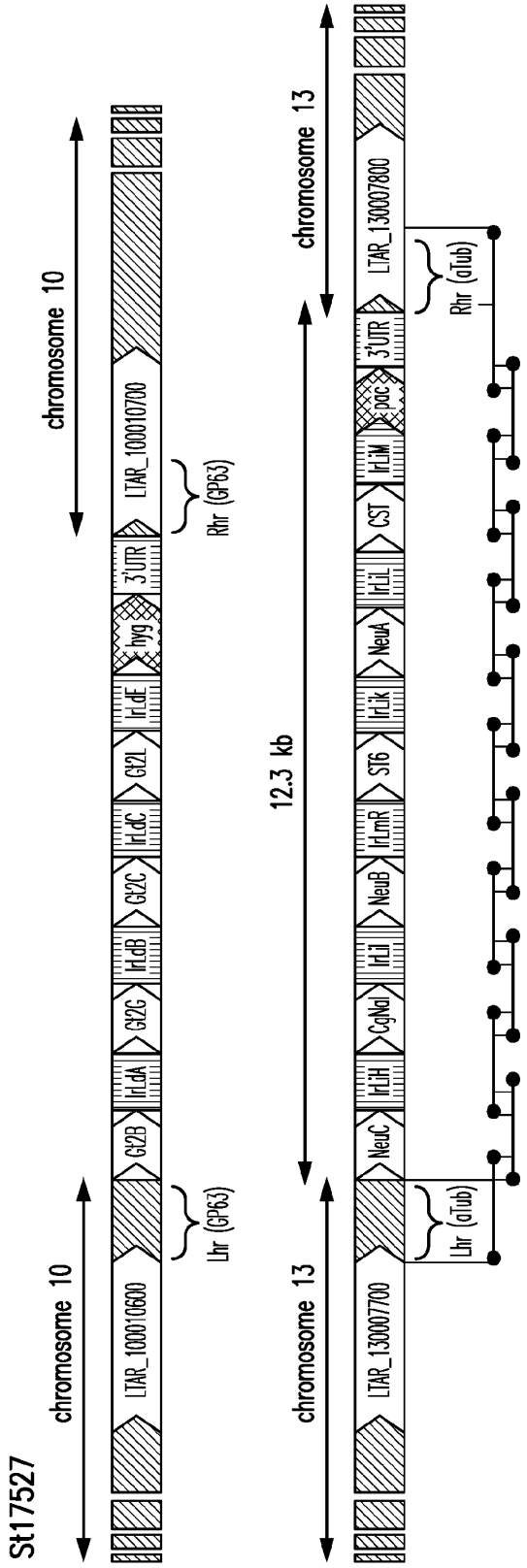
St17527
chromosome 10
chromosome 10
LTAR_100010600
Lhr (GP63)
Gt2B
IrLdA
Gt2G
IrLdB
Gt2C
IrLdC
Gt2L
IrLdE
hyg
3'UTR
LTAR_100010700
Rhr (GP63)
12.3 kb
chromosome 13
chromosome 13
LTAR_130007700
Lhr (aTub)
NeuC
IrLiH
CgNal
IrLi
NeuB
IrLmR
ST6
IrLik
NeuA
IrLiL
CST
IrLiM
pac
3'UTR
LTAR_130007800
Rhr (aTub)

FIG. 8A

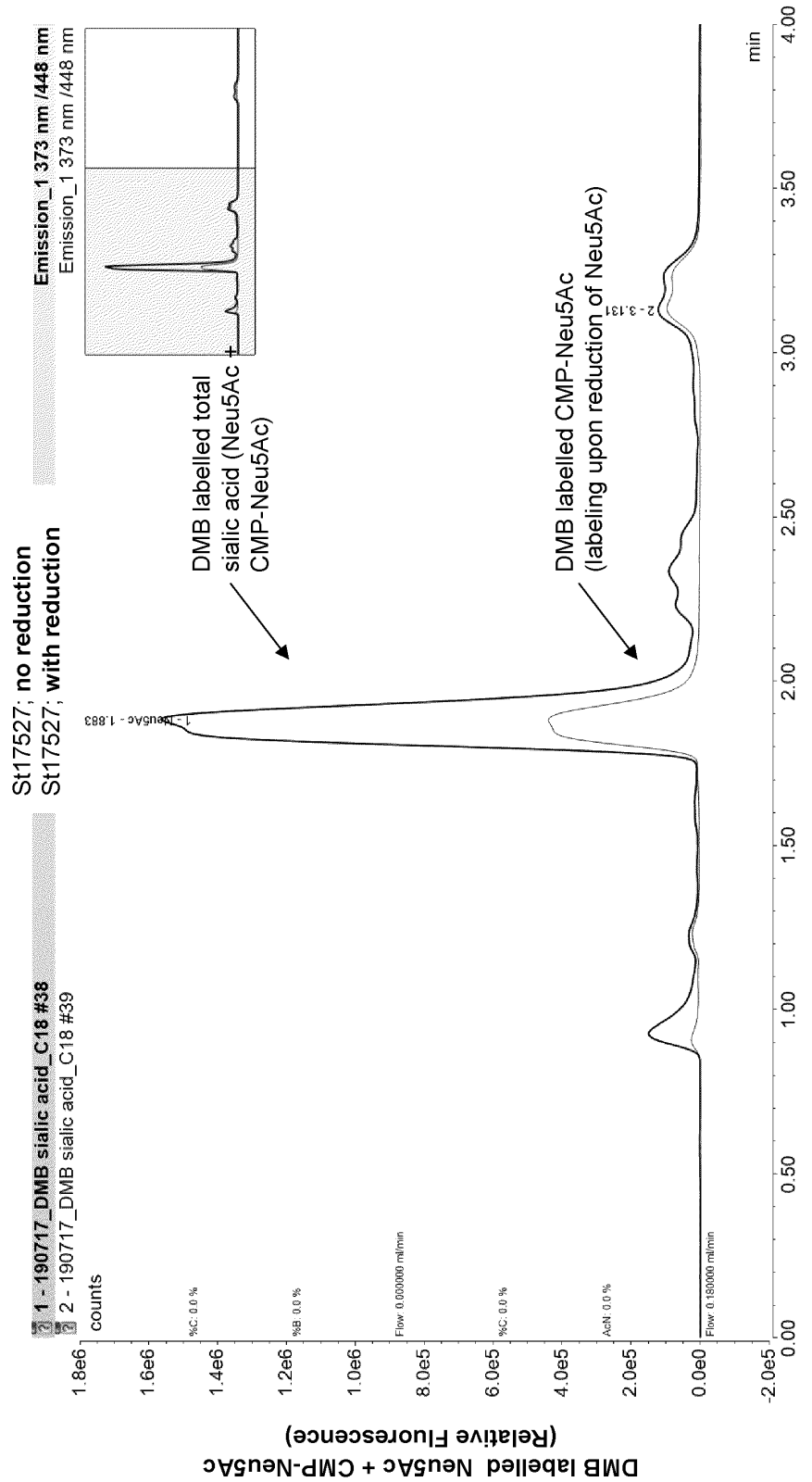
St17527; no reduction
St17527; with reduction
1 - 190717_DMB sialic acid_C18 #38
2 - 190717_DMB sialic acid_C18 #39
counts
Emission_1 373 nm /448 nm
Emission_1 373 nm /448 nm
DMB labelled total
sialic acid (Neu5Ac
CMP-Neu5Ac)
DMB labelled CMP-Neu5Ac
(labeling upon reduction of Neu5Ac)
1 - Neu5Ac - 1.883
2 - 3.131
%C 0.0 %
%B 0.0 %
Flow 0.000000 ml/min
%C 0.0 %
AcN 0.0 %
Flow 0.180000 ml/min
1.8e6
1.6e6
1.4e6
1.2e6
1.0e6
8.0e5
6.0e5
4.0e5
2.0e5
0.0e0
-2.0e5
0.00
0.50
1.00
1.50
2.00
2.50
3.00
3.50
4.00
min
DMB labelled Neu5Ac + CMP-Neu5Ac
(Relative Fluorescence)

FIG. 8B

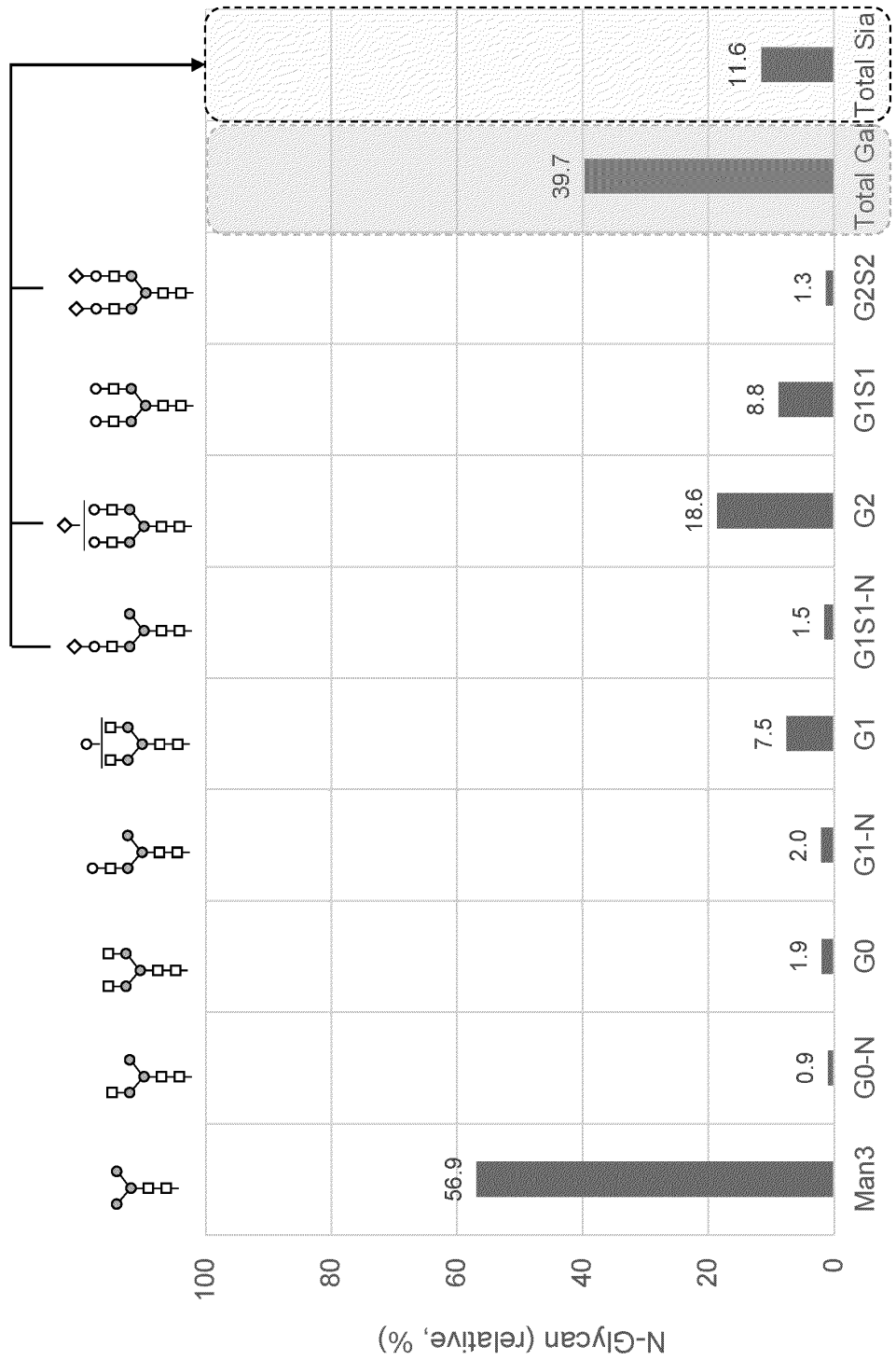
N-Glycan (relative, %)
0
20
40
60
80
100
Man3
G0-N
G0
G1-N
G1
G1S1-N
G2
G1S1
G2S2
Total Gal
Total Sia
56.9
0.9
1.9
2.0
7.5
1.5
18.6
8.8
1.3
39.7
11.6
St17527

FIG. 8C

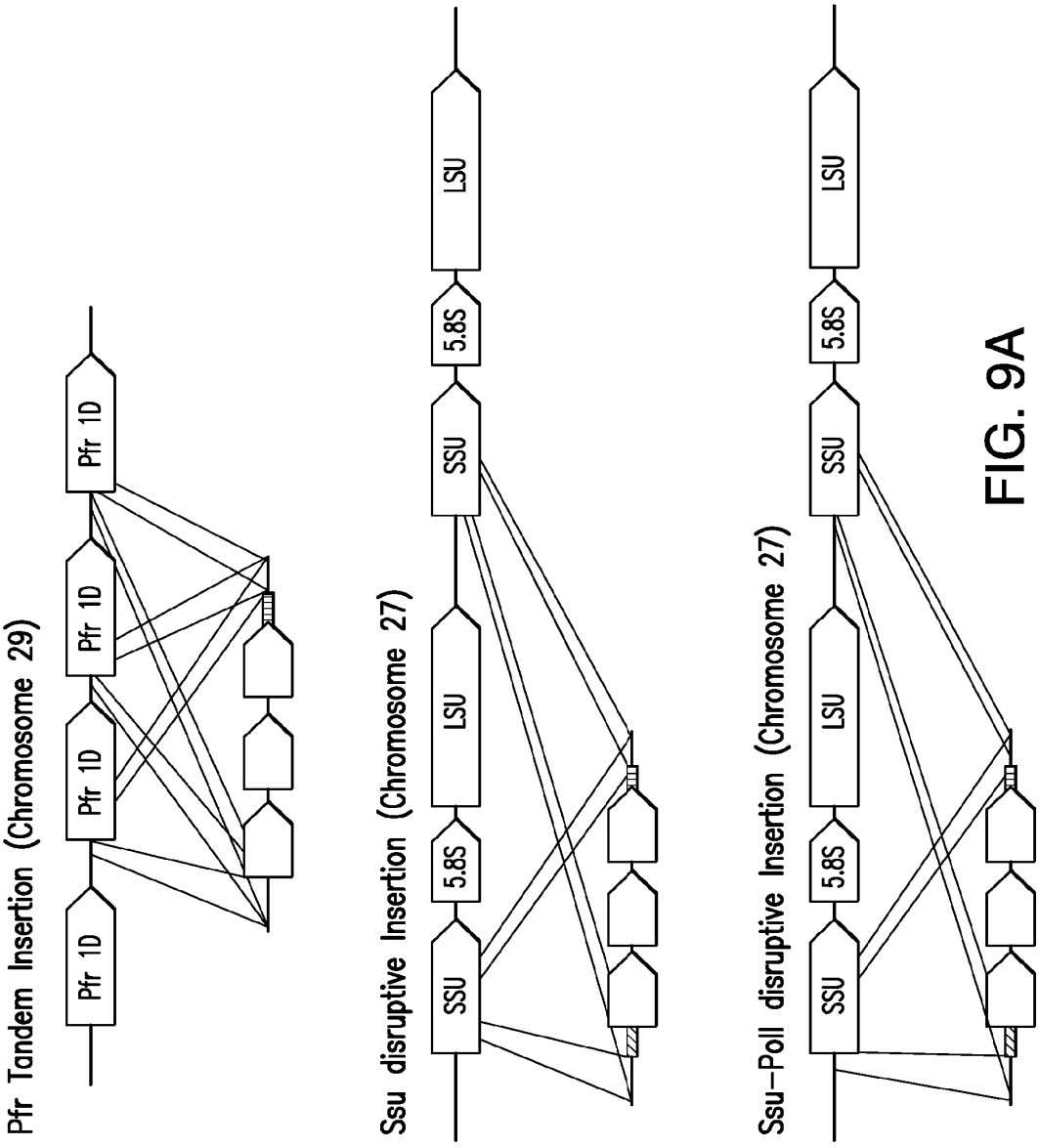
Pfr Tandem Insertion (Chromosome 29)
Pfr 1D
Pfr 1D
Pfr 1D
Pfr 1D
Ssu disruptive Insertion (Chromosome 27)
SSU
5.8S
LSU
SSU
5.8S
LSU
Ssu–Poll disruptive Insertion (Chromosome 27)
SSU
5.8S
LSU
SSU
5.8S
LSU

FIG. 9A

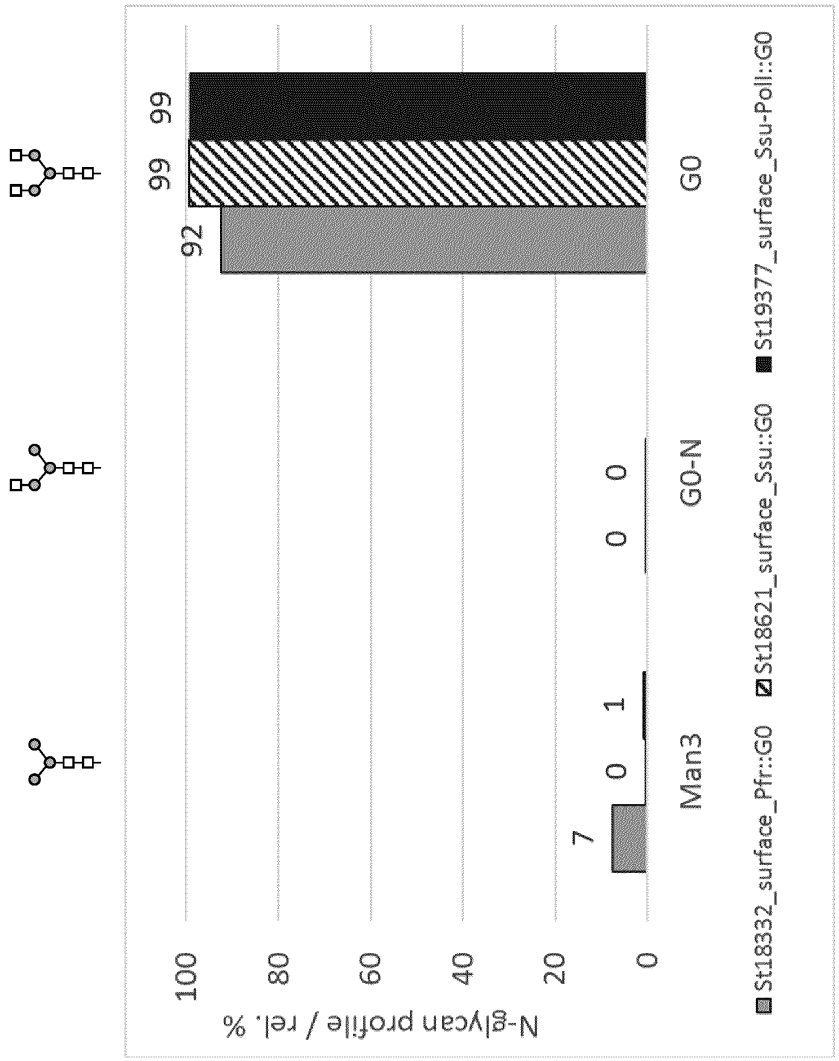
N-glycan profile / rel. %
100
80
60
40
20
0
7
0
1
0
0
0
92
99
99
Man3
G0-N
G0
St18332_surface_Pfr::G0
St18621_surface_Ssu::G0
St19377_surface_Ssu-PolI::G0

FIG. 9B

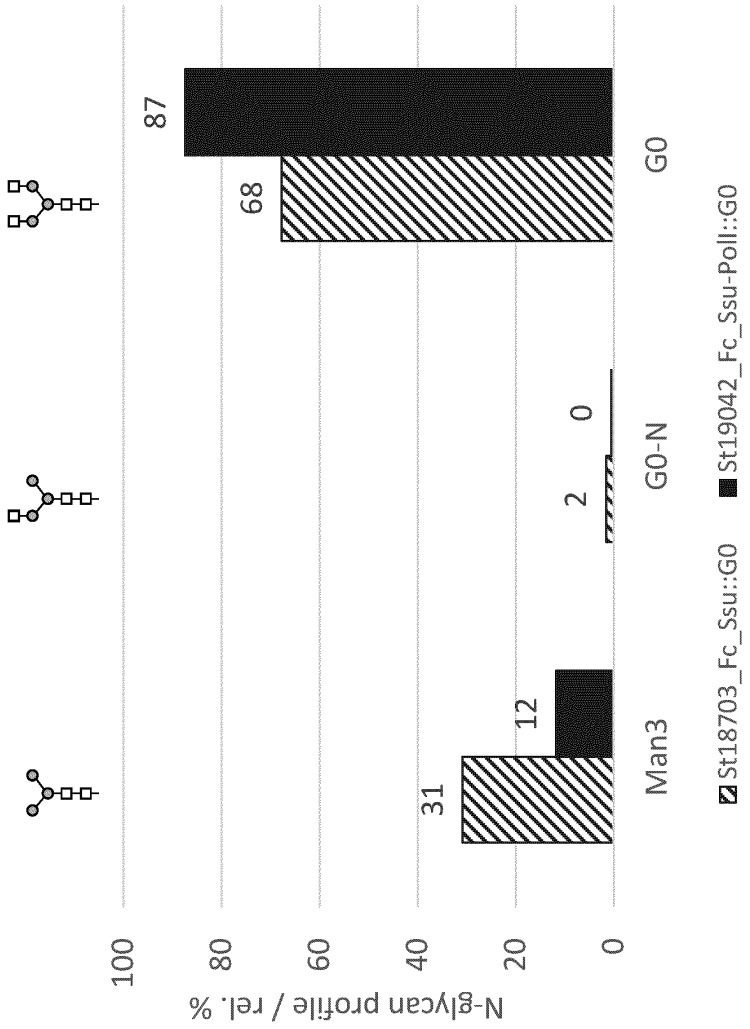
N-glycan profile / rel. %
100
80
60
40
20
0
87
68
2
0
12
31
Man3
G0-N
G0
St18703_Fc_Ssu::G0
St19042_Fc_Ssu-PoII::G0

FIG. 9C

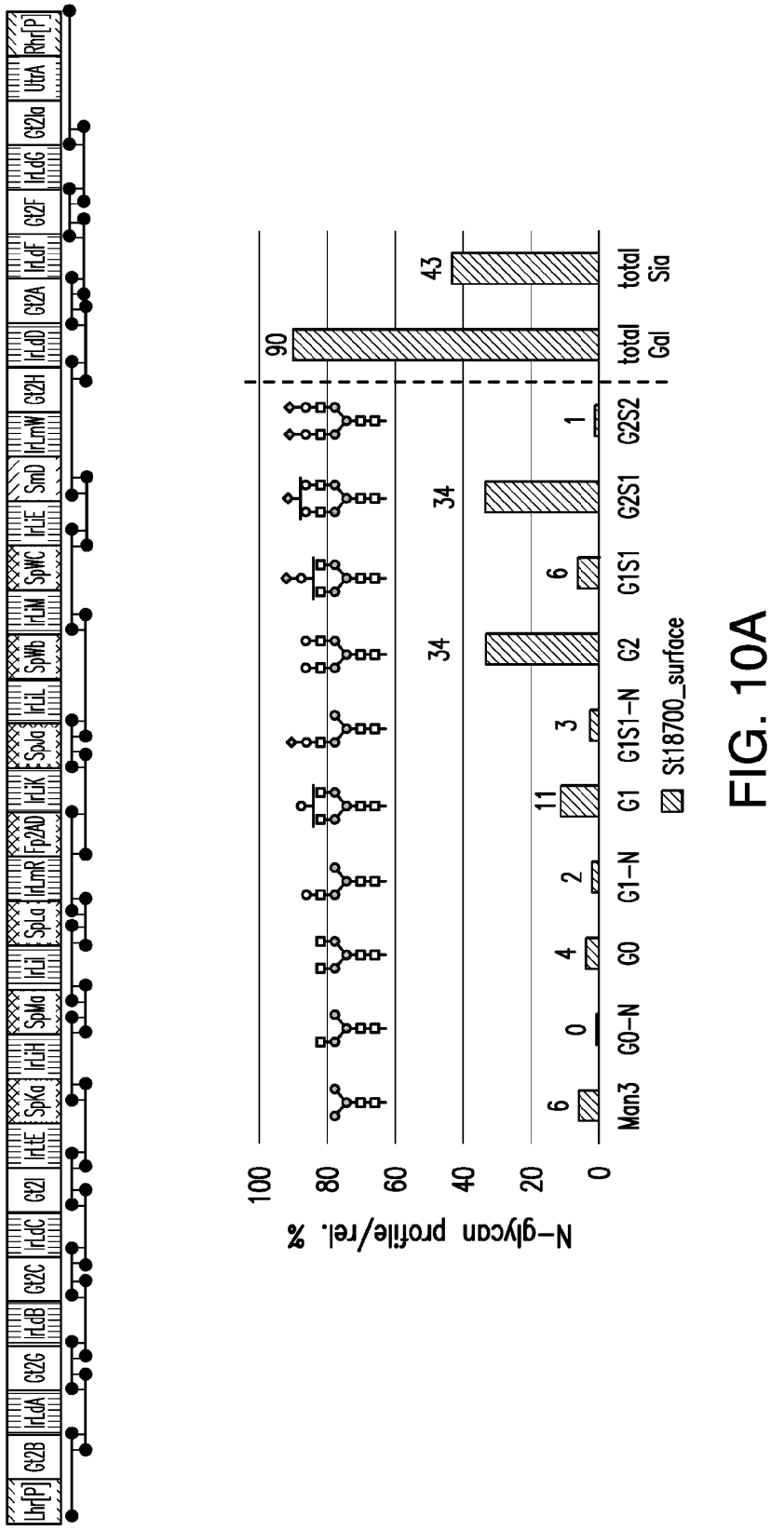
LhnP1
GI2B
IrLdA
GI2G
IrLdB
GI2C
IrLdC
GI2I
IrLtE
SpKa1
IrLiH
SpMa
IrLiJ
SpLa
IrLmR
Fp2AD
IrLiK
SpLa3
IrLiL
SpWb
IrLiM
SpWC
IrLiE
SmD
IrLmW
GI2H
IrLdD
GI2A
IrLdF
GI2F
IrLdG
GI2la
UtrA
RhrP1
N-glycan profile/rel. %
100
80
60
40
20
0
6
0
4
2
11
3
34
6
34
1
90
43
Man3
G0-N
G0
G1-N
G1
G1S1-N
G2
G1S1
G2S1
G2S2
total
Gal
total
Sia
St18700_surface

FIG. 10A

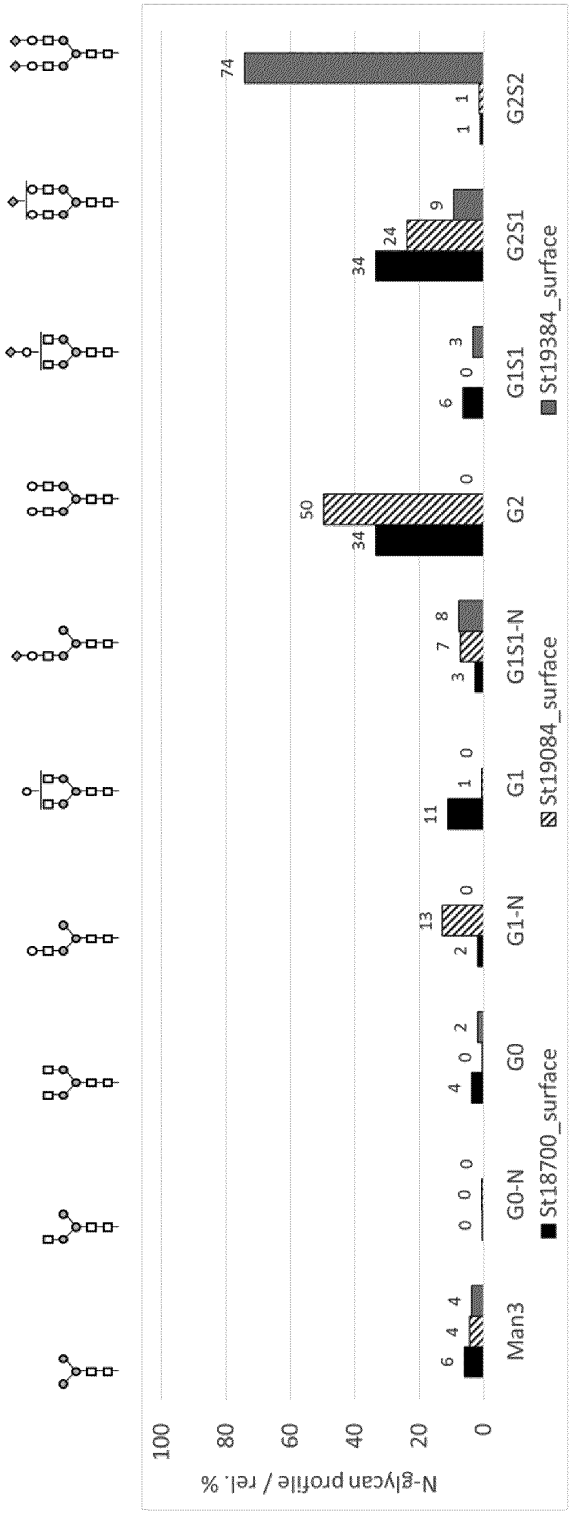
N-glycan profile / rel. %
0
20
40
60
80
100
Man3
G0-N
G0
G1-N
G1
G1S1-N
G2
G1S1
G2S1
G2S2
St18700_surface
St19084_surface
St19384_surface
6 4 4
0 0 0
4 0 2
2 13 0
11 1 0
3 7 8
50 34 0
6 0 3
34 24 9
74 1 1

FIG. 10B

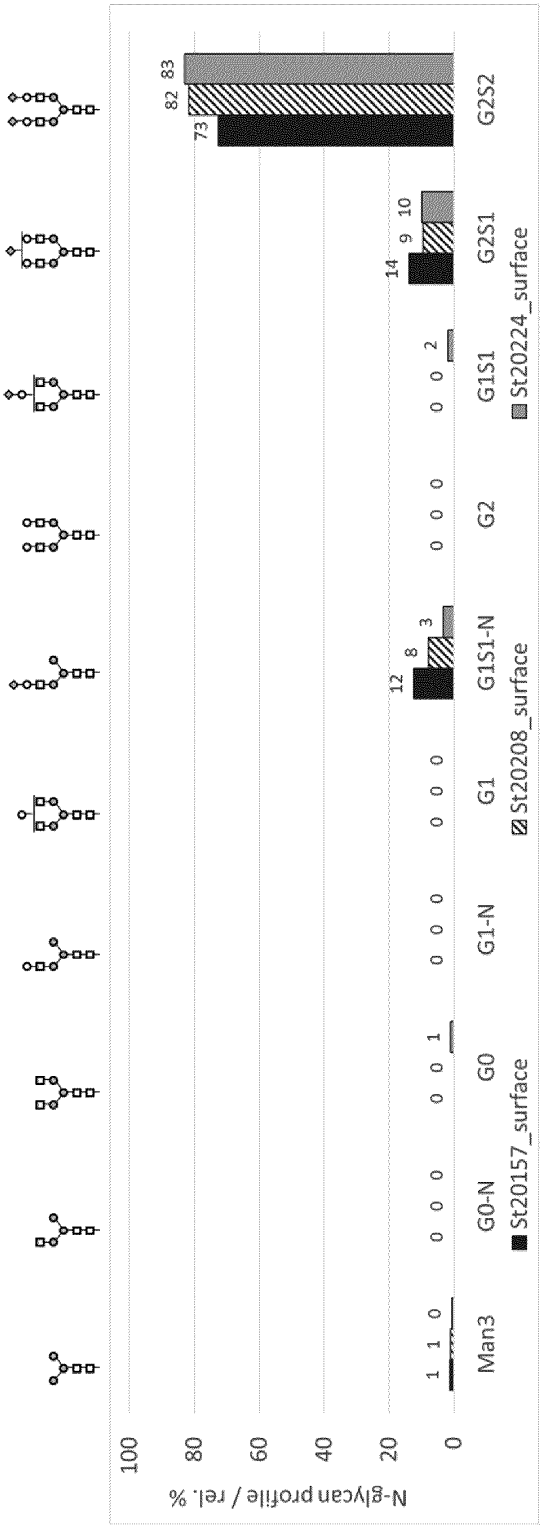
N-glycan profile / rel. %
100
80
60
40
20
0
1 1 0
0 0 0 0
0 0 1
0 0 0 0
0 0 0 0
12 8 3
0 0 0 0
0 0 2
14 9 10
73 82 83
Man3
G0-N
G0
G1-N
G1
G1S1-N
G2
G1S1
G2S1
G2S2
St20157_surface
St20208_surface
St20224_surface

FIG. 10C

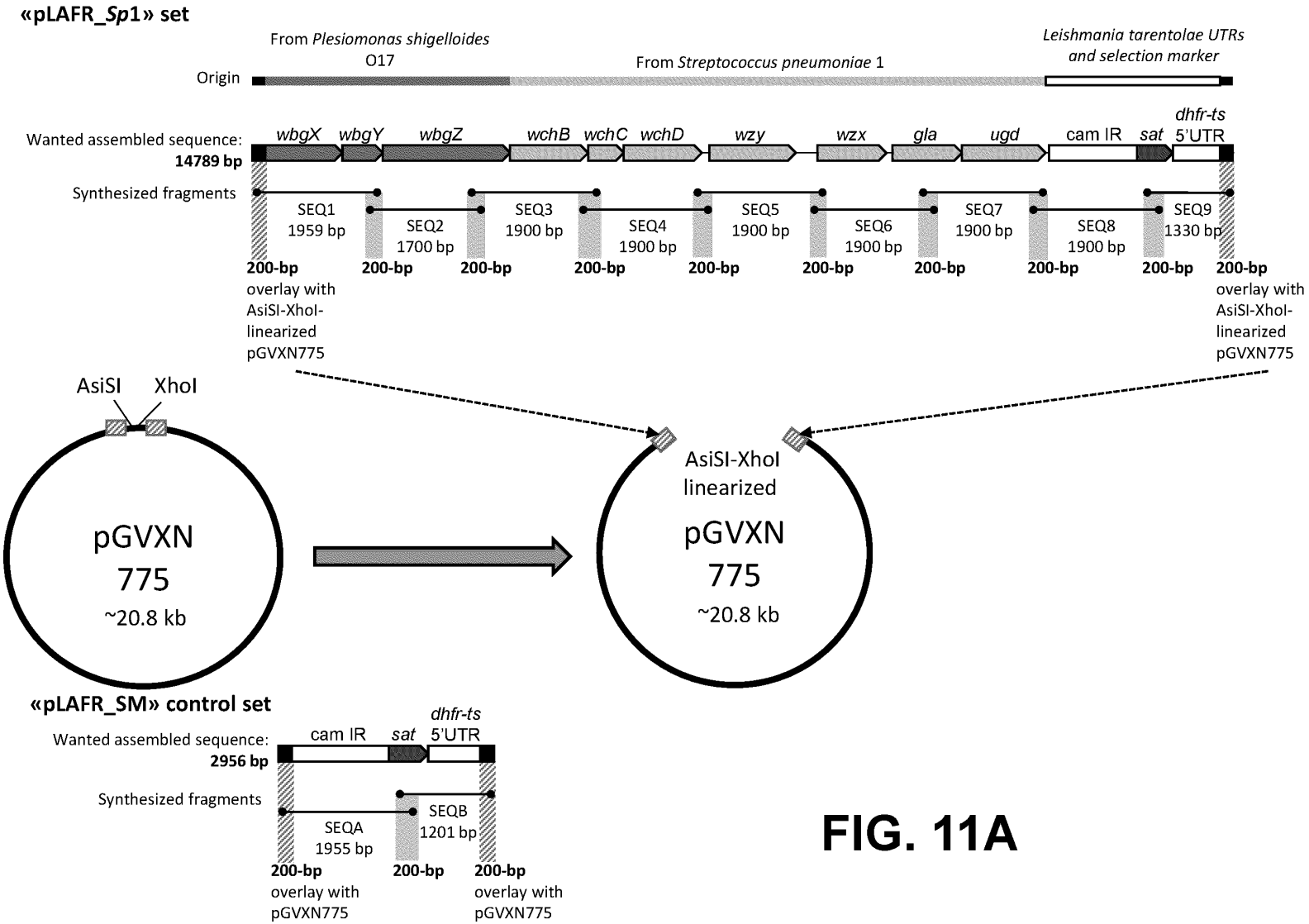
«pLAFR_Sp1» set
From Plesiomonas shigelloides O17
From Streptococcus pneumoniae 1
Leishmania tarentolae UTRs and selection marker
Origin
Wanted assembled sequence:
14789 bp
wbgX wbgY wbgZ wchB wchC wchD wzy wzx gla ugd cam IR sat dhfr-ts 5'UTR
Synthesized fragments
SEQ1 1959 bp
SEQ2 1700 bp
SEQ3 1900 bp
SEQ4 1900 bp
SEQ5 1900 bp
SEQ6 1900 bp
SEQ7 1900 bp
SEQ8 1900 bp
SEQ9 1330 bp
200-bp overlay with AsiSI-XhoI-linearized pGVXN775
AsiSI
XhoI
pGVXN 775 ~20.8 kb
AsiSI-XhoI linearized
pGVXN 775 ~20.8 kb
«pLAFR_SM» control set
Wanted assembled sequence:
2956 bp
cam IR sat dhfr-ts 5'UTR
Synthesized fragments
SEQA 1955 bp
SEQB 1201 bp
200-bp overlay with pGVXN775

FIG. 11A

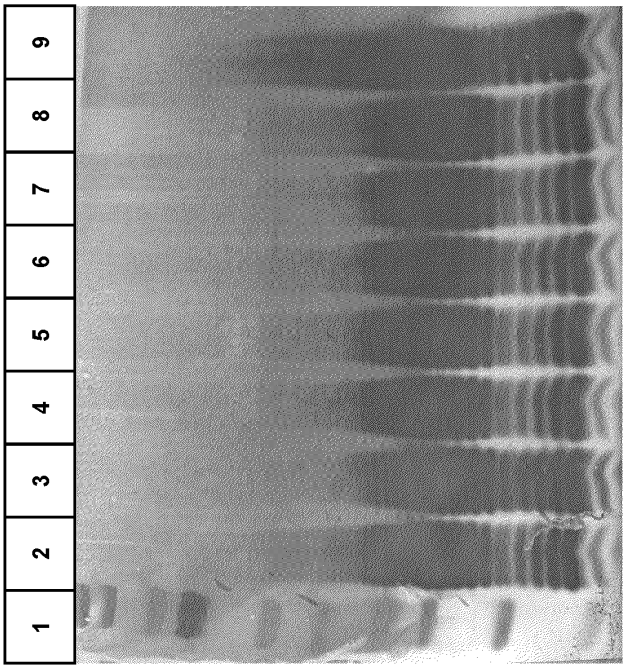

FIG. 11B

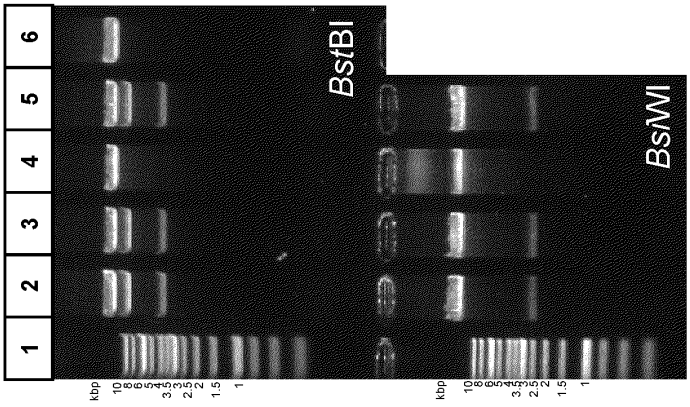

FIG. 11C

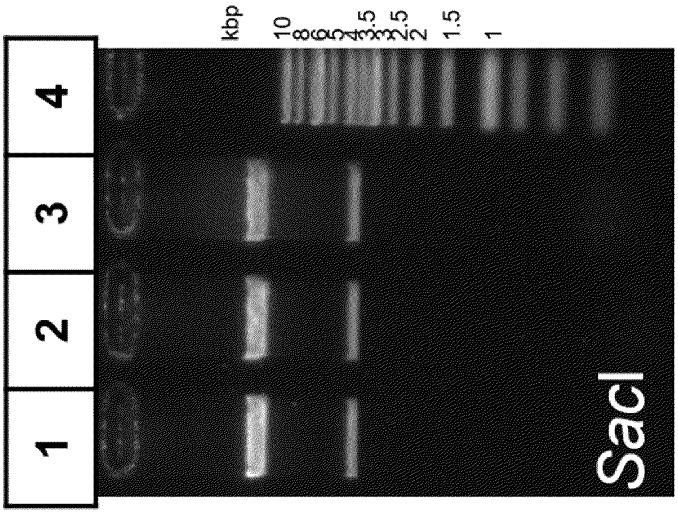

FIG. 11D