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(54) Title: GLYCOENGINEERING USING LEISHMANIA CELLS

(57) Abstract: The present application relates to *Leishmania* cells genetically engineered such that the formation of an O-linked GlcNAc on a polypeptide in the *Leishmania* cell is reduced or eliminated. The formation of the O-linked GlcNAc may be catalyzed in the *Leishmania* cell prior to said genetic engineering by at least one N-acetylglucosamine (GlcNAc)-transferase. Also provided herein are methods of making a polypeptide using a *Leishmania* cell described herein and polypeptides produced by the methods provided herein.

GLYCOENGINEERING USING LEISHMANIA CELLS

[0001] This application claims priority to U.S. Provisional Application No. 62/958,070, 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 "14197-010-228_SEQ_LISTING," was created on December 23, 2020, and is 1,350,529 bytes in size.

1. INTRODUCTION

[0003] The present application relates to *Leishmania* cells genetically engineered such that the formation of an O-linked GlcNAc on a polypeptide in the *Leishmania* cell is reduced or eliminated. The formation of the O-linked GlcNAc may be catalyzed in the *Leishmania* cell prior to said genetic engineering by at least one N-acetylglucosamine (GlcNAc)-transferase. 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] A glycoprotein is a glycoconjugate in which a protein carries one or more glycans covalently attached to a polypeptide backbone, usually via N- or O-linkages. An N-glycan (N-linked oligosaccharide, N-[Asn]-linked oligosaccharide) is a sugar chain covalently linked to an asparagine residue of a polypeptide chain, commonly involving a GlcNAc residue in eukaryotes, and the consensus peptide sequence: Asn-X-Ser/Thr (Varki, Ajit (2009): Essentials of glycobiology. 2ed. Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory Press).

[0005] O-glycosylation is one of the most abundant and diverse types of post-translational modifications of proteins. O-glycans modulate the structure, stability, and function of proteins and serve generalized as well as highly specific roles in most biological processes. In eukaryotes, all types of O-glycosylation are initiated by distinct polypeptide glycosyltransferases, and most glycans are further elongated/branched and capped in the Golgi by sequential addition of monosaccharides directed by distinct and/or common enzymes. An O-glycan (O-linked oligosaccharide) in vertebrates is frequently linked to the polypeptide via N-acetylgalactosamine (GalNAc) to a hydroxyl group of a serine or threonine

residue and can be extended into different structural core classes (Joshi, Hiren J et al (2018) Cell 172 (3), 632-632.e2).

[0006] Mucin-type O-glycosylation is a post-translational modification (PTM) that is predicted to occur in more than the 80% of the proteins that pass through the Golgi apparatus. This PTM is initiated by a family of polypeptide GalNAc-transferases (GalNAc-Ts) that modify Ser and Thr residues of proteins through the addition of a GalNAc moiety (Las Rivas, et al. (2019) In *Current opinion in structural biology* 56, pp. 87–96). A mucin is a large glycoprotein that carries many O-glycans that are clustered (closely spaced). Several other types of O-glycans also exist (e.g., O-linked fucose, glucose, or mannose) (Varki, Ajit (2009): Essentials of glycobiology. 2. ed. Cold Spring Harbor, N.Y.: Cold Spring Harbor Laboratory Press; Varki, Ajit, et al. (Eds.) (2015): Essentials of Glycobiology. Cold Spring Harbor Laboratory Press. 3rd. Cold Spring Harbor (NY)).

[0007] O-glycosylation is a frequent posttranslational modification but its control in the expression of therapeutic biologics has been challenging. Knockout of glycosylation genes to eliminate unwanted glycans has long been in the strategy to achieve clean expression hosts (Varki, Ajit, et al. (Eds.) (2015): Essentials of Glycobiology. Cold Spring Harbor Laboratory Press. 3rd. Cold Spring Harbor (NY)).

[0008] But engineering O-GalNAc glycans is challenging because up to 20 polypeptide GalNAc-transferases may synthesize O-GalNAc glycans. The result is that a protein that is naturally found with an O-glycan may not be O-glycosylated when expressed in a specific production cell line, and vice versa (Varki, Ajit, et al. (Eds.) (2015): Essentials of Glycobiology. Cold Spring Harbor Laboratory Press. 3rd. Cold Spring Harbor (NY)). Several examples show the problem:

[0009] Expression of human O-glycoproteins in yeast may result in O-mannosylation at sites that carry O-GalNAc in mammals. Examples of this include the hinge region of Ig and mucin sequences (Varki, Ajit, et al. (Eds.) (2015): Essentials of Glycobiology. Cold Spring Harbor Laboratory Press. 3rd. Cold Spring Harbor (NY)). In general, yeasts and fungi will exclusively perform O-mannosylation. Furthermore, yeast-type O-glycans are structurally different from human-type O-glycans, introducing concerns about the immunogenicity of O-glycosylated biopharmaceuticals produced by yeast. To address these problems, probably the most efficient manner is to change the sequence of the protein to avoid yeast-type O-glycans altogether. However, as the consensus sequence is rather unpredictable, this strategy depends on the ability to experimentally determine the sites of O-glycosylation, a less than trivial task. As yeast need O-glycosylated proteins to maintain their cell wall integrity and fitness,

deletion mutants have proven not to be the solution to the problem (Wachter, Charlot de;, et al. (2018) Advances in biochemical engineering/biotechnology. DOI: 10.1007/10_2018_69).

[0010] Plants do not have the types of O-glycosylation found in other eukaryotes, but produce unique O-glycans. O-glycosylation of plants and mammals is fundamentally different. In plants, serine residues from extensins and other members of the hydroxyproline-rich glyco-protein family can be glycosylated with a single galactose (Schoberer, Jennifer; Strasser, Richard (2017) Seminars in cell & developmental biology. DOI: 10.1016/j.semcdb.2017.07.005). In plants, the main anchor for O-glycosylation is 4-trans-hydroxyproline (Hyp). Indeed, undesired plant-typical prolyl-hydroxylation and in some cases subsequent arabinosylation of biopharmaceuticals was reported. Non-human prolyl-hydroxylation does not only alter the native sequence of the protein, but also serves as anchor for O-glycans, which in turn may be immunogenic. Plant-derived rhEPO from moss and *Nicotiana benthamiana* was shown to be hydroxylated within the motif SPP (amino acids 147–149). A targeted knockout of P4H1, the gene for non-human prolyl-hydroxylation of human erythropoietin recombinantly produced in *Physcomitrella patens*, eliminated the attachment of plantspecific O-glycosylation on rhEPO (Parsons, Juliana; et al. (2013) Scientific reports 3, p. 3019. DOI: 10.1038/srep03019). Although a number of the glycosyltransferases have been knocked out in different plants, no completely clean O-glycosylation free plant system has been achieved. And only if issues related to hydroxyproline can be resolved, plants would offer a suitable system in which different types of mammalian O-glycosylation can be engineered and exploited. It is unclear whether these modifications can be completely eliminated without affecting viability (Varki, Ajit, et al. (Eds.) (2015): Essentials of Glycobiology. Cold Spring Harbor Laboratory Press. 3rd. Cold Spring Harbor (NY)).

[0011] Insect cells perform similar range of O-glycosylation as mammalian cells, although the extent to which O-GalNAc glycans are attached at the same sites as in mammals is unexplored. Moreover, the degree of processing of O-glycans appears incomplete, at least using baculovirus expression (Varki, Ajit, et al. (Eds.) (2015): Essentials of Glycobiology. Cold Spring Harbor Laboratory Press. 3rd. Cold Spring Harbor (NY)). O-glycans with a GalNAc directly attached to the amino acid are referred to as mucin type O-glycans and are the most prevalent O-glycans in Drosophila embryos, constituting about 90% of total O-glycan profile (Li, Weidong, et al. (2019) Glycoconjugate journal. DOI: 10.1007/s10719-019-09867-1).

[0012] Mammalian cells perform many different types of O-glycosylation, and these exert diverse and important biological functions. Recombinant coagulation factors in clinical use carry O-GalNAc, O-Fuc, and/or O-Glc glycans, and many other approved drugs including erythropoietin and Enbrel have O-GalNAc type glycans (Varki, Ajit, et al. (Eds.) (2015): Essentials of Glycobiology. Cold Spring Harbor Laboratory Press. 3rd. Cold Spring Harbor (NY)).

[0013] Importantly, recent reports along with the development of high-end analytical tools point out the observations of diverse unwanted and/or elevated O-glycosylation in therapeutic proteins, some of them already approved (Hashii et al. (2019) Biologicals : journal of the International Association of Biological Standardization. DOI: 10.1016/j.biologicals.2019.01.005; Plomp et al. (2015) Mol Cell Proteomics 14 (5), pp. 1373–1384; Berlec and Strukelj (2013) J Ind Microbiol Biotechnol 40 (3-4), pp. 257–274.; Spahr, et al. (2013) Protein science : a publication of the Protein Society 22 (12), pp. 1739–1753. DOI: 10.1002/pro.2373; Spahr, et al (2014) mAbs 6 (4), pp. 904–914; Stavenhagen et al. (2019) mAbs 11 (6), pp. 1053–1063; Wen, et al (2013) Analytical chemistry 85 (9), pp. 4805–4812; Zhong, et al. (2013) The Journal Of Biological Chemistry 288 (2), pp. 1409–1419).

[0014] Provided in this application is a recombinant expression host that allows controlling O-glycosylation. The strategy is based on CustomGlycan *Leishmania* cell lines that are not capable of O-glycosylating proteins due to deletion of the native polypeptide GlcNAc-transferases while remaining fit and not suffering from any other phenotypic impact observed with other species. The technology provides a solution to express therapeutic proteins that should not be O-glycosylated, as undesired O-glycosylation in recombinantly expressed proteins appears to be a challenge in many cases. Modification control further increases product homogeneity and ensures product consistency and consequently leads to less risk of unwanted immune reactions when delivered to subjects.

[0015] The application describes O-glycosylation deficient *Leishmania* host cells for producing consistent therapeutic protein modalities where the absence of O-glycosylation is required and further avoids unwanted O-glycosylation of susceptible protein regions. O-glycosylation was identified and characterized as O-GlcNAc. This also provides the outlook of attaching relevant glycans onto O-GlcNAc in *Leishmania* host cells within the CustomGlycan Platform (International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein).

3. SUMMARY OF THE INVENTION

[0016] Provided herein are *Leishmania* cells, methods of making a polypeptide using a *Leishmania* cell, and polypeptides produced by the methods.

[0017] In one aspect, provided herein is a *Leishmania* cell genetically engineered such that the formation of an O-linked GlcNAc on a polypeptide in the *Leishmania* cell is reduced or eliminated.

[0018] In certain embodiments, the formation of O-linked GlcNAc in the *Leishmania* cell prior to genetic engineering is catalyzed by at least one N-acetylglucosamine (GlcNAc)-transferase.

[0019] In certain embodiments, the gene encoding the at least one GlcNAc-transferase is functionally inactivated. In certain embodiments, the gene encoding the at least one GlcNAc-transferase is downregulated. In certain embodiments, the gene encoding the at least one GlcNAc-transferase is deleted or mutated. In certain embodiments, the gene encoding the at least one GlcNAc-transferase is overexpressed.

[0020] In certain embodiments, the formation of the O-linked GlcNAc is reduced by at least 5%, 7%, 10%, 12%, 15%, 18%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% from the formation of the O-linked GlcNAc in a reference *Leishmania* cell.

[0021] In certain embodiments, the at least one GlcNAc-transferase is selected from the group consisting of OGNT1, OGNT2 and OGNTL, and homologous GlcNAc-transferases thereof. In certain embodiments, the at least one GlcNAc-transferase is a GlcNAc-transferase that is homologous to OGNT1, OGNT2 and/or OGNTL. In certain embodiments, the of the at least one GlcNAc-transferase is one, two or three.

[0022] In certain embodiments, the growth rate of the *Leishmania* cell is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of the growth rate of a reference *Leishmania* cell.

[0023] In certain embodiments, the cell is *Leishmania tarentolae*.

[0024] In certain embodiments, the polypeptide is selected from the group consisting of adalimumab, rituximab and erythropoietin (EPO).

[0025] In certain embodiments, the *Leishmania* cell comprises a recombinant nucleic acid encoding a heterologous glycosyltransferase. In certain embodiments, the heterologous glycosyltranferase is an N-acetyl glucosamine transferase; and/or a heterologous galactosyltransferase; and/or a heterologous sialyltransferase. In certain embodiments, the

Leishmania cell comprises one or more heterologous glycosyltransferases. In certain embodiments, the *Leishmania* cell comprises one or more N-acetyl glucosamine transferases; and/or one or more heterologous galactosyltransferases; and/or one or more heterologous sialyltransferases.

[0026] 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.

[0027] In yet another aspect, provided herein is a polypeptide produced by the method provided herein.

3.1 Definitions

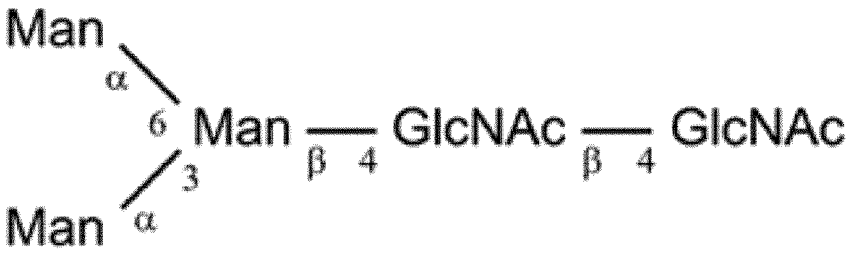
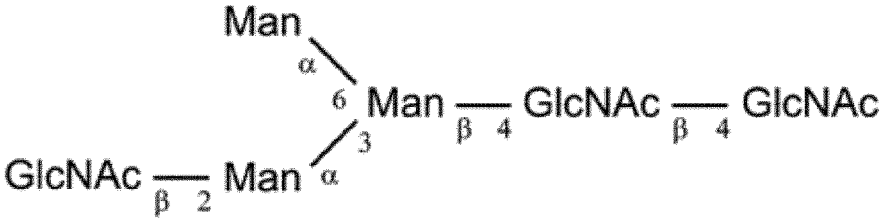
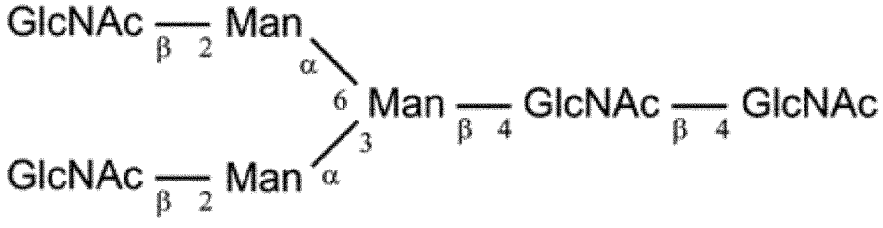
[0028] As used herein and unless otherwise indicated, the term "about," when used in conjunction with a number, refers to any number within ±1, ±5 or ±10% of the referenced number.

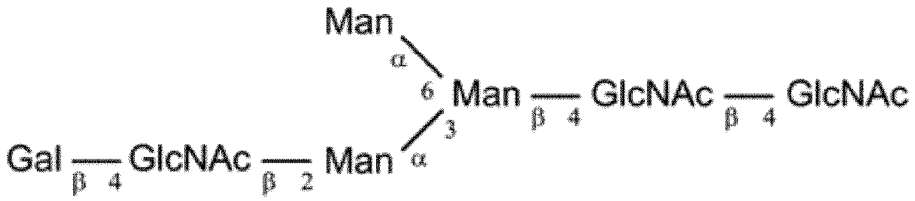
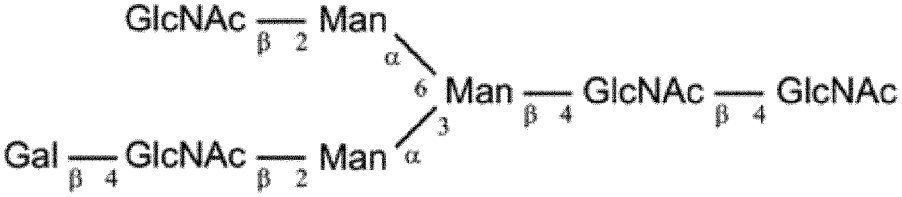
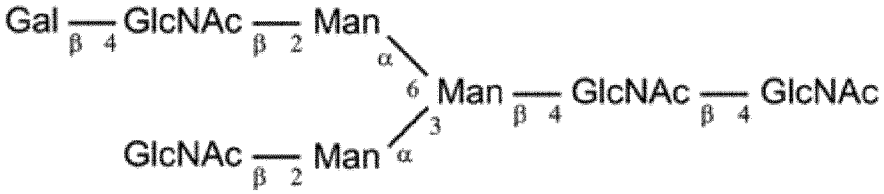
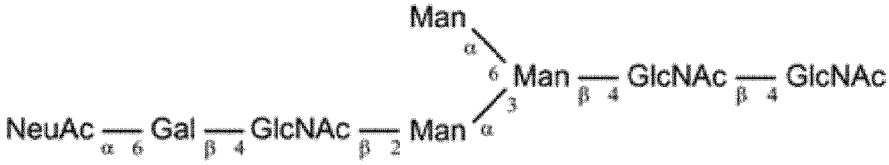
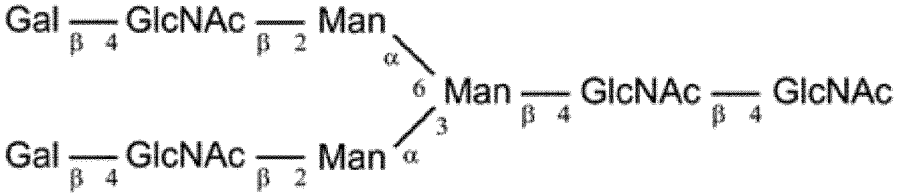
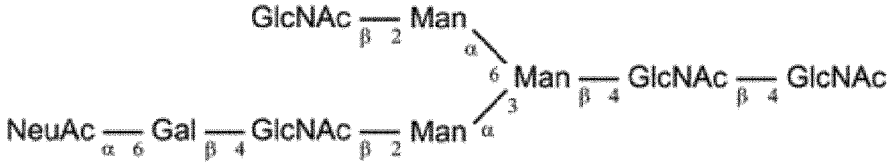
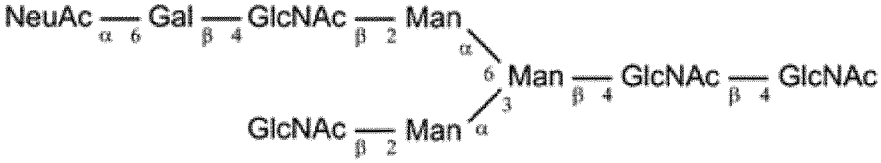
[0029] As used herein and unless otherwise indicated, the term "subject" refers to an animal (*e.g.*, birds, reptiles, and mammals). In another embodiment, a subject is a mammal including a non-primate (*e.g.*, a camel, donkey, zebra, cow, pig, horse, goat, sheep, cat, dog, rat, and mouse) and a primate (*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.

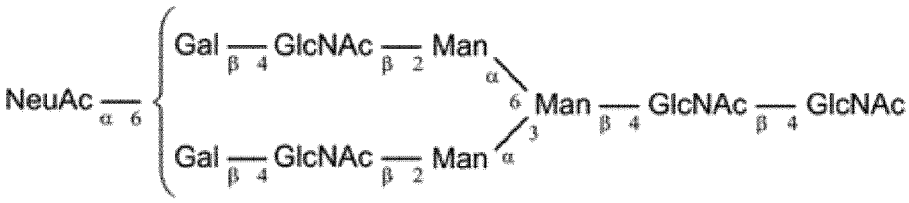
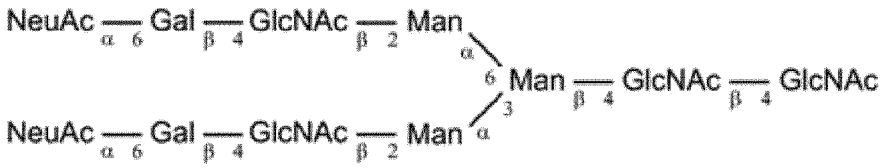
[0030] As used herein and unless otherwise indicated, the term "effective amount," in the context of administering a therapy (*e.g.*, a composition described herein) to a subject refers to the amount of a therapy which has a prophylactic and/or therapeutic effect(s). In certain embodiments, an "effective 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
CDS	Coding sequence
EPO	Erythropoietin
GlcNAc-transferase	N-acetylglucosamine-transferase
IR	Intergenic region
GalNAc	N-acetylgalactosamine
Fuc	Fucose
Glc	Glucose
GlcNAc	N-acetylglucosamine
HexNAc	N-acetylhexosamines
OGT or OGNT	O-glycosyltransferase
ORF	Open reading frames
UTR	Untranslated region
Man3	
G0-N	
G0	

Abbreviation	Convention
G1-N	
G1	 or 
G1S1-N	
G2	
G1S1	 or 

Abbreviation	Convention
G2S1	
G2S2	

4. BRIEF DESCRIPTION OF THE FIGURES

[0031] FIG. 1: An O-glycopeptide with the mass addition corresponding to one HexNAc was identified on recombinant Erythropoietin produced by the CustomGlycan host cells. Occupied glycopeptides in the enriched fractions are shown in acquired spectra both in reflectron positive (upper spectra R+) and linear positive (lower spectra L+) MALDI modes.

[0032] FIGs. 2A-2D: O-HexNAc is located at the Thr225 within the hinge region of CustomGlycan produced recombinant human IgG1 (FIG. 2A) Deconvoluted mass spectrum of intact mass measurement of full length antibody shows Adalimumab with two N-linked Man3 as the main species. Further, two forms are observed carrying additionally one or two HexNAc modifications (+203 Da). (FIG. 2B) Deconvoluted mass spectra for the two peaks observed in the intact mass measurement of the reduced Adalimumab sample showed the masses expected for the light chain (Peak A) and for the heavy chain + Man3 (Peak B). For the heavy chain peak, a form modified with a HexNAc (+203 Da) was also observed showing that the HexNAc modification is localized on the heavy chain. (FIG. 2C) Deconvoluted mass spectra of the Fd subunit derived from a IdeS digest confirmed the presence of the HexNAc (+203 Da) on the Fd part of the heavy chain. (FIG. 2D) The major glycosylation site for the HexNAc was confirmed to be localized on a Threonine N-terminal of the hinge region. The targeted peptide measurement of a tryptic digest using ETD fragmentation clearly confirmed the HexNAc on Thr225 by the presence of c- and z-ions origination from the break of the proximate peptide bonds.

[0033] FIGs. 3A-3B: High performance anion exchange chromatography coupled with pulsed amperometric detection (HPAEC-PAD) suggests GlcNAc being the monosaccharide in O-linked HexNAc containing Adalimumab. (FIG. 3A) An overlay of traces of HPAEC-

PAD runs of water blank, GlcNAc (black dotted), GalNAc (black dashed) and ManNAc (grey dashed) standards with buffer control (grey dotted), hydrolysis of Humira control (grey) and hydrolysis of Adalimumab carrying the O-HexNAc (black). One peak, indicated with a star, not present in buffer and Humira control was observed at RT 9.767 min, a bit shifted compared the GlcNAc standard (RT 9.95). (FIG. 3B) Overlay of traces of HPAEC-PAD runs of water blank, GlcNAc standard (black dotted), hydrolysis of Humira control (grey), hydrolysis of Adalimumab carrying the O-HexNAc (black), buffer control (grey dotted) and hydrolysis of Adalimumab carrying the O-HexNAc spiked with GlcNAc standard (black dashed). Spiking the GlcNAc standard into the sample matrix shifted the elution of GlcNAc slightly (RT 9.725), resulting in a match of RT between the O-HexNAc peak (Adalimumab, black) not present in the Humira control (grey) and the GlcNAc standard (black dotted).

[0034] FIGs. 4A-4C: Indicative pattern of oxonium ions in HCD MS/MS spectra support the presence of O-linked GlcNAc on Thr225 within recombinantly produced Adalimumab. (FIG. 4A) Pattern of the HexNAc oxonium ions in the MS/MS spectrum of the tryptic peptide (THTCPPCPAPELLGGPSVFLFPPKPK) (SEQ ID NO:227) carrying the O-HexNAc on Thr225 (m/z 762.641) from the HexNAc mAb sample (FIG. 4B) Intensity of the HexNAc oxonium ions in the MS/MS spectrum of the tryptic peptide (EEQYNSTYR) (SEQ ID NO:228) from the HexNAc mAb, carrying the N-glycan Man3, (FIG. 4C) Pattern of HexNAc oxonium ions of a tryptic peptide from CD43 (MoxYTTSITSDPK) (SEQ ID NO:229) carrying three GalNAc.

[0035] FIGs. 5A-5C: (FIG. 5A) Genomic location of three OGNT candidate genes in *Leishmania tarentolae* St10569. OGNT-2 (LTAR_170020900) is found on chromosome LTAR_17, OGNT-1 and OGNT-L (LTAR_020006800 and LTAR_020006900, respectively) is found on chromosome LTAR_2. Arrows denote directionality (5' to 3') of the genes. Double-headed arrows denote approximate distance to chromosome ends. (FIG. 5B) (FIG. 5C) OGNT homologues in other *Kinetoplastida*. *Kinetoplastida* genomes were downloaded from tritrypdb.org, *T. cruzi* OGNTs were used as reference query, the matches were tested by reciprocal best hits on *L. tarentolae* OGNTs. For each species, one representative isolate has been chosen and a total of 81 sequences were used to build a phylogenetic tree by multiple sequence alignment using T-coffee and the phylogenetic tree using RAxML. The phylogenetic relationship is depicted as rectangular tree (FIG. 5B) and radial tree (FIG. 5C).

[0036] FIG. 6: Schematic representation of genomic deletions of OGNT candidate genes. Lhr denotes left (upstream) homologous recombination sequence, Rhr denotes right (downstream) homologous recombination sequence. Light grey bars depict homologous

recombination events, replacing OGNT-2 with an intergenic region (IR), selection marker (SM), and IR (Variant A) or replacing OGNT-1 and OGNT-L by a selection marker only (Variant B). This results in an individual knockout of OGNT-2 and a double knockout of OGNT-1 and OGNT-L. Two fragments were used (depicted as line segments with 2 points at each end) to build the replacing fragment containing the selection marker. Variant C schematically demonstrates the replacement of OGNT-1 and OGNT-L by a functional construct for glycoengineering that contains 4 different enzymes (ORF1-ORF4) and a selection marker separated by intergenic regions (IR1-IR4).

[0037] FIGs. 7A-7B: OGNT deletion was verified by Illumina deep sequencing. Absence of reads matching to the respective OGNT region as displayed in the IGV genomics browser confirm the successful deletion of single OGNT genes in strains St16248, St16257 and St16249 (FIG. 7A) and a double knockout of OGNT-1 and OGNT-L in strain St16636 (FIG. 7B).

[0038] FIGs. 8A-8B: Confirmation of absence of O-HexNAc in a knock out (KO) cell line. (FIG. 8A) MALDI measurement of FabRICATOR (IdeS) and GingisKHAN (Kgp) double digest producing the 14 aa peptide THTCPPCPAPELLG (SEQ ID NO:230). For Adalimumab of the wt strain the peptide THTCPPCPAPELLG (SEQ ID NO:230) with and without HexNAc modification was observed (Na-adduct), for the triple KO cell line expressed Adalimumab only the THTCPPCPAPELLG (SEQ ID NO:230) peptide without an O-HexNAc modification was found. Marked sodium adducts of peptide with and without O-HexNAc are indicated. (FIG. 8B) The THTCPPCPAPELLGGPSVFLFPPKPK (SEQ ID NO:227) peptide (+ 2*carbamidomethylation) without O-HexNAc modification was found with high abundance in the triple OGNT knock out CustomGlycan host cells, the THTCPPCPAPELLGGPSVFLFPPKPK (SEQ ID NO:227) peptide (+ 2*carbamidomethylation) with O-HexNAc modification could not be confirmed. The selected ion chromatogram (SIC) for the peptide with and without O-HexNAc (+ 2*carbamidomethylation) are shown in duplicates.

[0039] FIGs. 9A-9D: Modification of OGNT levels has no phenotypic impact on N-glycoengineered CustomGlycan *Leishmania* host cells. (FIG. 9A) N-glycan engineering up to G0 in the absence and presence of OGNT-1 overexpression. Relative N-glycan profiles of Adalimumab purified from a strain (St16292) co-expressing constructs for OGNT-1 overexpression («OE») and N-glycan engineering on Adalimumab («Adalimumab G0 OGNT-1 OE») and the parental glycoengineering strain (St15882, «Adalimumab G0») demonstrate that overexpression of OGNT1 has no effect on N-glycan engineering. (FIG. 9B)

N-glycan engineering up to G0 in wt or OGNT triple knock-out background. Relative N-glycan profiles of Adalimumab purified from a glycoengineering strain mediating conversion up to G0 in wt background (St17607, «Adalimumab-G0») and upon knock-out of all three OGNT genes (St17863, "Adalimumab-G0, OGNT-1/2/L KO") demonstrate that knock-out of OGNTs has no effect on N-glycan engineering. (FIG. 9C) N-glycan engineering up to G2 in the wt or OGNT triple knock-out background. Relative N-glycan profiles of Adalimumab purified from a glycoengineering strain mediating conversion up to G2 in wt background (St15451, "Adalimumab-G2") and upon knock-out of all three OGNT genes (St17318, "Adalimumab-G2, OGNT-1/2/L KO") demonstrate that knock-out of OGNTs has no effect on N-glycan extension up to G2. (FIG. 9D) Representative PCR control for OGNT-2 replacement by selection marker (left) covers the whole endogenous locus by amplification with primers oLMTB6043 and oLMTB6044. It results for the wild type (wt) control in a fragment of 3.3 kbp, while the knock-out strains exhibit fragments of 2.2 kbp (exemplarily shown for clone St17317 from same transfection as St17318). Here in both cases, replacement was done by selection marker CDS without addition of IRs. Representative PCR control for OGNT-1+L replacement by selection marker (right) covers the whole endogenous locus by amplification with primers oLMTB6157 and oLMTB6156. It results for the wt control in a fragment of 8.1 kbp, while the knock-out strains exhibit fragments of 3.1 kbp for positive control St16704 where the CDS of the selection marker is flanked by additional IRs and 1.5 kbp for the analyzed strain St17317 where no extra IRs are used.

[0040] FIGs. 10A-10B: Replacement of OGNT genes by a glycosyltransferase expression cassette. (FIG. 10A) Relative N-glycan profile of Adalimumab purified from a strain (St17846) expressing a constructs for N-glycan engineering on Adalimumab from the endogenous OGNT-1/L locus. (FIG. 10B) PCR control for integration of the GT expression construct into the OGNT-1/L locus. Amplification with primers oLMTB4952 and oLMTB7163 does not result in a product in the wild type OGNT gene, but can amplify the 3' part of the correctly integrated construct between the selection marker hygromycin (hyg) and the 3' UTR of OGNT-L (2.4 kbp).

[0041] FIG. 11: Extracted ion chromatograms (XICs) of masses corresponding to unmodified (top panel; m/z 733.38) or O-HexNAc-modified (bottom panel; m/z 834.93) doubly charged tryptic peptides originating from LMSAP-rhEPO-Strep. The inset in the top panel shows the MS/MS fragmentation spectrum of the unmodified peptide [EAISPPDAASAAPLR] (SEQ ID NO:237). There was no evidence for the presence of

masses corresponding to the peptide carrying an O-HexNAc modification (represented by EAISPPDAASAAPLR+HexNAc) (SEQ ID NO:237 + HexNAc). (bottom panel).

[0042] FIGs. 12A-12E: ribonucleoprotein (RNP) mediated OGNT triple knock-outs in glycoengineering cell lines. (FIG. 12A) Schematic drawing of the transfection steps involved in the generation of strains St20097, St19855, St19931, St19915 and St19998, which are described in Example 9. Transfections are indicated by arrows and a short name of the transfected knock-out or construct is indicated in italics. (FIG. 12B) PCR control for the removal of WT OGNT-1, OGNT-2 and OGNT-L genes by transfection of RNPs. Primer pairs oLMTB7174/oLMTB7173 (probing for the endogenous sequence of OGNT-1), oLMTB7176/oLMTB7175 (probing for the endogenous sequence of OGNT-L) and oLMTB7492/oLMTB7495 (probing for the endogenous sequence of OGNT-2) produced amplicons of the proper sizes for WT gDNA from strain St18344, while no amplicon was obtained for St19855 derived gDNA or the technical control using H_2O instead of template DNA. (FIG. 12C) N-glycan engineering up to G0 before and after OGNT triple knock-out by RNP transfection. Relative N-glycan profiles of surface glycoproteins from parental glycoengineering strain St19462 and the derived OGNT knock-out strain St20097 demonstrate that overexpression of OGNT knock-out by RNP transfection has no effect on previously performed N-glycan engineering. (FIG. 12D) MALDI measurement of FabRICATOR (IdeS) and GingisKHAN (Kgp) double digest producing the 14 aa peptide THTCPPCPAPELLG (SEQ ID NO:230). After transfection of an Adalimumab expression construct into the triple KO cell line St19855, the expressed antibodies were analyzed for the presence of the O-HexNAc modification on the 14 aa peptide THTCPPCPAPELLG (SEQ ID NO:230). Only peptides without an O-HexNAc modification were detected. (FIG. 12E) N-glycan engineering after RNP mediated triple OGNT knock-out. Relative N-glycan profiles of Adalimumab (Fc) purified from the triple knock-out strain St19915 harboring the original 2 glycoengineering modules or the further modified triple knock-out strain St19998 containing in total 3 glycoengineering modules to G0 showed the desired improvement upon further glycoengineering. For St19915, 2% of other N-glycan biogenesis intermediates were detected (not shown).

5. DETAILED DESCRIPTION OF THE INVENTION

[0043] Provided herein are *Leishmania* cells, methods of making a target polypeptide using a *Leishmania* cell, and target polypeptides produced by the methods. In certain

embodiments, provided herein are *Leishmania* cells which have been modified to control O-glycosylation, such as reduction in O-glycosylation or deletion of O-glycans. These *Leishmania* cells can also produce homogeneous and fully function-customized N-glycans with a high site occupancy on recombinant therapeutic proteins by the properties of the host cell and the combination with the heterologous expression of a set of glycosyltransferases, including N-acetyl glucosamine transferases, galactosyltransferase, and sialyltransferases. For example, the *Leishmania* cells provided herein can be used within the CustomGlycan Platform (International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein). Also provided herein are nucleic acid sequences and methods, which can be used to delete or control O-glycosylation enzymes, for example O-glycosylation enzymes involved in N-acetyl glucosamine transfer to serine or threonine residues in polypeptides.

[0044] Provided herein is a *Leishmania* host cell in which a gene encoding an enzyme that catalyzes the formation of O-linked GlcNAc has been functionally inactivated. Such genes are described in Section 5.1. Methods for accomplishing such functional inactivation are described in Section 5.2. Properties of the resulting *Leishmania* cell are described in Section 5.3. Uses of such *Leishmania* cell as expression systems for, *e.g.*, therapeutic proteins are described in Section 5.4. Properties of the proteins expressed in *Leishmania* host cells provided herein are described in Section 5.5.

5.1 Enzyme that catalyzes the formation of O-linked GlcNAc

[0045] Provided herein is a *Leishmania* host cell genetically engineered such that the formation of an O-linked GlcNAc on a polypeptide in the *Leishmania* cell is reduced or eliminated. In certain embodiments, the formation of O-linked GlcNAc in the *Leishmania* cell prior to genetic engineering is catalyzed by at least one N-acetylglucosamine (GlcNAc)-transferase. In certain embodiments, the gene encoding an enzyme that catalyzes the formation of O-linked GlcNAc has been functionally inactivated.

[0046] In certain embodiments, the enzyme that catalyzes the formation of O-linked GlcNAc is an N-acetylglucosamine (GlcNAc)-transferase. In certain embodiments, the GlcNAc-transferase is selected from the group consisting of OGNT1, OGNT2, OGNTL, and homologous GlcNAc-transferases thereof. In certain embodiments, the GlcNAc-transferase is OGNT1. In other embodiments, the GlcNAc-transferase is OGNT2. In yet other embodiments, the GlcNAc-transferase is OGNTL. In certain embodiments, the GlcNAc-transferase is a GlcNAc-transferase that is homologous to OGNT1. In certain embodiments, the GlcNAc-transferase is a GlcNAc-transferase that is homologous to OGNT2. In certain

embodiments, the GlcNAc-transferase is a GlcNAc-transferase that is homologous to OGNTL. In certain embodiments, the GlcNAc-transferase is derived from *Leishmania tarentolae*. In certain embodiments, the GlcNAc-transferase is derived from other Trypanosomatida species. Nonlimiting examples of GlcNAc-transferases in Trypanosomatida are listed in Table 1, in which one representative genome per species is listed.

Table 1: Exemplary GlcNAc-transferases in Trypanosomatida.

Species	**Strain / TriTrypDB Genome accession**	**OGNT1**	**OGNT2**	**OGNTL**
Blechomonas ayalai	TriTrypDB-44_BayalaiB08-376_AnnotatedProteins	rna_Baya_228_0070-1-p1	rna_Baya_014_0750-1-p1	rna_Baya_228_0080-1-p1
Bodo saltans	TriTrypDB-44_BsaltansLakeKonstanz_AnnotatedProteins	*none*	BSAL_53670-t42_1-p1	*None*
Crithidia fasciculata	TriTrypDB-44_CfasciculataCfCl_AnnotatedProteins	CFAC1_160013000.1-p1	CFAC1_090018200.1-p1	CFAC1_160013300.1-p1
Endotrypanum monterogeii	TriTrypDB-44_EmonterogeiiLV88_AnnotatedProteins	EMOLV88_020005500.1-p1	EMOLV88_170014900.1-p1	EMOLV88_020005600.1-p1
Leishmania aethiopica	TriTrypDB-44_LaethiopicaL147_AnnotatedProteins	LAEL147_000030200.1-p1	LAEL147_000253000.1-p1	LAEL147_000030300.1-p1
Leishmania amazonensis	TriTrypDB-44_LamazonensisMHOMBR71973M2269_AnnotatedProteins	LAMA_000035900.1-p1	LAMA_000268900.1-p1	LAMA_000036200.1-p1
Leishmania arabica	TriTrypDB-44_LarabicaLEM1108_AnnotatedProteins	LARLEM1108_020007100.1-p1	LARLEM1108_170015900.1-p1	LARLEM1108_020007200.1-p1
Leishmania braziliensis	TriTrypDB-44_LbraziliensisMHOMBR75M2904_AnnotatedProteins	LbrM.02.0270:mRNA-p1	LbrM.17.1130:mRNA-p1	LbrM.02.0280:mRNA-p1
Leishmania donovani	TriTrypDB-44_LdonovaniCL-SL_AnnotatedProteins	LdCL_020007500-t42_1-p1	LdCL_170017200-t42_1-p1	LdCL_020007600-t42_1-p1
Leishmania enrietti	TriTrypDB-44_LenriettiiLEM3045_AnnotatedProteins	LENLEM3045_000029600.1-p1	LENLEM3045_170016400.1-p1	*None*
Leishmania gerbilli	TriTrypDB-44_LgerbilliLEM452_AnnotatedProteins	LGELEM452_020006800.1-p1	LGELEM452_170012100.1-p1	LGELEM452_020006900.1-p1

Species	Strain / TriTrypDB Genome accession	OGNT1	OGNT2	OGNTL
Leishmania infantum	TriTrypDB-44_LinfantumJPCM5_AnnotatedProteins	LINF_020007400-T1-p1	LINF_170017300-T1-p1	LINF_020007500-T1-p1
Leishmania major	TriTrypDB-44_LmajorFriedlin_AnnotatedProteins	LmjF.02.0240:mRNA-p1	LmjF.17.1020:mRNA-p1	LmjF.02.0250:mRNA-p1
Leishmania mexicana	TriTrypDB-44_LmexicanaMHOMGT2001U1103_AnnotatedProteins	LmxM.02.0240.1-p1	LmxM.17.1020.1-p1	LmxM.02.0250.1-p1
Leishmania panamensis	TriTrypDB-44_LpanamensisMHOMPA94PSC1_AnnotatedProteins	LPMP_020160-t37_1-p1	LPMP_170990-t37_1-p1	LPMP_020170-t37_1-p1
Leishmania pyrrhocoris	TriTrypDB-44_LpyrrhocorisH10_AnnotatedProteins	rna_LpyrH10_27_0530-p1	*none*	rna_LpyrH10_27_0550-p1
Leishmania seymouri	TriTrypDB-44_LseymouriATCC30220_AnnotatedProteins	rna_Lsey_0379_0030-1-p1	*none*	rna_Lsey_0379_0020-1-p1
Leishmania sp. MAR	TriTrypDB-44_LspMARLEM2494_AnnotatedProteins	*none*	LMARLEM2494_170015500.1-p1	LMARLEM2494_020006500.1-p1
Leishmania tropica	TriTrypDB-44_LtropicaL590_AnnotatedProteins	LTRL590_020007500.1-p1	LTRL590_000019100.1-p1	LTRL590_020007600.1-p1
Leishmania turanica	TriTrypDB-44_LturanicaLEM423_AnnotatedProteins	LTULEM423_020006600.1-p1	LTULEM423_170015700.1-p1	LTULEM423_020006700.1-p1
Paratrypanosoma confusum	TriTrypDB-44_PconfusumCUL13_AnnotatedProteins	*none*	PCON_0046770.mRNA-p1	*None*
Trypanosoma brucei	TriTrypDB-44_TbruceigambienseDAL972_AnnotatedProteins	Tbg.972.2.950:mRNA-p1	Tbg972.5.3320:mRNA-p1	Tbg.972.2.930:mRNA-p1
Trypanosoma congolense	TriTrypDB-44_TcongolenseIL3000_AnnotatedProteins	TcIL3000_0_43290.1-p1	TcIL3000_5_2160.1-p1	TcIL3000_2_200.1-p1
Trypanosoma evansi	TriTrypDB-44_TevansiSTIB805_AnnotatedProteins	TevSTIB805.2.1330-t26_1-p1	TevSTIB805.5.2740-t26_1-p1	TevSTIB805.2.1310-t26_1-p1
Trypanosoma grayi	TriTrypDB-44_TgrayiANR4_AnnotatedProteins	DQ04_09771010-t26_1-p1	DQ04_01951010-t26_1-p1	DQ04_042910001000-t26_1-p1
Trypanosoma rangeli	TriTrypDB-44_TrangeliSC58_AnnotatedProteins	TRSC58_00083-t26_1-p1	TRSC58_05317-t26_1-p1	TRSC58_03864-t26_1-p1

Species	Strain / TriTrypDB Genome accession	OGNT1	OGNT2	OGNTL
Trypanosoma theileri	TriTrypDB-44_TtheileriEdinburgh_AnnotatedProteins	TM35_000391720-t36_1-p1	TM35_000201600-t36_1-p1	TM35_000391740-t36_1-p1
Trypanosoma vivax	TriTrypDB-44_TvivaxY486_AnnotatedProteins	TvY486_0200430:mRNA-p1	TvY486_0501730:mRNA-p1	TvY486_0200410:mRNA-p1 (Pseudogene)

[0047] In certain embodiments, the enzyme that catalyzes the formation of O-linked GlcNAc is derived from species other than Trypanosomatida species. In certain embodiments, the enzyme is a human O-GlcNAc transferase (OGT, Uniprot: O15294) and homologous enzymes thereof. In certain embodiments, the O-GlcNAc transferase (OGT; uridine diphospho-N-acetylglucosamine:polypeptide β-N-acetylglucosaminyltransferase; EC 2.4.1.255) can catalyze the transfer of a single N-acetylglucosamine from UDP-GlcNAc to a serine or threonine residue in cytoplasmic and nuclear proteins resulting in their modification with a beta-linked N-acetylglucosamine (O-GlcNAc). In certain embodiments, the enzyme that catalyzes the formation of O-linked GlcNAc may be different isoforms of OGT. Exemplary isoforms of OGT include but are not limited to: (1) the nucleocytoplasmic or full-length variant (ncOGT), which may be 110 kDa; (2) a short isoform of OGT (sOGT), which may be 78 kDa; and (3) a variant of OGT that is targeted to the mitochondria (mOGT; which may be 90 kDa). In certain embodiments, OGT may appear to form multimers in the nucleus and cytoplasm, consisting of one or more 110-kDa subunits and 78-kDa subunits (Varki, Ajit, et al. (Eds.) (2015): Essentials of Glycobiology. Cold Spring Harbor Laboratory Press. 3rd. Cold Spring Harbor (NY)). In certain embodiments, the enzyme that catalyzes the formation of O-linked GlcNAc is human EOGT (Uniprot: Q5NDL2). In certain embodiments, the enzyme catalyzes the transfer of a single N-acetylglucosamine from UDP-GlcNAc to a serine or threonine residue in extracellular proteins resulting in their modification with a beta-linked N-acetylglucosamine (O-GlcNAc). In certain embodiments, the enzyme catalyzes Specific glycosylation of the Thr residue located between the fifth and sixth conserved cysteines of folded EGF-like domains.

[0048] In certain embodiments, the enzyme that catalyzes the formation of O-linked GlcNAc may transfer in alpha-linkage. In other embodiments, the enzyme that catalyzes the formation of O-linked GlcNAc may transfer in beta-linkage.

[0049] In certain embodiments, the formation of O-linked GlcNAc in the cell prior to genetic engineering is catalyzed by at least one enzyme as described in this Section, for

example one, two, three, four, five, six, seven, eight, nine or ten enzymes as described in this Section.

[0050] In certain embodiments, the formation of O-linked GlcNAc in the cell prior to genetic engineering is catalyzed by at least one GlcNAc-transferase derived from Trypanosomatida species, for example *Leishmania tarentolae*. In certain embodiments, the formation of O-linked GlcNAc in the cell prior to genetic engineering is catalyzed by at least one GlcNAc-transferase, for example one, two, three, four, five, six, seven, eight, nine or ten GlcNAc-transferases, one or more of which is derived from Trypanosomatida species. In certain embodiments, the number of the at least one GlcNAc-transferase is one, two or three. In certain embodiments, the at least one GlcNAc-transferase is selected from the group consisting of OGNT1, OGNT2, OGNTL and homologous GlcNAc-transferases thereof. In certain embodiments, at least one GlcNAc-transferase is a GlcNAc-transferase that is homologous to OGNT1, OGNT2 and/or OGNTL.

[0051] In certain embodiments, the formation of O-linked GlcNAc in the cell prior to genetic engineering is catalyzed by at least one GlcNAc-transferase derived from species that is other than Trypanosomatida species, for example human. In certain embodiments, the formation of O-linked GlcNAc in the cell prior to genetic engineering is catalyzed by at least one GlcNAc-transferase, for example one, two, three, four, five, six, seven, eight, nine or ten GlcNAc-transferases, one or more of which is derived from human. In certain embodiments, the number of the at least one GlcNAc-transferase is one, two or three. In certain embodiments, the at least one GlcNAc-transferase is selected from the group consisting of human O-GlcNAc transferase and human EOGT and homologous enzymes thereof. In certain embodiments, at least one GlcNAc-transferase is an enzyme that is homologous to human O-GlcNAc transferase and/or human EOGT.

[0052] In certain embodiments, the enzyme catalyzes the formation of O-linked GlcNAc prior to the genetic engineering of a *Leishmania* cell. In certain embodiments, the enzyme still catalyzes the formation of O-linked GlcNAc after the genetic engineering of a *Leishmania* cell. In certain embodiments, the enzyme does not catalyze the formation of O-linked GlcNAc after the genetic engineering of a *Leishmania* cell.

5.2 Method of Genetically Engineering a *Leishmania* Cell

[0053] Provided herein are also methods of genetically engineering a *Leishmania* cell as described in Section 5.3. In certain embodiments, the method may be used to accomplish the

functional inactivation of gene encoding an enzyme that catalyzes the formation of O-linked GlcNAc (as described in Section 5.1) in a *Leishmania* host cell.

5.2.1 Functional Inactivation of Gene Encoding an Enzyme that Catalyzes the Formation of O-linked GlcNAc

[0054] In certain embodiments, the gene encoding an enzyme that catalyzes the formation of O-linked GlcNAc may be functionally inactivated. In certain embodiments, the gene encoding the at least one GlcNAc-transferase is downregulated. In certain embodiments, the gene encoding the at least one GlcNAc-transferase is deleted. In certain embodiments, the gene encoding the at least one GlcNAc-transferase is mutated.

[0055] In certain embodiments, the gene encoding an enzyme that catalyzes the formation of O-linked GlcNAc may be functionally inactivated using the methods described in the Example Section (Section 6). In certain embodiments, the gene encoding an enzyme that catalyzes the formation of O-linked GlcNAc may be functionally inactivated using any method known in the art, for example methods described in International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein.

[0056] Non-limiting exemplary mutagenesis approaches include site directed mutagenesis using targeted gene editing techniques such as TALENs , ZFNs, CRISPR/Cas9; in combination with a repair scaffold for directed, homologous recombination mediated repair (Zhang, W et al. (2017) *mSphere* 2 (1); Gupta, R. and Musunuru, K. (2014) *The Journal of clinical investigation* 124 (10):4154–4161), transposon mutagenesis (Damasceno, J. et al. (2015) Christopher Peacock (Ed.): Parasite Genomics Protocols, vol. 1201. New York, NY: Springer New York (Methods in Molecular Biology), pp. 235–245); replacing the endogenous copy in situ with selectional markers, potentially in combination with a mutated gene version, that are integrated by homologous recombination (Roberts, S. (2011) *Bioeng Bugs* 2 (6): 320–326); RNA interference (RNAi) (Lye, L. et al. (2010) *PLoS Pathog* 6 (10), e1001161), conditional knock-down using Cre/LoxP or FRT/FLP (Duncan, S. (2017) *Molecular and Biochemical Parasitology* 216: 30–38).

[0057] In certain embodiments, the gene encoding the at least one GlcNAc-transferase is overexpressed. Such ovexpression may be accomplished by the following non-limiting exemplary approaches, such as gene copy number increase by introduction of additional copies into separate loci (Beverley, S. (1991): Gene amplification in Leishmania. In *Annu. Rev. Microbiol.* 45, pp. 417–444), high expression loci (ribosomal DNA loci) or episomal constructs (Lodes, M. et al. (1995) *Mol Cell Biol* 15 (12), pp. 6845–6853. DOI: 10.1128/mcb.15.12.6845; Boucher, N. (2004) *Nucleic Acids Res* 32 (9): 2925–2936),

modification of the native UTRs flanking the coding sequence; introduction of additional promoter regions such as the endogenous PolI promoter or a T7 promoter in combination with expression of bacterial T7 polymerase to increase the expression levels (Boucher, N. et al. (2002) *Molecular and Biochemical Parasitology* 119 (1): 153–158; Gu, P. et al. (2015) *Scientific reports* 5, p. 9684), use of transposable elements or recombinase based systems such as FRT-FLP or Cre/LoxP to introduce multiple copies of an expression construct (Duncan, S. et al. (2017) *Molecular and Biochemical Parasitology* 216, pp. 30–38), minichromosome integration (Zomerdijk, J. et al. (1992) *Nucleic acids research* 20 (11): 2725–2734), and forced chromosomal translocation by CRISPR (Zhang, W. et al. (2017) *mSphere* 2 (1). DOI: 10.1128/mSphere.00340-16)

[0058] Any method known in the art can be used to engineer the *Leishmania* cell, e.g., *Leishmania tarentolae*. In certain embodiments, nucleic acids are introduced into the host cells described herein using a plasmid, e.g., the heterologous nucleic acids are 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.

[0059] In specific embodiments, linearized nucleic acids are 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, heterologous nucleic acids are integrated site-specifically into the host cell genome by homologous recombination.

[0060] In certain embodiments, the genes encoding at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or at least 20 enzymes that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated. In certain embodiments, the genes encoding 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 enzymes that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated. In certain embodiments, the genes encoding three enzymes that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated. In certain embodiments, the genes and/or genetic loci that may be functionally inactivated include but are not limited to OGNT1, OGNT2, and OGNTL.

[0061] In certain embodiments, the genes encoding at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or at least 20 GlcNAc-transferase that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated. In certain embodiments, the genes encoding 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 GlcNAc-

transferase that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated. In certain embodiments, the genes encoding three GlcNAc-transferases that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated.

[0062] In certain embodiments, the genes encoding at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% of all enzymes that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated. In certain embodiments, the genes encoding 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% of all enzymes that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated.

[0063] In certain embodiments, the genes encoding at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% of all GlcNAc-transferases that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated. In certain embodiments, the genes encoding 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% of all GlcNAc-transferases that each catalyzes the formation of O-linked GlcNAc may be functionally inactivated.

5.2.2 Methods of Culturing Cells

[0064] Provided herein are methods for culturing host cells, for example *Leishmania* host cells.

[0065] 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 2.

[0066] In certain embodiments, host cells may be cultured using the methods described in the Assay and Examples Sections (Sections 5.6 and 6, respectively). Non-limiting exemplary *Leishmania* strains and plasmids used as donors for their production are provided in Table 3.

5.3 *Leishmania* Cell

[0067] Provided herein is a *Leishmania* host cell in which a gene encoding an enzyme that catalyzes the formation of O-linked GlcNAc prior to genetic engineering has been functionally inactivated.

5.3.1 Genetically Engineered *Leishmania* Cell

[0068] In certain embodiments, the *Leishmania* cells used herein are genetically engineered such that the formation of an O-linked GlcNAc on a polypeptide in the

Leishmania cell is reduced or eliminated. In certain embodiments, the formation of O-linked GlcNAc in the *Leishmania* cell prior to genetic engineering is catalyzed by at least one N-acetylglucosamine (GlcNAc)-transferase. In certain embodiments, the gene encoding the at least one GlcNAc-transferase is functionally inactivated.

[0069] In certain embodiments, the gene encoding the at least one GlcNAc-transferase in the *Leishmania* Cell is downregulated. In certain embodiments, the gene encoding the at least one GlcNAc-transferase in the *Leishmania* Cell is overexpressed.

[0070] In certain embodiments, the *Leishmania* cells provided herein comprise at least one gene deletion. In certain embodiments, the gene encoding the at least one GlcNAc-transferase is deleted.

[0071] In certain embodiments, the gene encoding the at least one GlcNAc-transferase is mutated.

[0072] In certain embodiments, additional modifications may be introduced (e.g., using recombinant techniques) into the *Leishmania* cell described herein.

[0073] In certain embodiments, in the genetically engineered *Leishmania* cells, the formation of the O-linked GlcNAc is reduced by at least 5%, 7%, 10%, 12%, 15%, 18%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% from the formation of the O-linked GlcNAc in a reference *Leishmania* cell. In certain embodiments, in the genetically engineered *Leishmania* cells, the formation of the O-linked GlcNAc is reduced by 5%, 7%, 10%, 12%, 15%, 18%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% from the formation of the O-linked GlcNAc in a reference *Leishmania* cell. In certain embodiments, the reference *Leishmania* cell is wild-type. In certain embodiments, the reference *Leishmania* cell is genetically engineered differently as the genetically engineered *Leishmania* cells described herein. In certain embodiments, some of the engineering of the reference *Leishmania* cell may be the same of the engineering of the genetically engineered *Leishmania* cells described herein, for example the deletion of one or more enzymes that catalyze the formation of O-linked GlcNAc. In certain embodiments, the reference *Leishmania* cell may comprise a recombinant nucleic acid encoding a heterologous glycosyltransferase, for example the *Leishmania* cells described in International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein. In certain embodiments, the formation of the O-linked GlcNAc is reduced by at least 5%, 7%, 10%, 12%, 15%, 18%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% from the formation of the O-linked GlcNAc in a wild-type *Leishmania* cell. In certain embodiments,

the formation of the O-linked GlcNAc is reduced by 5%, 7%, 10%, 12%, 15%, 18%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% from the formation of the O-linked GlcNAc in a wild-type *Leishmania* cell. In certain embodiments, the formation of the O-linked GlcNAc is reduced by at least 5%, 7%, 10%, 12%, 15%, 18%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% from the formation of the O-linked GlcNAc in a *Leishmania* cell that comprises a recombinant nucleic acid encoding a heterologous glycosyltransferase. In certain embodiments, the formation of the O-linked GlcNAc is reduced by 5%, 7%, 10%, 12%, 15%, 18%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% from the formation of the O-linked GlcNAc in a *Leishmania* cell that comprises a recombinant nucleic acid encoding a heterologous glycosyltransferase.

[0074] In certain embodiments, the growth rate of the genetically engineered *Leishmania* cells described herein is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of the growth rate of a reference *Leishmania* cell. In certain embodiments, the growth rate of the *Leishmania* cell is 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of the growth rate of a reference *Leishmania* cell. In certain embodiments, the reference *Leishmania* cell is wild-type. In certain embodiments, the reference *Leishmania* cell is genetically engineered differently as the genetically engineered *Leishmania* cells described herein. In certain embodiments, some of the engineering of the reference *Leishmania* cell may be the same of the engineering of the genetically engineered *Leishmania* cells described herein, for example the deletion of one or more enzymes that catalyze the formation of O-linked GlcNAc. In certain embodiments, the growth rate of the *Leishmania* cell is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of the growth rate of a wild-type *Leishmania* cell. In certain embodiments, the growth rate of the *Leishmania* cell is 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of the growth rate of a wild-type *Leishmania* cell.

5.3.2 *Leishmania* and Kinetoplastida Strains

[0075] In certain embodiments, a cell with reduced or eliminated ability to form O-linked GlcNAc on a polypeptide is a *Leishmania* cell. 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.

[0076] In certain embodiments, a cell with reduced or eliminated ability to form O-linked GlcNAc on a polypeptide 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.

5.4 Uses of the *Leishmania* cell as expression systems

[0077] In certain embodiments, a *Leishmania* cell with reduced or eliminated ability to form O-linked GlcNAc on a polypeptide (as described in Section 5.3) may be used as an expression system for the polypeptide. In certain embodiments, the polypeptide may be a heterologous, non-*Leishmania* protein, such as a therapeutic protein (e.g., an antibody or an antibody format).

5.4.1 Compositions comprising host cells

[0078] In one aspect, provided herein are compositions comprising the host cells described herein, for example, compositions comprising the *Leishmania* cells described herein. Such compositions can be used in methods for generating a target polypeptide as described in Section 5.3. 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.

[0079] 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.

5.4.2 Methods of Target Polypeptide Production

[0080] In one aspect, provided herein are methods for making a target polypeptide. In one embodiment, provided herein is a method of producing a target polypeptide *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 a heterologous glycosyltransferase. 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. In certain embodiments, the *Leishmania* cell comprises one or more heterologous glycosyltransferases. In certain embodiments, the *Leishmania* cell comprises one or more N-acetyl glucosamine transferases; and/or one or more heterologous galactosyltransferases; and/or one or more heterologous sialyltransferases.

[0081] 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 5.5.

5.5 Target Polypeptide

[0082] 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. In certain embodiments, the target the polypeptide is selected from the group consisting of adalimumab, rituximab and erythropoietin (EPO).

[0083] 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).

[0084] 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.

[0085] 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.

[0086] 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).

[0087] 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).

[0088] 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).

[0089] 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).

[0090] 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).

[0091] 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.

[0092] 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).

[0093] 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.

[0094] 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.

[0095] In certain embodiments, the target polypeptide is an Fc-fusion polypeptide.

[0096] In certain embodiments, the target polypeptide is a biologic comprising an Fc domain of an IgG.

[0097] 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.

5.5.1 Composition and/or formulation comprising the polypeptide

[0098] 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 5.5.2).

[0099] 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.

[00100] 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.

[00101] 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.

[00102] 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.

[00103] The compositions described herein can be included in a kit, container, pack, or dispenser together with instructions for administration.

[00104] 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.

5.5.2 Prophylactic and Therapeutic Uses

[00105] 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.

[00106] 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.

[00107] 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).

[00108] 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.

5.6 Assay

5.6.1 Strains, Growth and Genetic Methods

[00109] Provided herein are methods for culturing host cells.

[00110] 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. In

some embodiments, cultures contain Biopterin at a final concentration of 10 µM to support growth.

[00111] A non-limiting list of selective agents is provided in Table 2.

Table 2: 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
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

Table 3: Summary of strains presented in the examples and plasmids used as donors for their production. Some of the strains were produced by several rounds of transfection building on top of each other.

Strain	**Strain number**	**Plasmids for Cas9 expression**	**Plasmids for OGNT KO/OE**	**Plasmids for GT and target protein expression**
LMSAP-rhEPO-Strep	St11521			pLMTB4239
LMSAP-rhEPO-Strep	St12274	-	-	pLMTB4239
LMSAP-rhEPO-Strep Cas9-(hyg, integrated)	St17785	pLMTB8777		pLMTB4239
Triple OGNT-1/2/L KO **LMSAP-rhEPO-Strep**	St17917	pLMTB8777	pLMTB7805, 7807, 7811, 7812	pLMTB4239
Triple OGNT-1/2/L KO **LMSAP-rhEPO-Strep** *Monoclone of St17917*	St18143	pLMTB8777	pLMTB7805, 7807, 7811, 7812	pLMTB4239
LMSAP-rhEPO-Strep *G0-N N-glycan cell line*	St11895			pLMTB4239, 4123
Adalimumab	St15449	-	-	pLMTB7115

Strain	**Strain number**	**Plasmids for Cas9 expression**	**Plasmids for OGNT KO/OE**	**Plasmids for GT and target protein expression**
Rituximab	St12427	-	-	pLMTB5026
G0 N-glycan cell line	St15673	-	-	pLMTB6944, 6952, 6815, 6819, 6848, 6852, 7186, 6961
Adalimumab *G0 N-glycan cell line*	St15882	-	-	pLMTB7115, 6944, 6952, 6815, 6819, 6848, 6852, 7186, 6961
G2 N-glycan cell line	St15257	-	-	pLMTB6807, 6848, 6852, 6855, 6952, 6958, 6811, 6860, 6906, 6861
Adalimumab *G2 N-glycan cell line*	St15451	-	-	pLMTB7115, 6807, 6848, 6852, 6855, 6952, 6958, 6811, 6860, 6906, 6861
Cas9 (hyg, episomal)	St15392	pLMTB7101	-	
Cas9 (hyg, episomal) **Adalimumab**	St16568/ St16569	pLMTB7101	-	pLMTB7115
Cas9 (ble, episomal) **Adalimumab**	St16872	pLMTB7100	-	pLMTB7115
Cas9 (neo, episomal) **Adalimumab**	St16873	pLMTB7102	-	pLMTB7115
Cas9 (neo, episomal) **Adalimumab** *G0 N-glycan cell line*	St17607	pLMTB8640, 7102, 8225	-	pLMTB7115, 6944, 6952, 6815, 6819, 6848, 6852, 7186, 6961
Cas9 (neo, episomal) **Adalimumab** *G2 N-glycan cell line*	St17124	pLMTB7100	-	pLMTB7115, 6807, 6848, 6852, 6855, 6952,

Strain	**Strain number**	**Plasmids for Cas9 expression**	**Plasmids for OGNT KO/OE**	**Plasmids for GT and target protein expression**
				6958, 6811, 6860, 6906, 6861
Cas9 (hyg, episomal) **LMSAP-rhEPO-Strep**	St17785	pLMTB8777		pLMTB4239
OGNT-2 KO	St16248	pLMTB7101	pLMTB6460, 6471	-
OGNT-1 KO	St16257	pLMTB7101	pLMTB6463,6474	-
OGNT-L KO	St16249	pLMTB7101	pLMTB6463, 6474	-
OGNT-2 KO **Adalimumab**	St16478	pLMTB7101	pLMTB6460, 6471	pLMTB7115
OGNT-1 KO **Adalimumab**	St16700	pLMTB7101	pLMTB6463, 6474	pLMTB7115
OGNT-L KO **Adalimumab**	St16702	pLMTB7101	pLMTB6467, 6478	pLMTB7115
Double OGNT-1/L KO **Adalimumab**	St16704	pLMTB7101	pLMTB6474, 6466	pLMTB7115
Double OGNT-1/L KO (no IR) **Adalimumab**	St16770	pLMTB7101	pLMTB7811, 7812	pLMTB7115
Triple OGNT-1/2/L KO **Adalimumab**	St16636	pLMTB7101	pLMTB6460, 6471, 6474, 6466	pLMTB7115
Triple OGNT-1/2/L KO (no IR) **Adalimumab**	St17127	pLMTB7100	pLMTB7805, 7807, 7811, 7812	pLMTB7115
Triple OGNT-1/2/L KO **Adalimumab** *G0 N-glycan cell line*	St17863	pLMTB8640, 7102, 8225	pLMTB6467, 6475, 6470, 6459	pLMTB7115, 6944, 6952, 6815, 6819, 6848, 6852, 7186, 6961
Triple OGNT-1/2/L KO **Adalimumab** *G2 N-glycan cell line*	St17317/ St17318	pLMTB7100	pLMTB7805, 7807, 7811, 7812	pLMTB7115, 6807, 6848, 6852, 6855, 6952, 6958, 6811, 6860, 6906, 6861
OGNT-1/L:: G0 (heterozygous) **Adalimumab** *G0 N-glycan cell line*	St17846	-	-	pLMTB7115, 8223, 8381, 8301, 8234, 8629,

Strain	**Strain number**	**Plasmids for Cas9 expression**	**Plasmids for OGNT KO/OE**	**Plasmids for GT and target protein expression**
				8238, 8287, 8383, 8384, 8229
OGNT-2 OE **Adalimumab**	St15884	-	pLMTB5932	pLMTB7115
OGNT-1 OE **Adalimumab**	St15885	-	pLMTB5933	pLMTB7115
OGNT-L OE **Adalimumab**	St15886	-	pLMTB5934	pLMTB7115
OGNT-1 OE **Adalimumab** *G0 N-glycan cell line*	St16292		pLMTB5933	pLMTB7115, 6944, 6952, 6815, 6819, 6848, 6852, 7186, 6961
WT *Man3 N-glycan cell line*	St18344	-	-	-
Triple OGNT-1/2/L KO (RNP) *Man3 N-glycan cell line*	St19955	-	pLMTB9856, 9857, 7810, 7813	-
Triple OGNT-1/2/L KO (RNP) *Man3 N-glycan cell line*	St20107	-	pLMTB7805, 7807, 7811, 7812	-
G0 (2x) N-glycan cell line	St19462	-	-	pLMTB8389, 8310, 8234, 8311, 8235, 8631, 8632, 8313, 8236, 8314, 8633, 8297, 8392, 8223, 8564, 9070, 8568, 9072, 9080, 9082, 9083, 9077, 9305
Triple OGNT-1/2/L KO (RNP) *G0 (2x) N-glycan cell line*	St19855	-	pLMTB9852, 9853, 9854, 9855	pLMTB8389, 8310, 8234, 8311, 8235, 8631, 8632, 8313, 8236, 8314, 8633, 8297, 8392, 8223,

Strain	Strain number	Plasmids for Cas9 expression	Plasmids for OGNT KO/OE	Plasmids for GT and target protein expression
				8564, 9070, 8568, 9072, 9080, 9082, 9083, 9077, 9305
Triple OGNT-1/2/L KO (RNP) *G0 (2x) N-glycan cell line*	St20097	-	pLMTB7805, 7807, 7811, 7812	pLMTB8389, 8310, 8234, 8311, 8235, 8631, 8632, 8313, 8236, 8314, 8633, 8297, 8392, 8223, 8564, 9070, 8568, 9072, 9080, 9082, 9083, 9077, 9305
Triple OGNT-1/2/L KO (RNP) **Adalimumab** *G0 (2x) N-glycan cell line*	St19915	-	pLMTB9852, 9853, 9854, 9855	pLMTB8389, 8310, 8234, 8311, 8235, 8631, 8632, 8313, 8236, 8314, 8633, 8297, 8392, 8223, 8564, 9070, 8568, 9072, 9080, 9082, 9083, 9077, 9305, 8803, 8698, 7084, 6681, 6683
Triple OGNT-1/2/L KO (RNP) *G0 (3x) N-glycan cell line*	St19931	-	pLMTB9852, 9853, 9854, 9855	pLMTB8389, 8310, 8234, 8311, 8235, 8631, 8632, 8313, 8236, 8314, 8633, 8297, 8392, 8223, 8564, 9070, 8568, 9072, 9080, 9082, 9083, 9077,

Strain	Strain number	Plasmids for Cas9 expression	Plasmids for OGNT KO/OE	Plasmids for GT and target protein expression
				9305, 8223, 6948, 9839, 8608, 9840, 8582, 9841, 9836, 9832, 9838, 9303
Triple OGNT-1/2/L KO (RNP) **Adalimumab** *G0 (3x) N-glycan cell line*	St19998	-	pLMTB9852, 9853, 9854, 9855	pLMTB8389, 8310, 8234, 8311, 8235, 8631, 8632, 8313, 8236, 8314, 8633, 8297, 8392, 8223, 8564, 9070, 8568, 9072, 9080, 9082, 9083, 9077, 9305, 8223, 6948, 9839, 8608, 9840, 8582, 9841, 9836, 9832, 9838, 9303, 8803, 8698, 7084, 6681, 6683
Triple OGNT-1/2/L KO (RNP) *G2 N-glycan cell line*	St19885	-	pLMTB9852, 9853, 9854, 9855	pLMTB8389, 8310, 8234, 8311, 8235, 8631, 8632, 8313, 8236, 8314, 8633, 8297, 8392, 8223, 8564, 9070, 8568, 9072, 9080, 9082, 9083, 9077, 9305, 8391, 8831, 8832, 8834, 8836, 8281, 8821

Strain	Strain number	Plasmids for Cas9 expression	Plasmids for OGNT KO/OE	Plasmids for GT and target protein expression
Triple OGNT-1/2/L KO (RNP) *G2 N-glycan cell line*	St20201	-	pLMTB7805, 7807, 7811, 7812	pLMTB8389, 8310, 8234, 8311, 8235, 8631, 8632, 8313, 8236, 8314, 8633, 8297, 8392, 8223, 8564, 9070, 8568, 9072, 9080, 9082, 9083, 9077, 9305, 10054, 9833, 8608, 9834, 8582, 9835, 9836, 9832, 10055, 8831, 8832, 8834, 8836, 8281, 8821

(i) Plasmids

[00112] 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. The genes of interest are included as ORFs that were codon usage optimized for *L. tarentolae*. Optimized sequences were manually curated for avoidance of restriction sites and deletion of repeats or homopolymer stretches. The plasmids were generated and sequenced by a gene synthesis provider. Plasmids and descriptions are found in the sequence listings.

[00113] For codon usage optimization, 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.

(ii) DNA construct design for OGNT deletion

[00114] For OGNT deletions, three different ways of construct composition were employed. In all cases, the integration constructs were split into two or more fragments of approximately 1000-2500 bp with overlapping regions of 200 bp within the constructs to allow homologous recombination of the complete construct into the *L. tarentolae* genome.

[00115] Replacement with a selection marker flanked by 5' and 3' untranslated regions providing it with defined splice leader acceptor and polyadenylation sequences (transcription by endogenous PolII). 1.) a 5' homology region for specific integration into the OGNT gene (ideally immediately after 5' UTR to remove the full coding sequence), 2.) an intergenic region providing a 5'UTR with splice leader acceptor sequence to the gene of interest, 3.) the gene of interest encoding for a selection marker as ORF that was codon usage optimized for *Leishmania* (either *L. major* or *L. tarentolae)*, 4.) an intergenic region that provides a 3'UTR with polyadenylation site to the gene of interest, 5.) the 3' homology region for site specific recombination into the OGNT gene (see also FIG. 6, variant A).

[00116] Replacement with a selection marker without flanking untranslated regions (transcription by endogenous PolII). 1.) a 5' homology region for specific integration exactly after the 5' untranslated region of the OGNT gene, 2.) the gene of interest encoding for a selection marker as ORF that was codon usage optimized for *Leishmania* (either *L. major* or *L. tarentolae)*, 3.) a 3' homology region for site specific recombination before the 3' UTR of the OGNT gene (see also FIG. 6, variant B).

[00117] Replacement with an expression cassette for glycoengineering (counterclockwise integration, transcription by PolI). 1.) a 5' homology region for specific integration into the OGNT gene, 2.) a promoter region for PolI transcription comprising terminal repeats and a 5' UTR with splice leader acceptor sequence for the gene of interest 3.) the gene of interest encoding for a glycosyltransferase or enzymes of a sugar biosynthesis pathway as ORF that was codon usage optimized for *Leishmania* (either *L. major* or *L. tarentolae)*, 4.) an intergenic region providing a 3' polyadenylation site to the upstream gene and a splice leader acceptor site to the downstream gene, 5.) a selection marker as ORF that was codon usage optimized for *Leishmania* (either *L. major* or *L. tarentolae)*, 4.) an intergenic region that provides a 3'UTR with polyadenylation site to the gene of interest, 5.) the 3' homology region for site specific recombination into the OGNT gene. Repetition of several elements 3 and 4 before the selection marker are possible.

(iii) DNA construct design for OGNT overexpression

[00118] To assess the effect of overexpression on the three OGNT candidates, plasmids were generated that contained a) a 5' homologous recombination site targeting the ssu locus, b) a 5' UTR (aprt), c) the respective triple HA tagged OGNT gene, d) an intergenic region (CamIR) e) the selection marker gene, f) a 3'UTR (dhfr-ts) and g) a 3' homologous recombination site targeting the ssu locus to support stable expression.

(iv) DNA construct design for hCas9 expression

[00119] The plasmid for Cas9 expression was designed analogous to the overexpression plasmids described above, using a published Cas9 sequence codon usage optimized for *L. tarentolae* (Le, et al. (2013) Science 339 (6121), pp. 819–823). In contrast to the constructs for overexpression, the Cas9 expression constructs were usually transfected as circular DNA which should be retained episomally in *L. tarentolae*.

(v) crRNA design

[00120] crRNAs were designed based on the target regions (usually coding sequences of OGNT genes) for use with SpCas9 (PAM=NGG) by EuPaGDT (http://grna.ctegd.uga.edu/) and were counterchecked for on-/off-target effects by blast against the whole genome of *L. tarentolae*. crRNAs were then selected such that they are ideally targeting the extremities of the coding sequence to be replaced.

Table 4: crRNAs designed for knockout of OGNT genes.

gRNA_OGNT-1_3	GTTCTTCGCGAAATCCGATGCGG	SEQ ID NO:231
gRNA_OGNT-1_5	ACACGCATGCGGGTGAGGTGAGG	SEQ ID NO:232
gRNA_OGNT-2_5	AGTGGTTCACAACCGAATCCCGG	SEQ ID NO:233
gRNA_OGNT-2_3	GATGGGCACGGAACGGCCTGTGG	SEQ ID NO:234
gRNA_OGNT-L_5	ACGGTGACGCGAACTCGCAGAGG	SEQ ID NO:235
gRNA_OGNT-L_3	CTTGTCTCGGTGGCGCCAAGCGG	SEQ ID NO:236

(vi) Transfection method

(A) Preparation of DNA

[00121] 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 37°C and DNA was purified 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, pellet was dried for maximum 15 min and resuspended in ddH20). For optimized removal of circularized plasmid, 1 or 2 restriction enzymes with recognition sites in the vector backbones were chosen and 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) Preparation of gRNA for transfection into a cell line with constitutive Cas9 expression

[00122] gRNA for CRISPR/Cas9 mediated genome editing was assembled from tracrRNA and crRNA (Microsynth), by a denaturation step of 95°C for 5 min and subsequent slow cool down at 0.1°C/s in a thermo cycler. Per transfection 10 µg of tracrRNA and 10 µg of crRNAs (total) were used together with the DNA for integration (1 µg/fragment) that serves as template for homology directed repair.

(C) Preparation of ribonucleoprotein (RNP) complexes for transfection without constitutive Cas9 expression

[00123] gRNA for CRISPR/Cas9 mediated genome editing was assembled from equimolar amounts of tracrRNA and crRNA (Microsynth) as above by denaturation for 5 min at 95°C and subsequent slow cool down at 0.1°C/s in a thermo cycler. This was done separately for every crRNA used before the different gRNAs were subsequently mixed in equimolar amounts. Next, 122 pmol recombinantly expressed Cas9 protein (i.e. Alt-R® S.p. HiFi Cas9 Nuclease V3 (IDT, #1081061) were added to 360 pmol of the gRNA mix and incubated for 15 min at RT to allow RNP formation. The final volume used for a transfection by Nucleofector (see section E) should not exceed 6 µl. Lastly, the RNP mix was added to the repair DNA containing transfection solution described below along with 1 µl of Alt-R® Cas9 Electroporation Enhancer (IDT, #1081072).

(D) DNA preparation for transfection

[00124] The linear DNA fragments for integration are mixed for transfection in the needed combinations at 1 µg per fragment. If the CRISPR/Cas9 system was used, the gRNA was prepared as described above and mixed with the integration fragments. The volume of the mix was reduced to maximum 2 µl per transfection in a vacuum concentrator at 30°C. For episomal transfection of Cas9 plasmids, 0.1-1 µg of plasmid DNA were directly used for transfection.

(E) Transfection with Nucleofector

[00125] One day before transfection, a densely grown culture of the parental strain was diluted 1:10 into fresh media (BHIH) containing all antibiotics for which selection markers were previously integrated and cultured overnight at 26°C.

[00126] Transfection was performed using the 4D-Nucleofector™_Core_X with the P3 Primary Cell 4D-NucleofectorTM X Kit (Lonza). For this, DNA (or DNA/RNA or DNA/RNP) 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 20 µl of the DNA (or DNA/RNA or DNA/RNP) 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 ddH2O only.

[00127] 80 µl of fresh media (BHIH, parental 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 5). 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.

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

[00128] Preparation of the *Leishmania* culture for transfection was done by a 1:10 dilution of a densely grown culture in BHIH 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 ddH20 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 (200mM 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 (exp. decay: 450 V, 450 uF, 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 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 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 5min at RT and pellet resuspended in new BHIH media containing full selection marker concentration.

[00129] Similar methods are described in International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein. Clonal selection

[00130] For clonal selection, cells were streaked on BHIH 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, 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 is a flask and further grown statically as usual.

(vii) PCR and Sequence analysis of deletion strains

(A) Preparation of gDNA— Genomic DNA isolation by tissue kit

[00131] 2 ml of densely grown *L. tarentolae* culture were pelleted at 1800 g and the supernatant was discarded. The pellet was used for preparation of genomic DNA by the NucleoSpin® Tissue Kit (Macherey-Nagel). For this, the pellet is resuspended in 200 µl of Buffer T1 and further treated according to the manufacturer's instructions until elution. For efficient elution, 50 µl of prewarmed (50°C) Buffer BE are added to the column and incubated at RT for 3 min. The eluate is collected by centrifugation for 1 min at 11000g. Repetition of this step as well as reloading of the eluate can be used to increase the yield.

(B) Preparation of crude cell extracts for PCR analysis

[00132] 50 µl of culture were washed in 1ml PBS and pelleted at 1800 g for 5 min. The supernatant was removed and the pellet was resuspended in 50 µl of PBS and boiled at 95°C for 5 min with intermitted vortexing. 1µl was used instead of template DNA in the PCR reaction.

(C) PCR analysis of OGNT KOs

[00133] PCR confirmation of OGNT knock-outs was performed by either amplification of the complete locus (OGNT-1, OGNT-2, OGNT-L or OGNT-1+L) or by amplification of the shorter fragments covering the integration sites.

[00134] Usually the successful replacement of the wildtype OGNT sequence (OGNT-1 = 3.4 kbp, OGNT-2=1.9 kbp and OGNT-L=3.4 kbp) by the selection marker coding sequences (0.4-1.0 kbp) with or without the additional intergenic regions (together approx. 0.9 kbp) could be easily confirmed by the size of the amplicon resulting from the PCR targeting the whole native locus, since correct replacement of the wt gene would lead to a much shorter amplicon. For these PCRs LATaq DNA polymerase (TaKaRa) was used in combination with a buffer for amplification of GC rich sequences that allowed the amplification of the long wildtype regions (see Table 5). In some cases, amplification of shorter regions with primer binding within the OGNT coding sequence was preferred to test for presence of remaining wt genes (Table 5). For these, the DreamTaq DNA polymerase (Thermo Fisher Scientific) was used. Alternatively, the correct integration of the selection marker gene into the respective OGNT locus could be tested by combinations of a primer binding in the genome with one primer binding to the selection marker CDS or the intergenic regions of the integrated construct and the other one targeting the genome. This was for example done to confirm the correct integration of the selection marker cassette in the heterozygous KO produced in Example 2 (see "OGNT-2 KO (with IR)", Table 5; primers are listed in Table 6).

Table 5: PCRs for analysis of OGNT deletions. PCR primers used for confirmation OGNT knock-outs by absence of the respective OGNT wt gene and the expected amplicon sizes for the wt strain (St10569) are summarized. * KO amplicon length for whole locus PCRs depends on the combination of selection marker and intergenic regions used.

Target gene	**Target region**	**Primers**	**wt amplicon**	**KO amplicon**
OGNT-1	Whole locus	6154, 6156	4.9 kbp	shorter*
OGNT-1	3' end	7173, 7174	2.6 kbp	none
OGNT-2	Whole locus	6043, 6044	3.3 kbp	shorter*
OGNT-2	5' end	6043, 6047	1.3 kbp	none
OGNT-2	5' end	7492, 7495	0.9 kbp	none

Target gene	Target region	Primers	wt amplicon	KO amplicon
OGNT-L	Whole locus	6157, 6158	4.8 kbp	shorter*
OGNT-L	Whole locus	6073, 7163	5.5 kbp	shorter*
OGNT-L	5' end	7175, 7176	2.6 kbp	none
OGNT-1+L	Whole locus	6157, 6156	8.1 kbp	shorter*
OGNT-2 KO(with IR)	3' end (3'UTR-genome)	6045, 6044	none	0.8 kbp
OGNT-L	3' end (hyg)	4952, 7163	None	2.4 kbp

Table 6: Listing of primer sequences used in the described examples.

Primers	Sequence	Short name	SEQ ID NO:
4952	CCGATGGCTGTGTAGAAGTACTCG	Hyg_fw	53
6043	GCTCAGCTGCGAGAGCGTAAACCTCCGTAACAATG	OGNT-2_5'_fw	54
6044	AGCTAAACTCTGCACTCATCTGCGCTTCCGCAAGG	OGNT-2_3'_rev	55
6045	ACTATCATGCCCTACGTGGGCCACGCAGCGATGAG	3'UTR-dhfr_fw	56
6047	GCGTCTCACCGCTTGCCAGGTCTTCTACTCCAATG	OGNT-2_rev	57
6073	TGGTGGAGGAGGGTGCGGAGGATG	OGNT-L_3'_fw	58
6154	ATCTGGAGGATGTCTACGTGACACAGGCGCTCTGG	OGNT-1_5'(internal)_rev	59
6156	CGCACAGGGTGACGAGGAAAGCAGTATCGAAACAG	OGNT-1_3'_fw	60
6157	CGACCGCGATATCTGCTTTCCATTCTGCAGTTCTC	OGNT-L_5'_rev	61
6158	CTTTACACAGGCGGTCACGTGAGTGTCCATGAGAG	OGNT-L_3'(internal)_fw	62
7163	AGCACATGTTTCGGCAGGTC	OGNT-L_3'_rev	63
7173	CGCACCTCGGCTTCAACTGCCAATG	OGNT-1_rev	221
7174	AACGTGCCTGAAGCCCGTAGCTTTG	OGNT-1_fw	222
7175	GGCGACGGATGATGCCCACCATTTG	OGNT-L_rev	223
7176	GGAGGCAACCAAGAAGGCGTCAGAG	OGNT-L_fw	224
7492	CCATGGCCAGATGCCAAGCTTACTC	OGNT-2_5'_fw	225
7495	CGGAACACAGACCTGCCATCTGTGG	OGNT-2_5'_rev	226

(D) OGNT deletion sequencing

[00135] St16248, St16257, St16249, St16636, St16700, St16702 and St16704 genomic DNA was 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 (2013) Available online at http://arxiv.org/pdf/1303.3997v2) was used to align the reads to the reference sequence, resulting in an average coverage of 186-fold across the whole genome. Complete absence of reads matching to the respective OGNT region indicate a successful removal of the OGNT gene.

(viii) Expression analysis by Western blot

(A) Sample preparation and Expression analysis by Western Blot

[00136] 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) corresponding to 0.05 OD and cell free culture supernatants corresponding to 0.05 OD 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 Leammli (reducing) buffer, boiled again at 95°C for 10 min and vortexed intensively before loading 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. Polyclonal rabbit anti-HA antibody (H6908, Sigma) was used in 1:2000 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 secondary antibody detection with horse reddish peroxidase (HRP) coupled goat anti rabbit antibody (170-6515, BioRad) used 1:4000 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).

5.6.2 Anti-TNFa "Adalimumab" expression, purification and analysis in *L. tarentolae* derived CustomGlycan host cells

(i) Large Scale Expression and Purification

[00137] A 10 L bioreactor of St15449, a recombinant strain based on St10569 (wt), with ssu integrated adalimumab expression cassette (containing 5'UTR_Adalimumab_LC_intergenic region_Adalimumab HC_ intergenic region_sat_3'UTR; resistant to nouseotricin) was grown in BHIH for 50.8 h and harvested at an OD of 15. Cultures were harvested and centrifuged for 30 minutes at 8000 × g and SN filtrated through 0.45 µm + 0.22 µm filter cartridge (Sartorius, 544307H9--SS--A) and supplemented with 5

tablets PIC (Protease inhibitor cocktail, cOmplete, EDTA-free, Roche, 05056489001) and EDTA to 5 mM.

[00138] Media SN was loaded offline over night with peristaltic pump at 4°C continuously on 2x 5ml protein A Column (HiTrap MabSelect PrismA, GE Healthcare, 17-5498- 53). Column was connected to NGC System and washed with 10 CV 1xPBS pH 7.4. Elution was performed with 0.15M Glycine pH 2.5 and directly neutralized by adding 150 µl 1M Tris pH 8.5. Pooled fractions containing adalimumab were buffer exchanged to PBS pH 6. Adalimumab pools were adjusted with Tris and (NH4)2SO4 and loaded on a 2x 5ml HIC (HiTrap Capto Phenyl HP) with a flow rate of 1ml/minute, and eluted with a Buffer A 20mM Tris, 1M (NH4)2SO4 pH 7.0 and Buffer B 20mM Tris pH 7.0 gradient. Fractions were collected and analyzed by coomassie SDS PAGE and western blot. Final pools were buffer exchanged to PBS pH 6 and stored at -80°C.

(ii) Fed-batch fermentation for analysis of deletion strains

[00139] OGNT deletion strains St16704 (OGNT-1/L KO) and St16636 (OGNT-1/2/L KO) were subjected to fed-batch fermentations in a *bio-t® xpac* multi-bioreactor system. Cells were grown in BHIH (2/3 of total fermentation volume) for 50 h before a concentrated feed (56 g/L Yeast extract, 32 g/L soy peptone, 28.8g/L glucose, 15 mg/L hemin; 1/3 of total volume) was at a constant rate. The cultures were harvested after 94 h and centrifuged for 30 min at 3220x g, 4°C. 50 ml of the supernatant were subjected to small scale Protein A enrichment of Adalimumab as described below.

(iii) Small scale expression, purification of Adalimumab

[00140] Host cells were routinely grown in 50 ml culture in BHIH 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 4h 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 ProteinA 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. 3x1CV and 1x0.5 CV).

[00141] 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.

[00142] Samples were then subjected to analyses such as O-HexNac quantification as described below.

5.6.3 LMSAP-rhEPO-Strep expression, purification and analysis in *L. tarentolae* derived CustomGlycan host cells

[00143] Host cells were grown in 1 L culture in Yeast Extract media for 72 h at 26°C shaking at 140 rpm. Cultures were centrifuged at 8000g, 4°C for 30 min and the supernatant was harvested for precipitation with 40% ammonium sulfate (45 min at RT). The precipitate was collected by centrifugation for 1 h at 11000 g, 4°C and subsequently resuspended in 50 ml PBS pH7.4. The sample was dialysed (SpectraPor™ dialysis membrane, MWCO 3.5 kDa) against 5 l PBS pH7.4 for 2 h and against another 5 l PBS pH7.4 overnight at 4°C. After filtering through a 0.22 µm filter (Steriflip, SCGP00525), the sample was loaded overnight in recirculation at 4°C on a 1 ml StrepTrap™ HP (StrepTrap™ HP, GE Healthcare, 29-0486-53) column. After washing with 20 CV PBS pH7.4, LMSAP-rhEPO-Strep was eluted using 2.5 mM desthiobiotin in PBS pH7.4 (5 CV in 0.5 ml fractions) and concentrated using AmiconUltra-0.5 concentrators.

[00144] Samples were then subjected to glycopeptide analysis.

5.6.4 Analysis

(i) SDS PAGE and Capillary Gel Electrophoresis

[00145] SDS PAGE was performed under reduced or non-reducing conditions using 10 µg for Coomassie, 2.5 µg for WB, separated on 4-12% Gel with MOPS buffer for 55 minutes. Determination of Protein purity was done by Coomassie Stained SDS-PAGE with 10 µg protein sample and compared to a BSA standard curve. Impurities were quantified by ImageQuant. Capillary Gel Electrophoresis (CGE) was performed using an Agilent Protein 230 Kit (5067-1518), according to protocol.

(ii) Analytical SEC

[00146] MAbPac SEC-1 (4x300 mm) is a size exclusion chromatography (SEC) column specifically designed for separation and characterization of monoclonal antibodies (mAbs)

and was used according to manufacturer's recommendation (Temperature: 30 °C; Eluent: PBS 50mM NaPO4, 300 mM NaCl pH 6.8; Elution: isocratic, 30 minutes; Flow: 0.2 mL/minute; Detection: 215 nm; Injection V: 5 µL corresponding to 5 µg protein).

(iii) O-HexNAc identification

[00147] Intact monoclonal antibodies were analyzed by mass spectrometry employing the state-of-the-art instrumentation (Orbitrap FTMS), data processing and data analysis (bioinformatics) tools by SpectroSwiss. In addition to the intact measurement the antibody was reduced with TCEP or enzymatically cleaved (IdeS) to generate Fd, LC and Fc/2 subunits, which were analyzed using the same instrumentation.

(iv) Sample preparation for IdeS derived subunit analysis

[00148] To generate mAb subunits of about 25 kDa each, IdeS (FabRICATOR, Genovis, Lund, Sweden) digestion of mAbs was performed in formulation buffers. One unit of IdeS was added to each µg of mAbs and left to react for 30 minutes at 37° C. Then, mAbs were denatured and reduced by incubation with 6 M GdnCl and 30 mM TCEP at room temperature for 30 minutes. Finally, the reaction was quenched by acidifying the solution to 1 % TFA. For the analysis samples were diluted with 0.1% FA in water to a final concentration of 1 µg/µl.

(v) Mass spectrometry for intact and subunit analysis, Bioinformatics and Data processing.

[00149] A standard Orbitrap-based intact protein mass measurement set-up (a triplicate LC-MS experiment) was employed using:

[00150] - Analytical HPLC (Dionex) with 30 min run duration,

[00151] - Analytical column (Waters), C4 Aquity, BEH, 90 µl/min @60C,

[00152] - Q Exactive HF FTMS (Thermo),

[00153] - FTMS Booster (Spectroswiss), advanced data acquisition system

[00154] - Full MS resolution: 30'000 @ m/z 200 for intact mAb and 60'000 @ *m/z* 200 for subunit analysis

[00155] - Charge target number (ion number): AGC of 3e6

[00156] Intact Mass (Protein Metrics) was employed for mass spectra deconvolution of intact mAbs. MASH Suite software tool (open access, Wisconsin University, Ying Ge Group) was used for deconvolution of the mass spectra of the subunit analysis. The employed resolution enabled obtaining isotopically-resolved data. Peak-by-Peak software tool

(Spectroswiss) was employed for time domain signals and mass spectra processing. The employed methods enabled obtaining high spectral dynamic range data.

(vi) O-HexNAc localization by peptide mapping

[00157] To localize the HexNAc modification observed on the Fd subunit a bottom-up proteomics approach using trypsin and chymotrypsin digests and HCD and ETD fragmentation was carried out by SpectroSwiss employing the state-of-the-art instrumentation (Orbitrap FTMS), first untargeted and additionally targeted against the most promising peptides. A standard trypsin digestion protocol was employed using ~5µg of protein (concentration around 1µg/µl). 6 µl 2M Urea, 50 mM TEAB were added, the sample was reduced by adding 1.5 µl of 20 mM TCEP and alkylated with 1.5 µl of 80mM Chloroacetamide (incubation 1h at RT) before the digestion with 0.2 µg Trypsin for 2h at 37°C. The digestion was stopped using 10 µl 0.2% TFA and the sample centrifuged and the supernatant was used for the injections.

[00158] A standard Orbitrap-based bottom-up proteomics set-up (a triplicate LC-MS experiment) was employed using:

[00159] - Nano HPLC (Dionex) with 140 min run duration

[00160] - Q Exactive Plus FTMS with HCD employed as MS/MS technique

[00161] - Full MS resolution: 70'000 @ m/z 200

[00162] - Charge target number (ion number): AGC of 3e6

[00163] - MS/MS resolution: 17'500 @ m/z 200

[00164] - Charge target number (ion number): AGC of 1e5

[00165] - MS/MS method: HCD with 27 NCE

[00166] - Data dependent acquisition: top 10

[00167] - Dynamic exclusion: 60 s

[00168] Scaffold (Proteome Software Inc.) was employed for data analysis with the following parameters set:

[00169] Variable modifications: +1 on NQ (Deamidated), +16 on M (Oxidation), +42 on N (Acetyl)

[00170] Digestion Enzyme: SemiTrypsin

[00171] Max Missed Cleavages: 2

[00172] Scaffold: Version Scaffold_4.8.3

[00173] Protein Grouping Strategy: Experiment-wide grouping with binary peptide-protein weights

[00174] Peptide thresholds: 90.0% minimum

[00175] Protein thresholds: 95.0% minimum and 1 peptide minimum

[00176] Peptide FDR: 0.2% (Decoy)

[00177] Protein FDR: 9.2% (Decoy)

[00178] Peaks software was employed for a more detailed data analysis, specifically PTMs analysis.

[00179] Peak-by-Peak software tool (Spectroswiss) was employed for time domain signals and mass spectra processing. The employed methods enabled obtaining high spectral dynamic range data.

(vii) O-HexNAc characterization by monosaccharide analysis by high performance anion exchange chromatography coupled with pulsed amperometric detection, HPAEC-PAD

[00180] For confirmation of O-glycosylation and the determination of the amount of O-HexNAc found on T225 of the heavy chain of Adalimumab a 14 amino acid glycopeptide was generated using FabRICATOR (IdeS) (Genovis AB, Lund, Sweden) and GingisKHAN (Kgp) (Genovis AB, Lund, Sweden) following the product manuals in combination with several purification steps.

[00181] In short, 2 mg commercial Humira or Adalimumab purified from *L. tarentolae* were first incubated with PNGaseF (add 50 U, 3h at 37°C) for N-glycan removal to reduce possible interferences of N-glycan derived monosaccharides during the monosaccharide analysis. The PNGaseF treated sample was then incubated with FabRICATOR (2000 U) overnight in PBS pH 7.1 at 37°C. The digest was purified after via an in-batch CaptoL purification step (3h at RT) to remove the Fc/2 fragments. The remaining F(ab)2 fragments were concentrated with a Pierce PES 3kDa column and re-buffered to 0.1M Tris pH 8, 0.1M NaCl with a ZebaSpin column. The re-buffered sample was incubated with GingisKHAN (2000 U) overnight at 37°C in the presence or 2mM cysteine. The sample was reduced with TCEP for 20 min (20mM) before the 14 amino acid peptide containing the O-HexNAc site was purified using a 10kDa Pierce PES column, which retains LC and Fd fragment. The presence of the 14 amino acid peptide with and without the O-HexNAc modification was confirmed by MALDI. During the MALDI measurements no subunits (LC, Fc/2, Fd) were identified.

[00182] The monosaccharide found as a O-glycosylation on the 14 amino acid peptide ("10k permeate") was analyzed by HPAEC-PAD and the monosaccharide peak were identified by comparison to commercially available monosaccharide standards. The monosaccharides were released from the bioconjugate by TFA hydrolysis (2M TFA for 2h at

121°C). Commercial monosaccharide standards GlcNAc, GalNAc and ManNAc used were also treated with TFA to resemble the monosaccharides that were released from the mAb (GlcN, GalN and ManN after TFA hydrolysis). The resulting underivatized monosaccharides are separated on a CarboPac PA1 column 4 x 250 mm (Thermo Fisher Scientific) by eluting with NaOH/NaOAc and subsequent detection by pulsed amperometric detection (PAD). The sugar identity could be determined by overlaying the released monosaccharides from the mAb with the corresponding monosaccharide standards.

(viii) O-HexNAc characterization by MS fragmentation

[00183] An LC-MS/MS approach was carried out in the Group of Manfred Wuhrer at Leiden University (Medical Center (LUMC), Center for Proteomics and Metabolomics, Leiden, The Netherlands) to confirm the identity of the O-HexNAc, more specifically, whether it corresponds to an *N*-acetylglucosamine (GlcNAc) or *N*-acetylgalactosamine (GalNAc). It has previously been demonstrated that the pattern of oxonium ions obtained in the MS fragmentation can be used to discriminate between a GalNAc and a GlcNAc (Halim et al. (2014) J Proteome Res 13 (12), pp. 6024–6032). Especially the ratio between the intensities of the ions at m/z 138.055 and m/z 144.066 is very different between a GalNAc and a GlcNAc. Unfortunately, no such information for a peptide with *N*-acetylmannosamine (ManNAc) is currently available. The modification site has been identified on a threonine in the tryptic peptide THTCPPCPAPELLGGPSVFLFPPKPK (SEQ ID NO:227) (modified Thr underlined) from the antibody`s heavy chain. The same antibody produced in CHO cells was also available without this specific modification (Humira as Control Ab). A trypsin digestions was performed and a series of LC-MS/MS analyses of these two samples, followed by manual data analysis to look for the specific glycopeptides.

[00184] To obtain the glycopeptides an in-gel trypsin digestion was carried out after a reducing SDS-PAGE (10 µg protein in 10 µl were loaded) for the HC bands of Humira (Control Ab) and the LMTB Adalimumab with O-HexNAc modification (HexNAc Ab, which were analyzed in duplicate using an LC-MS/MS method on a Orbitrap Fusion Lumos mass spectrometer.

[00185] For in-gel digestion, an in-house digestion robotic system was used. During this procedure, gel plugs were first washed with 400 µl 25 mM NH_4HCO_3 and dehydrated using acetonitrile. Proteins were then reduced and alkylated using DTT (10 mM) and iodoacetamide (50 mM), respectively. Subsequently, trypsin was added and proteins were digested overnight. The next day, the tryptic peptides were collected and freeze dried. Prior to

LC-MS/MS analysis, tryptic peptides were reconstituted in 30 µl of 0.1% formic acid of which 1 µl was used for each individual LC-MS/MS analysis.

[00186] LC-MS/MS analysis was performed on Orbitrap Fusion Lumos mass spectrometer (Thermo). Tryptic peptides were separated using water + 0.1 % formic acid as solvent A and acetonitrile + 0.1 % formic acid as solvent B. The separation was performed using a linear gradient of 10-40% solvent B at 250 nl/min for 40 min. Peptides eluting from the gradient were analyzed by mass spectrometry on an Orbitrap Fusion Lumos instrument (Thermo). First, peptides were analyzed in a discovery type of MS/MS experiment. For this purpose, MS scans were recorded with a resolution of 120000. Further, an AGC target of $4*10^5$ and an injection time of 50 ms were used. Charge states of 2-5 were included and masses were dynamically excluded for 10 s after detection. An intensity threshold of $5*10^4$ was used. Data dependent MS/MS fragmentation (Cycle time, 3 sec between master scans) was performed using higher-energy collisional dissociation (HCD) with a collision energy of 32 %. For MS/MS scans, the orbitrap resolution was set to 30000, the AGC target was set to $5*10^4$ and the maximum injection time to 30 ms. Additionally, glycosylation modifications were specifically targeted by MS/MS via an MS2 inclusion list looking for HexNAc losses (m/z 204.087). The AGC target was set to $5*10^5$ with a maximum injection time of 200 ms. HCD collision energies of 32 %, 37 % and 42 % were used for fragmentation. Further, MS/MS scans with a CID collision energy of 35 % were acquired. Data analysis was performed manually.

(ix) Confirmation of absence of O-HexNAc in KO cell lines

[00187] To confirm the absence of the O-HexNAc on Adalimumab in KO-lines in addition to MALDI measurements a peptide mapping was carried out using a trypsin digest and HCD fragmentation employing the state-of-the-art instrumentation (Orbitrap FTMS) in a targeted approach (see sections on O-HexNAc localization by peptide mapping).

(x) Quantification of O-glycosylation on glycopeptide by MALDI-TOF MS

[00188] For the quantification of O-glycosylation with O-HexNAc found on T225 of the heavy chain of Adalimumab an 14 amino acid glycopeptide was generated using successively FabRICATOR (IdeS) (Genovis AB, Lund, Sweden) and GingisKHAN (Kgp) (Genovis AB, Lund, Sweden). For digesting the sample it was re-buffered in 0.1 mM Tris buffer (pH 8.0) and ~10 µg (10 µl) of sample was incubated for 1h at 37°C with 0.5 µl FabRICATOR (ca. 30 U). After that, 1 µl of GingisKHAN (ca. 10 U) and 2 mM reducing agent (cysteine) were

added and incubated for 3h at 37°C. To reduce the disulfide bridges of the hinge region 0.5 µl of 1M TCEP was added (50 mM final concentration) and incubated for 60min at RT.

[00189] Samples were desalted employing C18 ZipTip pipette tips (Millipore) according to the manufacturer's instructions and then spotted onto a ground steel target plate in α-Cyano-4-hydroxycinnamic acid (HCCA; 5 mg/ml HCCA in 40 % acetonitrile with 0.1 % trifluoroacetic acid). Matrix. MALDI-TOF MS was performed using an UltrafleXtreme Matrix-assisted laser desorption/ionization-time of flight/time of flight (MALDI-TOF/TOF) mass spectrometer (Bruker) operated in reflector positive ion mode. The instrument was operated with flexControl 3.4 (Bruker) using a laser intensity of 30-40 %, a mass range of *m/z* 700-3500, a two-fold detector gain and a sample rate of 2.5 GS/s. 3000 laser shots in 500 shot steps were summed up. The spectra were processed in flexAnalysis 3.4 (Bruker) with a signal/noise cut-off of 5 as well as smoothing and baseline subtraction using the TopHat algorithm. Picking of the peaks of interest was performed manually considering the unglycosylated and O-glycosylated versions of the same peptide. The relative abundances of O-glycosylated peptides was determined by integrating the areas of the monoisotopic masses of the H^+ and Na^+ ions and relating them to the sum of the intensities of all identified peptide forms.

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

[00190] 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. Enzymatic release of N-glycans from cell surfaces was performed using PNGase F (New England Biolabs). 50 mg of cells 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 pelleted by centrifugation and 75 µl of the supernatant was dried down in a SpeedVac concentrator. Glycans were re-suspended 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.

[00191] Procainamide-labeled N-glycans were analyzed by hydrophilic interaction chromatography-ultraperformance 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.

[00192] 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.

(xii) EPO glycopeptide analysis

(A) Determination of N- glycosylation site occupation and site specific glycosylation

[00193] Rapigest® SF was used to enhance enzymatic digestion of the proteins in 50 mM ammonium bicarbonate. 180 µg of protein corresponding to 250 µL of each sample were prepared in 50 mM ammonium bicarbonate buffer, pH 8 by Vivaspin 500 PES (5kDa) and four centrifugations (15'000 x g; 10 min, 4°C). The final concentration of the protein was about 3 mg/ml.

[00194] The protein was denatured in 0.1% Rapigest® SF, reduced by DTT (5 mM) at 60°C for 45 minutes and alkylated by iodoacetamide (15 mM) in the dark for 45 minutes at room temperature according to Rapigest® SF protocol (WATERS). The sample was incubated for 16 hours, at 37°C with 6.4 µg Trypsin/Lys-C Mix, Mass Spec Grade (Promega

V507A #201254) to obtain the digested protein. The hydrolytic surfactant was removed by adding 0.5% TFA to the digested protein sample and incubated at 37°C for 30 minutes and centrifugation at 15000 g for 10 minutes. All tryptic peptides were purified on SEP Pack C18, 200 mg (Waters) in 0.1% TFA in water. The elution volume, 2 mL of 70% acetonitrile, 0.1% TFA, was completely dried by lyophilisation.

[00195] Peptides were solubilized in 40 µL ultra-pure water and 30 µl were used for glycopeptide enrichment according to ProteoExtract® Glycopeptide Enrichment Kit protocol 72103-3 (Novagen).

[00196] 30 µL of sample were added to 150 µL of ZIC Glycocapture Resin and the flow through containing non-bound peptides was collected. Glycopeptides were eluted with 225 µL ZIC Elution Buffer. The flow through and eluted samples were completely evaporated in speed vac. Glycopeptides were resuspended in 15 µL of MilliQ water. After purification on Zip Tips MILLIPORE C18 to improve the signal/noise ratio, the glycopeptide solution in 50% methanol was dried on maldi plate and 1µl of CHCA (LaserBiolabs) matrix solution (7 mg/mL 50% acetonitrile) was added.

[00197] Five µL of suspended glycopeptides were adjusted to 50 mM sodium acetate buffer and 1 µL of PNGase F (Promega V483A#226517) and 1 µL of PNGase A (Sigma # 01000353) were added to deglycosylate during 16 hours at 37°C. The deglycosylated peptides after preparation on Zip Tips MILLIPORE C18 (SOP P17/2) were mixed with CHCA (1:1) (LaserBiolabs) matrix solution (7 mg/mL 50:50 acetonitrile/water, 0.1% TFA).

[00198] The flowthrough fractions were prepared and analysed with CHCA (1:1) (LaserBiolabs) matrix solution (7 mg/mL 50:50 acetonitrile/water, 0.1% TFA).

[00199] Peptides in the flow through fraction, deglycosylated glycopeptides and occupied glycopeptides were analysed by MALDI-TOF MS mass spectrometry in positive mode reflectron and linear modes. Linear mode MALDI mass spectra were acquired on MALDI-TOF/TOF Autoflex III (Bruker Daltonics). Acquisition conditions were: 14.3 x 2904V, laser 49%, 6000 shots. Positive ion reflectron MALDI mass spectra were acquired on MALDI-TOF/TOF Autoflex III (Bruker Daltonics) (SOP 44/1). Acquisition conditions with RP850-3500 Bruker method were 40 x 2160V; laser 97%, 5000 shots.

(B) Sample preparation and EPO- O-glycosylation peptide analysis by LC-MS

[00200] For EPO O-glycopeptide analysis a filter aided sample preparation (FASP) for purified protein using trypsin digest was applied. The Amicon 30kd centrifuge filter unit (Millipore, Cat. UFC503096) was primed by washes with water for two times, centrifuged

each time at 10,000g for 10min while FT was discarded. 100 ug of purified EPO sample was added on the Amicon filter, and ABC-Buffer (0.05M NH_4HCO_3 in water pH 8.0) was added up to 400µl. Filters were centrifuged at 10,000g for 10min, washed once with 400 ul ABC-buffer, centrifuged again and FT discarded. All further centrifugation steps were performed at 10,000g for 10min

[00201] Proteins were then reduced with 100 µl of 50mM DTT in ABC-Buffer for 30min at 37°C and filters thereafter centrifuged, washed with 400 µL ABC-Buffer and centrifuged again. Next, proteins were alkylated with 100 µl of 65mM IAA in ABC-Buffer for 1hr at RT in the dark and filters were then centrifuged, washed three times with 400 µl ABC-Buffer and centrifuged each time and FT was discarded.

[00202] The column was transferred to a new collection tube, in which 2ul Trypsin (1ug/ul) and 98ul ABC-Buffer was added to hEPO (wt) to obtain an Enzyme : Protein ratio of 1:20. More trypsin (1.5ul, 1ug/ul) and 98.5ul ABC-Buffer was added to hEPO derived from the triple OGNT-KO to retain an Enzyme : Protein ratio of 1:20. Samples were incubated the overnight at 37°C, for 16h without shaking. The peptides were collected by centrifugation and the FT was transferred to a low binding tube. 400ul H2O was added on the Amicon, and rinsed by pipetting, centrifuged and the FT was transferred to the same low binding tube. Then, 400ul 10% AcN was added on the Amicon, carefully rinsed by pipetting and followed by centrifugation to collect remaining FT in the same low binding tube. Samples were dried in the SpeedVac at RT overnight. Resuspension of the sample was performed with 25ul 5% acetonitrile + 0.1% formic acid and 10ul of which 10 ul were injected into the LC-MS.

[00203] Tryptic peptides were analyzed using am Acquity UPLC System (Waters) with UV detection coupled to a Synapt G2-Si mass spectrometer (Waters). Peptides were separated using an Acquity UPLC Peptide BEH column (130 Å, 1.7 µm, 2.1 mM × 150 mM; Waters) with 0.1 % formic acid in water as solvent A and 0.1 % formic acid in acetonitrile as solvent B. The separation was performed using a linear gradient of 0-38 % solvent B over 120 min. 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* 50-2000; scan time: 0.5 sec; cone voltage: 37 V. MSe was used for fragmentation with 4 V in the trap and 2 V in the transfer cell for low energy scans; and a ramped collision energy of 15-45 V in the trap cell for high energy scans. Data analysis was performed using Byonic and Byologic (Proteinmetrics).

6. EXAMPLES

6.1 EXAMPLE 1 – Identification of O-HexNAc modification on rhEPO and recombinant IgG1

6.1.1 rhEPO

[00204] The CustomGlycan platform is developed for manufacturing recombinant and function customized glycoprotein therapeutics and the composition and methods of producing glycoproteins in vivo have been described (International Publication No. WO2019/002512 A2, incorporated by reference in its entirety herein). Recombinant human Erythropoietin (rhEPO) contains three N-glycosylation sites, and one O-glycosylation site, latter was being modified upon expression in *L. tarentolae* with an single HexNAc attached to Serine 126, exemplified in CustomGlycan host cells St11521 and St11895 (International Publication No. WO2019/002512 A2, for example Fig. 19 and method section 8.11.9: Determination of N-glycosylation site occupation and site specific glycosylation). In both cases, St11521 and St11895 the mass of a peptide ion at m/z 1668.892 corresponded to the tryptic O-glycopeptide, position [117-131] [EAISPPDAASAAPLR] (SEQ ID NO:237) with one HexNAc residue bound. EPO O-glycopeptide was present in the flow through fraction and in the enriched glycopeptide fraction as peptide occupied with one HexNAc residue. This peptide was not detected in its non-glycosylated form (FIG. 1).

6.1.2 Rituximab

[00205] Recombinant expression of human IgG1 antibodies such as Rituximab and Adalimumab was also performed in *L. tarentolae* derived CustomGlycan host cells. Purified mAbs were in-depth characterized for (post-translational) modifications such as glycosylation. While Rituximab led to some variants at the N-terminus due to the suboptimal cleavage of the secretion peptides preceding heavy chain (HC) and light chain (LC) sequences (International Publication No. WO2019/002512 A2, for example Table 12 and Fig. 44), some additional hints from subunit analysis were obtained, pointing towards an additional modification matching the mass of a HexNAc for approximately 20% of the total mAb (data not shown). Further analyses using high-end MS methods were not undertaken on Rituximab due to the heterogeneity of the sample leading to high complexity in MS data interpretation.

6.1.3 Adalimumab

(i) Identification

[00206] Next, anti-TNF alpha IgG1, Adalimumab, heavy and light chains were co-expressed in *L. tarentolae* CustomGlycan host cells with optimized secretion peptides. Adalimumab was Protein A and HIC purified from the supernatant for the characterization of the recombinant mAb preparation by MS, such as intact protein, subunit analysis and peptide mapping methods.

[00207] Intact antibody MS measurement showed the expected mass matching the N-glycosylation on the HC with Man3. However, two additional peaks were prominent, which fit to the mass increment of one or two HexNAc (FIG. 2A). In addition to the intact measurement, the antibody was reduced with TCEP or enzymatically cleaved (IdeS) to generate Fd, LC and Fc/2 subunits. Using the reduced antibody, this modification was found to be present on the heavy chain of the antibody. No HexNAc modification was observed on the light chain (FIG. 2B).The analysis of IdeS derived subunits showed that the additional HexNAc is localized on the Fd subunit of Adalimumab suggesting that either one or two heavy chains are modified with an additional HexNAc glycosylation event (FIG. 2C). These analyses indicated that the additional and unexpected HexNAc modification was located within the HC, more precisely within the Fd part.

[00208] In order to identify the localization of the additional HexNAc modification observed on the Fd subunit of Adalimumab, a bottom-up proteomics approach using trypsin and chymotrypsin digests and HCD and ETD fragmentation was carried out employing the state-of-the-art Orbitrap FTMS instrumentation, first untargeted and additionally targeted against the most promising peptides. These results clearly indicated a HexNAc modification of a threonine within a peptide of the hinge area of the heavy chain: TH**T**CPPCPAPELLGGPSVFLFPPKPK (SEQ ID NO:227) with the O-HexNAc attached to a Threonine (bold and underlined), corresponding to the Thr225 (EU numbering) (FIG. 2D). Such modification (O-glycosylation) was previously suggested in the mAb literature (Plomp, et al. (2015) Mol Cell Proteomics 14 (5), pp. 1373–1384). The detected peptide shows a strong intensity, supporting the intact Fd measurements (relatively high abundance of HexNAc modified Fd). The bottom-up data suggested that two additional sites could also be O-glycosylated with HexNAc. The degree of the O-glycosylation on these sites was however very low and thus difficult to confirm. On the peptide TKPREEQYNSTYR (SEQ ID NO:228) a HexNAc was assigned to the Tyrosine (Y) residue next to the N-glycosite. Further, on the peptide LTVDKSRWQQGNVFSCSVMHEALHNHYTQK (SEQ ID NO:238) an O-glycosylation is likely taking place, but the exact site could not be determined.

[00209] Thus, the O-glycosylation in Adalimumab was confidently located at the Thr225 within the hinge region of the antibody.

(ii) Characterization

[00210] The HexNAc modification found on Adalimumab produced by LimmaTech Biologics' CustomGlycan platform was subjected to specific analyses to address the identity, more specifically, whether it corresponds to an N-acetylglucosamine (GlcNAc), N-acetylgalactosamine (GalNAc) or N-acetylmannosamine (ManNAc). For this purpose two different approaches were used, first, the monosaccharide analysis by high performance anion exchange chromatography coupled with pulsed amperometric detection (HPAEC-PAD) and secondly, by MS LC-MS/MS analysis.

(A) Monosaccharide analysis by high performance anion exchange chromatography coupled with pulsed amperometric detection (HPAEC-PAD).

[00211] To approach the identity by different methods, the Adalimumab was first characterized for the O-HexNAc by monosaccharide analysis by high performance anion exchange chromatography coupled with pulsed amperometric detection, HPAEC-PAD. For identifying the nature of the O-HexNAc found on T225 of the heavy chain of Adalimumab, a 14 amino acid glycopeptide was generated using FabRICATOR (IdeS) and GingisKHAN (Kgp) following the product manuals in combination with several purification steps.

[00212] TFA was used for hydrolysis of HexNAc from the mAb; during TFA treatment the N-Ac is lost and the respective amino-sugar is generated. On the HPAEC the standards GlcNAc, GalNAc and ManNAc, which were also treated with TFA, were chromatographically well separated. In the hydrolyzed Adalimumab sample three peaks were observed with low intensities, two of which were also present in the buffer control and the hydrolysis of the commercial Humira®, not carrying an O-HexNAc. The third peak (RT 9.767 min) in the Adalimumab sample was not present in the controls and eluted at a similar RT as the TFA treated GlcNAc standard, however with a slightly shifted in RT (RT 9.95). Spiking the treated GlcNAc standard in a hydrolyzed Adalimumab sample showed that the slight shift originates from the difference of the matrix between the hydrolyzed sample and the standard and it could thus be hypothesized that the HexNAc present on Adalimumab is a GlcNAc (FIGs. 3A-3B).

(B) Identity of O-HexNAc characterized by MS fragmentation

[00213] To check for the identity of the O-HexNAc, a targeted method was applied in which additional MS/MS events of an ion were triggered once the initial MS/MS scan of this

ion shows the characteristic HexNAc oxonium ion at m/z 204.087. It has previously been demonstrated that this pattern of oxonium ions can be used to discriminate between a GalNAc and a GlcNAc (Halim et al. (2014) J Proteome Res 13 (12), pp. 6024–6032). Especially the ratio between the intensities of the ions at m/z 138.055 and m/z 144.066 is very different between a GalNAc and a GlcNAc.

[00214] First, the specific tryptic peptide (THTCPPCPAPELLGGPSVFLFPPKPK) (SEQ ID NO:227) with the HexNAc modification was identified. The calculated m/z of this peptide is 762.6397 ($[M+4H]^{4+}$). This peptide was found in the Adalimumab samples (eluting around 29.2 min) but not in the commercial control (Humira®) samples, confirming that this single HexNAc modification is unique for the Adalimumab derived from CustomGlycan host cells. As an internal reference, the species at m/z 1467.0175 ($[M+3H]^{3+}$) was used, which eluted around 35.2 minutes in all samples.

[00215] Subsequently, the glycopeptides were looked up in each run by checking for the presence of the characteristic HexNAc oxonium ion at m/z 204.087 in the high collision dissociation (HCD) MS/MS data. Also the tryptic glycopeptides containing the conserved N-glycosylation site in the heavy chain could be observed.

[00216] The samples were then analyzed with a more targeted LC-MS/MS method where additional MS/MS events of an ion was triggered once the initial MS/MS scan of this ion showed the characteristic HexNAc oxonium ion at m/z 204.087. For these additional MS/MS experiments, different collision energies were used (HCD normalized collision energies, NCE, of 32, 37 and 42%) and a higher number of ions were selected for fragmentation.

[00217] Previous experiments using electron transfer dissociation (ETD) demonstrated that the HexNAc is present on Thr-3 within the following tryptic peptide containing the HexNAc (THTCPPCPAPELLGGPSVFLFPPKPK+HexNAc) (SEQ ID NO:227). Using HCD for fragmentation, ions that lost the HexNAc (as neutral loss ions) are primarily observed. To investigate the identity of the HexNAc, the relative intensity of the HexNAc oxonium ions (Table 7) in the low mass region of the MS/MS spectra were evaluated.

Table 7: HexNAc oxonium ions.

Name	***m/z***	**Composition**
HexNAc	204.087	[C8H14NO5]+
HexNAc-H2O	186.076	[C8H12NO4]+
HexNAc-2H2O	168.066	[C8H10NO3]+
HexNAc-C2H4O2	144.066	[C6H10NO3]+

Name	*m/z*	Composition
HexNAc-CH6O3	138.055	[C7H8NO2]+
HexNAc-C2H6O3	126.055	[C6H7NO2]+

[00218] In FIG. 4A, the pattern of HexNAc oxonium ions is shown for the tryptic peptide (THTCPPCPAPELLGGPSVFLFPPKPK) (SEQ ID NO:227) carrying the HexNAc (m/z 762.641), acquired at an NCE of 32%. (The patterns at NCE's of 37 and 42% are not shown). A similar pattern was also observed in the fragmentation spectra of the tryptic peptide with one missed cleavage (SCDKTHTCPPCPAPELLGGPSVFLFPPKPK) (SEQ ID NO:239) and the HexNAc (data not shown).

[00219] Previously, it was demonstrated that the Adalimumab contains a homogeneous glycan on the conserved N-glycosylation site within the tryptic peptide EEQYNSTYR (SEQ ID NO:228). The fragmentation spectrum of this peptide carrying a glycan structure composed of GlcNAc2Man3 was also analyzed (m/z 1041.4221 $[M+2H]^{2+}$). As expected, the pattern of the HexNAc oxonium ions (low intensity of the ion at m/z 144 compared to that of the ion at m/z 138) in this MS/MS spectrum matches with that of a GlcNAc (FIG. 4B). Moreover, the value integrating the intensities of the ions at m/z 138.055 and 168.066 and the ions at m/z 126.055 and 144.066, as described above, was 3.8 in this spectrum.

[00220] As a reference to a peptide carrying a GalNAc, which was measured with the same method on the same instrument in previous experiments, the pattern of HexNAc oxonium ions for a peptide from CD43 (MoxYTTSITSDPK) (SEQ ID NO:229) carrying three GalNAc is shown in FIG. 4C.

[00221] Based on the pattern observed in FIG. 4A, especially the low intensity of the ion at m/z 144 compared to that at m/z 138, it is highly likely that the HexNAc on this peptide in the Adalimumab sample is a GlcNAc. This is further supported by the numerical value displaying the combined intensities of the ions at m/z 138.055 and 168.066 divided by the combined intensities of the ions at m/z 126.055 and 144.066. In the paper by Halim et al (Halim et al. (2014) J Proteome Res 13 (12), pp. 6024–6032), it was shown that for peptides with a GlcNAc, this value was ≥ 2. For the spectrum shown in FIG. 4A this value is 2.6. On the contrary, a value of 0.6 was found in the spectrum with the GalNAc in FIG. 4C, in line with the study by Halim et al..

[00222] Taken together, these complementary data unambiguously identified an O-linked GlcNAc to the Threonine 225 (EU numbering) within IgG1 hinge area of the heavy chain of Adalimumab produced by CustomGlycan host cells.

6.2 EXAMPLE 2 – Bioinformatic screen and analysis of OGNT candidate genes in *Leishmania tarentolae*

[00223] In eukaryotes, all types of O-glycosylation are initiated by distinct polypeptide glycosyltransferases, and most glycans are further elongated/branched and capped in the Golgi by sequential addition of monosaccharides directed by distinct and/or common enzymes (Joshi, et al (2018) *Cell* 172 (3), 632-632.e2). An O-glycan (O-linked oligosaccharide) in vertebrates is frequently linked to the polypeptide via N-acetyl galactosamine (GalNAc) to a hydroxyl group of a serine or threonine residue and can be extended into different structural core classes.

[00224] The main problem in identifying an O-glycosyltransferase ("OGT" or "OGNT") is that there seems to be no unique identifying feature that generally separates OGT from common glycosyltransferases ("GTs"). One may rely on homology to known O-glycosyltransferases.

[00225] In humans, there is a wide range of OGTs known transferring GalNAc, Man, Fuc, Glc, Xylose and GlcNAc (Bennett et al. (2012) *Glycobiology* 22 (6), pp. 736–756), but there were no homologues found in *Leishmania tarentolae*.

[00226] In addition, some more exotic OGT candidates in KEGG were evaluated and screened against the LTAR genome. 1) For KEGG orthology K09667, protein O-GlcNAc transferase, the representative of this family, the human OGT (Uniprot: O15294) gave several matches, but likely due to coincidental congruence of their secondary structure. The relevant active protein domain is PF13844 (GT family 41 as described by PFAM) but there were no matches in *L. tarentolae* to this domain. 2) For K18134, protein O-GlcNAc transferase, the representative of this family human EOGT (Uniprot: Q5NDL2), which transfers a single N-acetyl glucosamine from UDP-GlcNAc to a serine or threonine residue in proteins and specifically glycosylates the Thr residue located between the fifth and sixth conserved cysteines of folded EGF-like domains, there was one match in *L. tarentolae* genome that show the same GT-family-domain: LTAR_110011600, but there were no reverse hits back to the human enzyme, so this was not further regarded. 3) For COLGALT2 (human Gal OGT, transfers beta-galactose to hydroxylysine residues on collagen) there were also two matches:

LTAR_130014000; LTAR360049600. The reverse hits matched back to COLGALT2. However they share the GT25 family domain, which is very broadly defined.

[00227] Importantly, candidates were found to be homologues to OGNT-1, OGNT-2, OGNT-L, which are characterized *Trypanosoma cruzi* GlcNAc O-glycosyltransferases (Heise, et al. (2009) *Glycobiology* 19 (8), pp. 918–933). Based on these *T. cruzi* sequences, homologues were identified and confirmed by reciprocal best hits (phmmer v3.1b; Table 8 and FIG. 5A)

Table 8: Identification of *L. tarentolae* OGNT candidate genes.

Reference		**Best hit**	**E-value**	**Reciprocal best hit**
TcOGNT2-1	Tc00.1047053511309.70	LTAR_170020900.1	5.20E-106	Yes
TcOGNT2-2	Tc00.1047053511759.30	LTAR_170020900.1	1.70E-105	Yes
TcOGNT1-1	Tc00.1047053503511.10	LTAR_020006800.1	9.00E-116	Yes
TcOGNT1-2	Tc00.1047053508741.340	LTAR_020006800.1	1.70E-115	Yes
TcOGNT-L-1	Tc00.1047053503509.10	LTAR_020006900.1	4.90E-27	Yes
TcOGNT-L-2	Tc00.1047053508741.360	LTAR_020006900.1	5.30E-27	Yes

[00228] We therefore focused on the closely related *Trypanosoma* enzymes that were biochemically well characterized to transfer GlcNAc. The biosynthesis of O-glycans in mucins in *T. cruzi* initiates with the addition of a GlcNAc residue from UDP-GlcNAc (the activated sugar donor) to serine or threonine residues in the protein by a uridine diphospho-N-acetylglucosamine:polypeptide-α-N-acetylglucosaminyltransferase (ppGlcNAc-transferase) (Previato, et al (1998) *Journal of Biological Chemistry* 273 (24), pp. 14982–14988). This reaction represents a major difference between O-glycosylation in *T. cruzi* and mammals. In mammals the orthologue enzyme is an UDP-GalNAc transferase that transfers N-acetyl galactosamine (GalNAc) from UDP-GalNAc to the peptide (Hagen (2002) *Glycobiology* 13 (1), 1R-16). This difference may have been originated by the fact that T. *cruzi* is incapable of interconverting UDP-GlcNAc to UDP-GalNAc (Roper, et al (2002) *Proc Natl Acad Sci U S A* 99 (9), pp. 5884–5889). The *T. cruzi* enzyme, in common with most glycosyltransferases, requires divalent metal cations for activity, with Mn2+ being the

most effective. This is in contrast to the human cytosolic O-GlcNAc-transferase, which shows no metal ion dependence. Most strikingly, the *T. cruzi* enzyme attaches GlcNAc to the hydroxylated amino acid via an alpha-linkage, whereas the anomeric specificity of the cytosolic enzyme is beta (Previato, et al (1998) *Journal of Biological Chemistry* 273 (24), pp. 14982–14988). A TcOGNT-2 gene that encodes a ppGlcNAc-transferase activity was also described in *T. cruzi*. Enzymatic analysis showed high levels of UDP-GlcNAc transferase and UDP-GlcNAc hydrolase activities, both specific for UDP-GlcNAc (Heise, et al. (2009) Glycobiology 19 (8), pp. 918–933). The peptide preference and the optimum pH are comparable to the native GlcNAc-transferase activity previously reported in *T. cruzi* microsomal fraction (Previato, et al (1998) *Journal of Biological Chemistry* 273 (24), pp. 14982–14988).

[00229] We also assessed the sequence features of the OGNT homologues identified in the *L. tarentolae* genome using sequence alignments to human GalNAcT1 (UniProt ID Q10472), which with OGNT-1 did not lead to meaningful results. However, for OGNT-2 with human GalNAcT1, the catalytic residues for Mn2+ coordination and UDP-GalNAc binding seem to be conserved in OGNT-2. A structure prediction with Phyre for the three OGNT candidates was performed and the resulting hits for OGNT-1 and OGNT-2 comprise different members of the UDP-GalNAc polypeptide GalNAc transferase family (GalNAc T1, T2, T4, T10 and PGANT9). Of OGNT-2 223 residues (35% of the sequence) were modelled with 99.0% confidence by the single highest scoring template. No meaningful hits were identified for OGNT-L.

[00230] By InterProScan following regions were identified:

[00231] OGNT-2 (638 amino acids, 72.2 kDa): IPR021067; Family: GlcNAc (PF11397 aa 160-316) that share a GT-A fold. Phobius combined transmembrane (TM) and signal peptide (SP) predictor for aa 1-28 cytoplasmic, 29-50 TM, 51-638 non-cytoplasmic.

[00232] OGNT-1 (1136 amino acids, 124.8 kDa): IPR021067; Family: GlcNAc (PF11397 aa 742-1121) that share a GT-A fold. Phobius aa 1-302 non-cytoplasmic, 303-325 TM, 326-1136 cytoplasmic. OGNT-1 has also signatures to the Nucleotide-diphospho-sugar transferases (IPR029044) superfamily.

[00233] OGNT-L (1136 amino acids, 124.4 kDa): IPR021067; Family: GlcNAc (PF11397) that share a GT-A fold. Phobius 1-20 cytoplasmic, 21-42 TM, 43-1136 non-cytoplasmic.

[00234] Additionally, the available proteomes of 96 isolates from the TriTryp database (release 44) were analyzed to identify OGNT homologues in other *Kinetoplastida*. The search

for OGNT variants used T. cruzi OGNTs as reference, the hits were tested by reciprocal best hits on *L. tarentolae* genome, indicating meaningful hits for 47 *Kinetoplastida* (dated Sept 2019). For each species, one representative isolate has been chosen and a total of 81 sequences were used to build a phylogenetic tree by multiple sequence alignment using T-coffee and RAxML (FIGs. 5B and 5C)

[00235] Next, phenotypic effects or even lethality upon deletions of the O-glycosylation enzymes were considered. Interestingly, a high-throughput phenotyping approach termed RNA interference target sequencing, or RIT-seq, could map fitness-costs associated with RNAi in *Trypanosoma brucei* (Alsford et al. (2011) Genome research 21 (6), pp. 915–924). In T. brucei RNAi against the OGNT-2 (Tb927.5.2350) and OGNT-1 (Tb927.2.2400) was associated with loss-of-fitness in individual samples, which hints these enzymes are not essential, but suggests that double knock-out is potentially harmful for cells. OGNT-L (Tb927.2.2380), described as being inactive, does not seem to be essential in *T. brucei*. Single knock-out and especially heterozygous mutations were therefore expected to lead to viable mutants in *L. tarentolae* cells.

6.3 EXAMPLE 3 – Controlling O-HexNAc levels on mAb by targeted deletions. Methods and Compositions of knock out (KO) host cells

[00236] Deletions of the OGNT candidates in *Leishmania tarentolae* were performed by homologous recombination of DNA constructs into the untranslated regions flanking the coding sequence of the respective gene. Due to the tandem organization of OGNT-L and OGNT-1 on chromosome 2 (FIG. 5A and FIG. 6) the two ORFs could also be targeted simultaneously. For this, integration constructs were synthesized that contain a selection marker that ultimately replaces the OGNT coding sequence (CDS) and can be used to select for positive transfectants. Three different versions of integration constructs were used:

[00237] Replacement with a selection marker flanked by 5' and 3' untranslated regions providing it with defined splice leader acceptor and polyadenylation sequences (transcription by endogenous PolII).

[00238] Replacement with a selection marker without flanking untranslated regions (transcription by endogenous PolII). These constructs receive the spliced leader acceptor and polyadenylation sequences from the endogenous OGNT 3' and 5' UTRs.

[00239] Replacement with an expression cassette for glycoengineering that is integrated in counterclockwise orientation and equipped with a promoter region for PolI transcription and

untranslated regions providing spliced leader addition as well as polyadenylation sequences to the gene(s) of interest.

[00240] The genetic integration constructs described above are split into two DNA fragments within the coding sequence of the selection marker, leaving an overlap of 200 bp for homologous recombination between the two fragments. This was necessary to avoid expression of the selection marker from the plasmid (episome) and thus false positive transfectants.

[00241] DNA fragments were prepared for transfection by restriction digest of the cloning plasmids and mixing of the fragments in the appropriate combinations. Transfection was standardly performed using the 4D-Nucleofector™_Core_X.

[00242] Transfection of the DNA fragments for replacement of the OGNT-2 gene by homologous recombination generated positive transfectants that were able to grow in the respective selection antibiotic. PCR analysis on crude DNA preparations revealed that one allele of OGNT-2 was replaced by the selection marker construct, while another wild type allele remained (heterozygous KO, data not shown). Attempts to create homozygous knock-outs by either raising the selection marker concentration or transfection of a second construct carrying a different selection marker were not successful. Since high throughput RNAi screens had indicated non-lethality but potential growth defects under certain conditions for the homologous genes in *T. brucei*, achievement of homologous OGNT knock-outs might be complicated by growth impairment of the transfectants.

[00243] Thus, due to the high efficiency of double strand break formation by CRISPR/Cas9 and the assumption that homology mediated repair is the main DNA repair mechanism in *Leishmania* (Zhang and Matlashewski (2015) MBio 6 (4), e00861; Duncan et al (2017) Molecular and Biochemical Parasitology 216, pp. 30–38), it was attempted to achieve homozygous knock-outs by this mechanism, which had previously been used in other *Leishmania* species (Beneke, et al (2017) R. Soc. open sci. 4 (5), p. 170095; Ishemgulova (2018) PloS one 13 (2), e0192723; Peng, et al (2015) mBio 6 (1), p. 409; Fernandez-Prada, et al (2018) International Journal for Parasitology: Drugs and Drug Resistance 8 (2), pp. 165–173). For this, a 3xflag-hCas9 expression construct containing a nuclear localization signal (Le, et al. (2013) Science 339 (6121), pp. 819–823) was transfected episomally into St10569. The resulting strain St15392 was subsequently transfected with a mixture of guide RNAs (gRNA) and the DNA fragments for replacement of the individual OGNT genes by selection marker integration (flanked by IRs). To confirm the absence of the OGNT genes in these strains (St16248 OGNT-2 KO; St16257 OGNT-1 KO; St6249 OGNT-L KO), were

sequenced on Illumina NextSeq. High genomic coverage was achieved and thus the complete absence of reads matching to the respective OGNT region indicated a successful and complete removal of the respective OGNT gene for all three strains (FIG. 7A). Alternative to sequencing, PCR analysis can be used to confirm homozygous knock-out of the respective OGNT genes (see representative figure in example 6, FIG. 9D).

[00244] In order to analyze whether the knockout of any of these genes is sufficient to prevent O-glycosylation of the Adalimumab hinge region, individual knock-out strains were engineered that co-express Adalimumab from the ssu locus. Additionally, a cell line was created where the tandemly arranged OGNT-L and OGNT-1 genes were replaced simultaneously by a selection marker integration construct. For this, the homologous recombination sites and gRNAs targeting the 5' end of OGNT-L and the 3' end of OGNT-1 were combined.

[00245] From the resulting cell lines (St16478 OGNT-2 KO + Adalimumab; St16700 OGNT-1 KO + Adalimumab, St16702 OGNT-L KO + Adalimumab; St16704 OGNT-1+L KO + Adalimumab), Adalimumab was enriched by ProteinA affinity chromatography and subjected to MALDI based relative O-HexNAc quantification. In preparation for the MALDI based relative O-HexNAc quantification, Adalimumab is subjected to a double digest with FabRICATOR and GingisKHAN during which a 14 aa peptide with the sequence THTCPPCPAPELLG (SEQ ID NO:230) is produced that includes the O-glycosylation site of the IgG hinge region.

[00246] MALDI spectra obtained after the FabRICATOR/GingisKHAN double digest were analyzed and the relative abundances of unglycosylated and O-glycosylated versions of the same peptide were determined by integrating the areas of the monoisotopic masses of the H+ and Na+ ions and relating the summed intensities of all identified peptide forms. Although the MALDI can be considered suitable for a relative quantification of the modified and unmodified peptide, the absolute intensities obtained and the noise level might differ between samples due to differences in quality of the crystals formed during spotting on the target. Therefore, samples where O-HexNAc is expected at low levels might lead to a positive confirmation in some cases and for weaker spots not lead to a confirmation due to changes in the signal-to noise level. Therefore, for some of the KO lines O-HexNAc levels were determined also by the targeted glycopeptide analysis or subunit analysis. Table 3 summarizes the obtained results.

[00247] While for the OGNT-2 KO 15.8% of the hinge region peptides were still found to be modified with an O-HexNAc, no O-HexNAc modification could be detected on the

antibodies prepared from the OGNT-1 KO and OGNT-L KO cell lines. However, in the samples generated from the simultaneous OGNT-1+L KO cell line 0.3% of the peptides were still carrying the O-HexNAc modification. To further assess the amount of the O-HexNAc modification by a more sensitive method, the purified antibodies of the OGNT-1 KO and the OGNT-1+L KO were additionally analyzed by peptide mapping. In these measurements, both strains were found to have almost undetectable remaining O-HexNAc modified hinge regions with around 0.04-0.05%.

[00248] Since the remaining OGNT-2 gene in the OGNT-1+L KO cell line could be responsible for the residual modifications, a triple KO cell line was generated by transfection of the construct for simultaneous OGNT-1+L knock-out into the previously produced OGNT-2 KO strain (St16478). The resulting strain St16636 was confirmed by Illumina NextSeq to have all three OGNT genes knocked out (FIG. 7B).

[00249] In FIG. 8A MALDI spectra from the FabRICATOR/GingisKHAN double digest are shown for a wt background and a triple KO, respectively. While in the wt background the unmodified 14 aa peptide and the peptide with a HexNAc modification was observed, only the unmodified 14 aa peptide was present for the KO line. Additionally, confirmatory targeted glycopeptide analysis was performed to confirm the absence of the O-HexNAc modification. In FIG. 8B the selected ion chromatograms (SIC) of the peptide THTCPPCPAPELLGGPSVFLFPPKPK (SEQ ID NO:227) (+ 2*carbamidomethylation) with and without O-HexNAc are shown for the triple KO line, that was subjected to a tryptic digest and measured with a very sensitive ESI-LC-MS method (Orbitrap FTMS system). While the SIC for the peptide without HexNAc modification showed a good signal, no signal could be confirmed for the peptide with modification, confirming the hypothesis that a knock-out of all three OGNT candidate genes can completely abolish unwanted O-glycosylation on IgG. No other O-HexNAc modification was found in a search for the peptide data. For Adalimumab expressed in CustomGlycan host cells without the OGNT knockout a signal was obtained for the SIC of the peptide THTCPPCPAPELLGGPSVFLFPPKPK (SEQ ID NO:227) (+ 2*carbamidomethylation) with and without O-HexNAc modification.

[00250] For the generation of all previously mentioned strains, integration constructs were used that integrated the selection markers flanked by additional untranslated regions to ensure proper expression. Next it was tested whether these can be omitted and the selection markers can be expressed under the control of the native OGNT UTRs. For this, an integration construct containing only the selection marker coding sequence flanked by homologous

recombination sites for the 5' intergenic region of OGNT-L and the 3' intergenic region of OGNT-1 was transfected into a strain that co-expresses 3xflag-hCas9 and Adalimumab (St16569). Correct replacement of the OGNT-1 and OGNT-L genes in the resulting strain (St16770) was confirmed by PCR and the antibody prepared from this strain was analyzed by MALDI. As in the OGNT-1+L KO cell line that was produced with additional intergenic regions (St16704), the strain without these intergenic regions was found to contain only low amounts of O-HexNAc modified hinge peptides (0.2-0.3%). This confirms that the integration of additional intergenic regions can be omitted for the creation of OGNT KO cell lines.

[00251] Since the CRISPR/Cas9 based knock-out strategy reproducibly produced homozygous knock-out of the individual or tandemly arranged genes, it was next attempted to create a knock-out of all three candidate genes at once by including the gRNAs and homologous recombination constructs targeting the 5' and 3' ends of OGNT-2 as well as the 5' end of OGNT-L and the 3' end of OGNT-1 into the transfection of the Adalimumab, 3xflag-hCas9 co-expressing strain (St16872, cas9 episomal). In this case, the same selection marker was used to target both loci and integration constructs without additional intergenic regions were used. The transfection successfully obtained viable clones that were by PCR confirmed to have all OGNT genes replaced by the selection marker. MALDI based analysis of Adalimumab purified from this strain St17127 confirmed the functional knock-out of all three OGNT genes by the absence of detectable HexNAc modification.

[00252] Taken together, complete OGNT deletion cell lines were generated that show complete absence of O-glycans within the recombinant Adalimumab, making these host cells ideal for manufacturing recombinant antibodies or antibody formats devoid of unwanted modifications.

Table 9: Summary of O-HexNAc quantification of OGNT deletion strains.
n.a. = not available (no measurement performed); n.d.= not detected, *targeted glycopeptide analysis, #data (additionally) measured for fed-batch fermentation derived Adalimumab.

Strain	**Strain number**	**Illumina Sequencing**	**Rel. O-HexNAc % (MALDI)**	**Rel. O-HexNAc % (subunit analysis or * targeted glycopeptide)**
Wt **Adalimumab**	St15449	n.a.	20.9-21.7	17.4

Strain	Strain number	Illumina Sequencing	Rel. O-HexNAc % (MALDI)	Rel. O-HexNAc % (subunit analysis or * targeted glycopeptide)
OGNT-2 KO	St16248	Confirmed	n.a.	n.a.
OGNT-1 KO	St16257	Confirmed	n.a.	n.a.
OGNT-L KO	St16249	Confirmed	n.a.	n.a.
OGNT-2 KO **Adalimumab**	St16478	confirmed for parental (St16248)	15.8	19.4
OGNT-1 KO **Adalimumab**	St16700	Confirmed	0 (n.d.)	0.04*
OGNT-L KO **Adalimumab**	St16702	Confirmed	0 (n.d.)	n.a.
Double OGNT-1/L KO **Adalimumab**	St16704	Confirmed	0#-0.3	0.05 *
Double OGNT-1/L KO (no IR) **Adalimumab**	St16770	n.a.	0.3	n.a.
Triple OGNT-1/2/L KO **Adalimumab**	St16636	Confirmed	0# (n.d.)	0 (n.d.)*
Triple OGNT-1/2/L KO (no IR) **Adalimumab**	St17127	n.a.	0 (n.d.)	n.a.
Triple OGNT-1/2/L KO **Adalimumab** *G0 N-glycan cell line*	St17863	n.a.	0 (n.d.)	n.a.
Triple OGNT-1/2/L KO **Adalimumab** *G2 N-glycan cell line*	St17317/St17318	n.a.	0 (n.d.)	n.a.
OGNT-1/L:: G0 **Adalimumab** *G0 N-glycan cell line*	St17846	n.a.	7	n.a.

6.4 EXAMPLE 4 – Controlling O-HexNAc levels on mAb by overexpression of OGNTs

[00253] To assess the effect of overexpression on the three OGNT candidates, DNA fragments were generated that contained the respective triple HA tagged OGNT genes as well as the selection marker "ble" flanked by intergenic regions (aprt 5' UTR, CamIR, dhfr-ts

3'UTR) to support stable expression. The extremities of the constructs contained homologous recombination sites for the ssu locus which is known to support high level protein expression.

[00254] The linearized constructs (p5932, p5933, p5934) were transfected into a strain that expresses Adalimumab (also ssu locus, St15449). By Western blot it could be confirmed that the resulting strains were expressing either OGNT-2_3xHA (St15884), OGNT-1_3xHA (St15885) or OGNT-L_3xHA (St15886) as expected. Next, Adalimumab was enriched from these strains by Protein A affinity chromatography and the O-HexNAc level was quantified by subunit analysis. While the OGNT-L overexpression strain exhibited almost wild type O-HexNAc modification levels on Adalimumab, both OGNT-1 and OGNT-2 overexpressing strains performed less O-glycosylation on the Adalimumab hinge region. This effect was very pronounced in the OGNT-1 overexpression strain where the O-HexNAc amount was 10x reduced to 1.9% compared to the wt control derived Adalimumab (Table 4). Without further analysis one might speculate that this effect results from a regulation by self-glycosylation as protein primary sequence contains a stretch of THT repeats. Alternatively, another hypothesis could be based on Heise (Heise, et al. (2009) *Glycobiology* 19 (8), pp. 918–933), who described that OGNT-1 has not only transferase but also hydrolysis activity on UDP-GlcNAc, causing UDP-GlcNAc breakdown if there is a lower peptide concentration (less protein substrate). One might expect that OGNT-1 overexpression, while the protein substrate concentration stays the same, shifts the OGNT-1 activity to hydrolysis of UDP-GlcNAc so UDP-GlcNAc might be depleted in the cell. However, these hypotheses warrant further investigation.

[00255] In conclusion, modification of OGNT variant expression levels can be used to tune and reduce the O-glycosylation levels in *L. tarentolae*.

Table 10: Summary of O-HexNAc quantification of OGNT overexpression strains. n.a. = not available (no measurement performed)

Strain	**Strain number**	**Illumina Sequencing**	**Rel. O-HexNAc % (MALDI)**	**Rel. O-HexNAc % (subunit analysis)**
wt **Adalimumab**	St15449	n.a.	20.9-21.7	17.4
OGNT-2 OE **Adalimumab**	St15884	n.a.	n.a.	8.5
OGNT-1 OE **Adalimumab**	St15885	n.a.	n.a.	1.9
OGNT-L OE **Adalimumab**	St15886	n.a.	n.a.	13.2

Strain	Strain number	Illumina Sequencing	Rel. O-HexNAc % (MALDI)	Rel. O-HexNAc % (subunit analysis)
OGNT-1 OE **Adalimumab** *G0 N-glycan cell line*	St16292	n.a.	2.8	1.5

6.5 EXAMPLE 5 – No phenotypic impact of OGNT deletion strains – growth in bioreactor

[00256] To analyze if there was a phenotypic impact of OGNT deletion strains St16704 (OGNT-1/L KO) and St16636 (OGNT-1/2/L KO) were subjected to fed-batch fermentations. Both strains exhibited stable growth in the bioreactor and reached maximum ODs of 18 and 20 at the end of fermentation. This is fully comparable to strains with wild type OGNT genotype such as St12427 grown under the same conditions. Furthermore, full length antibody could be isolated by Protein A enrichment from the supernatant after fermentation and was subjected to MALDI based relative O-HexNAc quantification. In both samples, the O-HexNAc modified peptide was not detectable (Table 9). Thus, knock-out of OGNTs depletes the O-HexNAc modification independent of the culture scale and has no effect on growth during fermentation.

6.6 EXAMPLE 6 – No phenotypic impact of OGNT deletion and overexpression on N-glycan engineering

[00257] Overexpression

[00258] In order to identify whether OGNT overexpression has an effect on other strain modifications such as N-glycan engineering, a strain expressing Adalimumab and the glycosyltransferases sfGnt1, rnMGAT2 and drMGAT1 (St15882, "Adalimumab G0") was transfected with SmiI linearized plasmid pLMTB5933 to achieve integration of an OGNT-1 overexpression construct into the ssu locus (St16292, "Adalimumab G0 OGNT-1 OE"). The resulting strain and the parental strain were grown in 50 ml shake flask cultures and the secreted antibody was enriched via ProteinA affinity chromatography. Samples were subjected to N-glycan analysis (RFMS) as described previously and demonstrated almost identical N-glycan profiles. Thus, the overexpression of OGNT-1 does not affect the expression and function of glycosyltransferases modifying the N-glycan on Adalimumab (FIG. 9A).

[00259] Knock-out

[00260] To assess the effect of OGNT deletion on the expression and function of N-glycan modifying enzymes, CRISPR/Cas9 mediated knock-out of all three OGNT candidates (1/2/L) in the background of a strain expressing Adalimumab and the glycosyltransferases sfGntI, rnMGAT2, drMGAT1 was performed. Protein A enriched Adalimumab prepared from the resulting strain St17863 ("Adalimumab-G0, OGNT-1/2/L KO") and the precursor strain St17607 ("Adalimumab-G0") was subjected to N-glycan analysis (PC-labeling) and displayed almost indistinguishable N-glycan profiles (FIG. 9B). No O-HexNAc could be detected on the purified antibody from strain St17863 by MALDI based analysis. The absence of the putative O-glycosyltransferases thus does not affect glycoengineering of N-glycans. The same was observed for a glycoengineering strain expressing sfGntI, drMGAT1, rnMGAT2 and hsB4GalT1 for N-glycan conversion up to G2 St17318 ("Adalimumab-G2, OGNT-1/2/L KO") in comparison with the precursor strain St15451 ("Adalimumab-G2") (FIG. 9C). Thus also galactosylation of N-glycans is not affected by OGNT knock-outs. In both cases, the absence of the OGNT encoding genes was assessed by PCR (see representative example in FIG. 9D).

6.7 EXAMPLE 7 – replacement of OGNTs by expression cassette for glycoengineering

[00261] In previous examples, the OGNT coding sequences were replaced by selection markers with the intention to remove OGNT function. By this, it was found that selection marker expression can be driven from this chromosomal locus, by exploiting the native intergenic regions. In order to assess, whether the OGNT loci can also be used for functionalization of the cell, i.e. by expression of a glycoengineering construct, an Adalimumab expressing strain (St15449) was transfected with linear fragments derived from plasmids pLMTB8223, 8381, 8301, 8234, 8629, 8238, 8287, 8383, 8384, 8229. This multiple fragment assembly (as described in Provisional Application entitled "Engineered Leishmania Cells" filed even date herewith) targeted an expression construct for drMGAT1, drMGAT2, gjMGAT1 and agMGAT1to the native OGNT-1/L locus on chromosome 2. The resulting strain St17846 was subjected to N-glycan analysis based on Protein A purified Adalimumab and almost homogeneous G0 glycans were detected (92%) (FIG. 10A). Furthermore, construct integration into the OGNT locus was confirmed by PCR covering the selection marker including 3' end of the integrated construct (FIG. 10B) and a relative O-HexNAc content of 7% was determined by MALDI on hinge region peptides from ProteinA enriched Adalimumab from this strain (see Table 9). Taken together, these data corroborate that we

successfully replaced one of the two alleles encoding OGNT-1 and OGNT-L by a functional expression cassette for glycoengineering and thereby reduced, but not abolished the O-HexNAc modification.

6.8 EXAMPLE 8 – OGNT deletion prevents O-glycosylation on erythropoietin

[00262] In contrast to the unexpected O-glycosylation of the IgG hinge region, the native O-glycosylation site of rhEPO was completely modified with O-HexNAc upon expression in wildtype *L. tarentolae* (see Example 1). In order to assess whether the modification of this highly occupied native site can also be controlled by targeted knock out of the *L. tarentolae* OGNTs, strain St17785 expressing LMSAP-rhEPO-Strep was transfected with a Cas9 expression cassette (St17785) and subsequently all three OGNTs were simultaneously knocked out as described in previous examples (St17917). Upon monoclone selection, strain St18143 was obtained which was PCR positive for replacement of all OGNT genes by the selection maker neo (OGNT-1/2/L KO).

[00263] Next, LMSAP-rhEPO-Strep was enriched from the cell culture supernatant of St18143 by ammonium sulfate precipitation and StrepTrap affinity purification and subsequently analyzed by targeted peptide mapping with LC-MS. While the unglycosylated form of the peptide containing the native rhEPO O-glycosylation site was readily detected, no evidence for the presence of masses corresponding to the peptide carrying an O-HexNAc modification (FIG. 11) nor for the presence of oxonium ions originating from O-HexNAc in the expected elution time range was found (data not shown). This corroborates that with these three enzymes the true O-glycosyltransferases of *L. tarentolae* could be knocked out. Thus, the CustomGlycan Platform can be utilized to prevent unwanted O-glycosylation on mammalian target proteins.

6.9 Example 9 – Improved methods for CRISPR/Cas9 mediated OGNT triple knock-outs

[00264] The above-provided method for CRISPR/Cas9 based knock-out of *Leishmania* OGNTs has proven to be very efficient. However, the procedure requires two sets of transfections for introduction of the constitutively expressed 3xflag-hCas9 and generation of the actual knock-out in any given target strain. This requires the use of two different selection markers and thus limits the possibilities for further modifications of the cell lines. Additionally, the constitutive expression of Cas9 and therefore modified host cell protein composition may be unfavorable for stable cell lines. For these reasons, knock-out generation

in *L. tarentolae* by ribonucleoprotein complexes (RNP) was attempted. The above-provided CRISPR guide RNAs targeting OGNT-1, OGNT-2 and OGNT-L were complexed with recombinantly produced Cas9 protein (Alt-R® S.p. HiFi Cas9 Nuclease, Cat. No. 1081061, Integrated DNA Technologies, Inc.) and were directly transfected into the cells along with the same DNA repair constructs used for the above-provided CRISPR mediated replacements of all three OGNT genes by the same selection marker without using additional untranslated regions.

[00265] While previously high knock-out efficiencies in *Leishmania (major)* were only published for the use of SaCas9/sgRNA RNPs (Soares Medeiros, et al (2017) mBio 8:e01788-17), but not for SpCas9, we were able to reproducibly obtain full knock-outs of all three OGNT genes within a single transfection with SpCas9/gRNA RNPs.

[00266] The example shown here demonstrates the triple OGNT knock-out in strain St19462, which already contains two expression constructs encoding the following glycosyltransferases: drMGAT1 (2x) , drMGAT2, rnMGAT1, rnMGAT2 (3x), hsMGAT1, hsMGAT2 and sfGntI. The resulting strain St19855 thus is capable of N-glycan modification to G0, while natural O-glycosylation should be abolished (FIG. 12A). The absence of the OGNT genes was proven by PCR analysis probing for the open reading frames of OGNT-1, OGNT-2 and OGNT-L in the resulting cell line St19855 in comparison with a WT strain (St18344) (FIG. 12B).

[00267] Analogously, cell line St20097 was created by RNP mediated replacement of all three OGNTs with the selection marker for Geneticin resistance. Comparison of the N-glycan profiles released from *L. tarentolae* surface proteins of the parental cell line St19462 and the triple OGNT knock-out cell line St20097 demonstrated that the efficiency of N-glycan conversion to G0 was not affected by OGNT knock-outs introduced by the RNP transfection method (FIG. 12C). This confirmed reproducibility of the approach.

[00268] Next, an Adalimumab expression construct was transfected into the knock-out cell line St19855 (FIG. 12A). The antibodies purified from the resulting cell line (St19915) were subjected to the FabRICATOR/GingisKHAN double digest described above. The MALDI spectrum shown in FIG. 12D confirmed the absence of O-HexNAc modification on the 14 aa peptide.

[00269] To assess how far a cell line that has undergone OGNT triple KO by RNP transfection can be further modified, the knock-out cell line St19855 was further modified by transfection of another glycoengineering module containing several copies of MGAT1 (drMGAT1, gjMGAT1, agMGAT1) and another copy of MGAT2. In order to analyze the

resulting cell line St19931 (FIG. 12A) for its proficiency in glycoengineering, it was furthermore transfected with an Adalimumab expression construct, resulting in cell line St19998. Comparison of the N-glycan profiles released from antibodies (Fc) produced in cell lines St19915 and St19998 clearly demonstrated that further improvement of the entry strain St19855 was obtained by transfection of the additional glycoengineering module, since St19998 exhibits 100% conversion to G0, while in St19915 only 96% of the N-glycans are fully converted (FIG. 12E). This confirmed, that after undergoing CRISPR/Cas9 mediated OGNT removal by RNP transfection, the resulting cell lines were still fully modifiable. Moreover, these OGNT deleted and O-glycosylation deficient strains fully retained growth and target protein expression performance.

[00270] In order to assess whether the RNP transfection can be used to establish O-glycosylation free cell lines with alternative N-glycan phenotypes, the following cell lines were produced in addition to the previously shown G0 variants: A) St19955 (triple OGNT replacement with selection marker conferring resistance to Zeocin in WT *L.tarentolae* St18344) and St20107 (triple OGNT replacement with selection marker conferring resistance to Geneticin in WT *L.tarentolae* St18344), which homogeneously produce Man3 N-glycans and B) St19885 (transfection of galactosyltransferase expression cassette into a G0 N-glycan producing strain, in which all 3 OGNTs were replaced by the Zeocin resistance marker, St19855) and St20201 (transfection of galactosyltransferase expression cassette into a G0 N-glycan producing strain, in which all 3 OGNTs were replaced by the Geneticin resistance marker, St20097), which exhibit homogenous conversion of their surface N-glycans to G2. Table 11 summarizes the resulting strains and their characteristics. This further corroborated reproducibility of the RNP mediated OGNT removal procedure as well as the fact that this method can be utilized at any point of the cell line engineering process and does not interfere with other modifications. Importantly, O-glycosylation deficient and N-glycoengineered cell lines retained full capabilities for growth, viability and further target protein expression.

Table 11: Summary of triple OGNT knock-out cell lines with different N-glycan profiles and different resistance genes replacing the O-HexNAc transferase genes.

Strain	**OGNT triple KO (resistance)**	**N-glycan profile**	**PCR confirmation**
St19955	Ble (Zeocin)	n.a. (parental, St18344 = 100% Man3)	yes
St20107	Neo (Geneticin)	n.a. (parental, St18344 = 100% Man3)	yes

St19855	Ble (Zeocin)	n.a. (parental, St19462 = 100% G0)	yes
St20097	Neo (Geneticin)	100% G0	yes
St19885	Ble (Zeocin)	95% G2, 4% G1-N, 1% Man3	Parental (St19855)
St20201	Neo (Geneticin)	99% G2, 1% G1-N	Parental (St20097)

[00271] In conclusion, the RNP mediated knock-out procedure in combination with introduction of an antibiotic resistance marker is as efficient as the one using constitutively expressed Cas9. Since it however requires only the expression of a single selection marker, additionally saves time by avoiding a second transfection step and finally also avoids retention of the Cas9 expression construct, this method is therefore preferred. As the method was proven to be highly effective in removing the three OGNT genes at once, it could also provide a useful tool for the knock-out of other targets.

7. EQUIVALENTS

[00272] 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.

[00273] 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	pLMTB4123	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATTGGATAACT TGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTGTTCTCCACTC CAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCGAATGAATGACA GTAAAACCAATGCCTTCACTGGCAGTAACACCCAGCAGTGTTGACTCA ATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGTCTTTTGACGAACA ACTGCCCTATCAGCTGGTGATGGCCGTGTAGTGGACTGCCATGCATGG CGTTGACGGGAGCGGGGGATTAGGGTTCGATTCCGGAGAGGGAGCCTG AGAAATAGCTACCACTTCTACGGAGGGCAGCAGGCGCGCAAATTGCCC AATGTCAAAACAAAACGATGAGGCAGCGAAAAGAAATAGAGTTGTCAG TCCATTTGGATTGTCATTTCAATGGGGGATATTTAAACCCATCCAATA TCGAGTAACAATTGGAGGACAAGTCTGGTGCCAGCACCCGCGGTAATT CCAGCTCCAAAAGCGTATATTAATGCTGTTGCTGTTAAAGGGTTCGTA GTTGAACTGTGGGCTGTGCAGGTTTGTTCCTGGTCGTCCCGTCCATGT CGGATTTGGTGACCCAGGCCCTTGCAGCCCGTGAACATTCAAAGAAAC AAGAAACACGGGAGTGGTTCCTTTCCTGATTTACGCATGTCATGCATG CGTCGAAGATCCAGTCGCAGCCTGACCGCATCACACATCAAGGCGTTA CAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTT GAGGGATCTAATGGATTCGGAACTTTGGTCGTTTGGTCTCTCATGCTG CCCAATCCCATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCCGTT CTATTTGGACAACGATGTGTACTGTAATGCGTGCGCCATCTGACAACG AATAGATCAGCAGCATTCGCACACTTGCACATACCCAGTGAAGCTTTT GTGTCTGTCGTATTGACAACACCGACTGCAACAAGGTGTAGATAGAAG TTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCTCCTGCTTTCCTTG CTGTGCCTTGCCACCAGATCTAAGCTTATGCGGCTCAACGTCAAGAAG GCGCTCATCTTCGTCGGCTGCGTGGTCTTCCTCTGGGTCCTGCTCTCG TACGCGAGCGTGATTGAGGTGCCGCGCGCGGTCCCGCAGAAGGACCCG GCCGTGGAGATCGAGAAGAAAATCATTAAGCTGCAAAAGCAGGTGGAC GCCCAGATGGCCGAGAGCAAATCGCTGCTGGCGAAGGTCAAGAAGCTG AAGAAGATTAGCGAGGGCGAGAACGTGGGTGGCGAAGAGGACAGCCTG AAGGACTCGGAGGTGATGCAGCACCTGTCGCAGCCGATCCTGCCGGTC CTCGTCATCGCGTGTGACCGGGTGACCGTCCAGCGCTGCCTGGACAAC CTCGTCAAGTTCCGCCCCAGCAAGGAGACGTTCCCGATCATTGTGAGC CAAGACTGTGGCCACAACGCCACCTACGAAGTGATCACGAGCTACACG GCGAGCGACCCGACGATCAGCGTGGTGCGCCAACCGGACCTCAGCGAG ATCGTGCTGCCCCGCGTGAAGGTGAAGTTCCGGGGCTACTACAAGATC GCCCGCCACTATAAGTTCGCGCTGAACCACGTCTTTGAGACGCTGGGC

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	pLMTB 4239	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATTGGATAACT TGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTGTTCTCCACTC CAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCGAATGAATGACA GTAAAACCAATGCCTTCACTGGCAGTAACACCCAGCAGTGTTGACTCA ATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGTCTTTTGACGAACA ACTGCCCTATCAGCTGGTGATGGCCGTGTAGTGGACTGCCATGCATGG CGTTGACGGGAGCGGGGGATTAGGGTTCGATTCCGGAGAGGGAGCCTG AGAAATAGCTACCACTTCTACGGAGGGCAGCAGGCGCGCAAATTGCCC AATGTCAAAACAAAACGATGAGGCAGCGAAAAGAAATAGAGTTGTCAG TCCATTTGGATTGTCATTTCAATGGGGGATATTTAAACCCATCCAATA TCGAGTAACAATTGGAGGACAAGTCTGGTGCCAGCACCCGCGGTAATT CCAGCTCCAAAAGCGTATATTAATGCTGTTGCTGTTAAAGGGTTCGTA GTTGAACTGTGGGCTGTGCAGGTTTGTTCCTGGTCGTCCCGTCCATGT CGGATTTGGTGACCCAGGCCCTTGCAGCCCGTGAACATTCAAAGAAAC AAGAAACACGGGAGTGGTTCCTTTCCTGATTTACGCATGTCATGCATG CGTCGAAGATCCAGTCGCAGCCTGACCGCATCACACATCAAGGCGTTA CAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTT GAGGGATCTAATGGATTCGGAACTTTGGTCGTTTGGTCTCTCATGCTG CCCAATCCCATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCCGTT CTATTTGGACAACGATGTGTACTGTAATGCGTGCGCCATCTGACAACG AATAGATCAGCAGCATTCGCACACTTGCACATACCCAGTGAAGCTTTT GTGTCTGTCGTATTGACAACACCGACTGCAACAAGGTGTAGATAGAAG TTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCTCCTGCTTTCCTTG CTGTGCCTTGCCACCAGATCTGCCATGGCCTCGAGGCTCGTCCGTGTG CTGGCCGCCGCCATGCTGGTTGCAGCGGCCGTGTCGGTCGACGCGGCG CCGCCACGCCTGATCTGCGACAGCCGCGTGCTGGAGCGCTACCTGCTG GAGGCGAAGGAAGCGGAGAACATCACCACCGGCTGCGCGGAGCACTGC AGCCTGAACGAGAACATCACGGTGCCGGACACGAAGGTGAACTTCTAC GCGTGGAAGCGCATGGAGGTCGGCCAGCAGGCGGTGGAGGTCTGGCAG GGCCTGGCGCTGCTGAGCGAGGCGGTGCTGCGCGGCCAGGCCCTGCTG GTGAACAGCAGCCAGCCGTGGGAGCCGCTGCAGCTGCACGTGGACAAG GCCGTGAGCGGCCTGCGCAGCCTGACCACCCTGCTGCGCGCCCTGGGC GCCCAGAAGGAAGCGATCAGCCCGCCGGACGCCGCCAGCGCCGCCCCG CTGCGCACGATCACGGCCGACACGTTCCGCAAGCTGTTCCGCGTGTAC AGCAACTTCCTGCGCGGCAAGCTGAAGCTGTACACCGGCGAGGCCTGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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3	pLMTB 5026	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGGAGATCGGTACTTCGCGAATGCGTCGAGATG GTACCAAATTGGATAACTTGGCGAAACGCCAAGCTAATACATGAACCA ACCGGGTGTTCTCCACTCCAGACGGTGGGCAACCATCGTCGTGAGACG CCCAGCGAATGAATGACAGTAAAACCAATGCCTTCACTGGCAGTAACA CCCAGCAGTGTTGACTCAATTCATTCCGTGCGAAAGCCGGCTTGTTCC GGCGTCTTTTGACGAACAACTGCCCTATCAGCTGGTGATGGCCGTGTA GTGGACTGCCATGCATGGCGTTGACGGGAGCGGGGGATTAGGGTTCGA TTCCGGAGAGGGAGCCTGAGAAATAGCTACCACTTCTACGGAGGGCAG CAGGCGCGCAAATTGCCCAATGTCAAAACAAAACGATGAGGCAGCGAA AAGAAATAGAGTTGTCAGTCCATTTGGATTGTCATTTCAATGGGGGAT ATTTAAACCCATCCAATATCGAGTAACAATTGGAGGACAAGTCTGGTG CCAGCACCCGCGGTAATTCCAGCTCCAAAAGCGTATATTAATGCTGTT

SEQ ID NO.	Description	Sequence
		GCTGTTAAAGGGTTCGTAGTTGAACTGTGGGCTGTGCAGGTTTGTTCC TGGTCGTCCCGTCCATGTCGGATTTGGTGACCCAGGCCCTTGCAGCCC GTGAACATTCAAAGAAACAAGAAACACGGGAGTGGTTCCTTTCCTGAT TTACGCATGTCATGCATGCGTCGAAGATCCAGTCGCAGCCTGACCGCA TCACACATCAAGGCGTTACAGCCTCTCCGTCTTTGCTGCACCCAAGTG TATTCGTGTGACCGCGTTGAGGGATCTAATGGATTCGGAACTTTGGTC GTTTGGTCTCTCATGCTGCCCAATCCCATGCGCTTTTCTCCGTGCCTC TCTGTCTCCCCTTCCGTTCTATTTGGACAACGATGTGTACTGTAATGC GTGCGCCATCTGACAACGAATAGATCAGCAGCATTCGCACACTTGCAC ATACCCAGTGAAGCTTTTGTGTCTGTCGTATTGACAACACCGACTGCA ACAAGGTGTAGATAGAAGTTGGCCTTCTCGCTCGCTCGCACGCTCTTC ACGCTCCTGCTTTCCTTGCTGTGCCTTGCCACCAGATCTGCCATGATC GCGGGCAGCGTGCGCCGCGGCGTGATCCTGCTGCTGGTGGCGGTGGCG GTGGCGACGATGGCGGCGGCGGTGAGCGCGGCGCAGATCGTGCTGAGC CAGAGCCCGGCGATCCTGAGCGCGAGCCCGGGCGAGAAGGTGACGATG ACGTGCCGCGCGAGCAGCAGCGTGAGCTACATCCACTGGTTCCAGCAG AAGCCGGGCAGCAGCCCGAAGCCGTGGATCTACGCGACGAGCAACCTG GCGAGCGGCGTGCCGGTGCGCTTCAGCGGCAGCGGCAGCGGCACGAGC TACAGCCTGACGATCAGCCGCGTGGAGGCGGAGGACGCGGCGACGTAC TACTGCCAGCAGTGGACGAGCAACCCGCCGACGTTCGGCGGCGGCACG AAGCTGGAGATCAAGCGCACGGTGGCGGCGCCGAGCGTGTTCATCTTC CCGCCGAGCGACGAGCAGCTGAAGAGCGGCACGGCGAGCGTGGTGTGC CTGCTGAACAACTTCTACCCGCGCGAGGCGAAGGTGCAGTGGAAGGTG GACAACGCGCTGCAGAGCGGCAACAGCCAGGAGAGCGTGACGGAGCAG GACAGCAAGGACAGCACGTACAGCCTGAGCAGCACGCTGACGCTGAGC AAGGCGGACTACGAGAAGCACAAGGTGTACGCGTGCGAGGTGACGCAC CAGGGCCTGAGCAGCCCGGTGACGAAGAGCTTCAACCGCGGCGAGTGC TGATCGAGGGAGGAGGAGGAGGCGCGTAGCATTGCGTGCGGGTTATGT GTGCGTGCGTGTGTGTGTGCGGTGCGCGCCTTTCCTCTTTTTTTTCTC CCTCTCGTCGGTTTTTTTTTTCTGAGGAGACGGGGCGAAGACGCGAGC GGGGGGCGGCGTTTGTGTGTGTGTGTGCGCGTGTCGGGGGCAGCGGTG TTGGCGGAACGGCCAACGCCCTGCCCCCTCCCCGCCCTGCGACGTTTC TGCGCACCCGTTCTCTCCTTCCTGCGTGCGTGTCTGCGCGCATGCACA TCTGTCCGCGTGTGCCGCAGCGCTGGTATTTTTGTGAGGGCAGAGCCC TGCCTCCCCGCCTCTCTGCCGTTGGCAGGTGAAGCGAAAACGAAGCGA GAGGGCAGTCTGCATGTGTGTGCGAGGGCATGCGGAGCCCCCCTCCCC CCGCCCCCTGCCGTGCTGCACCGCTATTGTGGCGTCTTCTCTCGTTGT GCGCAAGTGTGGCTGCACCACGGCCGCCTCATGTGCGTGTGTGCGCAT GTACACACACACACACACACACACACACACACACGGGCAGGCGCACGCTC CTCTCTCTTCAGGGAGCGCCGCCCCGCTGGTGTCATTGGACGAGCATC CGCCGCGCATCTCTTCACCCCTCACCCCTCATCCCTCTCCCCTCTCCC CGCACACACACGCAGTCCTTCGCTTTCACTCTTCGAACAAACACCTCA ACCATCTTATCACCTTTCTCTCTTCCTTGTCAACCATGCGTGAGGCCA TGATCGCGGGCAGCGTGCGCCGCGGCGTGATCCTGCTGCTGGTGGCGG TGGCGGTGGCGACGATGGCGGCGGCGGTGAGCGCGGCGCAGGTGCAGC TGCAGCAGCCGGGCGCGGAGCTGGTGAAGCCGGGCGCGAGCGTGAAGA TGAGCTGCAAGGCGAGCGGCTACACGTTCACGAGCTACAACATGCACT GGGTGAAGCAGACGCCGGGCCGCGGCCTGGAGTGGATCGGCGCGATCT

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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4	pLMTB 5932	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATTGGATAACT TGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTGTTCTCCACTC CAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCGAATGAATGACA GTAAAACCAATGCCTTCACTGGCAGTAACACCCAGCAGTGTTGACTCA ATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGTCTTTTGACGAACA ACTGCCCTATCAGCTGGTGATGGCCGTGTAGTGGACTGCCATGCATGG CGTTGACGGGAGCGGGGGATTAGGGTTCGATTCCGGAGAGGGAGCCTG AGAAATAGCTACCACTTCTACGGAGGGCAGCAGGCGCGCAAATTGCCC AATGTCAAAACAAAACGATGAGGCAGCGAAAAGAAATAGAGTTGTCAG TCCATTTGGATTGTCATTTCAATGGGGGATATTTAAACCCATCCAATA TCGAGTAACAATTGGAGGACAAGTCTGGTGCCAGCACCCGCGGTAATT CCAGCTCCAAAAGCGTATATTAATGCTGTTGCTGTTAAAGGGTTCGTA GTTGAACTGTGGGCTGTGCAGGTTTGTTCCTGGTCGTCCCGTCCATGT CGGATTTGGTGACCCAGGCCCTTGCAGCCCGTGAACATTCAAAGAAAC AAGAAACACGGGAGTGGTTCCTTTCCTGATTTACGCATGTCATGCATG CGTCGAAGATCCAGTCGCAGCCTGACCGCATCACACATCAAGGCGTTA CAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTT GAGGGATCTAATGGATTCGGAACTTTGGTCGTTTGGTCTCTCATGCTG CCCAATCCCATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCCGTT CTATTTGGACAACGATGTGTACTGTAATGCGTGCGCCATCTGACAACG AATAGATCAGCAGCATTCGCACACTTGCACATACCCAGTGAAGCTTTT GTGTCTGTCGTATTGACAACACCGACTGCAACAAGGTGTAGATAGAAG TTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCTCCTGCTTTCCTTG CTGTGCCTTGCCACCAGATCTATGAAGCCAGAAATGCTAGACCATGGC CAGATGCCAAGCTTACTCAAGCGGCCTCTGCGCATGCCGCGGCGTCGC CTCAGCGCACGTCGGCGACAGGCGCTTAAAGTCTTCATCGTTATTCTG TGCTTGTGTGCGTTTCTTTTCATTTTTTTCTTCTCAGCGCGGCTGCCC GGCATTCTGCACGAGCGCATTACTCCAAGTGAAAAGCCGTGGCTCACC CGAGCAGGGAACTCGACGCTCTTCGAGAAAGTGGTTCACAACCGAATC CCGGGGACCGCGTGGCGCGATGCTCACCTGAACACCATTATCTCCCTC GCGAAGTCTGGTGACGTGGTGCACTTGACTCCCACTAAACACGTTCGC CACCGCCGAGCCAGCGGCAGCAACTCTAGCACATTCCAGAAGTGGGAA TCACTCTATAGACCGAGCGACAGGTACCATATCCCTGCCTGGGCCACG CCGGAAGACCGTGACACGCTGCAGCACGCGTCTATCTTTACCTCCTTA GCTTCTTTCCGCGACCACGAGTGTGCGCTGACGCTGCGCAACCTTTTC GACATGGCTGTTGCTCCGCACCGCCTGTACGTTGGTGTGAGCGAGGAG

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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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5	pLMTB 5933	ATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATAT TTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTC CCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACAT TAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTT TCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGG TCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGG GCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGG CATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATAC CGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCAT TCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGC TATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTT GGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCA GTGAATTGACGCGTATTGGGATATTTAAATTGGATAACTTGGCGAAAC GCCAAGCTAATACATGAACCAACCGGGTGTTCTCCACTCCAGACGGTG GGCAACCATCGTCGTGAGACGCCCAGCGAATGAATGACAGTAAAACCA ATGCCTTCACTGGCAGTAACACCCAGCAGTGTTGACTCAATTCATTCC GTGCGAAAGCCGGCTTGTTCCGGCGTCTTTTGACGAACAACTGCCCTA TCAGCTGGTGATGGCCGTGTAGTGGACTGCCATGCATGGCGTTGACGG GAGCGGGGGATTAGGGTTCGATTCCGGAGAGGGAGCCTGAGAAATAGC TACCACTTCTACGGAGGGCAGCAGGCGCGCAAATTGCCCAATGTCAAA ACAAAACGATGAGGCAGCGAAAAGAAATAGAGTTGTCAGTCCATTTGG ATTGTCATTTCAATGGGGGATATTTAAACCCATCCAATATCGAGTAAC AATTGGAGGACAAGTCTGGTGCCAGCACCCGCGGTAATTCCAGCTCCA AAAGCGTATATTAATGCTGTTGCTGTTAAAGGGTTCGTAGTTGAACTG TGGGCTGTGCAGGTTTGTTCCTGGTCGTCCCGTCCATGTCGGATTTGG TGACCCAGGCCCTTGCAGCCCGTGAACATTCAAAGAAACAAGAAACAC GGGAGTGGTTCCTTTCCTGATTTACGCATGTCATGCATGCGTCGAAGA TCCAGTCGCAGCCTGACCGCATCACACATCAAGGCGTTACAGCCTCTC CGTCTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTTGAGGGATCT AATGGATTCGGAACTTTGGTCGTTTGGTCTCTCATGCTGCCCAATCCC ATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCCGTTCTATTTGGA CAACGATGTGTACTGTAATGCGTGCGCCATCTGACAACGAATAGATCA GCAGCATTCGCACACTTGCACATACCCAGTGAAGCTTTTGTGTCTGTC GTATTGACAACACCGACTGCAACAAGGTGTAGATAGAAGTTGGCCTTC TCGCTCGCTCGCACGCTCTTCACGCTCCTGCTTTCCTTGCTGTGCCTT GCCACCAGATCTGCCATGGGTATGGTGCGCAGTGGTGTCTTCGACCCC CCCCCCCCCCCCCCGCCCCCAACAGCCAAGCGTTGTGCTCCGCCGCCGC CGTGGCACTTGGCGTCTACGGAGTCGATTCCGTGTAGGCGCGGACTCA CCCACCCGCCAACACCTGCGCATGCTGCTTCACTTATCTCTGCTGTTC GATGCGACATCCTCCGCACCCTCCTCCACGCGGACGACACACACACAC ACACACACACACACACACACACACGGACTTTCTGTGACTTCATTGCAC ACAGGCGCTCGCGCCACCGCAGTTGGGAGGGCTCCTCGCACGCGCGAC GCTCTCATGGACACTCACGTGACCGCCTGTGTAAAGCGGGTGCCCTCA

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	pLMTB 5934	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATTGGATAACT TGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTGTTCTCCACTC CAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCGAATGAATGACA GTAAAACCAATGCCTTCACTGGCAGTAACACCCAGCAGTGTTGACTCA

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	pLMTB 6459	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGTGAAATGGTGTATCCCATGACACGTCTTACGTCATGTTCCTCC CTCCTTCGTATGCGTACGACTCTCCTCCGCCTCCGCCTCCGCCTCCGC CTCCGCCTCCGCCTCCGCCTTCTCTGCGCCGGTTTCCTGGAGGATGGA GAGCTCTTGCTCATAGATTGAAGAAAGACCAGGCAAGCCACGGAAAAC TCCGAACAAAAGCGGACTCACGCGGCCGTCTGCATTTGACGTGCTTGC ATACATATACGCACCAACCTTGTGCACGTCTTGTTGACATCCGTAACA CTTGCCTCATTTTTTCCGTGCTGCTCGGATGCACACTCCTGGTGTGGG GCGTAGTCACTATTCGTCTCTCACCAACACACACACACACACACACAC ACACCTGTACATCTCTCTCTCTCTCCTTTTCTGTGTGCCCCGGCGGAC GTGCGTGCGTGTCTAATCACTGAAATTCTTCACATTGCATAGAACGTA GCGTCAGGACGCAGCCTCGAACGGCGAAGTCGCAGCCTGACCGCATCA CACATCAAGGCGTTACAGCCTCTCCGTCTTTGCTGCACCCAAGTGTAT TCGTGTGACCGCGTTGAGGGATCTAATGGATTCGGAACTTTGGTCGTT TGGTCTCTCATGCTGCCCAATCCCATGCGCTTTTCTCCGTGCCTCTCT GTCTCCCCTTCCGTTCTATTTGGACAACGATGTGTACTGTAATGCGTG CGCCATCTGACAACGAATAGATCAGCAGCATTCGCACACTTGCACATA CCCAGTGGAGCTTTTGTGTCTGTCGTATTGACAACACCGACTGCAACA AGGTGTAGATAGAAGTTGGCCTTCTCGCTCGCTCGCACGCTCTTCACG CTCCTGCTTTCCTTGCTGTGCCTTGCCACCACCTAGGCTCGAGATGGC CAAGTTGACCAGTGCCGTTCCGGTGCTCACCGCGCGCGACGTCGCCGG AGCGGTCGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGT GGAGGACGACTTCGCCGGTGTGGTCCGGGACGACGTGACCCTGTTCAT CAGCGCGGTCCAGGACCAGGTGGTGCCGGACAACACCCTGGCCTGGGT GTGGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGGAGGTCGT GTCCACGAACTTCCGGGACGCCTCCGGGCCGGCCATGACCGAGATCGG CTTCGAAATTTAAATGGTACCATCCCAATGGCGCGCCGAGCTTGGTCG AGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAT

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8	pLMTB 6460	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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9	pLMTB 6463	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGACCGCACCGACATCTTCTTCCGTGGCCGAGGATAGCGTGCCAG CCGAGCTGCGTGATGCGCGCACCTTCACACACGACAAGTTCTGGGCTT TGCTGATGGCCCACCGCGATGCGGGTACGCCGCTTGGCGCCACCGAGA CAAGGCAGCAGGCCTCTGCGCCGCGGGAGAGCTCGCTGTTGCTCTACC CCTTACGCCGAACTATGAAGGAGTGGGAGCTGTTCGCTGGCATGCCGC TGACAACCCTCCGTGATGCGCTGCACCCGACCTGACGCATGCAGGGAT ATCGTCCCCAACTTGCGAGGACCTCCTGCACAACGACCTGGATCTCGG CGCACGCGCAACCAGCGCATGCGTTGTGCATCAGAAACATCGTACGCC ATCGATCGTCTGCTTTCTCTGGTAAGCCTGGCGCATCGGCGCCGACGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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10	pLMTB 6466	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGCGGTGGGCGCGCGCGTAATCGGGCACGCGTCAGGCAGCGCCAC AGAGGCCTGCCCAGACAGCGAACGGGTCCATCGTACACCCTCGGTCCC CGGCATTCGCAGGACTGTGGGCCATGCGGTCACGACTTCTTCCGAGTC GGCGGCCTCGCGCCGCCCGCTGGGCCCGCTGCACCGTTTTCTGTCTGG GCTTTTTCATTGGCGCTATTACTCTCTGCGGCGTCGTTGCGTGGAGGA TCATGAGTGACATGAGCGAGGACGTGAAGGGCCGCAGAACGCTGACGC AGCACCCTTCCCCAGGCAAGCCAGGGTGCCACGGGTGACTGACGCTGG CGCTGACGACGACGCTGGGTTGTTGCGCAGCAGTGGAGGGGCAGCTCC ATACACGGAAGGCTTAGAGGAGCTGGTCCTGCTGCTCCGTATCTACGC CGAAGAAACTGGTGTCCGGGTAACCGACACGTCTTATGCGCTTCCAGA GGGCGTGTCTGCAGGTGCAGGCCTCAGTCGCAGCCTGACCGCATCACA CATCAAGGCGTTACAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTC GTGTGACCGCGTTGAGGGATCTAATGGATTCGGAACTTTGGTCGTTTG GTCTCTCATGCTGCCCAATCCCATGCGCTTTTCTCCGTGCCTCTCTGT CTCCCCTTCCGTTCTATTTGGACAACGATGTGTACTGTAATGCGTGCG CCATCTGACAACGAATAGATCAGCAGCATTCGCACACTTGCACATACC CAGTGAGGCTTTTGTGTCTGTCGTATTGACAACACCGACTGCAACAAG GTGTAGATAGAAGTTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCT CCTGCTTTCCTTGCTGTGCCTTGCCACCACCTAGGCTTCAGCTCGAGA GTATGGGATCGGCCATTGAACAAGATGGATTGCACGCAGGTTCTCCGG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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11	pLMTB6467	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGCGGTGGGCGCGCGCGTAATCGGGCACGCGTCAGGCAGCGCCAC AGAGGCCTGCCCAGACAGCGAACGGGTCCATCGTACACCCTCGGTCCC CGGCATTCGCAGGACTGTGGGCCATGCGGTCACGACTTCTTCCGAGTC GGCGGCCTCGCGCCGCCCGCTGGGCCCGCTGCACCGTTTTCTGTCTGG GCTTTTTCATTGGCGCTATTACTCTCTGCGGCGTCGTTGCGTGGAGGA TCATGAGTGACATGAGCGAGGACGTGAAGGGCCGCAGAACGCTGACGC AGCACCCTTCCCCAGGCAAGCCAGGGTGCCACGGGTGACTGACGCTGG CGCTGACGACGACGCTGGGTTGTTGCGCAGCAGTGGAGGGGCAGCTCC ATACACGGAAGGCTTAGAGGAGCTGGTCCTGCTGCTCCGTATCTACGC CGAAGAAACTGGTGTCCGGGTAACCGACACGTCTTATGCGCTTCCAGA GGGCGTGTCTGCAGGTGCAGGCCTCAGTCGCAGCCTGACCGCATCACA CATCAAGGCGTTACAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTC GTGTGACCGCGTTGAGGGATCTAATGGATTCGGAACTTTGGTCGTTTG GTCTCTCATGCTGCCCAATCCCATGCGCTTTTCTCCGTGCCTCTCTGT CTCCCCTTCCGTTCTATTTGGACAACGATGTGTACTGTAATGCGTGCG CCATCTGACAACGAATAGATCAGCAGCATTCGCACACTTGCACATACC CAGTGAGGCTTTTGTGTCTGTCGTATTGACAACACCGACTGCAACAAG GTGTAGATAGAAGTTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCT CCTGCTTTCCTTGCTGTGCCTTGCCACCACCTAGGCTCGAGATGGCCA AGTTGACCAGTGCCGTTCCGGTGCTCACCGCGCGCGACGTCGCCGGAG CGGTCGAGTTCTGGACCGACCGGCTCGGGTTCTCCCGGGACTTCGTGG AGGACGACTTCGCCGGTGTGGTCCGGGACGACGTGACCCTGTTCATCA GCGCGGTCCAGGACCAGGTGGTGCCGGACAACACCCTGGCCTGGGTGT GGGTGCGCGGCCTGGACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGT CCACGAACTTCCGGGACGCCTCCGGGCCGGCCATGACCGAGATCGGCT TCGAAATTTAAATGGTACCATCCCAATGGCGCGCCGAGCTTGGTCGAG CATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTC CACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTT TCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAAC GCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGC

SEQ ID NO.	Description	Sequence
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12	pLMTB 6470	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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13	pLMTB 6471	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAATGAAGACTACAGCGTCGCCAGCGCAGCTCTCTCTAGCGACGGC CGCATCTTCACTGGTGTCAATGTATATCATTTTACTGGGGGACCTTGT GCAGAACTCGTGGTGCTGGGCACTGCTGCTGCTGCGGCAGCTGGCAAC CTGACTTGTATCGTCGCGATCGGAAATGAGAACAGGGGCATCTTGAGC CCCTGCGGACGGTGCCGACAGGTGCTTCTCGATCTGCATCCTGGGATC AAAGCCATAGTGAAGGACAGTGATGGACAGCCGACGGCAGTTGGGATT CGTGAATTGCTGCCCTCTGGTTATGTGTGGGAGGGCTAACCTCGGAGA TCCATGGCCTAAGGCTCGTGTGAGCGTTCGCGGAATCGGTCGCTCGTG TTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAGCAGGATAC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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14	pLMTB 6474	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAAGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTT GCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGTTGC TATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTC CTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCA TCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATG ATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCA GGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCGTGACGCATG GCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTG GATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACA TAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGG CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGC GCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGACCTCGGAGAT CCATGGGAAGTCCTAAGGCTCGTGTGAGCGTTCGCGGAATCGGTCGCT CGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAGCAGG ATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAATTCGCGA TCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTTTTCCCA CCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAGAAGGGAC GGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCTTCTCTTGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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15	pLMTB 6475	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACGACTTCGCC GGTGTGGTCCGGGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGAC CAGGTGGTGCCGGACAACACCCTGGCCTGGGTGTGGGTGCGCGGCCTG GACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGTCCACGAACTTCCGG GACGCCTCCGGGCCGGCCATGACCGAGATCGGCGAGCAGCCGTGGGGG CGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGCACTTCGTG GCCGAGGAGCAGGACTGACCATGGCCTAAGGCTCGTGTGAGCGTTCGC GGAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAG GCGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTT CTTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCAC CCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCC GTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCG CATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGCCCC ACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGA TGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAG GGCACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTT CGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCT TGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCA CACACACACACACACACACACACACACACAAGGGCTACAACATCTACTCC CCCGCGCGAGGCGCCTGCTTCCATATATACACTCGCTCATCCGCGCCA AAGGTGTGGGCCGAGTCGCCTCAGTGGTACAGCATGCAGGCCCGCGTG CACGAGCGGATTCAGTTCTTGGTGCAGGCGCACCTCCTCAACAAGGAA GACGTGATGGTAGCGGCGAACAGCACGAGCTCTTTCGTCATAATGGAC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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16	pLMTB 6478	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAACCGGCTCGGGTTCTCCCGGGACTTCGTGGAGGACGACTTCGCC GGTGTGGTCCGGGACGACGTGACCCTGTTCATCAGCGCGGTCCAGGAC CAGGTGGTGCCGGACAACACCCTGGCCTGGGTGTGGGTGCGCGGCCTG GACGAGCTGTACGCCGAGTGGTCGGAGGTCGTGTCCACGAACTTCCGG GACGCCTCCGGGCCGGCCATGACCGAGATCGGCGAGCAGCCGTGGGGG CGGGAGTTCGCCCTGCGCGACCCGGCCGGCAACTGCGTGCACTTCGTG GCCGAGGAGCAGGACTGACCATGGCCTAAGGCTCGTGTGAGCGTTCGC GGAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAG GCGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTT CTTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCAC CCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCC GTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCG CATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGCCCC ACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGA TGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAG GGCACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTT CGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCT TGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCA CACACACACACACACACACACACACACACAAGTGAAGGAGTGGGAGCTGT TCGCTGGCATGCCGCTGACAACCCTCCGTGATGCGCTGCACCCGACCT GACGCATGCAGGGATATCGTCCCCAACTTGCGAGGACCTCCTGCACAA CGACCTGGATCTCGGCGCACGCGCAACCAGCGCATGCGTTGTGCATCA GAAACATCGTACGCCATCGATCGTCTGCTTTCTCTGGTAAGCCTGGCG CATCGGCGCCGACGCATCATCTGGACCTCCTCCTCGGCGTCACACGCG AAGGTGCATCAACGCGCCCGGTGCTTCAGCTCTCCTGATGTATGGTGC GCAGTGGTGTCTTCGACCCCCCCCCCCCCCCCCGCCCCCAACAGCCAA GCGTTGTGCTCCGCCGCCGCCGTGGCACTTGGCGTCTACGGAGTCGAT TCCGTGTAGGCGCGGACTCACCCACCCGCCAACACCTGCGCATGCTGC TTCACTTATCTCTGCTGTTCGATGCGACATCCTCCGCACCCTCCTCCA CCCCTGCAGGATTTAAATGGTACCATCCCAATGGCGCGCCGAGCTTGG TCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG TGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCC CGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGG

SEQ ID NO.	Description	Sequence
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17	pLMTB 6807	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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18	pLMTB6811	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCGCT CCGGCCCCTTCCGGGTCCAGTATTCCTCCCGGGACTCCTTCAAGGTCC TGGCCCGGAACCTGGGCGTCATGGACGACCTGAAGTCCGGCGTCCCCC GGGCCGGCTATCGGGGCGTCGTCTCCTTCATCTCCCGGGGCCGGCGGA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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19	pLMTB6815	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCCAA AGACATACCAGCGTGCCGCGAAGAAGCTCGGTCTGATGGACGACTTTC GATCAGGTGTTCCCCGCACGGCGTACCGTGGGATAGTAACATGCTTCA TTCGCGGCCGCCGGGTGTACCTTGCCCCCAGTTTCGAGTGGAACAAGT ACGACCCGACTTGGGGCGCGGGTGCCTGGTCGCATCCCCAATTTGAGA AGTAGGAGACAAACGTGGCGGATGTGATGTTTTCAGTTTACTTCGCCT CTTTTCGTTTTCCTTTCAGGCGACTTCCCTTTTGAGTTTTCGTGTATG CAATTGTTGCTGTTCTACTGTGCAGTTGTCACCAGCGCCGCTTTTGGG CTTGTGGCGTCGGTGATTCTGCCTACGTGATTCTTCTCCACGTTAACC ACACGTGTTATTGCCCTTCGCTTTTGCGTGCGCGGTCTGGGCAGCCAC

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SEQ ID NO.	Description	Sequence
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20	pLMTB 6819	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCGCT GCCCACTCACCATCACCGGCCTCCTTCGTTGGCAGAGCAACATTTGTT CATGAGCAGCTCTCCGTACTGTGTGTGTGCCCACTAGCCGGTGCAGAG TAGGAGCCGCGCTTTTGTTGTTGTACGTATCTTTTGACGTGGGTGTGC GTGCAAGCAAGGATCTACGCGCAACAAGTAGCAGGCAAGCGGATCTGT TCGCCATGCGGTTCCGGATCTATAAGCGGAAGGTCCTGATCCTGACCC TGGTCGTCGCCGCCTGCGGCTTCGTCCTGTGGTCCTCCAACGGCCGGC AGCGGAAGAACGACGCCCTGGCCCCCCCCCTGCTGGACTCCGAGCCCC TGCGGGGCGCCGGCCACTTCGCCGCCTCCGTCGGCATCCGGCGGGTCT CCAACGACTCCGCCGCCCCCCTGGTCCCCGCCGTCCCCCGGCCCGAGG TCGACAACCTGACCCTGCGGTATCGGTCCCTGGTCTATCAGCTGAACT TCGACCAGATGCTGCGGAACGTCGACAAGGACGGCACCTGGTCCCCCG GCGAGCTGGTCCTGGTCGTCCAGGTCCACAACCGGCCCGAGTATCTGC GGCTGCTGATCGACTCCCTGCGGAAGGCCCAGGGCATCCGGGAGGTCC TGGTCATCTTCTCCCACGACTTCTGGTCCGCCGAGATCAACTCCCTGA TCTCCTCCGTCGACTTCTGCCCCGTCCTGCAGGTCTTCTTCCCCTTCT

SEQ ID NO.	Description	Sequence
		CCATCCAGCTGTATCCCTCCGAGTTCCCCGGCTCCGACCCCCGGGACT GCCCCCGGGACCTGAAGAAGAACGCCGCCCTGAAGCTGGGCTGCATCA ACGCCGAGTATCCCGACTCCTTCGGCCACTATCGGGAGGCCAAGTTCT CCCAGACCAAGCACCACTGGTGGTGGAAGCTGCACTTCGTCTGGGAGC GGGTCAAGGTCCTGCAGGACTATACCGGCCTGATCCTGTTCCTGGAGG AGGACCACTATCTGGCCCCCGACTTCTATCACGTCTTCAAGAAGATGT GGAAGCTGAAGCAGCAGGAGTGCCCCGGCTGCGACGTCCTGTCCCTGG GCACCTATACCACCATCCGGTCCTTCTATGGCATCGCCGACAAGGTCG ACGTCAAGACCTGGAAGTCCACCGAGCACAACATGGGCCTGGCCCTGA CCCGGGACGCCTATCAGAAGCTGATCGAGTGCACCGACACCTTCTGCA CCTATGACGACTATAACTGGGACTGGACCCTGCAGTATCTGACCCTGG CCTGCCTGCCCAAGGTCTGGAAGGTCCTGGTCCCCCAGGCCCCCCGGA TCTTCCACGCCGGCGACTGCGGCATGCACCACAAGAAGACCTGCCGGC CCTCCACCCAGTCCGCCCAGATCGAGTCCCTGCTGAACAACAACAAGC AGTATCTGTTCCCCGAGACCCTGGTCATCGGCGAGAAGTTCCCCATGG CCGCCATCTCCCCCCCCCCGGAAGAACGGCGGCTGGGGCGACATCCGGG ACCACGAGCTGTGCAAGTCCTATCGGCGGCTGCAGGCGGGAGCGTATC CTTATGACGTCCCTGATTACGCATATCCTTATGACGTCCCTGATTACG CATATCCTTATGACGTCCCTGATTACGCATAAGGTACCATTTAAATAT CCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCT GTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGA AGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTG CGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATA CGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGC TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCG CTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC TCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGC GCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG TATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACC GCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGAC GCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTA TCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAA AACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTA TCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAAC TCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCG ATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCA

SEQ ID NO.	Description	Sequence
		AAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCC GGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACA GGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCG TTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTG TTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAAC ACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCT AATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCAT GCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATA AATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTG GCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGC TTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCG CGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAAT CGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTC CTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGC GGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCG CGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATT ATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGT C
21	pLMTB 6848	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCTCA TCGGCGAGAAGTTCCCCATGGCCGCCATCTCCCCCCCCCGGAAGAACG GCGGCTGGGGCGACATCCGGGACCACGAGCTGTGCAAGTCCTATCGGC GGCTGCAGGCGGGAGCGTATCCTTATGACGTCCCTGATTACGCATATC CTTATGACGTCCCTGATTACGCATATCCTTATGACGTCCCTGATTACG CATAAGGAGACTGAGCTTTAGCGAGGGAACCCGCATGGCATACGTTGC CATAACAAGTGACCATCTACTCTCCTTAAAGTCATGGGGGTGCTGCTG CTTGGCCGGTGCTGATCACTCTTGTTGAGGTTCCTTCAGGTGCGGGGA CTCTCTTTGGCGCCTTCCCTGCTTGCCGTGCTCTCTCGACTTGTTCTA ATTCCCACGTGTGCTCTCTTCCGCTTTCGTTGTAGTGGTGTACGCTGC GGTTGAGCTTGTTGTGCTTGCGCTACATTTCTCTTCGAAGGCGGAGGC AGGCGCGCCTGCGCAGTGCCGTGACGAGAGCCACTGCCGTGTCGAGCT GCGAGCAAGAGCAGTTAAGGCAAAAGGGTAGGTGAGAAAGATGACTCT GTGCGGTGCTCTCTTGTCCATGCCTGTCCGTTGTTGTCTCCCCTGTCT CTCCCTTTTTTCGGCTTGAGTGACGTTTTGCTGCCTTTGTACGTTGTT GTAGTGTCCTTACTGCTCTCGATTGCCGTCACGTTGATGCCCCTATGT GTCTCCTTTTCTTGCCTCGCACATTGCGGATGTGCTCCCTTCTCCGCC CCCTTTTTTTTTTTTTTGCCACAGCCGGTGCTGCCTTGTTGCGAGAGC ATGCGCATTTGGAACAAATGGCACATAGTCGTAGCATCTGCGCTCTGG CCTCGGCGCCTCTCTACACCTTTGCTCACCGTGCATCACGCCATCTAC ACCATGTTCTCTTCGTGTTCTGCCACTCTTTTAAATGCTTTGCCTTCC CTTGGAATCCCATGCTCAGCCCTCCCCTGCTTCTCACGGTGCCTGTGG

SEQ ID NO.	Description	Sequence
		CTCTCGGCTGCGCTCTCCTGTCGCCTGTTCTTCTTCTTCCGTCCCTGT GGATGCTGCCGATTTCCCGTCTGCCCCCGTCTTTCGTTTGCCGCCTCC CCCTTCTGTGACGAATGCCGTCTCTGTATCCCGGACGCTCCCTCACGC CAACCCACTCCTCTTTTGCGTTCTTGCGTGTGCGTCGGGCTTCTCTCC CTCCCCCTCCCCCTCCCCCTCCCCTGCCTACCCCATCACCGATGGGTG TGTGGGAGAGAGGTGGCAGGGGAAGAGGGAGTGCAGATAATGTGAGAC AGAATTGAAATATCTGCTCTCCGACACACAGGGAGTAAATGCATTCAA CAGGGATGGTAAGGACACGCACTGGCGTGACATGGAGAAAAAATAATG GAGTAATGCATGCAGGGCTGAACTCGGCACAGAGGTACGCACCCGTGG GCACCCTCTTCTCTACGGCCCTACCTCTTTGTCTCCAATCGTTTTGTC CCCGTATGTCATTATTATTGCTCACCTCGCGGCATTCTTGATGTAGCC GCCTCTTGACATGTATAGTGTTGTTCATTAGTATCCACCGCAAGAAAA GAAATCCTGCATACCACCAATCGCGCGCACTGGACGTTGCCGAAAGCA GTCAGTGGGCACCTTGGACGTTGCCGCCGGTGTGGAAGTGGCCGCGTC GCAAGCAGGCCTCCATGACGTTGACTGCACGTCCCTCCCGGAAAGGGG ATGGCTTTGGTGCCATTTAGGACACAAATGGAGCTTCTTGTCGACCCT TGCTTCGAGGAATGAGGCTGCGTGTATGTGTCTTGGTGACCCCTTTGG GCTGTGCAGCTTGTGGCGTGTGCGCACCGGCGTGTGCCAACGCCCAGG TACTGTGCGCACGTTCGTATCTCCATACGCTAGCTGACCGAGACGCAT GCCCTCCGCCACCCTCAGTGGCGCGCACCTTCTCTCGTTTGAGCTCTT TATGCTCTCGTGAATGGCACACAACATCCCGTGACTATCACGATGATC CTTCTCAAGCCACACCGCTTGCCTTTTCTACAGCTCTGCGTTCTCTGG CCCATCCTCCTCTTGTTTGCTTTCCCTCTTTGCACATCCGTGTGCGCG TCCTTGTTCTTCTCTTCTGCGCACACTATTCTGCGCCCGCGACCCGCG CTTCGACTGCTGTCGGGTCATGCCTTGTGCTGCGCGTTCAGCTCTTCA TTGCCCCTCGGCCTTGTACATAGCGGCTCTCCGTCATCGACGTTTTCC TCTCTCTTCAGCTCTATACACTCCCTCCCTTGTCAACACACTACACTG TGTCTCCCCCTTTCATCTCTCCTCCCCTGTCACAGGTACCATTTAAAT ATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTC CTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCG GAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCA CATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGT CGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTT TGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCT CGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAA TACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAG CAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGG CGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGAC GCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGG CGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGC CGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGC TTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTC GCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCT GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACG ACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGA GGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACG GCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAG TTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCA

SEQ ID NO.	Description	Sequence
		CCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCA GAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTG ACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGAT TATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTT TTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGA AAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGAT TATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAA ACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTG CGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGT CAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAAT CCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAA CAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAAC CGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGC TGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGA ACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTT CTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACC ATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCA TAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCAT TGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGG GCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTAT CGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTA ATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCT TCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGA GCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTC CGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTA TTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTC GTC
22	pLMTB 6852	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCTAT TCTGCGCCCGCGACCCGCGCTTCGACTGCTGTCGGGTCATGCCTTGTG CTGCGCGTTCAGCTCTTCATTGCCCCTCGGCCTTGTACATAGCGGCTC TCCGTCATCGACGTTTTCCTCTCTCTTCAGCTCTATACACTCCCTCCC TTGTCAACACACTACACTGTGTCTCCCCCTTTCATCTCTCCTCCCCTG TCACAATGGTCCGGAAGAAGGGCTCCCTGATCCTGTGCGGCGCCTTCC TGTTCGTCGCCTGGAACGCCCTGCTGCTGCTGTTCCTGTGGGGCCGGC CCCCCATCGGCCGGCTGGGCGAGGGCGGCGGCGCCGAGCCCGGCGCCG GCGAGGAGTGGGGCGCCGGCAAGTCCAAGGTCGGCGGCGCCAACGGCC TGGCCGGCGAGGTCATCCGGCTGGCCGAGGAGGTCGAGTCCGAGCTGG AGACCCAGAAGAAGCTGCTGAAGCAGATCCAGTCCCACCGGGAGCTGT GGGAGCAGCGGAAGGAGCTGGAGAAGCGGGAGTCCGAGGACACCAAGG ACGAGAAGATCGACGTCGAGCCCAAGAAGCCCCGGCAGATCCCCGCCG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		GTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAA AAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCT GACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTC ATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAAT GAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGG TATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAAT TTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTG ACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAG ACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCA TCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAAT ACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAAC CGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCA GGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTG GTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTC GGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCT GTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCT GGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGC CCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATG TTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGG CTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTAT TGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAA ATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAA GAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACG AGGCCCTTTCGTC
23	pLMTB 6855	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCAGC AAGCAGGCGCTGTGGGGTTTATCCACACAGAAGAGAAAATAGGGTCCG TGAAGCCTGCCTACAAAGGGCGTGGAATGATAAACACGACGTACAAGA ACATGCCGAGCAGGGCACCAACAAATGGGACGATAAGGGGTAACCAAA AGTAGTGGTCGTGCAACGTGAAGGGCTCTGAGCCCCAGAGCATCGCGG AGAGGACGCGAGGTGCAAAGTCACGTGCGGGATTGAGGCAATACCCTG AGTTAATGCCTGTAGTGGCACCAATAACCACCAGCAGCAGCCCAATAG CCACCGGCTTGTAGTTTGTAGCCGGCGTCATGCGGTCATCTGTAATGG CGAGAATGCCCATCAGTAGTGCCATGGTGTTGAACACCTCGCTCCACA CCGCATAGCCGGTCGCCACCTTCGGGTAGGTGACGAAGATCCCGCCAT ACTTGGACGCCATCGTCTCTGTTGGAAGTAAGTTCCTCTCGCCCTCGT CAAAGTGGGACTTGAACGCGTGGGGATGGATCGCGAGGGACGCGGGGT TTGAGGGCCGTGGGTGGTGTGGAGAGTGTGGTTGATTATTGTATGGTG GTGAGGGTGGAAGGTGTGGCGGGGATGGTGGTGCGGTGGTGTCGGAAG GGGTGTGTGAGAGGGCGCGGGTCCTTGAGGGAGGGTGGGTGTGTTGTT GTTTTGCGGGTGTTATCCGGGGCTTGGGTGTTGGTGTGATTGGTGACT

SEQ ID NO.	Description	Sequence
		ATGTAGGGGTGAAGGGTGAGTGGAGGGGGTCGCCAGAGGCGTTCCGTT CTACGAAGCTTCATTCCTATGTCCGACTCCGAAGCATGCCTGCAGTTC TGCTGGCTATGTGGGCGTGTCTGGGCAACGACTGAATTGAGAAGGGGA GTCGAAACGGTGCGTGGATGCTGTGTTTGTGCTACACACAAGCAAAGG CAACAACACAAGCGCATCGAGCCAGACGAACCAACCCAATATTCACAC AACTGTACGTGGCCGCGCGCTGTATCTCCGATGGGATGATGCGTGTGC GTGTGCCACCACCACGTACTAGTTTCCAGCCTTACTGCTTGTATACCT TGTCTTTTGCGTTGTGCTTGCGCGTGCTGTGTACCTCTGCTCGTGCGT TCCGTATCCCGGGACCTGCGGGCGGTGGGTGCCACACAACCCGTCACA TTCAACATCACTCATACATCTCACCGATGTGTGCGTGTGCTTGCTGTG TGCGTGTGTTGTGTGGCGTCAAACCTGTTTGAAAACACACCCCTAGCA CTATTCGACCGCGAAAGCGCCCCCCCAAAGGGGCCGGTGTGCAATGCG AGCTACATGTATGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTGC TGAACATGTTTTGTGTGTGCTGCCGTGTCTACACGTTTGCAGCGGAAA CTCGGTTGAACCAGAAACAGAACTTGATTGTTGCTGCATTTCGAGGAA TTTCAGCCAAACAAGAGGTCAACAACCAAGCCGCGTGTACACATATAC ACACACCGCGTGTATGTATATATGCGTTTGTTTTGTTACCACAAATAC TGAGTTGTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGGAAATAC AACAAAATACAACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTG TGTGTGTGTGCGAGCGCACACACACATGCACACGACTCACGTTGTCAC ACAATTGAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTC TCTCCAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTC TCCAGAGCTCGAGCCACCGGTACCATTTAAATATCCCAATGGCGCGCC GAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAA AGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCG CTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTA ATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTC TTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGA ATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAA GGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT CCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAG CTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCT GTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACG CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTG TGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGC TACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGG TTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCA AGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTT CACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAG TATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCAT

SEQ ID NO.	Description	Sequence
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24	pLMTB 6860	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCGCT GCCCACTCACCATCACCGGCCTCCTTCGTTGGCAGAGCAACATTTGTT CATGAGCAGCTCTCCGTACTGTGTGTGTGCCCACTAGCCGGTGCAGAG TAGGAGCCGCGCTTTTGTTGTTGTACGTATCTTTTGACGTGGGTGTGC GTGCAAGCAAGGATCTACGCGCAACAAGTAGCAGGCAAGCGGATCTGT TCGCCATGCGCCTGCGCGAGCCGCTGCTGAGCGGCAGCGCGGCGATGC CGGGCGCGAGCCTGCAGCGCGCGTGCCGCCTGCTGGTGGCGGTGTGCG CGCTGCACCTGGGCGTGACGCTGGTGTACTACCTGGCGGGCCGCGACC TGAGCCGCCTGCCGCAGCTGGTGGGCGTGAGCACGCCGCTGCAGGGCG GCAGCAACAGCGCGGCGGCGATCGGCCAGAGCAGCGGCGAGCTGCGCA CGGGCGGCGCGCGCCCGCCGCCGCCGCTGGGCGCGAGCAGCCAGCCGC GCCCGGGCGGCGACAGCAGCCCGGTGGTGGACAGCGGCCCGGGCCCGG CGAGCAACCTGACGAGCGTGCCGGTGCCGCACACGACGGCGCTGAGCC TGCCGGCGTGCCCGGAGGAGAGCCCGCTGCTGGTGGGCCCGATGCTGA TCGAGTTCAACATGCCGGTGGACCTGGAGCTGGTGGCGAAGCAGAACC CGAACGTGAAGATGGGTGGTCGTTACGCGCCGCGCGACTGCGTGAGCC CGCACAAGGTGGCGATCATCATCCCGTTCCGCAACCGCCAGGAGCACC TGAAGTACTGGCTGTACTACCTGCACCCGGTGCTGCAGCGCCAGCAGC TGGACTACGGCATCTACGTGATCAACCAGGCGGGCGACACGATCTTCA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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25	pLMTB 6861	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCCGC AAGGAATCGGTCAATACACTACATGGCGTGATTTCATATGCGCGATTG CTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACACCGTCA GTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTTGGGCCGAGG ACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGCTCCAACA ATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTGACTGGAGCG AGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACATCTTCTTCT GGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGCTACTTCGAGC GGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCGGGCGTATATGC TCCGCATTGGTCTTGACCAACTCTATCAGAGCTTGGTTGACGGCAATT TCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCAATCGTCCGAT CCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGCAGAAGCGCGG CCGTCTGGACCGATGGCTGTGTAGAAGTACTCGCCGATAGTGGAAACC GACGCCCCAGCACTCGTCCGAGGGCAAAGGAATAGCTAGCCTCGGAGA TCCACTAGTTCTAGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCG TTCGCGGAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTC GCAAGGCGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCT CTGTTCTTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTC CTCACCCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGT CTGCCGTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGC GCGCGCATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCG GCCCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGC GCGGATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTC AAGAGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCC GGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGCC TTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTC TCTCACACACACACACACACACACACACACACACAAGCCCGTAAGTATTG GCGGCACCAACAAAAGCTCCCAGAAACTGAGCGAGAAAATAGCCTGGT AGCTTCTTCCAAGGGAACCCGGCAAACACGCAGTTTGCCAGCGTCACA GCCGGGTTCAAGTGACCACCGGACACACCCATGGTCAGGAAAAGGCTG

SEQ ID NO.	Description	Sequence
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26	pLMTB 6906	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCTCC GCCACAGCCGCGACAAGAAGAACGAGCCGAACCCGCAGCGCTTCGACC GCATCGCGCACACGAAGGAGACGATGCTGAGCGACGGCCTGAACAGCC TGACGTACCAGGTGCTGGACGTGCAGCGCTACCCGCTGTACACGCAGA TCACGGTGGACATCGGCACGCCGAGCTGGTCCCACCCGCAGTTCGAGA AGTAACCTCCTCCTCCTTTCTTGTTCCTTTCACGTCGCCTTCTCGGTT GTAGCTGGCAGACGACGAGTCTTACTTTTACGTGTACTTCTCTATAGA TGATGTATGATCTCTCTGCATGCGTGTTCGTGCATGTGTCCGTGTGTT GTGTACGCGTGCGTCTCGCCTCAGCTCTCCGCGTGAAAGGGTTTGACT GCCCATGATGCGTGTGTATATCCACGCGCAGGCACGCACACACACACA CACACACACACACACAGGCACACACAGGCACACAAACGCATCTCAGGC CGAGCCGCATACGTCTCTCGCACGGTCTCGTTTATTTGATCATGTAGT TGAGTATTAAATTGGGAAGACAAAAACATAATAGCACGAAGAGTCGGG CACGAAAAGCCCGATCTCTCTCTCTCTCTCTCGTGCGCGCAGGGGCGT GTGGGTGCACGACGACGAGGACGGAGGGGGGAAGGGAGGCATAAACGG ATCGATCCCCCATCGCACATGCGGGTACGAGCATTATCTGCTGTGTCT GGTCCTTTATCATATCGCTACCCGCCCGCCCCCCGCCCCCCTCCCCCC CCCCCCCCCGCGGCTCCTGTCACTGTCGTTCCTGCGACTCCCCACACA CCCGCGCAACGCTCATGTCACGAAGAGAAAAGTAGAAGGCGTGGCGAT GCGTTGCGCGGCCCCCTGTCCGCTGGCATGCAGACGTCGAGCCGTGGA ACGGATGGTAGCGAGAGACAACGCGGCGATGCAGGAAAGGAGATTTAC TGCAGGACGTCTACACACGCGCGCACACCACTGCGAATGGCACCGTGC TGAGGAAAATTGGGGGGGAGGGCGCACGGGGGCGGGGCAGGAAACGGT TGGATCAGCAGCACTCTCAACTTGTGTCCGTATTGCGAAGGAGGGAGA GGAGCCTGCCCGTATTATGGGCGCTGAAACGTCGGAACCACCTATGAA TCCCACTTCTGCGTCGCGGAGGCGTACTGCTTCCGACCACCTCCGCAG CTCACGCGCGTCGAGCTCCCTCCCTTTCCCCTTCTTTCCGTTGTGTGT GTGTGTGTGTGTGTGTCTTGTCACGATGCATGGCCATCTCTCCTCCAA CCCTCCACGCCTTCCTCTCCCCCGCCCATCAAACGCGCTACGGCCACA ACCATTTCTTCAAGTATCACATCCACCACCACTCTTACCCACCTACCC TCTTCGACTCTGACACAGCCACTGACGCCCTCTCCGCCTCTCTCGCTC GCTGCACATTGACTCTCCACAGCCCCCCCTCCCTCGCACAGCCAGCCC CACCCACCCACCCACCCACCCACCGCTCTACACACCTCCACAGCAGCC ATGAAAAAGCCTGAACTCACCGCGACGTCTGTCGAGAAGTTTCTGATC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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27	pLMTB 6944	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCAGC AAGCAGGCGCTGTGGGGTTTATCCACACAGAAGAGAAAATAGGGTCCG TGAAGCCTGCCTACAAAGGGCGTGGAATGATAAACACGACGTACAAGA ACATGCCGAGCAGGGCACCAACAAATGGGACGATAAGGGGTAACCAAA AGTAGTGGTCGTGCAACGTGAAGGGCTCTGAGCCCCAGAGCATCGCGG AGAGGACGCGAGGTGCAAAGTCACGTGCGGGATTGAGGCAATACCCTG AGTTAATGCCTGTAGTGGCACCAATAACCACCAGCAGCAGCCCAATAG CCACCGGCTTGTAGTTTGTAGCCGGCGTCATGCGGTCATCTGTAATGG CGAGAATGCCCATCAGTAGTGCCATGGTGTTGAACACCTCGCTCCACA CCGCATAGCCGGTCGCCACCTTCGGGTAGGTGACGAAGATCCCGCCAT ACTTGGACGCCATCGTCTCTGTTGGAAGTAAGTTCCTCTCGCCCTCGT CAAAGTGGGACTTGAACGCGTGGGGATGGATCGCGAGGGACGCGGGGT TTGAGGGCCGTGGGTGGTGTGGAGAGTGTGGTTGATTATTGTATGGTG GTGAGGGTGGAAGGTGTGGCGGGGATGGTGGTGCGGTGGTGTCGGAAG GGGTGTGTGAGAGGGCGCGGGTCCTTGAGGGAGGGTGGGTGTGTTGTT GTTTTGCGGGTGTTATCCGGGGCTTGGGTGTTGGTGTGATTGGTGACT ATGTAGGGGTGAAGGGTGAGTGGAGGGGGTCGCCAGAGGCGTTCCGTT CTACGAAGCTTCATTCCTATGTCCGACTCCGAAGCATGCCTGCAGTTC TGCTGGCTATGTGGGCGTGTCTGGGCAACGACTGAATTGAGAAGGGGA GTCGAAACGGTGCGTGGATGCTGTGTTTGTGCTACACACAAGCAAAGG CAACAACACAAGCGCATCGAGCCAGACGAACCAACCCAATATTCACAC AACTGTACGTGGCCGCGCGCTGTATCTCCGATGGGATGATGCGTGTGC GTGTGCCACCACCACGTACTAGTTTCCAGCCTTACTGCTTGTATACCT TGTCTTTTGCGTTGTGCTTGCGCGTGCTGTGTACCTCTGCTCGTGCGT TCCGTATCCCGGGACCTGCGGGCGGTGGGTGCCACACAACCCGTCACA TTCAACATCACTCATACATCTCACCGATGTGTGCGTGTGCTTGCTGTG TGCGTGTGTTGTGTGGCGTCAAACCTGTTTGAAAACACACCCCTAGCA CTATTCGACCGCGAAAGCGCCCCCCCAAAGGGGCCGGTGTGCAATGCG AGCTACATGTATGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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28	pLMTB 6952	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCAAC ACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTGTGTGCGA GCGCACACACACATGCACACGACTCACGTTGTCACACAATTGAGAGCT CTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTCT CTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTCGAG CCACCATGCGCTTGAACGTAAAGAAGGCACTCATTTTCGTCGGCTGCG TTGTCTTTCTGTGGGTGCTCCTCTCCTACGCGAGCGTCATTGAAGTGC CGCGCGCTGTGCCACAGAAGGATCCCGCAGTAGAAATTGAGAAGAAGA TCATAAAGCTGCAGAAGCAGGTGGATGCCCAGATGGCCGAGTCTAAGA GTCTGCTTGCGAAGGTCAAGAAGCTTAAGAAGATATCGGAGGGAGAGA ACGTGGGTGGCGAGGAGGACTCCCTGAAAGACAGCGAAGTGATGCAGC ACCTGTCCCAGCCGATTCTCCCTGTCCTTGTGATCGCGTGCGACCGTG TGACGGTGCAGCGATGCCTGGACAATCTCGTGAAGTTTCGCCCATCCA AGGAGACCTTTCCGATCATTGTGTCGCAGGACTGCGGCCACAACGCTA CATACGAGGTGATAACTAGCTACACGGCTTCAGATCCGACGATCTCGG TGGTACGACAACCGGACTTGTCCGAGATCGTGCTGCCGCGGGTGAAGG TGAAGTTCCGAGGGTACTATAAGATCGCCCGCCACTACAAATTTGCCT TGAACCACGTTTTTGAGACACTGGGTCACGAGGCTGTGATCATCGTAG AGGACGACCTCGATATCAGCCCGGACTTCTTCGAATACTTTTTGGGCA CGTACCCTTTGCTTCTCAAGGACCCGAGCCTTTGGTGTATCTCTGCCT GGAACGACAATGGTAAGATGGAGGTGATCGATATGAGCCGGCCAGATC TGCTCCACCGGACAGATTTCTTCCCCGGTCTTGGGTGGGTTTTGCGCC GGGAGATGTGGCGGAAGCTTGCACCCAAGTGGCCTACAGCTTTTTTTG ACGACTGGCTTCGGAACCCAGTGAACATCGACGGCAAGGCATGTATTC GCCCAGAGATTAGCCGCACGTACTCATTCGGAAAAGTGGGAGTCTCGA AAGGGCTCTTTTTTGACCTTCATCTCCGGAACATTCAGCTCAATATGG AATATGTGGAGTTTACGAAGCTTAACCTGACCTACCTCCTGAAGGAGC ACTACGACGACGCTCTCGTGAGTACGGTGTACAATCTGCCCGAGATGT CAGCCTCGGAAGTTGTGGCGGGGAGTGATCTCAGCGCAGACCCCGTGC GAGTCATGTACTCGAACGCAAAGACATACCAGCGTGCCGCGAAGAAGC TCGGTCTGATGGACGACTTTCGATCAGGTGTTCCCCGCACGGCGTACC GTGGGATAGTAACATGCTTCATTCGCGGCCGCCGGGTGTACCTTGCCC

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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30	pLMTB 6961	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCCGC AAGGAATCGGTCAATACACTACATGGCGTGATTTCATATGCGCGATTG CTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACACCGTCA GTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTTGGGCCGAGG ACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGCTCCAACA ATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTGACTGGAGCG AGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACATCTTCTTCT GGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGCTACTTCGAGC GGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCGGGCGTATATGC TCCGCATTGGTCTTGACCAACTCTATCAGAGCTTGGTTGACGGCAATT TCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCAATCGTCCGAT CCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGCAGAAGCGCGG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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31	pLMTB 7100	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATTGGATAACT TGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTGTTCTCCACTC CAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCGAATGAATGACA GTAAAACCAATGCCTTCACTGGCAGTAACACCCAGCAGTGTTGACTCA ATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGTCTTTTGACGAACA ACTGCCCTATCAGCTGGTGATGGCCGTGTAGTGGACTGCCATGCATGG CGTTGACGGGAGCGGGGGATTAGGGTTCGATTCCGGAGAGGGAGCCTG AGAAATAGCTACCACTTCTACGGAGGGCAGCAGGCGCGCAAATTGCCC AATGTCAAAACAAAACGATGAGGCAGCGAAAAGAAATAGAGTTGTCAG TCCATTTGGATTGTCATTTCAATGGGGGATATTTAAACCCATCCAATA TCGAGTAACAATTGGAGGACAAGTCTGGTGCCAGCACCCGCGGTAATT CCAGCTCCAAAAGCGTATATTAATGCTGTTGCTGTTAAAGGGTTCGTA GTTGAACTGTGGGCTGTGCAGGTTTGTTCCTGGTCGTCCCGTCCATGT CGGATTTGGTGACCCAGGCCCTTGCAGCCCGTGAACATTCAAAGAAAC AAGAAACACGGGAGTGGTTCCTTTCCTGATTTACGCATGTCATGCATG CGTCGAAGATCCAGTCGCAGCCTGACCGCATCACACATCAAGGCGTTA

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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32	pLMTB 7101	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATTGGATAACT TGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTGTTCTCCACTC CAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCGAATGAATGACA GTAAAACCAATGCCTTCACTGGCAGTAACACCCAGCAGTGTTGACTCA ATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGTCTTTTGACGAACA ACTGCCCTATCAGCTGGTGATGGCCGTGTAGTGGACTGCCATGCATGG CGTTGACGGGAGCGGGGGATTAGGGTTCGATTCCGGAGAGGGAGCCTG AGAAATAGCTACCACTTCTACGGAGGGCAGCAGGCGCGCAAATTGCCC AATGTCAAAACAAAACGATGAGGCAGCGAAAAGAAATAGAGTTGTCAG TCCATTTGGATTGTCATTTCAATGGGGGATATTTAAACCCATCCAATA TCGAGTAACAATTGGAGGACAAGTCTGGTGCCAGCACCCGCGGTAATT CCAGCTCCAAAAGCGTATATTAATGCTGTTGCTGTTAAAGGGTTCGTA GTTGAACTGTGGGCTGTGCAGGTTTGTTCCTGGTCGTCCCGTCCATGT CGGATTTGGTGACCCAGGCCCTTGCAGCCCGTGAACATTCAAAGAAAC AAGAAACACGGGAGTGGTTCCTTTCCTGATTTACGCATGTCATGCATG CGTCGAAGATCCAGTCGCAGCCTGACCGCATCACACATCAAGGCGTTA CAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTT

SEQ ID NO.	Description	Sequence
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		AATAGATCAGCAGCATTCGCACACTTGCACATACCCAGTGAAGCTTTT
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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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33	pLMTB 7102	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATTGGATAACT TGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTGTTCTCCACTC CAGACGGTGGGCAACCATCGTCGTGAGACGCCCAGCGAATGAATGACA GTAAAACCAATGCCTTCACTGGCAGTAACACCCAGCAGTGTTGACTCA

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	pLMTB 7115	GGGACCCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATG CAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGC AGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGC TGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCAT

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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35	pLMTB 7186	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCGCT CCGGCCCCTTCCGGGTCCAGTATTCCTCCCGGGACTCCTTCAAGGTCC TGGCCCGGAACCTGGGCGTCATGGACGACCTGAAGTCCGGCGTCCCCC GGGCCGGCTATCGGGGCGTCGTCTCCTTCATCTCCCGGGGCCGGCGGA TCTATCTGGCCCCCCCCGAGGGCTGGACCAAGTATGACGTCTCCTGGT CCTAATTAGCGCTCCGTAGCTCGCTGCGTATGAGAGGTACTGAGCTCC AATGCATCACACGGCGTACGGCAACACACACTATCTTTTCAGTTTATT TTTTTAATTATCCCTCCAAAAAGAAGCAACTGACACTTCAAAATATTC CCAACAAGGAGCGTGAGGTCAGTGACCAGTCTCGGACTTCACACCGCG CATGTAGAAGCACGCGGCTTGCGCGCCAGGCTTCTTTTGGCAAACCAC GCTGCACAGAATGTCTGTGTACAGCAGCCAGGCTGTGATCGATCTATT ATGCTCGCCCCTCGCTCCTCCGGCATTCTCGAGTCCATGTCGAGCTTG TCTGGCTCCGTGCACATGCAAGCGTTTGTGCGCGCCTCTAATGTAACC ACACGTCAAAACATTGTGTGTCTTCCGAAGTGGGAGACACCGGGGCCA CCAACTCCGGTGGTTTACAGCCTCCTCCCTCAACCAACGCTGCCGATT GTACCACCTTTCATTGCGTCTTTGTGCCCCTCCCTATCTTCATGTTTC CACTGCGCTTCGTTTCCGAATACTATTTTCGTGTACTGTTTCATCACT TTCTCACAACAGCTCTTTTTTTTCACCCGCAGGCCATGAAAAAGCCTG AACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCGAAAAGTTCGACA GCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGTGCTT TCAGCTTCGATGTAGGAGGGCGTGGATATGTCCTGCGGGTAAATAGCT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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36	pLMTB7805	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGTGAAATGGTGTATCCCATGACACGTCTTACGTCATGTTCCTCC CTCCTTCGTATGCGTACGACTCTCCTCCGCCTCCGCCTCCGCCTCCGC CTCCGCCTCCGCCTCCGCCTTCTCTGCGCCGGTTTCCTGGAGGATGGA GAGCTCTTGCTCATAGATTGAAGAAAGACCAGGCAAGCCACGGAAAAC TCCGAACAAAAGCGGACTCACGCGGCCGTCTGCATTTGACGTGCTTGC ATACATATACGCACCAACCTTGTGCACGTCTTGTTGACATCCGTAACA CTTGCCTCATTTTTTCCGTGCTGCTCGGATGCACACTCCTGGTGTGGG GCGTAGTCACTATTCGTCTCTCACCAACACACACACACACACACACAC ACACCTGTACATCTCTCTCTCTCTCCTTTTCTGTGTGCCCCGGCGGAC GTGCGTGCGTGTCTAATCACTGAAATTCTTCACATTGCATAGAACGTA GCGTCAGGACGCAGCCTCGAACGGCGATGAAGCCAGAACTCGAGAGTA TGGGATCGGCCATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCG CTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCG GCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGG TTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGG ACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCG CAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGTTGCTAT TGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTG CCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGC TTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCG AGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC TGGATTCGAAATTTAAATGGTACCATCCCAATGGCGCGCCGAGCTTGG TCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG TGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCC CGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGG CCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTC CTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGT ATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGA TAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAA CCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCC

SEQ ID NO.	Description	Sequence
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37	pLMTB 7807	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAAGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTT GCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGTTGC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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38	pLMTB7811	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAAGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTT GCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGTTGC TATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTC CTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATA CGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCA TCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATG ATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCA GGCTCAAGGCGCGCATGCCCGACGGCGAGGATCTCGTCGTGACGCATG GCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTG GATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACA TAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGG CTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGC GCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGACCTCGGAGAT CCATGGAGGGAGAATGATGATGTGACCGAGGTGGCGCGCTCGCACGTG TCCTCCTCCTCCCCCTCCTCCTCCTCTTCTTCTTCCTCCTCATGGCCG CCCTCTGCGGTGGTCCTCTCTCACCTTTTCATGTGTTCCTGTGTGGCG TGCGTGTCGCTCAGGGGATTCCCGTGTGTGTGTGGGGGGGGGGGATGC CGGCCACTGGGGCGTGGGGCGTGCGGGCGCGGCAGCAGGCTCTCGAGG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		CCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAG CGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCC GCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTAT TATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCG TC
39	pLMTB 7812	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGCTCTCTCGTGCTGGACGCCTCTGCACCACTGCGTCGCACACGA ATCGCCGGTAGTGATGGTGCTTTTTCGTACACCGATGCGCGCGAGCAC CTCCGCTCTTGCCGCGTCCTTCTGAGCTTTGCTGCTACGCGTCGCCGT GGCGTCCTTCCATCGTGTTGCTTTTCTTTCAACGTTCCTTCTGCAGCG ATGCGACTGGCATCCCCTTCGTATTAGCACCAGCACCAACAACACGGC AGCTGCGCGCACTTTTGTCGCACGTGACTGCGCGACCGCGATATCTGC TTTCCATTCTGCAGTTCTCTACACACTTCTTTGTGTCTTTCCTTCCCC CCTTTCGAGCGCACACACGCGGGCGCGCTCAGAATCCGCCTCGCCTGC TGTCCTCCTGTGGGCGCGCGCGTAATCGGGCACGCGTCAGGCAGCGCC ACAGAGGCCTGCCCAGACAGCGAACGGGTCCATCGGACACCCTCGGTC CCCGGCATTCGCAGGACTGTGGGTCCTCGAGAGTATGGGATCGGCCAT TGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAG GCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGC CGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAA GACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCG GCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGA CGTTGTCACTGAAGCGGGAAGGGACTGGTTGCTATTGGGCGAAGTGCC GGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATC CATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC CTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAC TCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGATTCGAAATT TAAATGGTACCATCCCAATGGCGCGCCGAGCTTGGTCGAGCATGGTCA TAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG GGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGG AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGAC TCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA AGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA

SEQ ID NO.	Description	Sequence
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40	pLMTB 8223	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATCCACACAAT ACCACCGTGCACACGCACAGCTTCTCTCTCCCCCCCCCACCTATACAC ACATACTCACACAGAGAGAGAGACAGAGACAGAGAGGGGAGGAGAGGG GCACAGAGAGCGACGCACAGGGTGACGAGGAAAGCAGTATCGAAACAG TGACCAGCAGGAACGTTCCTGCCGGTGTCCACTTGTGCCCGTGCTCCA CTACGGGCCGGTCAACCAACGGACACCCGCACCGCCCCCCACGCCAAG

SEQ ID NO.	Description	Sequence
		AGTCCAACCAGCCATCACCTCGAGAGCCTGCTGCCGCGCCCGCACGCC CCACGCCCCAGTGGCCGGCATCCCCCCCCCCCCACACACACACGGGAAT CCCCTGAGCGACACGCACGCCACACAGGAACACATGAAAAGGTGAGAG AGGACCACCGCAGAGGGCGGCCATGGGGAGGAAGAAGAAGAGGAGGAG GAGGGGGAGGAGGAGGACACGTGCGAGCGCGCCACCTCGGTCACATCA TCATTCTCCCTGCGTGGGGATGGATCGCGAGGGACGCGGGGTTTGAGG GCCGTGGGTGGTGTGGAGAGTGTGGTTGATTATTGTATGGTGGTGAGG GTGGAAGGTGTGGCGGGGATGGTGGTGCGGTGGTGTCGGAAGGGGTGT GTGAGAGGGCGCGGGTCCTTGAGGGAGGGTGGGTGTGTTGTTGTTTTG CGGGTGTTATCCGGGGCTTGGGTGTTGGTGTGATTGGTGACTATGTAG GGGTGAAGGGTGAGTGGAGGGGGTCGCCAGAGGCGTTCCGTTCTACGA AGCTTCATTCCTATGTCCGACTCCGAAGCATGCCTGCAGTTCTGCTGG CTATGTGGGCGTGTCTGGGCAACGACTGAATTGAGAAGGGGAGTCGAA ACGGTGCGTGGATGCTGTGTTTGTGCTACACACAAGCAAAGGCAACAA CACAAGCGCATCGAGCCAGACGAACCAACCCAATATTCACACAACTGT ACGTGGCCGCGCGCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGC CACCACCACGTACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCTT TTGCGTTGTGCTTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCGTA TCCCGGGACCTGCGGGCGGTGGGTGCCACACAACCCGTCACATTCAAC ATCACTCATACATCTCACCGATGTGTGCGTGTGCTTGCTGTGTGCGTG TGTTGTGTGGCGTCAAACCTGTTTGAAAACACACCCCTAGCACTATTC GACCGCGAAAGCGCCCCCCCAAAGGGGCCGGTGTGCAATGCGAGCTAC ATGTATGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTGCTGAACA TGTTTTGTGTGTGCTGCCGTGTCTACACGTTTGCAGCGGAAACTCGGT TGAACCAGAAACAGAACTTGATTGTTGCTGCATTTCGAGGAATTTCAG CCAAACAAGAGGTCAACAACCAAGCCGCGTGTACACATATACACACAC CGCGTGTATGTATATATGCGTTTGTTTTGTTACCACAAATACTGAGTT GTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGGAAATACAACAAA ATACAACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTG TGTGCGAGCGCACACACACATGCACACGACTCACGTTGTCACACAATT GAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCA GAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGA GCTCGAGCCACCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCG AGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAT TCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGC CTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGC TTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCA ACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTC GCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATC AGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAA CGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCG TAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGA CGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC AGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCG CTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCT CCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT CAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACC CCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA

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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42	pLMTB 8229	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATCGCAAGGAA TCGGTCAATACACTACATGGCGTGATTTCATATGCGCGATTGCTGATC CCCATGTGTATCACTGGCAAACTGTGATGGACGACACCGTCAGTGCGT CCGTCGCGCAGGCTCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCC CCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGCTCCAACAATGTCC TGACGGACAATGGCCGCATAACAGCGGTCATTGACTGGAGCGAGGCGA TGTTCGGGGATTCCCAATACGAGGTCGCCAACATCTTCTTCTGGAGGC CGTGGTTGGCTTGTATGGAGCAGCAGACGCGCTACTTCGAGCGGAGGC ATCCGGAGCTTGCAGGATCGCCGCGGCTCCGGGCGTATATGCTCCGCA TTGGTCTTGACCAACTCTATCAGAGCTTGGTTGACGGCAATTTCGATG ATGCAGCTTGGGCGCAGGGTCGATGCGACGCAATCGTCCGATCCGGAG CCGGGACTGTCGGGCGTACACAAATCGCCCGCAGAAGCGCGGCCGTCT GGACCGATGGCTGTGTAGAAGTACTCGCCGATAGTGGAAACCGACGCC CCAGCACTCGTCCGAGGGCAAAGGAATAGCTAGCCTCGGAGATCCACT AGTTCTAGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGCG GAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGG

SEQ ID NO.	Description	Sequence
		CGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTC TTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCACC CTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCCG TCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGC ATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGCCCCA CGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGAT GCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAGG GCACACTATCATGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTC GGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCTT GACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCAC ACACACACACACACACACACACACACACAAGACCCACAGTCCTGCGAATG CCGGGGACCGAGGGTGTCCGATGGACCCGTTCGCTGTCTGGGCAGGCC TCTGTGGCGCTGCCTGACGCGTGCCCGATTACGCGCGCGCCCACAGGA GGACAGCAGGCGAGGCGGATTCTGAGCGCGCCCGCGTGTGTGCGCTCG AGAGGGGGGAAGGAAAGACACAAAGAAGTGTGTAGAGAACTGCAGAAT GGAAAGCAGATATCGCGGTCGCGCAGTCACGTGCGACAAAAGTGCGCG CAGCTGCCGTGTTGTTGGTGCTGGTGCTAATACGAAGGGGATGCCAGT CGCATCGCTGCAGAAGGAACGTTGAAAGAAAAGCAACACGATGGAAGG ACGCCACGGCGACGCGTAGCAGCAAAGCTCAGAAGGACGCGGCAAGAG CGGAGGTGCTCGCGCGCATCGGTGTACGAAAAAGCACCATCACTACCG GCGATTCGTGTGCGACGCAGTGGTGCAGAGGCGTCCAGCACGAGAGAG ATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATA GCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACAT ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG CTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGG AAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAG AGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTC GCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAA GGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAA CATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGC GTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAA AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG ATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCC GACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAG CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTA GGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCC CGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGT AAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCC TAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCT GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA ACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGAT TACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC GGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGT CATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAA ATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGA CAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCAT ATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGA

SEQ ID NO.	Description	Sequence
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43	pLMTB 8234	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATATGCGGTTC CGGATTTACAAGCGCAAAGTGGTCATCTTGACCCTCGTCGTGATTATA TGCGGTTTTGCAGTGTGGAACAGTGGCAAACCGAAGAAGGCCAGCACG GTGTTTCCGAAAGAGGTGGAGACAGTGAAGCGCAGTAGTGTGGGCAGC CAAATCCAGGCGACCATTCCTGTCACGCGGAAGCCGATCAACGAGTCG ATCCCAGAGAAGCAGCAGCAGCAACAGCCTGTGGCAAAGTCTGAAGCA GACAACACGACACTTGTCTACCGGGGCATCGTGTTCCAGTTGAACTTT GACCAGAACCTCAAAAACGAGGAGAAGTTTCGAGCGGTTCGCCAGAAG GACGACCTGGTTATCGTCGTCCAGGTGCACAACCGCCCGGAGTATCTG CGTCTTCTGGTGGATAGCTTGCGAAAGAGCAAGGGTATTGAGAACATA CTCCTTATTTTCAGCCACGACTTCTGGTCGCCTGAGATCAATCAAATC GTAGCTTCGGTAGATTTCTGCCTCGTGCTGCAAATCTTCTTTCCATTC TCCATCCAGTTGTATCCCCAAGAGTTTCCCGGCAACGACCCCCGAGAC TGCCCCCGCGACATCCCTAAAAAGGAGGCACTGACACTTGGCTGCATC AACGCAGAATACCCGGATTCATTTGGCCACTACCGCGAGGCCAAATTT AGTCAGACGAAGCACCATTGGTGGTGGAAGCTGCATTTTGTGTGGGAC CGGGTGCGGGTGCTGAAGGACCATAAGGGGCTGGTGCTGCTGATCGAG GAGGACCACTACCTCGCTCCCGATTTCTACCACCTTCTGAAGCTGATG GCAAGTCTCAAGAAGGAGCAGTGCCCTGACTGTGATATACTCTCTCTG GGGTCGTATGGCCACATCGGCTACTCATCAAAGGCAAATAAGGTTGAG

SEQ ID NO.	Description	Sequence
		GTCAAGGCCTGGAAGTCCACGGAGCACAACATGGGCATGGCCCTCAAC CGCGATGCCTACCAGAAACTCCTCCGCTGCACGGACGCGTTTTGCACC TATGATGACTATAACTGGGACTGGAGCCTGCAGCATCTGACAGTCACG TGTCTGCCCGCGTTTCTCAAGGTGATGGTTTCGGAGGCACCACGGATA TTTCACGCTGGCGACTGCGGGATGCACCACAAGAAGTCTGCCTGCATG CCGAGCGGCCAGAAGACAAAGATTGAGAACGTGCTCCAGAATAGCGGT AATCAGCTCTTCCCTAAGCAGCTCTTGATCACGAAGCGACTGCCCGCG TCGGGGGCGAAGGGCGTAGCCCCCCATGTGAAGAACGGCGGTTGGGGC GACATCCGGGACCACGAACTGTGCAAGTCTTACCTGCGCCTTCAGTAG ATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATA GCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACAT ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG CTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGG AAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAG AGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTC GCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAA GGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAA CATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGC GTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAA AAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG ATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCC GACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAG CGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTA GGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCC CGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGT AAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAG CAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCC TAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCT GAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAA ACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGAT TACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTAC GGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGT CATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAA ATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGA CAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCAT ATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGA AGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTA TCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTT CCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGAC GACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGAC TTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATC AACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATAC GCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCG GCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGG ATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGT GAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGG AAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGT AACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGG

SEQ ID NO.	Description	Sequence
		CGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCC GACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTT GGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCT CATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTG TCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAAT AGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGA AACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAG GCCCTTTCGTC
44	pLMTB 8238	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATATGCTGAAG AAGAGCTCGCTCGTGCTGTGGGGTGTGGTACTGTTCGTGGCATGGAAC GCCCTTATCTTGTTCTTCCTGTGGACTCGACCGCAAAGCCTCTCCGAT CACAGCCATCTCACGGAGGAGGTGATTCGGCTTGCGCAGGATGCCGAG TCTGAATTGGAGCGTCAGAAGGACCTGTTGCAGCAGATCTACCGTTAT TCTGCACTGTGGTCCCGGCGCAAGGCGTCCGAAGCCAAGCTCCATCCG CCGGTCGCCGCAAGTGCGCAGCCTTCAACGGCGGCACCCCTCAGCCAT CACTCGCAGATCAGCCCGGATGCGGTTTTGCCAGTGCTCGTGATCGCG TGCGATCGGTCGACAGTCCGTCGCTGCCTGGACAAGTTGCTGCACTAC CGCCCGTCACAGGAGCGTTTCCCAATCATCGTGTCGCAGGACTGTGGG CACGACGAGACAGCGCGAGTCATAGCTAGTTATGGCGACGCCATCATG CACATCAAACAGCCAAACTTGAGCGACATTCCGGTGCCGACCGACCAT CGTAAGTTCCAGGGCTACTACAAGATCGCGCGGCATTACCATTGGGCA CTCTCACAGGTGTTCCGTACGTTTCAGTATCAGGCGGCGATTGTCGTG GAGGATGACTTGGAGGTTGCCCCTGATTTCTTCGAGTACTTTCAAGCT GCCTTTCCGCTTCTCCTGGCAGACCCAACACTGTGGTGTGTCTCCGCG TGGAACGATAATGGGAAAGAGCAAATGGTGGATGCCGCGCACCCAGAT CTGCTCTACCGTACCGATTTTTTCCCGGGGCTCGGATGGCTTCTCCTG AGCGATTTGTGGAACGAACTCGAGCCCAAGTGGCCAAAGGCCTTCTGG GACGACTGGATGCGACAGCCTGAGCAGCGGCAGGGACGATCTTGTATA CGCCCAGAGGTTAGCCGAACTATGACTTTCGGTCGAAAGGGCGTCTCC CACGGGCAGTTTTTTGATCAGCACCTCAAGTTTATCAAGCTGAACGAT CACTTCGTCCCATTCACCCAAATGGACCTCAGCTACCTCAAGAAGAAC GAGTACGACCGGTCTTTTCTGGACCAGGTGTACGGTGCACCCGAGCTG CGAGTTGAGGAGCTTCAGGGTAACCGGCGCCGCGAGCTGGGCACGGTG CGAGTGCAGTACACAACTCGCGACTCCTTCAAGGCGTTCGCTAAGGCG CTGGGTGTCATGGACGACCTTAAGTCCGGTGTGCCGCGTGCCGGTTAC CGTGGCATCGTTTCGTTTCTCTATCAGAGCCGCCGGGTCTATCTGGCC CCGCCTTCCGACTGGACAGGATACGATCCCAGCTGGAGCTAGATTTAA ATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTT TCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGC CGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACT

SEQ ID NO.	Description	Sequence
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45	pLMTB 8287	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT

SEQ ID NO.	Description	Sequence
		GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGCTGGGCAC GGTGCGAGTGCAGTACACAACTCGCGACTCCTTCAAGGCGTTCGCTAA GGCGCTGGGTGTCATGGACGACCTTAAGTCCGGTGTGCCGCGTGCCGG TTACCGTGGCATCGTTTCGTTTCTCTATCAGAGCCGCCGGGTCTATCT GGCCCCGCCTTCCGACTGGACAGGATACGATCCCAGCTGGAGCTAGTT CCTTTCACCTATACACGTGGTTCATATATTATCGGCTTTTTACCTGAG AGAGCAAAGAAAGCTTATTAGCACGGAAAAACGTAATGTGCTGATAGG GGAAAGAAACAAAAACAACCGCAGCCGAGACATTTTGTTTGTGTTGGA GGAAGTAGAGGAGGCCCATCGGTGTCTAGAAGACAATACCGCAGTGTG AGACAGTGACAGAGGTGGCAGAGGAGAGGTAGGGGGAAGCTCAAATGA GTGCTGTATCATGTATGCATGTCTCTCTGGCTGCTTCTCAGCTTTTCG TTCCGGCTTCCACTGGACTGTGGCCCTGCTCCAAACCTTCGACGTGGG ATGATTCGATGACTCTTTCTTTTATCAGTGACTGATACCGATACTGTG CTGCAGAGAATCGAGAAAAAAAGCGGAAAAGGCGGCAGGGCCTCGATG GCAAATCGTTTAGTTGTGTGTGTCAGTGATGCCTCTCTAGGTGGCGGA GTGGGGCTGCACGTGATGGACGACGACGTAGCGCAATACGCGCCTTCA GTCGACAGATCGAACAAGCACCGTGCTGGTTTCAGTATCCCTGCGCAC TCTCCTGGTTATGGGCGCCTTGAATGCGAGCCTTTGTTTGAGCTCCAC TTGCTGCTCATCAAATGGCCACACTTCCGACCTCCCTTGCTCTTTTTT TTTGCACTTTTGTGGCACCTGTGTCCTTGCTGTCGGTCCTTTCCAACT TCAGCACACGGAGAAACCACCCTGACTGTAGCAATCACGATCCAGTGG GGACAAAGGAGACGAGGTGTCGAGTGCCATTTCGACGATCGGAATGCG ACCACGTAAGACCATACTGCTCGTGGGTGTCCTGGTGATATGGGTGCT TATGACCTACCTTGCCTTTATGCGGAGCGTTCGGGGCACAGACGGGTC GCGCCCACGCCCGGCTTTCGCCAGTAATAAGCTCATGCTCGAGAAGGT ACAGGATTTCGAGCAGAACCTGAAGTCGTTCGCCGACAGCCGTCAGAA TCTATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTC ATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAA CATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGT GAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTC GGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGG GAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGA CTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTC AAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAA GAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGC CGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCA CAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA AAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGT TCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGG AAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGT GTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCA GCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCC GGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGAT TAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG

SEQ ID NO.	Description	Sequence
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46	pLMTB 8301	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGCAGCGGCC CCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCAAGGTCCTTGCCC GCAACCTCGGGGTGATGGATGACCTGAAGTCAGGCGTGCCACGCGCCG GTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCCGGCGCATCTACC TCGCGCCCCCTGAGGGTTGGACGAAATACGACGTGAGCTGGAGCTAAT GAACTGCCTGTCGCAACGACCACGGCCCTCTCGCTTTCCCTTGGTTGG TTCGTCAAACGGCTGAACCGGCTTCTCTTCCTCTGTCGCTCCTTGTCC TCATTTCTGTTTCACACGACATACTTGTCTATTATGTCGCTGCCTGTA TGTGTGTGTGTGTGTGCTGCAATGACGGGTAGGGGGCTGAGGCGGCAA GGTAAGCAGGGGCGCCGAGGCACGGGTAGAGGCCAAAGGCAGGCGTCG GCGATGATGGACCTTCCTCGACTTTCTTCGTTGTGGTCTTATCTTTGC

SEQ ID NO.	Description	Sequence
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47	pLMTB 8381	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATAACACTTGA TCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTGTGTGCGAGCGCAC ACACACATGCACACGACTCACGTTGTCACACAATTGAGAGCTCTCTCT TCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTCTCTCTTC TCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTCGAGCCACCA TGGTCCGCAAGAAGGGATCTCTGATCCTGTGTGGGGCGTTTCTGTTCG TGGCCTGGAACGCGCTCTTGCTCCTTTTTTTGTGGGGCCGCCCGCCCA TTGGTCGACTCGGCGAGGGTGGGGGGGCGGAGCCGGGCGCGGGCGAGG AGTGGGGTGCGGGGAAGAGCAAAGTGGGTGGCGCTAACGGCCTGGCGG GTGAGGTTATCCGCCTGGCGGAGGAGGTCGAGAGTGAGCTGGAGACGC AGAAGAAGCTTCTGAAACAGATACAGTCGCACCGCGAGCTTTGGGAAC AGCGTAAGGAACTGGAGAAGCGTGAAAGCGAGGATACCAAGGACGAGA AGATTGACGTTGAGCCTAAGAAGCCCCGCCAGATCCCGGCCGTGCACC TGTCCCACAAGGTGGTGGAAGACGCCCAGACAGTAACCAAGAAAATGC AAACGCTGATGGTGACACCGCCTCAGCTGGTGATGAAGGAGCAGGAGA CAGATCAGAAGAATAAGCAGATGATGGAGGACCAGCTGGGGCTCACCA CGCCATCTCCGCAAATCATCATCCCGATTCTCGTGATCGCGTGCGATC GCGTGACCGTGAAGCGGTCCCTCGACCGTCTGATCCAGTACCGGCCAA GCGCAGAGTTGTACCCAATTATCGTCAGCCAGGATTGTGGCCACGCTG ACACAGCCCGCGTGATCGGGTCCTATGGCAGCCAGATCACGCACATAA GCCAGCCTGACCTTGCAGATATACCGGTGCGGCCAGATCATCGCAAGT TTCAGGGGTACTACAAGATCGCCCGCCATTACCGTTGGGCGCTCAACC AGGTGTTCAACGTGTTTGCCTACTCAACGGTGGTGATAGTCGAGGACG

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48	pLMTB8383	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATATGCGACCA CGTAAGACCATACTGCTCGTGGGTGTCCTGGTGATATGGGTGCTTATG ACCTACCTTGCCTTTATGCGGAGCGTTCGGGGCACAGACGGGTCGCGC CCACGCCCGGCTTTCGCCAGTAATAAGCTCATGCTCGAGAAGGTACAG GATTTCGAGCAGAACCTGAAGTCGTTCGCCGACAGCCGTCAGAATCTG TATCGCGACATCATTAACATCCTGCGCCGGACAGACAAGGTGAGTTCT GTGCCAGCTCAGCCGATACCGGCTGTACCGTCGCAAGAGTCCCCTGGC GCGGCCGTGCAGGAGAGCGAGGTCCCGAAGGAGCGCCAAGCGCCGCCG CAACGCTACCTGAACAACGATCCAGCCTTCCCGGTGATCCCTGTGGTC GTTTTTGCTTGCAACCGCATTTCTGTCAACAAGTGCCTTGACGATCTT ATCCGCTATCGACCCTCGGCCGAACAATTCCCTATCATTGTGTCACAA GACTGTGACGATGAAGCGACGCGTAATACGATTCTGAGCTACCGTGAC GAAGTGACTCTGATTCAGCAGCCTGACCAGTCAGATATCCCGGTGCCG CCTAAGGAGAAGAAATACAAGGGCTACTACAAGATTTCGCGGCACTAC GGCTGGGCGCTCCGCGCAGTGTTCGGTCAAGGCTTCGATTCCGTCATT TTGGTTGAGGACGACCTCTCGGTTGCTCCTGACTTCTACGAATACTTT CTCGGAACCTACCCTATCCTGAAGCGTGATAAGTCCCTCTGGTGTGTA TCCGCATGGAACGACAATGGCAAGGAGGGTCTCATCGACACGACGGCG CACGACCTTTTGTACCGCTCGGATTTTTTTCCTGGCCTGGGCTGGATG ATGACAAAGGATTTGTGGGACGAGCTGGAGCCGAAGTGGCCAAAGGCG TTTTGGGACGACTGGATCCGCCAGCCAGAACAACGCAAGGAGCGCGCC TGCATCCGGCCCGAGCTTCCACGTACCCGCACGTTCGGCAAGATCGGC GTTTCTAACGGCCTGTTTTTTGACAAGCATCTGAAGTTTATTAAGCTG AGTGAGGAGTTCGTGTCCTTTACCAAGACGAACCTTAGCTACCTCGTG AAGAGTGCGTACGATGATGCGTTTCTGAAGACAGTGTACCAAAGTCCT GTAGTGACTCTTGACGAGCTCAAACGGGGCATGGTCATGACACGCGAG

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SEQ ID NO.	Description	Sequence
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49	pLMTB 8384	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTAGACTC GTGCCGCGCGCTGATGATGTAGGTGCACGCGTGCGTGTGCTGCAGCGG AGCCGCCGCCACCGCGACTGTGTGTGTGTGCGCGCGTGACGACCGGCT CGAGGAAGGAGGAGCGCGCGTGTGCGTGCGATGCGCCTCCTCTTTTTT TTTCGCCCTCGTCGGTTTTTTTTTTTCTGAGAGGACGGCGGCGGCGGA TGGCGGGGCGGCGGCGCTGACGGAGCGGCCACGCTCTGCACCTCCCCG CCCTCCGCCGTCTCTCCGTTCGCCGTCCTCTCCTTCCTCGTGCGTGCG TCTGCCGCGCATGCACACGCGCGCGCGTTGCCGTAGCGCTGTGTATCT GTGGAGGAGGGCCTTGTCTCTCCCTCCCCGTCGCTGAGAGATGAAGGG GCAAAAAGAGAGAGCAGTGCGCATGTGTGCCTCCGCTCCCTGGAGCTC CCCACGAGCCCCCTGCGCCACGCACCTGCGAACCTGCACAGCGGCCCA CCTGCCCGCACACGTGAGCAGAAATGGGTGTGTGGAGCGGGTGATGTC GGCGCGCACACGCGCGCGCGCTGACCACTCCGACGTGAAAACACGGAA GAGCGAGGCTGGCAAGGCAGGGCAGGAACCTGATCACGTGCGCGCGCA CAAACGGAATGAGCAGCTCCTGAAGAGGAGATGGGGCTCATGCACGCA GACACGCACGTGCACACTCCTCCGTCTTCACGGAGCGCGGCCCTGCTG CTGCTGCCATGTGCCGGACGTCTGCCACGCGTCTCTTCCCCACACCTT GCTCTTCCCCCCCCCCCTTCCCTCCCGGCGAACACAAAACACGCGCAC GCCCACCGAAACAACAACGCGCAGCTCTTCGCTCTCGTTCTTCGAACA AACACCTTTAAACCGCCTTCCAACCCCTCTTTCTTCTTTTTCAGCCAT GAAAAAGCCTGAACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCGA AAAGTTCGACAGCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGA ATCTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATATGTCCTGCG GGTAAATAGCTGCGCCGATGGTTTCTACAAAGATCGTTATGTTTATCG GCACTTTGCATCGGCCGCGCTCCCGATTCCGGAAGTGCTTGACATTGG GGAATTCAGCGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGG TGTCACGTTGCAAGACCTGCCTGAAACCGAACTGCCCGCTGTTCTGCA GCCGGTCGCGGAGGCGATGGATGCGATCGCTGCGGCCGATCTTAGCCA GACGAGCGGGTTCGGCCCATTCGGACCGCAAGGAATCGGTCAATACAC TACATGGCGTGATTTCATATGCGCGATTGCTGATCCCCATGTGTATCA CTGGCAAACTGTGATGGACGACACCGTCAGTGCGTCCGTCGCGCAGGC TCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGCA CCTCGTGCACGCGGATTTCGGCTCCAACAATGTCCATTTAAATATCCC

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		AATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTG TGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGC ATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTA ATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGC CAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGT ATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTC GTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGG TTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAA GGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTT TTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCA AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTT CCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTT ACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCT CATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC AAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCC TTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTA TCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTAT GTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTAC ACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC TTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCT GGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAA AAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCT CAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCA AAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAA TCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAAC TCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCA ATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCA CCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATT CCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAA ATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGT GAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGC CAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTA TTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTA AAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACT GCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAAT ACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCA TCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAAT TCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCA ACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTC CCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGA GCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGC GGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTT TTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGA TACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGC ACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATC ATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
50	pLMTB8629	CTGCATGCCGAGCGGCCAGAAGACAAAGATTGAGAACGTGCTCCAGAA TAGCGGTAATCAGCTCTTCCCTAAGCAGCTCTTGATCACGAAGCGACT

SEQ ID NO.	Description	Sequence
		GCCCGCGTCGGGGGCGAAGGGCGTAGCCCCCCATGTGAAGAACGGCGG TTGGGGCGACATCCGGGACCACGAACTGTGCAAGTCTTACCTGCGCCT TCAGTAGCGAGCGCGTTGCCTCTGCGCTGGTGAACGTGCCTGCGCACT TACATCTCAGCCGTGCTTTCTGGGAAGACCTTCTGCGACGCGGGGCGC TGTGCTGGTACAGATGGAAAGATGTGCGCCATCACGGATGCATCCTTG CATGGTGCGTGCTCACGTGCTCACCACAGTTTGTGTGTGTGTGTGTGT GAGTGTGAGTGTGAGTGAGAGAGAGAGTGTGTTTCGGCGCACCTCCCA TCCAACAGTGGCGTGAACGGCTTTCTCTGTATGCGCCCTTTCGTTTTA ACTCTTTCTTTTTCCGCCTTTGTTTTTTGTGATTTTTGATGAACTCAA ACACAAAATGAACATCCATGCTGAAGAAGAGCTCGCTCGTGCTGTGGG GTGTGGTACTGTTCGTGGCATGGAACGCCCTTATCTTGTTCTTCCTGT GGACTCGACCGCAAAGCCTCTCCGATCACAGCCATCTCACGGAGGAGG TGATTCGGCTTGCGCAGGATGCCGAGTCTGAATTGGAGCGTCAGAAGG ACCTGTTGCAGCAGATCTACCGTTAATTTAAATATCCCAATGGCGCGC CGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTT ATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTA AAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGC GCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATT AATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCT CTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGC GGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAG AATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAA AGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGC TCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGT GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAA GCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACC TGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCAC GCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCT GTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTA ACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGG CAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTG CTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAA CAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAA GAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTG GTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTC AAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACG AAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCT TCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAA GTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCA TCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATT TTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGT TCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTC CAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTAT CAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCA AAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTAC GCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTG ATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAAT TACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCAT

SEQ ID NO.	Description	Sequence
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51	pLMTB 8640	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATACCTCGAGA GCCTGCTGCCGCGCCCGCGCGCCCCACGCCCCAGTGGCCGGCATCCCC CCCCCCTCACGGTGGAGGAGGGTGCGGAGGATGTCGCATCGAACAGCA GAGATAAGTGAAGCAGCATGCGCAGGTGTTGGCGGGTGGGTGAGTCCG CGCCTACACGGAATCGACTCCGTAGACGCCAAGTGCCACGGCGGCGGC GGAGCACAACGCTTGGCTGTTGGGGGCGGGGGGGGGGGGGGGGGGGTC AAGACACCACTGCGCACCATACATCAGGAGAGCTGAAGCACCGGGCGC GTTGATGCACCTTCGCGTGTGACGCCGAGGAGGAGGTCCAGATGATGC GTCGGCGCCGATGCGCCAGGCTTACCAGAGAAAGCAGACGATCGATGG CGTACGATGTTTCTGATGCACAACGCATGCGCTGGTTGCGCGTGCGCC GAGATCCAGGTCGTTGTGCAGGAGGTCCTCGCAAGTTGGGGACGATAT CCCTGCATGCGGCGTGGGGATGGATCGCGAGGGACGCGGGGTTTGAGG GCCGTGGGTGGTGTGGAGAGTGTGGTTGATTATTGTATGGTGGTGAGG GTGGAAGGTGTGGCGGGGATGGTGGTGCGGTGGTGTCGGAAGGGGTGT GTGAGAGGGCGCGGGTCCTTGAGGGAGGGTGGGTGTGTTGTTGTTTTG CGGGTGTTATCCGGGGCTTGGGTGTTGGTGTGATTGGTGACTATGTAG GGGTGAAGGGTGAGTGGAGGGGGTCGCCAGAGGCGTTCCGTTCTACGA AGCTTCATTCCTATGTCCGACTCCGAAGCATGCCTGCAGTTCTGCTGG CTATGTGGGCGTGTCTGGGCAACGACTGAATTGAGAAGGGGAGTCGAA

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		ACGGTGCGTGGATGCTGTGTTTGTGCTACACACAAGCAAAGGCAACAA CACAAGCGCATCGAGCCAGACGAACCAACCCAATATTCACACAACTGT ACGTGGCCGCGCGCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGC CACCACCACGTACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCTT TTGCGTTGTGCTTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCGTA TCCCGGGACCTGCGGGCGGTGGGTGCCACACAACCCGTCACATTCAAC ATCACTCATACATCTCACCGATGTGTGCGTGTGCTTGCTGTGTGCGTG TGTTGTGTGGCGTCAAACCTGTTTGAAAACACACCCCTAGCACTATTC GACCGCGAAAGCGCCCCCCCAAAGGGGCCGGTGTGCAATGCGAGCTAC ATGTATGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTGCTGAACA TGTTTTGTGTGTGCTGCCGTGTCTACACGTTTGCAGCGGAAACTCGGT TGAACCAGAAACAGAACTTGATTGTTGCTGCATTTCGAGGAATTTCAG CCAAACAAGAGGTCAACAACCAAGCCGCGTGTACACATATACACACAC CGCGTGTATGTATATATGCGTTTGTTTTGTTACCACAAATACTGAGTT GTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGGAAATACAACAAA ATACAACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTG TGTGCGAGCGCACACACACATGCACACGACTCACGTTGTCACACAATT GAGAGTCGCAGCCTGACCGCATCACACATCAAGGCGTTACAGCCTCTC CGTCTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTTGAGGGATCT AATGGATTCGGAACTTTGGTCGTTTGGTCTCTCATGCTGCCCAATCCC ATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCCGTTCTATTTGGA CAACGATGTGTACTGTAATGCGTGCGCCATCTGACAACGAATAGATCA GCAGCATTCGCACACTTGCACATACCCAGTGAAGCTTTTGTGTCTGTC GTATTGACAACACCGACTGCAACAAGGTGTAGATAGAAGTTGGCCTTC TCGCTCGCTCGCACGCTCTTCACGCTCCTGCTTTCCTTGCTGTGCCTT GCCACCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATG GTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACA CAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATG AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCA GTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGC GGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCAC TGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCA CTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAA GGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCA TCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCC TGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC GGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTC GGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGT TCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAG GATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGC TCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATC CGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTT TTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGAT

SEQ ID NO.	Description	Sequence
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52	pLMTB 8777	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCAGC AAGCAGGCGCTGTGGGGTTTATCCACACAGAAGAGAAAATAGGGTCCG TGAAGCCTGCCTACAAAGGGCGTGGAATGATAAACACGACGTACAAGA ACATGCCGAGCAGGGCACCAACAAATGGGACGATAAGGGGTAACCAAA AGTAGTGGTCGTGCAACGTGAAGGGCTCTGAGCCCCAGAGCATCGCGG AGAGGACGCGAGGTGCAAAGTCACGTGCGGGATTGAGGCAATACCCTG AGTTAATGCCTGTAGTGGCACCAATAACCACCAGCAGCAGCCCAATAG CCACCGGCTTGTAGTTTGTAGCCGGCGTCATGCGGTCATCTGTAATGG CGAGAATGCCCATCAGTAGTGCCATGGTGTTGAACACCTCGCTCCACA CCGCATAGCCGGTCGCCACCTTCGGGTAGGTGACGAAGATCCCGCCAT ACTTGGACGCCATCGTCTCTGTTGGAAGTAAGTTCCTCTCGCCCTCGT CAAAGTGGGACTTGAACTACGTAGCGTGGGGATGGATCGCGAGGGACG CGGGGTTTGAGGGCCGTGGGTGGTGTGGAGAGTGTGGTTGATTATTGT ATGGTGGTGAGGGTGGAAGGTGTGGCGGGGATGGTGGTGCGGTGGTGT CGGAAGGGGTGTGTGAGAGGGCGCGGGTCCTTGAGGGAGGGTGGGTGT GTTGTTGTTTTGCGGGTGTTATCCGGGGCTTGGGTGTTGGTGTGATTG

SEQ ID NO.	Description	Sequence
		GTGACTATGTAGGGGTGAAGGGTGAGTGGAGGGGGTCGCCAGAGGCGT TCCGTTCTACGAAGCTTCATTCCTATGTCCGACTCCGAAGCATGCCTG CAGTTCTGCTGGCTATGTGGGCGTGTCTGGGCAACGACTGAATTGAGA AGGGGAGTCGAAACGGTGCGTGGATGCTGTGTTTGTGCTACACACAAG CAAAGGCAACAACACAAGCGCATCGAGCCAGACGAACCAACCCAATAT TCACACAACTGTACGTGGCCGCGCGCTGTATCTCCGATGGGATGATGC GTGTGCGTGTGCCACCACCACGTACTAGTTTCCAGCCTTACTGCTTGT ATACCTTGTCTTTTGCGTTGTGCTTGCGCGTGCTGTGTACCTCTGCTC GTGCGTTCCGTATCCCGGGACCTGCGGGCGGTGGGTGCCACACAACCC GTCACATTCAACATCACTCATACATCTCACCGATGTGTGCGTGTGCTT GCTGTGTGCGTGTGTTGTGTGGCGTCAAACCTGTTTGAAAACACACCC CTAGCACTATTCGACCGCGAAAGCGCCCCCCCAAAGGGGCCGGTGTGC AATGCGAGCTACATGTATGTGTAGAGAGCGCTGCGCCGAACTAGTCGT GCGTGCTGAACATGTTTTGTGTGTGCTGCCGTGTCTACACGTTTGCAG CGGAAACTCGGTTGAACCAGAAACAGAACTTGATTGTTGCTGCATTTC GAGGAATTTCAGCCAAACAAGAGGTCAACAACCAAGCCGCGTGTACAC ATATACACACACCGCGTGTATGTATATATGCGTTTGTTTTGTTACCAC AAATACTGAGTTGTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGG AAATACAACAAAATACAACACTTGATCATCAATGCGCAATGTGCGCGT GTTGTGTGTGTGTGTGCGAGCGCACACACACATGCACACGACTCACGT TGTCACACAATTGAGAGTCGCAGCCTGACCGCATCACACATCAAGGCG TTACAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTCGTGTGACCGC GTTGAGGGATCTAATGGATTCGGAACTTTGGTCGTTTGGTCTCTCATG CTGCCCAATCCCATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCC GTTCTATTTGGACAACGATGTGTACTGTAATGCGTGCGCCATCTGACA ACGAATAGATCAGCAGCATTCGCACACTTGCACATACCCAGTGAAGCT TTTGTGTCTGTCGTATTGACAACACCGACTGCAACAAGGTGTAGATAG AAGTTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCTCCTGCTTTCC TTGCTGTGCCTTGCCACCAGATCTACCATGGACTATAAGGACCACGAC GGAGACTACAAGGATCATGATATTGATTACAAAGACGATGACGATAAG ATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCA GCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTG GGCTGGGCCGTGATCACCGACGAGTACAAGGTGCCCAGCAAGAAATTC AAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATC GGAGCCCTGCTGTTCGACAGCGGCGAAACAGCCGAGGCCACCCGGCTG AAGCGCACCGCCCGCCGCCGCTACACCCGCCGGAAGAACCGGATCTGC TATCTGCAAGAGATTTTCAGCAACGAGATGGCCAAGGTGGACGACAGC TTCTTCCACCGCCTGGAAGAGTCCTTCCTGGTGGAAGAGGATAAGAAG CACGAGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTAC CACGAGAAGTACCCCACCATCTACCACCTGCGCAAGAAACTGGTGGAC AGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCCAC ATGATCAAGTTCCGGGGCCACTTCCTGATCGAGGGCGACCTGAACCCC GACAACAGCGACGTGGACAAGCTGTTCATCCAGCTGGTGCAGACCTAC AACCAGCTGTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGGACGCC AAGGCCATCCTGTCTGCCCGCCTGAGCAAGAGCCGCCGGCTGGAAAAT CTGATCGCCCAGCTGCCCGGCGAGAAGAAGAATGGCCTGTTCGGAAAC CTGATTGCCCTGAGCCTGGGCCTGACCCCCAACTTCAAGAGCAACTTC GACCTGGCCGAGGATGCCAAACTGCAGCTGAGCAAGGACACCTACGAC

SEQ ID NO.	Description	Sequence
		GACGACCTGGACAACCTGCTGGCCCAGATCGGCGACCAGTACGCCGAC CTGTTTCTGGCCGCCAAGAACCTGTCCGACGCCATCCTGCTGAGCGAC ATCCTGCGCGTGAACACCGAGATCACCAAGGCCCCCCTGAGCGCCTCT ATGATCAAGCGCTACGACGAGCACCACCAGGACCTGACCCTGCTGAAA GCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTC GACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGC CAGGAAGAGTTCTACAAGTTCATCAAGCCCATCCTGGAAAAGATGGAC GGCACCGAGGAACTGCTCGTGAAGCTGAACCGCGAGGACCTGCTGCGG AAGCAGCGGACCTTCGACAACGGCAGCATCCCCCACCAGATCCACCTG GGAGAGCTGCACGCCATTCTGCGGCGGCAGGAAGATTTTTACCCATTC CTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATC CCCTACTACGTGGGCCCTCTGGCCCGCGGAAACAGCCGCTTCGCCTGG ATGACCCGCAAGAGCGAGGAAACCATCACCCCCTGGAACTTCGAGGAA GTGGTGGACAAGGGCGCTTCCGCCCAGAGCTTCATCGAGCGGATGACC AACTTCGATAAGAACCTGCCCAACGAGAAGGTGCTGCCCAAGCACAGC CTGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAA TACGTGACCGAGGGAATGCGCAAGCCCGCCTTCCTGAGCGGCGAGCAG AAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACC GTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGAC TCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTCCCTGGGC ACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTGGAC AATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACA CTGTTTGAGGACCGCGAGATGATCGAGGAACGGCTGAAAACCTATGCC CACCTGTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGCGCTAC ACCGGCTGGGGCCGCCTGAGCCGGAAGCTGATCAACGGCATCCGGGAC AAGCAGTCCGGCAAGACAATCCTGGATTTCCTGAAGTCCGACGGCTTC GCCAACCGCAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTT AAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTG CACGAGCACATTGCCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGC ATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGC CGGCACAAGCCCGAGAACATCGTGATCGAAATGGCCCGCGAGAACCAG ACCACCCAGAAGGGACAGAAGAACAGCCGCGAGCGCATGAAGCGGATC GAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCC GTGGAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTG CAGAATGGGCGGGATATGTACGTGGACCAGGAACTGGACATCAACCGG CTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGAAG GACGACTCCATCGACAACAAGGTGCTGACCCGCAGCGACAAGAACCGG GGCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAG AACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCAGCGCAAG TTCGACAATCTGACCAAGGCCGAGCGCGGCGGCCTGAGCGAACTGGAT AAGGCCGGCTTCATCAAGCGCCAGCTGGTGGAAACCCGGCAGATCACA AAGCACGTGGCACAGATCCTGGACTCCCGGATGAACACTAAGTACGAC GAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCCTGAAGTCC AAGCTGGTGTCCGATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGC GAGATCAACAACTACCACCACGCCCACGACGCCTACCTGAACGCCGTC GTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTC GTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAG AGCGAGCAGGAAATCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGC

SEQ ID NO.	Description	Sequence
		AACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAG ATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATC GTGTGGGATAAGGGCCGGGATTTTGCCACCGTGCGGAAAGTGCTGAGC ATGCCCCAAGTGAATATCGTGAAAAAGACCGAGGTGCAGACAGGCGGC TTCAGCAAAGAGTCTATCCTGCCCAAGCGCAACAGCGATAAGCTGATC GCCCGCAAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGC CCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGAAAAGGGC AAGTCCAAGAAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATC ATGGAACGCAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCC AAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCTAAG TACTCCCTGTTCGAGCTGGAAAACGGCCGGAAGCGCATGCTGGCCTCT GCCGGCGAACTGCAGAAGGGAAACGAACTGGCCCTGCCCTCCAAATAT GTGAACTTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGGGCTCC CCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAGCAC TACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGCGCGTG ATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTACAACAAG CACCGGGATAAGCCCATCCGCGAGCAGGCCGAGAATATCATCCACCTG TTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGAC ACCACCATCGACCGGAAGCGCTACACCAGCACCAAAGAGGTGCTGGAC GCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATC GACCTGTCTCAGCTGGGAGGCGACAAACGCCCGGCGGCCACGAAAAAG GCCGGCCAGGCAAAAAAGAAAAAGTAAGCGGCCGCCCTCCTCCTCCTT TCTTGTTCCTTTCACGTCGCCTTCTCGGTTGTAGCTGGCAGACGACGA GTCTTACTTTTACGTGTACTTCTCTATAGATGATGTATGATCTCTCTG CATGCGTGTTCGTGCATGTGTCCGTGTGTTGTGTACGCGTGCGTCTCG CCTCAGCTCTCCGCGTGAAAGGGTTTGACTGCCCATGATGCGTGTGTA TATCCACGCGCAGGCACGCACACACACACACACACACACACACACAGG CACACACAGGCACACAAACGCATCTCAGGCCGAGCCGCATACGTCTCT CGCACGGTCTCGTTTATTTGATCATGTAGTTGAGTATTAAATTGGGAA GACAAAAACATAATAGCACGAAGAGTCGGGCACGAAAAGCCCGATCTC TCTCTCTCTCTCTCGTGCGCGCAGGGGCGTGTGGGTGCACGACGACGA GGACGGAGGGGGGAAGGGAGGCATAAACGGATCGATCCCCCATCGCAC ATGCGGGTACGAGCATTATCTGCTGTGTCTGGTCCTTTATCATATCGC TACCCGCCCGCCCCCCGCCCCCCTCCCCCCCCCCCCCCCGCGGCTCCT GTCACTGTCGTTCCTGCGACTCCCCACACACCCGCGCAACGCTCATGT CACGAAGAGAAAAGTAGAAGGCGTGGCGATGCGTTGCGCGGCCCCCTG TCCGCTGGCATGCAGACGTCGAGCCGTGGAACGGATGGTAGCGAGAGA CAACGCGGCGATGCAGGAAAGGAGATTTACTGCAGGACGTCTACACAC GCGCGCACACCACTGCGAATGGCACCGTGCTGAGGAAAATTGGGGGGG AGGGCGCACGGGGGCGGGGCAGGAAACGGTTGGATCAGCAGCACTCTC AACTTGTGTCCGTATTGCGAAGGAGGGAGAGGAGCCTGCCCGTATTAT GGGCGCTGAAACGTCGGAACCACCTATGAATCCCACTTCTGCGTCGCG GAGGCGTACTGCTTCCGACCACCTCCGCAGCTCACGCGCGTCGAGCTC CCTCCCTTTCCCCTTCTTTCCGTTGTGTGTGTGTGTGTGTGTGTCT TGTCACGATGCATGGCCATCTCTCCTCCAACCCTCCACGCCTTCCTCT CCCCCGCCCATCAAACGCGCTACGGCCACAACCATTTCTTCAAGTATC ACATCCACCACCACTCTTACCCACCTACCCTCTTCGACTCTGACACAG CCACTGACGCCCTCTCCGCCTCTCTCGCTCGCTGCACATTGACTCTCC

SEQ ID NO.	Description	Sequence
		ACAGCCCCCCCTCCCTCGCACAGCCAGCCCCACCCACCCACCCACCCA CCCACCGCTCTACACACCTCCACAGCAGCCGGATCCACCATGAAAAAG CCTGAACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCGAAAAGTTC GACAGCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGT GCTTTCAGCTTCGATGTAGGAGGGCGTGGATATGTCCTGCGGGTAAAT AGCTGCGCCGATGGTTTCTACAAAGATCGTTATGTTTATCGGCACTTT GCATCGGCCGCGCTCCCGATTCCGGAAGTGCTTGACATTGGGGAATTC AGCGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCACG TTGCAAGACCTGCCTGAAACCGAACTGCCCGCTGTTCTGCAGCCGGTC GCGGAGGCGATGGATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGC GGGTTCGGCCCATTCGGACCGCAAGGAATCGGTCAATACACTACATGG CGTGATTTCATATGCGCGATTGCTGATCCCCATGTGTATCACTGGCAA ACTGTGATGGACGACACCGTCAGTGCGTCCGTCGCGCAGGCTCTCGAT GAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTG CACGCGGATTTCGGCTCCAACAATGTCCTGACGGACAATGGCCGCATA ACAGCGGTCATTGACTGGAGCGAGGCGATGTTCGGGGATTCCCAATAC GAGGTCGCCAACATCTTCTTCTGGAGGCCGTGGTTGGCTTGTATGGAG CAGCAGACGCGCTACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCG CCGCGGCTCCGGGCGTATATGCTCCGCATTGGTCTTGACCAACTCTAT CAGAGCTTGGTTGACGGCAATTTCGATGATGCAGCTTGGGCGCAGGGT CGATGCGACGCAATCGTCCGATCCGGAGCCGGGACTGTCGGGCGTACA CAAATCGCCCGCAGAAGCGCGGCCGTCTGGACCGATGGCTGTGTAGAA GTACTCGCCGATAGTGGAAACCGACGCCCCAGCACTCGTCCGAGGGCA AAGGAATAGACTAGTTCTAGTTCTAGGGGCCGAATTCAGATCCTCGTG TGAGCGTTCGCGGAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTT GTGCTCGCAAGGCGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTT GCTTCTCTGTTCTTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACG CCCTTCCTCACCCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCG TTCCGTCTGCCGTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTC TCTCGCGCGCGCATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTC AAGGCGGCCCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATC CGTAGCGCGGATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGT GCCCTCAAGAGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGAT GAGGCCGGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGC TACGCCTTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTC TCTCTCTCTCACACACACACACACACACACACACACACACAATACGTAGC CCGTAAGTATTGGCGGCACCAACAAAAGCTCCCAGAAACTGAGCGAGA AAATAGCCTGGTAGCTTCTTCCAAGGGAACCCGGCAAACACGCAGTTT GCCAGCGTCACAGCCGGGTTCAAGTGACCACCGGACACACCCATGGTC AGGAAAAGGCTGATGGTCAGCCCCAAACCCCAGCCAAAGTTGATAGCC AGGTAGCTCGGGTTCGACTGGCCGGCGCCAGTGGCACCAGCGTTGAAC ACAGTGGTCGCCACCACGCCGGTGCCGAAGGCAATCAGGAAAAACGTT CCAAAGAACTCGCTGAAGTACTCGCGTAACTGCCATCGGAACTCGTAG AGAGGCCATTTGCTCTGTGACATCCAGTTCCATTTGCTCTCCTTCTCC TGCGGATCTTCCTCATTCATGTGAACTCCAGTGGCCACCTCGTCCGGG TCCTCTTTTTTGCTCATATAACTGAGCCTCGACATCGTATTGCGAGGGA GCCGTACCTTTATGCGCGGGTACCATTTAAATATCCCAATGGCGCGCC GAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA

SEQ ID NO.	Description	Sequence
		TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAA AGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCG CTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTA ATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTC TTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGA ATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAA GGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT CCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAG CTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCT GTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACG CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTG TGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGC TACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGG TTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCA AGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTT CACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAG TATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCAT CAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTT TTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTT CCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCC AACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATC AAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAA AAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACG CTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGA TTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATT ACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATC AACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGC TGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGT ACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCA GTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTT GCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCG ATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATA CCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCA AGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTA TTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGA ATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCG AAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAAC CTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
53	oLMTB 4952	CCGATGGCTGTGTAGAAGTACTCG

SEQ ID NO.	Description	Sequence
54	oLMTB6043	GCTCAGCTGCGAGAGCGTAAACCTCCGTAACAATG
55	oLMTB6044	AGCTAAACTCTGCACTCATCTGCGCTTCCGCAAGG
56	oLMTB6045	ACTATCATGCCCTACGTGGGCCACGCAGCGATGAG
57	oLMTB6047	GCGTCTCACCGCTTGCCAGGTCTTCTACTCCAATG
58	oLMTB6073	TGGTGGAGGAGGGTGCGGAGGATG
59	oLMTB6154	ATCTGGAGGATGTCTACGTGACACAGGCGCTCTGG
60	oLMTB6156	CGCACAGGGTGACGAGGAAAGCAGTATCGAAACAG
61	oLMTB6157	CGACCGCGATATCTGCTTTCCATTCTGCAGTTCTC
62	oLMTB6158	CTTTACACAGGCGGTCACGTGAGTGTCCATGAGAG
63	oLMTB7163	AGCACATGTTTCGGCAGGTC
64	IrA	TCGAGGGAGGAGGAGGAGGCGCGTAGCATTGCGTGCGGGTTATGTGTG CGTGCGTGTGTGTGTGCGGTGCGCGCCTTTCCTCTTTTTTTTCTCCCT CTCGTCGGTTTTTTTTTTCTGAGGAGACGGGGCGAAGACGCGAGCGGG GGGCGGCGTTTGTGTGTGTGTGTGCGCGTGTCGGGGGCAGCGGTGTTG GCGGAACGGCCAACGCCCTGCCCCCTCCCCGCCCTGCGACGTTTCTGC GCACCCGTTCTCTCCTTCCTGCGTGCGTGTCTGCGCGCATGCACATCT GTCCGCGTGTGCCGCAGCGCTGGTATTTTTGTGAGGGCAGAGCCCTGC CTCCCCGCCTCTCTGCCGTTGGCAGGTGAAGCGAAAACGAAGCGAGAG GGCAGTCTGCATGTGTGTGCGAGGGCATGCGGAGCCCCCCTCCCCCCG CCCCCTGCCGTGCTGCACCGCTATTGTGGCGTCTTCTCTCGTTGTGCG CAAGTGTGGCTGCACCACGGCCGCCTCATGTGCGTGTGTGCGCATGTA CACACACACACACACACACACACACACACACGGGCAGGCGCACGCTCCTC TCTCTTCAGGGAGCGCCGCCCCGCTGGTGTCATTGGACGAGCATCCGC CGCGCATCTCTTCACCCCTCACCCCTCATCCCTCTCCCCTCTCCCCGC ACACACACGCAGTCCTTCGCTTTCACTCTTCGAACAAACACCTCAACC ATCTTATCACCTTTCTCTCTTCCTTGTCAACC
65	IrB	GAGACAAACGTGGCGGATGTGATGTTTTCAGTTTACTTCGCCTCTTTT CGTTTTCCTTTCAGGCGACTTCCCTTTTGAGTTTTCGTGTATGCAATT GTTGCTGTTCTACTGTGCAGTTGTCACCAGCGCCGCTTTTGGGCTTGT GGCGTCGGTGATTCTGCCTACGTGATTCTTCTCCACGTTAACCACACG TGTTATTGCCCTTCGCTTTTGCGTGCGCGGTCTGGGCAGCCACTAGGT ATAGGGGTGTGGTGGAGTGCACCCGTGACGGTGACATCCCTTCGACCC GCGTCTGCTGCCTCAGACGTTCGTGGAGAGCTGACATGTCGACATCCC TTTGGTGTGAGCATTTGTGAGCGTGTGGGTGTTTAGTGTTTTTGTTAC CGGTTTTGTTGCGCTTGTGTGCTCTAGTAGTGTTTGTGCGCGTGCGTG GGGCACTATGAAGCAAGCTGCGGTAGATGCGCTGCGTGGGGTGGTAGG CTGCAGGACTACAACCATTAAGATTCCTCTCTCTCTCCTTGGCTCGCT

SEQ ID NO.	Description	Sequence
		CTACATTGACCCTCTGCGGTGGTCTGCTTCTCTACAATCGATATGCCC GACACCTCCCGTTGTGTGTTCGTTCTCCTTTATCACTAGGCCATTGCA TTCGGCCCTGTTGATGTGGCTACGGTCTTAGACACGCACAAATGGTTT GCATTATTTATCGGCCATGGTGTGTGTCACACTCGCTTGATTGATTTT GTTCTGATGTGCAGCATGAAATGTCGGGAGAATAAAACATAGTGCCTT CATCATAGGATGACGGATGCTTGAATCCGTCTTTGTCTTCTGAACAAC TCTCTGCAGAGGGCGCGGGTGGCTGACTTCTCTCCCCCTTCGTATGGC GAAAGGATGGCTTTGGCGTCCTTCCGGGCTTCGCGCGCATAGGGGAGC AGAATATGTGCTGCAAAGAAGACGCCTGGCGGCTGCGTGCGTGCGTAC GTGTGAGTGTGTGTGTGTGTGAGGGCTACGCTGCCGGCACCACTACTC GTGCCTATCTTCACCACCTTCTCGTTCTCCTCCGTCTTCTCTTTTGCC TGGTGAGCATTTGTGTTCACCATACCTCAACGCGCTTCGCATAGCTGC CCAACCTCCTACTACTCTGTTTGGCTAATCTCAGCTCGTTAGTTTCTC TCGTTAATCATAACGAGTTTGCCCCTCCCCCCCCATTGTGTGTGTGTGT CTTGTAAAAAAAAAAAAAAAACATTATCTTCTACCTTTCCGCGCCTCA CATCCGCATCTTTCGTGTGCTGCCCACTCACCATCACCGGCCTCCTTC GTTGGCAGAGCAACATTTGTTCATGAGCAGCTCTCCGTACTGTGTGTG TGCCCACTAGCCGGTGCAGAGTAGGAGCCGCGCTTTTGTTGTTGTACG TATCTTTTGACGTGGGTGTGCGTGCAAGCAAGGATCTACGCGCAACAA GTAGCAGGCAAGCGGATCTGTTCGCC
66	IrC	CCTCCTCCTCCTTTCTTGTTCCTTTCACGTCGCCTTCTCGGTTGTAGC TGGCAGACGACGAGTCTTACTTTTACGTGTACTTCTCTATAGATGATG TATGATCTCTCTGCATGCGTGTTCGTGCATGTGTCCGTGTGTTGTGTA CGCGTGCGTCTCGCCTCAGCTCTCCGCGTGAAAGGGTTTGACTGCCCA TGATGCGTGTGTATATCCACGCGCAGGCACGCACACACACACACACAC ACACACACACAGGCACACACAGGCACACAAACGCATCTCAGGCCGAGC CGCATACGTCTCTCGCACGGTCTCGTTTATTTGATCATGTAGTTGAGT ATTAAATTGGGAAGACAAAAACATAATAGCACGAAGAGTCGGGCACGA AAAGCCCGATCTCTCTCTCTCTCTCTCGTGCGCGCAGGGGCGTGTGGG TGCACGACGACGAGGACGGAGGGGGGAAGGGAGGCATAAACGGATCGA TCCCCCATCGCACATGCGGGTACGAGCATTATCTGCTGTGTCTGGTCC TTTATCATATCGCTACCCGCCCGCCCCCCGCCCCCCTCCCCCCCCCCC CCCCGCGGCTCCTGTCACTGTCGTTCCTGCGACTCCCCACACACCCGC GCAACGCTCATGTCACGAAGAGAAAAGTAGAAGGCGTGGCGATGCGTT GCGCGGCCCCCTGTCCGCTGGCATGCAGACGTCGAGCCGTGGAACGGA TGGTAGCGAGAGACAACGCGGCGATGCAGGAAAGGAGATTTACTGCAG GACGTCTACACACGCGCGCACACCACTGCGAATGGCACCGTGCTGAGG AAAATTGGGGGGGAGGGCGCACGGGGGCGGGGCAGGAAACGGTTGGAT CAGCAGCACTCTCAACTTGTGTCCGTATTGCGAAGGAGGGAGAGGAGC CTGCCCGTATTATGGGCGCTGAAACGTCGGAACCACCTATGAATCCCA CTTCTGCGTCGCGGAGGCGTACTGCTTCCGACCACCTCCGCAGCTCAC GCGCGTCGAGCTCCCTCCCTTTCCCCTTCTTTCCGTTGTGTGTGTGTG TGTGTGTGTGTCTTGTCACGATGCATGGCCATCTCTCCTCCAACCCTC CACGCCTTCCTCTCCCCCGCCCATCAAACGCGCTACGGCCACAACCAT TTCTTCAAGTATCACATCCACCACCACTCTTACCCACCTACCCTCTTC GACTCTGACACAGCCACTGACGCCCTCTCCGCCTCTCTCGCTCGCTGC ACATTGACTCTCCACAGCCCCCCCTCCCTCGCACAGCCAGCCCCACCC ACCCACCCACCCACCCACCGCTCTACACACCTCCACAGCAGCC

SEQ ID NO.	Description	Sequence
67	IrD	GGAGACTGAGCTTTAGCGAGGGAACCCGCATGGCATACGTTGCCATAA CAAGTGACCATCTACTCTCCTTAAAGTCATGGGGGTGCTGCTGCTTGG CCGGTGCTGATCACTCTTGTTGAGGTTCCTTCAGGTGCGGGGACTCTC TTTGGCGCCTTCCCTGCTTGCCGTGCTCTCTCGACTTGTTCTAATTCC CACGTGTGCTCTCTTCCGCTTTCGTTGTAGTGGTGTACGCTGCGGTTG AGCTTGTTGTGCTTGCGCTACATTTCTCTTCGAAGGCGGAGGCAGGCG CGCCTGCGCAGTGCCGTGACGAGAGCCACTGCCGTGTCGAGCTGCGAG CAAGAGCAGTTAAGGCAAAAGGGTAGGTGAGAAAGATGACTCTGTGCG GTGCTCTCTTGTCCATGCCTGTCCGTTGTTGTCTCCCCTGTCTCTCCC TTTTTTCGGCTTGAGTGACGTTTTGCTGCCTTTGTACGTTGTTGTAGT GTCCTTACTGCTCTCGATTGCCGTCACGTTGATGCCCCTATGTGTCTC CTTTTCTTGCCTCGCACATTGCGGATGTGCTCCCTTCTCCGCCCCCTT TTTTTTTTTTTTGCCACAGCCGGTGCTGCCTTGTTGCGAGAGCATGCG CATTTGGAACAAATGGCACATAGTCGTAGCATCTGCGCTCTGGCCTCG GCGCCTCTCTACACCTTTGCTCACCGTGCATCACGCCATCTACACCAT GTTCTCTTCGTGTTCTGCCACTCTTTTAAATGCTTTGCCTTCCCTTGG AATCCCATGCTCAGCCCTCCCCTGCTTCTCACGGTGCCTGTGGCTCTC GGCTGCGCTCTCCTGTCGCCTGTTCTTCTTCTTCCGTCCCTGTGGATG CTGCCGATTTCCCGTCTGCCCCCGTCTTTCGTTTGCCGCCTCCCCCTT CTGTGACGAATGCCGTCTCTGTATCCCGGACGCTCCCTCACGCCAACC CACTCCTCTTTTGCGTTCTTGCGTGTGCGTCGGGCTTCTCTCCCTCCC CCTCCCCCTCCCCCTCCCCTGCCTACCCCATCACCGATGGGTGTGTGG GAGAGAGGTGGCAGGGGAAGAGGGAGTGCAGATAATGTGAGACAGAAT TGAAATATCTGCTCTCCGACACACAGGGAGTAAATGCATTCAACAGGG ATGGTAAGGACACGCACTGGCGTGACATGGAGAAAAAATAATGGAGTA ATGCATGCAGGGCTGAACTCGGCACAGAGGTACGCACCCGTGGGCACC CTCTTCTCTACGGCCCTACCTCTTTGTCTCCAATCGTTTTGTCCCCGT ATGTCATTATTATTGCTCACCTCGCGGCATTCTTGATGTAGCCGCCTC TTGACATGTATAGTGTTGTTCATTAGTATCCACCGCAAGAAAAGAAAT CCTGCATACCACCAATCGCGCGCACTGGACGTTGCCGAAAGCAGTCAG TGGGCACCTTGGACGTTGCCGCCGGTGTGGAAGTGGCCGCGTCGCAAG CAGGCCTCCATGACGTTGACTGCACGTCCCTCCCGGAAAGGGGATGGC TTTGGTGCCATTTAGGACACAAATGGAGCTTCTTGTCGACCCTTGCTT CGAGGAATGAGGCTGCGTGTATGTGTCTTGGTGACCCCTTTGGGCTGT GCAGCTTGTGGCGTGTGCGCACCGGCGTGTGCCAACGCCCAGGTACTG TGCGCACGTTCGTATCTCCATACGCTAGCTGACCGAGACGCATGCCCT CCGCCACCCTCAGTGGCGCGCACCTTCTCTCGTTTGAGCTCTTTATGC TCTCGTGAATGGCACACAACATCCCGTGACTATCACGATGATCCTTCT CAAGCCACACCGCTTGCCTTTTCTACAGCTCTGCGTTCTCTGGCCCAT CCTCCTCTTGTTTGCTTTCCCTCTTTGCACATCCGTGTGCGCGTCCTT GTTCTTCTCTTCTGCGCACACTATTCTGCGCCCGCGACCCGCGCTTCG ACTGCTGTCGGGTCATGCCTTGTGCTGCGCGTTCAGCTCTTCATTGCC CCTCGGCCTTGTACATAGCGGCTCTCCGTCATCGACGTTTTCCTCTCT CTTCAGCTCTATACACTCCCTCCCTTGTCAACACACTACACTGTGTCT CCCCCTTTCATCTCTCCTCCCCTGTCACA
68	IrE	TTAGCGCTCCGTAGCTCGCTGCGTATGAGAGGTACTGAGCTCCAATGC ATCACACGGCGTACGGCAACACACACTATCTTTTCAGTTTATTTTTTT AATTATCCCTCCAAAAAGAAGCAACTGACACTTCAAAATATTCCCAAC

SEQ ID NO.	Description	Sequence
		AAGGAGCGTGAGGTCAGTGACCAGTCTCGGACTTCACACCGCGCATGT AGAAGCACGCGGCTTGCGCGCCAGGCTTCTTTTGGCAAACCACGCTGC ACAGAATGTCTGTGTACAGCAGCCAGGCTGTGATCGATCTATTATGCT CGCCCCTCGCTCCTCCGGCATTCTCGAGTCCATGTCGAGCTTGTCTGG CTCCGTGCACATGCAAGCGTTTGTGCGCGCCTCTAATGTAACCACACG TCAAAACATTGTGTGTCTTCCGAAGTGGGAGACACCGGGGCCACCAAC TCCGGTGGTTTACAGCCTCCTCCCTCAACCAACGCTGCCGATTGTACC ACCTTTCATTGCGTCTTTGTGCCCCTCCCTATCTTCATGTTTCCACTG CGCTTCGTTTCCGAATACTATTTTCGTGTACTGTTTCATCACTTTCTC ACAACAGCTCTTTTTTTTCACCCGCAGAAG
69	PolB	GCGTGGGGATGGATCGCGAGGGACGCGGGGTTTGAGGGCCGTGGGTGG TGTGGAGAGTGTGGTTGATTATTGTATGGTGGTGAGGGTGGAAGGTGT GGCGGGGATGGTGGTGCGGTGGTGTCGGAAGGGGTGTGTGAGAGGGCG CGGGTCCTTGAGGGAGGGTGGGTGTGTTGTTGTTTTGCGGGTGTTATC CGGGGCTTGGGTGTTGGTGTGATTGGTGACTATGTAGGGGTGAAGGGT GAGTGGAGGGGGTCGCCAGAGGCGTTCCGTTCTACGAAGCTTCATTCC TATGTCCGACTCCGAAGCATGCCTGCAGTTCTGCTGGCTATGTGGGCG TGTCTGGGCAACGACTGAATTGAGAAGGGGAGTCGAAACGGTGCGTGG ATGCTGTGTTTGTGCTACACACAAGCAAAGGCAACAACACAAGCGCAT CGAGCCAGACGAACCAACCCAATATTCACACAACTGTACGTGGCCGCG CGCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGCCACCACCACGT ACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCTTTTGCGTTGTGC TTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCGTATCCCGGGACCT GCGGGCGGTGGGTGCCACACAACCCGTCACATTCAACATCACTCATAC ATCTCACCGATGTGTGCGTGTGCTTGCTGTGTGCGTGTGTTGTGTGGC GTCAAACCTGTTTGAAAACACACCCCTAGCACTATTCGACCGCGAAAG CGCCCCCCCAAAGGGGCCGGTGTGCAATGCGAGCTACATGTATGTGTA GAGAGCGCTGCGCCGAACTAGTCGTGCGTGCTGAACATGTTTTGTGTG TGCTGCCGTGTCTACACGTTTGCAGCGGAAACTCGGTTGAACCAGAAA CAGAACTTGATTGTTGCTGCATTTCGAGGAATTTCAGCCAAACAAGAG GTCAACAACCAAGCCGCGTGTACACATATACACACACCGCGTGTATGT ATATATGCGTTTGTTTTGTTACCACAAATACTGAGTTGTCTGATGTGA GCTTCTGCTACAGACGCAATTCAGGAAATACAACAAAATACAACACTT GATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTGTGTGCGAGCGC ACACACACATGCACACGACTCACGTTGTCACACAATTGAGAGTCGCAG CCTGACCGCATCACACATCAAGGCGTTACAGCCTCTCCGTCTTTGCTG CACCCAAGTGTATTCGTGTGACCGCGTTGAGGGATCTAATGGATTCGG AACTTTGGTCGTTTGGTCTCTCATGCTGCCCAATCCCATGCGCTTTTC TCCGTGCCTCTCTGTCTCCCCTTCCGTTCTATTTGGACAACGATGTGT ACTGTAATGCGTGCGCCATCTGACAACGAATAGATCAGCAGCATTCGC ACACTTGCACATACCCAGTGAAGCTTTTGTGTCTGTCGTATTGACAAC ACCGACTGCAACAAGGTGTAGATAGAAGTTGGCCTTCTCGCTCGCTCG CACGCTCTTCACGCTCCTGCTTTCCTTGCTGTGCCTTGCCACC
70	5UTR	AGTCGCAGCCTGACCGCATCACACATCAAGGCGTTACAGCCTCTCCGT CTTTGCTGCACCCAAGTGTATTCGTGTGACCGCGTTGAGGGATCTAAT GGATTCGGAACTTTGGTCGTTTGGTCTCTCATGCTGCCCAATCCCATG CGCTTTTCTCCGTGCCTCTCTGTCTCCCCTTCCGTTCTATTTGGACAA CGATGTGTACTGTAATGCGTGCGCCATCTGACAACGAATAGATCAGCA

SEQ ID NO.	Description	Sequence
		GCATTCGCACACTTGCACATACCCAGTGAAGCTTTTGTGTCTGTCGTA TTGACAACACCGACTGCAACAAGGTGTAGATAGAAGTTGGCCTTCTCG CTCGCTCGCACGCTCTTCACGCTCCTGCTTTCCTTGCTGTGCCTTGCC ACC
71	PolA	GCGTGGGGATGGATCGCGAGGGACGCGGGGTTTGAGGGCCGTGGGTGG TGTGGAGAGTGTGGTTGATTATTGTATGGTGGTGAGGGTGGAAGGTGT GGCGGGGATGGTGGTGCGGTGGTGTCGGAAGGGGTGTGTGAGAGGGCG CGGGTCCTTGAGGGAGGGTGGGTGTGTTGTTGTTTTGCGGGTGTTATC CGGGGCTTGGGTGTTGGTGTGATTGGTGACTATGTAGGGGTGAAGGGT GAGTGGAGGGGGTCGCCAGAGGCGTTCCGTTCTACGAAGCTTCATTCC TATGTCCGACTCCGAAGCATGCCTGCAGTTCTGCTGGCTATGTGGGCG TGTCTGGGCAACGACTGAATTGAGAAGGGGAGTCGAAACGGTGCGTGG ATGCTGTGTTTGTGCTACACACAAGCAAAGGCAACAACACAAGCGCAT CGAGCCAGACGAACCAACCCAATATTCACACAACTGTACGTGGCCGCG CGCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGCCACCACCACGT ACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCTTTTGCGTTGTGC TTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCGTATCCCGGGACCT GCGGGCGGTGGGTGCCACACAACCCGTCACATTCAACATCACTCATAC ATCTCACCGATGTGTGCGTGTGCTTGCTGTGTGCGTGTGTTGTGTGGC GTCAAACCTGTTTGAAAACACACCCCTAGCACTATTCGACCGCGAAAG CGCCCCCCCAAAGGGGCCGGTGTGCAATGCGAGCTACATGTATGTGTA GAGAGCGCTGCGCCGAACTAGTCGTGCGTGCTGAACATGTTTTGTGTG TGCTGCCGTGTCTACACGTTTGCAGCGGAAACTCGGTTGAACCAGAAA CAGAACTTGATTGTTGCTGCATTTCGAGGAATTTCAGCCAAACAAGAG GTCAACAACCAAGCCGCGTGTACACATATACACACACCGCGTGTATGT ATATATGCGTTTGTTTTGTTACCACAAATACTGAGTTGTCTGATGTGA GCTTCTGCTACAGACGCAATTCAGGAAATACAACAAAATACAACACTT GATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTGTGTGCGAGCGC ACACACACATGCACACGACTCACGTTGTCACACAATTGAGAGCTCTCT CTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTCTCTCT TCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTCGAGCCAC C
72	UtrA	CTAGCCTCGGAGATCCACTAGTTCTAGTTCTAGGGGCCGAATTCAGAT CCTCGTGTGAGCGTTCGCGGAATCGGTCGCTCGTGTTTATGCCCGTCT TGGTGTTGTGCTCGCAAGGCGGTGCAGCAGGATACCGTCGCCCTCCTC TCTCCTTGCTTCTCTGTTCTTCAATTCGCGATCTCACAGAGGCCGGCT GTGCACGCCCTTCCTCACCCTCCTTTTCCCACCTCTCGGCCACCGGTC GGCTCCGTTCCGTCTGCCGTCGAGAAGGGACGGGCATGTGCAGCTCCT CCCTTTCTCTCGCGCGCGCATCTTCTCTTGCTTGTGGCACTCACGCTC ATGCGTCAAGGCGGCCCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTT GCGCATCCGTAGCGCGGATGCCGTCGATGCGCAAGGCCGGCATGAAGG AGCGCGTGCCCTCAAGAGGGCACACTATCATGCCCTACGTGGGCCACG CAGCGATGAGGCCGGCTTCGGCGGAGATGCGTCACGCACGTGCCAGAT GATGCGCTACGCCTTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCT CTCACTCTCTCTCTCTCACACACACACACACACACACACACACACAA
73	IrLmA	TGAACTGCCTGTCGCAACGACCACGGCCCTCTCGCTTTCCCTTGGTTG GTTCGTCAAACGGCTGAACCGGCTTCTCTTCCTCTGTCGCTCCTTGTC CTCATTTCTGTTTCACACGACATACTTGTCTATTATGTCGCTGCCTGT

SEQ ID NO.	Description	Sequence
		ATGTGTGTGTGTGTGTGCTGCAATGACGGGTAGGGGGCTGAGGCGGCA AGGTAAGCAGGGGCGCCGAGGCACGGGTAGAGGCCAAAGGCAGGCGTC GGCGATGATGGACCTTCCTCGACTTTCTTCGTTGTGGTCTTATCTTTG CTCGTTTCAATTCTTGTTTTCATTTCTCGTCGTCTGAAAAGAAAGGCA AAAAAAAACAAAGAAGGGGCGCAGAAGAGCGGGATCGCGACGTGCGTA CACGTATCGAGGTCGCTTCCCTTTTTTGCGAAGTCTTTTCGACCTCTC GTACACATCTTTCGTGGGCTGTTGTGCACCATGTTCAGCGCGCGACGT CGAGCTGTGCTCGCTTCCTGCAATGACTTCCCGCCCTTCGTCTTTGTC TTCCACTGGAAGAGTGTGGCACTTCACTCGCCAGTGATGAGGGGAAGG GGGAGCGGACCAACACCGTCTTTTTTATAGCGATAAGGAGGTGAGGAG GTGGTCTGTGTGGCGTTCCTCGTGATGATAGGCTTCATGGTCGACTTA CTTACCGCGTGAGGAGCAGCATATCCATCCACCTCCAAGTTCCTCGAA GAGGTCAGGAAACGCCACTTCTCATGCCCCGCCAGTCTCTTGTGTAAC CTTCGTCCCTCTTATTCTTCATCTCACTCATCCGTGCCTCGTTGACCA CTTCACCGTAACCCGCTCCCTCCCTTTCAATCTCTCCTGCCCCCCCCC CCCCCACACACACACTATCGCTCACTCGCGCCCCTTTGTTCGTGTTTC CCTCCCTATCATATGCGTGCGCATTCCATAAAGTGTTGCAATC
74	IrLmB	CGAGCGCGTTGCCTCTGCGCTGGTGAACGTGCCTGCGCACTTACATCT CAGCCGTGCTTTCTGGGAAGACCTTCTGCGACGCGGGGCGCTGTGCTG GTACAGATGGAAAGATGTGCGCCATCACGGATGCATCCTTGCATGGTG CGTGCTCACGTGCTCACCACAGTTTGTGTGTGTGTGTGTGTGAGTGTG AGTGTGAGTGAGAGAGAGAGTGTGTTTCGGCGCACCTCCCATCCAACA GTGGCGTGAACGGCTTTCTCTGTATGCGCCCTTTCGTTTTAACTCTTT CTTTTTCCGCCTTTGTTTTTTGTGATTTTTGATGAACTCAAACACAAA ATGAACATCC
75	IrLmJ	TTCCTTTCACCTATACACGTGGTTCATATATTATCGGCTTTTTACCTG AGAGAGCAAAGAAAGCTTATTAGCACGGAAAAACGTAATGTGCTGATA GGGGAAAGAAACAAAAACAACCGCAGCCGAGACATTTTGTTTGTGTTG GAGGAAGTAGAGGAGGCCCATCGGTGTCTAGAAGACAATACCGCAGTG TGAGACAGTGACAGAGGTGGCAGAGGAGAGGTAGGGGGAAGCTCAAAT GAGTGCTGTATCATGTATGCATGTCTCTCTGGCTGCTTCTCAGCTTTT CGTTCCGGCTTCCACTGGACTGTGGCCCTGCTCCAAACCTTCGACGTG GGATGATTCGATGACTCTTTCTTTTATCAGTGACTGATACCGATACTG TGCTGCAGAGAATCGAGAAAAAAAGCGGAAAAGGCGGCAGGGCCTCGA TGGCAAATCGTTTAGTTGTGTGTGTCAGTGATGCCTCTCTAGGTGGCG GAGTGGGGCTGCACGTGATGGACGACGACGTAGCGCAATACGCGCCTT CAGTCGACAGATCGAACAAGCACCGTGCTGGTTTCAGTATCCCTGCGC ACTCTCCTGGTTATGGGCGCCTTGAATGCGAGCCTTTGTTTGAGCTCC ACTTGCTGCTCATCAAATGGCCACACTTCCGACCTCCCTTGCTCTTTT TTTTTGCACTTTTGTGGCACCTGTGTCCTTGCTGTCGGTCCTTTCCAA CTTCAGCACACGGAGAAACCACCCTGACTGTAGCAATCACGATCCAGT GGGGACAAAGGAGACGAGGTGTCGAGTGCCATTTCGACGATCGGA
76	IrLmK	GGTAGACTCGTGCCGCGCGCTGATGATGTAGGTGCACGCGTGCGTGTG CTGCAGCGGAGCCGCCGCCACCGCGACTGTGTGTGTGTGCGCGCGTGA CGACCGGCTCGAGGAAGGAGGAGCGCGCGTGTGCGTGCGATGCGCCTC CTCTTTTTTTTTCGCCCTCGTCGGTTTTTTTTTTTCTGAGAGGACGGC GGCGGCGGATGGCGGGGCGGCGGCGCTGACGGAGCGGCCACGCTCTGC ACCTCCCCGCCCTCCGCCGTCTCTCCGTTCGCCGTCCTCTCCTTCCTC

SEQ ID NO.	Description	Sequence
		GTGCGTGCGTCTGCCGCGCATGCACACGCGCGCGCGTTGCCGTAGCGC TGTGTATCTGTGGAGGAGGGCCTTGTCTCTCCCTCCCCGTCGCTGAGA GATGAAGGGGCAAAAAGAGAGAGCAGTGCGCATGTGTGCCTCCGCTCC CTGGAGCTCCCCACGAGCCCCCTGCGCCACGCACCTGCGAACCTGCAC AGCGGCCCACCTGCCCGCACACGTGAGCAGAAATGGGTGTGTGGAGCG GGTGATGTCGGCGCGCACACGCGCGCGCGCTGACCACTCCGACGTGAA AACACGGAAGAGCGAGGCTGGCAAGGCAGGGCAGGAACCTGATCACGT GCGCGCGCACAAACGGAATGAGCAGCTCCTGAAGAGGAGATGGGGCTC ATGCACGCAGACACGCACGTGCACACTCCTCCGTCTTCACGGAGCGCG GCCCTGCTGCTGCTGCCATGTGCCGGACGTCTGCCACGCGTCTCTTCC CCACACCTTGCTCTTCCCCCCCCCCCTTCCCTCCCGGCGAACACAAAA CACGCGCACGCCCACCGAAACAACAACGCGCAGCTCTTCGCTCTCGTT CTTCGAACAAACACCTTTAAACCGCCTTCCAACCCCTCTTTCTTCTTT TTCAGCC
77	OGNT-1	MCCLLRSVHRCSVVAFCLTSPACVCVRRTSAALRRTPPSSAAAAPALP WRRPRAHMRTELSASSLALFLCAQHDADMRVIPHRHRQKNSREDVRTH THTHTHTHTHTHGLSVTSLHTGARATAVGRAPRTRDALMDTHVTACVK RVPSPAPFRDGLDAVATAGAAVVGDAALCMDAEVGSGLDERGRGPAGF TPASVAFAKEGNGRLASLAQPSHSSNYRGPSTVALRTAAMGHDDARTH VTHTTPALSSSATVHSRGSVRPLKHWMCCASRVHHVLRSLGILNDDAD PANMSRILACSCATIGALLVLLIISFAALVVLLVVVVPDAQHRLSRTV SPLLDLNSKRNDRAAGGGRGGDDTASGLSVFDLQIRRLLASEGLEGFL RKAHRAADLRRRVQRNATLLAALRRANATRGKGAGDDVDWASLAQTLP ELEHLSFLLAEVCAHVRAVQEHDPVMGLVKLSDFLLNVKGRKAALEKA AERARSLAANATSPAAAASDIGDAVARWNAALKESLAGRSEAARLRAQ LRGFIGVSPWETERLTEQPFDDLALLQYRHAWAQSEVLPILRGRLGRA GARAAEEDPNAAVLRNNAVRHPPQNRSAHARSARLSPQEVAERIAMKA DLYEVASIFNHVYYYPLRRYSALRPYGGSSVADTDAWYTAITAVVQTR FGVPITSNAAQTTETAAAALPLLQRDSPLSTLALQRLGLERAEEVARL HAEDRPLMPQALHSDAAESTHSIFVSLASYRDMECAPTLMSLFRTARN PHRLYVGVAQQNRAGDAPCLVPEMYTPYLCPSEGVPDSPRERGARART LYGEGVDFMKSANVPEARSFDGGVCFLAEQVRLREIDARQAKGPTYGR YMAMLLYRGETLALVLDSHNRFRPMWDVLSATMLMRMEDPKAVLSHYP ESYQGEQVDLQPYRTTTSYLCRANFLNNFGYLRLEAIVIESASDFAKN NVYNDPYVRVQSTDIDPATNHRLPQPWVAGGFLVSFGRIFRDVPFDPH LPYVFDGEEVLYSMRLWTHGYNIYSPARGACFHIYTRSSAPKVWAESP QWYSMQARVHERIQFLVQAHLLNKEDVMVPANSTSSFVIMDSSRYGMG KQRTVAQWYDYAGVDPVRYTLDGRWCGKSKRD
78	OGNT-L	MRSRLLPSRRPRAARWARCTVFCLGFFIGAITLCGVVAWRIMSDMSED VKGRRTLTQHPSPGKPAVPRVTDAGADDDAGLLRSSGGAAPYTESLEE LVLLLRIYAEETGVRVTDTSYALPEGVSAGAGLMDGDANSQRGAETNG ADLHLPGMALLRGRHGNGGPTGDHLSATWVLEDPETIRTEQEMYVERY LAPTQADVELTPLRVISSYYNTQGSRSLHRMAAETEKAMNDDGYATYI QRSSTFYDVSHAARRGYGQEGSIFVAVPFTLTDITPQMVGIIRRRASA VPTSSKTQKPTSSNSPLKERDNSVTDDGFHELRLTAARCAMTVESLFR QAHRGVAVTVGTLDVVTASGISSAVDLDFSKPSDVLFPLKPEDRASLG ARRRRYTRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLTQLEGL SATPTDPLRGEDAAATLERRFPLQYMGRYATLQLYRGESYVFFLRTGA

SEQ ID NO.	Description	Sequence
		LVLPNWDLMLRLLYLRTPARDRAVLSSRPTPRVAWIALAASVAKMWDT EPFLRLSLTASWHRNGKGATDRDGEGAATAPPPDQVGQRLLAALPADV ASWLSAAREEAELVLWLVTPSWLWPTMAETLADWRQLTASSDAQPPPG ATASTLRLLFASDAVNGVLGDAASTLMTADLDTVQTTPVKRSDAAAAS LHGQRVVSLRGGTNPTTNSTPQAVVAASLTPSEVYELLFLAEKRPPTP EQPIVQVPSSEPTLHRVPSQDLGPSVEPLCGEATSEAPYYSAADKALL KRSFEYCWLKEHRKVLRQQLHRLLHSTKATTVLKTTQATKVPAAGARG AKGGREGGPVVAEVAPRSSVCLADMRYLAPMEATLLTGADEGTSDSGP SAHHEEHAADQPSLRQENAWLTSAANVGKVHGVATSLVSKAARGTKER QGGSPQSPKDAASTPPEPTPYVLQSAASLDLLFGPAEAFFEFDTAHRL RTRARSLSEQLEERRLRREGLTATAAHAQVPEAVELDTSLQFMDGDLE DVYVTQALWTRGWNIFGTTEPVAVGTGEEEFSRSASAATTAPTSSSVA EDSVPAELRDARTFTHDKFWALLMAHRDAGTPLGATETRQQASAPRES SLLLYPLRRTMKEWELFAGMPLTTLRDALHPT
79	OGNT-2	MLDHGQMPSLLKRPLRMPRRRLSARRRQALKVFIVILCLCAFLFIFFF SARLPGILHERITPSEKPWLTRAGNSTLFEKVVHNRIPGTAWRDAHLN TIISLAKSGDVVHLTPTKHVRHRRASGSNSSTFQKWESLYRPSDRYHI PAWATPEDRDTLQHASIFTSLASFRDHECALTLRNLFDMAVAPHRLYV GVSEERNLSDESCLSSIGVEDLASGETRRVLYGAEAPDTLGVEVRSLT WAAVAGSRQLLDVDQEPRVFTGSAAESGAQPTGVFVHPSHAMERVTCI AGELETTRDRLLLAEDDAKESTDGRSVFRRGRGGPQQQPSHALAGCRV TTRVTYPTSARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSHYPNGYREGHDREEFDKTSVMLMCTAQVLSNGMPK LGARWANVSPRPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYIFDGEEV LYSARMWTAGWDLYGPGQPDVFHHYGRMHTPKYFEVLTPTKAARRELS EKRALHLLRRAHPWIEELVRRGYVSSDGQSTLKPLPPEEAPETRLIVT DEVAADTQEIRVWATYYGMGTERPVAAYWKHTELSDEFVKAKDDEQRW MGGTGLCEKSDVLA
80	OGNT-1/L region	TGCAGAGAGAGAGAGAGAGAGCGAGGGGGGGGAGCACGACTACCTT CGCTGCACTCCAGCAGCACCACAGCAGGCGAGTGTAGCCTTTCCAGCT CGCTCGCAGAATGTGAAAGCCGCACCACGCACTCCTTTTCCAGGGATG TCAGCGCATTGACCGCCCCCGCCCGTTCAAACTTCTCTGCACATCATA GTCGCCACCTTGTGCGGCACCCCAGCCGCAGCAGCGGCACCGCCCTCT TCGCTGGTTTGAGCAGGCACCACACAACCCGTGGTGCACACAACGCAG AGGCGATCGGCAGCTCTCACATGAATAGGTGACCACTCCAGCCCACGT GTCATTAGCCTCATCGCAGGTGAGAACGTACGGTGTTGCCACTCGCGC CTCCGGCTCACGTCCGGTTCGACGACGAGAAACAGGAATGTAGGAAGC AGGCACACCCGCGTGAGGCGGCGAACGAGCGTGGCACAGCCGTGGTCA CGCCGAAGCACAGAGGACGCCGTTCGGTGAGTGAGACACTTGTTTCAC ATGCCTGCTCGTTCGGCTTCCGCCCACCCCTCCCTCCCTCCCTCCCCC CTCCCCTGCCGTACGGCACACGTGCGGCCGCCTCCCTACCCCACCCCC TAGCCACAGACACACACGCACATACACGGGGGCCTAGAGGAAGGAAAG AGTTGAAAACAGCCAGAGTCTCGGAGGTGTCTAGTCGGCTGGAGCGGT GGAAAAGCGCCAAAGGAGGAAGAACCCCACGAACGTTTGTCGGCTTGG CTGCACGCAGCGAGGAGGAGGAGGAGGAGGAGGAGGGGGGCGGGG GGCATCGCACGCGTATGCCAGGCGCCTCGCTTGGCAGCCGCGCACGCA TCCCCCCCCCCCACTGTCACGCTTCATCATCGCGCGCGGCCCCCATCA TCAGCACGCCAGCGCGCAAAACGCTTACGCTCTGAATACCGGGGGGGA

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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81	OGNT-2 region	GACACGTGGAGGATACAAGCACTGTTACTGGCACACATCACCCGGCAC CACCCGGTTTCTCTGCTCCCTTCACATACAGCACTGCCCGCACGCATC ACGCACCCTCATGAGGTGCTGTACTTCACTATTGTGTCCCCTTCGATA CAGAGCCGTCTATTTTTGAATGGGAAGCAGCGAAAGCGCTGCGGTGAG GTAACTCCTCTTTCGCAGTGGCGCCTCTTACCACGTCATCTGTGGCCG AACTTGCCGTGGCGCTACTGAGTGTGCAACAGCATCCCCGCTGCTCCC GTTGGATGGCAACCTTCATGCCCGTCTGCACTTGTGCGTATATTTGAG CTGCTGCTGTTGCCGGCAGTGCACTGACGCTCCCGTCTTACTCGCTGC GGTCTACACGTCCTCTTCTGTGCTTCTCGCACACCGTCACGCAGGCTC CGGGAACACGATCGCGGTAGCCCCCCCCCCCCCCCCCCCCCCCCCCC AAAGTGACCGCAGCCTGTGTGCGAGGACGAGTATGCCCGCGCGAGCTT CGTGGTCGGGGCGAGCCGATGCCGGACGACAAGTTTGTGAAGGCTGGG AGGCTCCCTAGCATGGGAATGGAGGTGATTATGCGCTGCCGAACGTAC AGTAGTCCCTCCGACTCCTGTATGCTGCTCGTCCTCGGCTTCGGTGGC ACCCTTACGTCACTGGGTCGAAGCAGTTCGTGACGACCTCCTCCTCCA GGGAGACGTGTACCTTGTTCGCTTTGACCACCCCGACTCGGGCGTGCC

SEQ ID NO.	Description	Sequence
		GGCCCACGTGGACGGCTCTCCAACCCTATGCTTCTCCTGCATGGTACT CCAATCGCGCCCCCTCCCCTTCGCACAGGCTCGCACCCTACACGCTCT ACAACCCAGCGAGCGATGCCTGTGGTTTGCTGACGGTACTCGAGGTCC GTTGTATGCACACCTTCACCACCTCCACGGGTGGCAGGAGCGTGCTTG GCAGAACCCTAGAACATGCTGATCCGGCGCTTAGCCTCATAGTTGGTT ATTCACTCAGCAGCCGCCTTCGCGTGGAGCCACGGATATGTCCGTGTG ACGCTGGCGTTGCTCTACAAGTCTGCTAGCATGCCCATGAGGGACGTC GTGGACTACGCTCTGCGCAGTGGCTGCTGCTTCAGAGAGAGAGGGGGG GGCGGGCAACTGCGTGCTGGAGGAGCACCGTGTGGGCGGGCTTGCCAG GGCTTAGCGTCATGCGATGCGCTCTCGACATGAGTGGGCAGTGCAGCG CGCCCCCCAAAAAAAAATGAAGGGTGTGCACTCCGCCTACCGAGGCGT TTCTCAGCACTCATCGTACACGACAGAGAAGTCCTACGGATACCATGC TACAGCGGCTTGCGTGATGCGTGATGCACAGCATACTCATCCTCACAT GGGCGGTGGTATCTCGAGGCAACTCTGCCGTAAAATCGCGGCAGAGGT CGACGTACAGGCGCTGCACACGGTGGAGTAAATGCGCCGTTGTAGGGG GGATGGTCTCCGCGGCGAGCGCGACGGATGCCTCCTTCCACGACCGGA GACACAACCAGGGCGTGAAGACAAAGGGAAGGGGGAGGCAAAGAAGGG AGGTGCCGCTTGTTTCACTTATTATTATTATTGGTTGCTGTGTGTCTT CGCGGCAGTCAACAAGAACTTCACGTTTCTGGAGAGGGACGACGTGGC AGCCTACATGCGGTCGTGTGGGTGGCGTTGATGCTGTTCTTTGGCTCT AGCGGAGTCGGAGGGCGTGGAGAGCCAAGCCCCTGCAATCGTGGTGAC ACGTGGGTGGCTGCGGTGGGGTGGGGGTGGGGGGTCTGGAGAAAGTGG CTGCTCACGTCACCGATTGTGCTGTGCCCCCTTCAGCACTGTGTGCTT GCCTGTGGACGCTGCCCACAATCTCTTCGAATGCCTCAGTGCAGATGA CTACCGGCACCAAACGAAATAGTGCGTACCAGATATGTTGCAGAGCCA CTCTCTCCCCTCGTCCGCACACCTTCATGCTCACCTCCCGCCCGCCAT CGCTGCCCTCGTTGGTCTAGGCCTGTTCCCACCCTTATTATTATTATT AGTTTTCGCACCCTTCCTCCTCCTCCACCATCGCCACCAACCTTACAC TCCGTAGGACGTACGCGAAGATGGAGGTGACTGAGCGCATGGACCACG AGAGGATGCGATTGCCTTCCTGCTTCCTTTCGTTGTGCTTCATCGTTT ATATTCTTTGAACACGTTTCATGGGCCACCATTTCTTTCTGCCCCATG AGTTCCCTAACGACCCCCTCCCCTCTCCCCCGCTGCCTGACGCCCTCG CGGTCACTCAACAGCCCACGCTTCTCTGCTGTGGTGTTGAGTGACGGT GTGCATGTGCGAGGTTGTGCGCCTCGACTGTATCATCTCCCTCACTCC CCTTGCTTCGTTGTCTTCCTGGTCCACCATCAACTTTTTCTACGCGCA CGTGCTTCTCGTTCCTCTGCCACTCTCTGCCTTCCTACTCTCTGTGTC GGTCGGCTCCCTCTGTGCCCAGGCCTTGCTTTCACCTTCGCCTGTGCA GGCGTACTGCTTCAGGTGTATCGCTGCTCTACTCCAACGAACGAACAA AGAAGATGCAGCAGTGGGAGGATACGAAGGCAGAGAGGGAGACGGAGG GGAGAGGGAGGCGCAGCGCGCTCCCTGCAGCTGGATGCGCGTTGTCCC GCATACGCAATCGTTCTTCCGCTTTCCGCCGCCTCCGTCTGCTGCTGT CTTTGATGGCATGCGCGGGACTGCTTTGACGGCGTCACCTATTTCTGA ATTTGTCACACGTACAAATGTATATATATATATATATACATACATATA CGTGCATGTGCACTGATGACGGTGGGGGTTACCCGCCACGCTCAGCTG CGAGAGCGTAAACCTCCGTAACAATGATACTTTACGCATAGCACCACT GCGCAGCGCTTCCATGGGCCGCCCCCTTCACCTCTCGCTTCGTTGGCG GACCTGTGCGCGCTCGCCGTGCGTAACGAGGGGCGTCTCTCTCTTTGC CCGATGAGTGGTTTGTGTCTCGGAAGTACTTGAAATGGTGTATCCCAT

SEQ ID NO.	Description	Sequence
		GACACGTCTTACGTCATGTTCCTCCCTCCTTCGTATGCGTACGACTCT CCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTCCGCCTTCT CTGCGCCGGTTTCCTGGAGGATGGAGAGCTCTTGCTCATAGATTGAAG AAAGACCAGGCAAGCCACGGAAAACTCCGAACAAAAGCGGACTCACGC GGCCGTCTGCATTTGACGTGCTTGCATACATATACGCACCAACCTTGT GCACGTCTTGTTGACATCCGTAACACTTGCCTCATTTTTTCCGTGCTG CTCGGATGCACACTCCTGGTGTGGGGCGTAGTCACTATTCGTCTCTCA CCAACACACACACACACACACACACACACCTGTACATCTCTCTCTCTC TCCTTTTCTGTGTGCCCCGGCGGACGTGCGTGCGTGTCTAATCACTGA AATTCTTCACATTGCATAGAACGTAGCGTCAGGACGCAGCCTCGAACG GCGATGAAGCCAGAAATGCTAGACCATGGCCAGATGCCAAGCTTACTC AAGCGGCCTCTGCGCATGCCGCGGCGTCGCCTCAGCGCACGTCGGCGA CAGGCGCTTAAAGTCTTCATCGTTATTCTGTGCTTGTGTGCGTTTCTT TTCATTTTTTTCTTCTCAGCGCGGCTGCCCGGCATTCTGCACGAGCGC ATTACTCCAAGTGAAAAGCCGTGGCTCACCCGAGCAGGGAACTCGACG CTCTTCGAGAAAGTGGTTCACAACCGAATCCCGGGGACCGCGTGGCGC GATGCTCACCTGAACACCATTATCTCCCTCGCGAAGTCTGGTGACGTG GTGCACTTGACTCCCACTAAACACGTTCGCCACCGCCGAGCCAGCGGC AGCAACTCTAGCACATTCCAGAAGTGGGAATCACTCTATAGACCGAGC GACAGGTACCATATCCCTGCCTGGGCCACGCCGGAAGACCGTGACACG CTGCAGCACGCGTCTATCTTTACCTCCTTAGCTTCTTTCCGCGACCAC GAGTGTGCGCTGACGCTGCGCAACCTTTTCGACATGGCTGTTGCTCCG CACCGCCTGTACGTTGGTGTGAGCGAGGAGCGCAACCTGTCTGACGAG AGCTGTCTCTCGAGCATTGGAGTAGAAGACCTGGCAAGCGGTGAGACG CGGCGTGTGCTCTACGGTGCAGAAGCGCCAGACACACTTGGCGTGGAG GTGCGCTCGCTGACGTGGGCAGCTGTGGCTGGATCACGGCAGTTGCTG GACGTGGATCAAGAGCCGAGAGTGTTCACCGGCAGTGCTGCCGAATCT GGCGCGCAACCTACGGGGGTGTTTGTACACCCGTCGCACGCAATGGAG AGGGTGACGTGCATTGCCGGGGAGCTGGAAACAACGCGTGACAGGTTG CTCTTAGCGGAGGATGACGCGAAGGAATCCACAGATGGCAGGTCTGTG TTCCGACGCGGGCGCGGGGGCCCCCAGCAACAGCCGTCGCACGCACTG GCTGGGTGCCGCGTGACGACGCGCGTGACGTACCCCACGTCCGCGCGC GGGCCGACATTTGGCCGGTACATCACAAGCCTGTTCTTTTTTGACCAG GACTACTACATGGTGGTGGACAGCCACACGCGGTTCTCTGTGGACTGG GACATGAAGCTGATCACACGCGTGTTTCAGCTGCCGACGCGGGGCGTG CTGTCGCACTACCCGAACGGTTACCGAGAGGGGCATGACCGTGAGGAA TTCGACAAGACGAGCGTTATGCTGATGTGCACCGCACAGGTGCTCAGT AATGGGATGCCAAAACTTGGGGCGCGGTGGGCCAACGTATCGCCACGC CCGGTCCTGCAGGGCTTTGCTGCCGCGGGCTTCATGTTTGGGGATGCG CAGTTCATGCTGGACACGCCGTTCGACCCTTTCCTGCCGTACATTTTC GACGGCGAGGAGGTGCTGTACTCTGCGCGGATGTGGACGGCCGGCTGG GACCTCTACGGGCCGGGGCAGCCGGACGTGTTTCACCACTACGGGCGA ATGCATACACCAAAGTACTTTGAGGTCCTAACGCCAACTAAGGCTGCG CGGCGTGAGTTGTCAGAGAAGCGGGCACTGCACCTTCTGCGGCGTGCG CACCCGTGGATCGAGGAGCTTGTACGCCGCGGCTATGTGAGCTCTGAC GGGCAGTCGACTTTGAAGCCTTTGCCGCCGGAGGAGGCGCCGGAGACG CGACTCATCGTGACAGATGAAGTGGCCGCCGATACGCAGGAGATCCGG GTGTGGGCGACATACTACGGGATGGGCACGGAACGGCCTGTGGCAGCT

SEQ ID NO.	Description	Sequence
		TACTGGAAGCACACGGAGCTGTCCGATGAGTTCGTGAAGGCGAAGGAC GACGAGCAGAGGTGGATGGGTGGTACTGGGCTGTGTGAAAAAAGTGAC GTCCTGGCGTGAGGTGTGCTTTCCAGGCCGCTGAGCGGAGAGGTGCGG AGGGCAGTCCAGGAAGGTGGGGAGGGAGGAGGGATGGTACCCAAGCGA GAAGGGGACGGACGAGCTCAAGGCTGAAAGTTTCAGCCAACGGTTTCC GGCGCTGCATCCGTTCTCATGTTTTGGCACTCGTCATATGCTTTTATT TCTGTAATCGTTTTTGGAGGAGGGAGGAGGGGAGGAGATGTGGGCGAG CAGAGACGGCGGCAGCAGCAAAAAAAAGGGGGGGCGCCCACCGGCGCT GGTGAGGCGTGCAGGGGGAAGAGGGTGGCATGCGACATGCACAACCAA ACGTGCGCGTGTGCAGATGTGCTGGCGTGCGTCGTGAGTGTGTGATTT ATTTTTGAATGACACCTTATCATTGCTCTCTCTGCCTCACACTCTCTC GCTTCCACCGCTTTACCTTGCTACGAGTGTCGCTTCGGTATACCGTCA CTGACGTTGCCTCTCCCCTCTCCATACTTTCGCTGTCACTCGCCGCAG GACCGGACTGGTGAGTCCGGGGTGGGGGGGGTAGACTTGAGCACACCG TCACTCATCCTCAGCATCACACGCTTGCATCTGGGCAAGGGAGAGAGG AGCTCCGCCTTGCGGAAGCGCAGATGAGTGCAGAGTTTAGCTTTCCAT TCATGCTCATGCTCATGCTCTGGCGTGCACCGGTGTGCTCACCTCTCC ATGTACATACACCTTCGGGCTTGCGCGTGCACCCCGAAGACGGAGAGC GACAGCGAAGACATCTCTGTGCGGGCTGCCCCTGTCTTTGTTTTGGGC TGCTTCCAACCTCCCGCCCCCCTCTCCTCCATCAGACCCGTGCATTAC TGAGATGCTCGCCGCACAAAATCACGTTCACAGGAGAGACCTCCACTT TCGAAGTAGCGATAGGAAAGAGAATGTCTAACCATGCCCGATACGCTT TGTGGGCCCTCGCCATTGCTGCGCTTCCGTGCTTTTGTCGTCACAGAA TGGCGGCCTCCACGTCCGCCACCATGGCGGGCACGCAGCCATGCCATT CACGGTCTCTCACTGCGCTCTAGTTCCTTTCGTCTCAACCGGATCTTT TCCTGCTTTCTTCGTTTTTCTCGAGCATGAGCGTTGTCGACAGCGTCT TCATAGCGATCGTGCCCCCCCCCCCATCGAGCAGGCGACTGCTTTCGA GTTCACACGCGTGGCCATGCGTACTGACGTATTTCAGGTCCAAAGCTA GGCCAGCTTCTGAGGTGCGCCACCTGCTCATCGATGTGGGGTAAGACG CCGTGCGACGGCGGCAGCACGGACTTGTGAGCGCAGGGCTGCAAGAGG GGGTGCCCGAGACGAAGTGAAAAGGAATGGGGGACGGCCTCGCAAACG CTGCGGCTCCCTTCCTCCTCCTCCTCCTCATCTCCACAACTTTAGCGA CATCGAGGGCGACGCAGATTGTGTGCGGCGTCGTTTTCCCGAATCGCT CACGGTTTCGTGGCCCGCAGTCCACACTTTGGCAATGCGACCGGCTTG GACGTGTATGGCTGGCGCGTGCGAGACTGAAGACAACGCTTTCGGGTG TGACGTTAACAATGCGTCAAAAAAAAAAACTGCGTTGACGCCTTTGAC ATGTTTTTGACAGCGTAATGCCGTCAGAGGCTGGCAGCTGCTCTTGCG TCTCTCATGCCTACCGAAGACCACCGGCTCGCTGAAGGTCAGACGGAG ATGGCGGGTGGTTGGGCATAGTGGGAACAGGGGAGGGGGGGGGACGCG TGCCATACGTGTCTGCGCGTAGAAGGGAAGAGGGGGTGGGGGTGGGGG TGGGGAGTGGCGCCCAAACCCACCGACGTCTCTACAGGCATATCGGCA AACAGCACGACATGGCAGCTCCGCAGAGGAAGGAGGCAGACCGTTGCT CAGACAACCGTATCTCACCGTGTTCATTACGCGCCAGCTCCTGGACGC GGAAGTACACACCGGCGAAGGCGTCTGTTGTACATTCGACTACATCCA CCCGGGAGCGAGGACGAGAGCAGCGTGCAGAGGATGGGGGTTTTCTGT GCGGGCTGTACACATGTGCGCTGGCCTCCTTTTGCCCCGCCCTCGTGC TTTCGTCACCGTATTCGTTTGATGTTGTGTGGTTGTGTGCGCCCGGGC TTCTCGTTACCCCAACAGCCATCCCCATTCGTGGGATTCAGCGGTTGT

SEQ ID NO.	Description	Sequence
		CGACCACTCACTACTTCTTTCCCATTCTTCTTCTTTTCGATATCGTGG GCATATCCTTTTACGACGTGCCGGCATTCTGAAGAACACCAAAGACCT GATGCGATGTGTAGGAGGGGCATGCGGACGCAGCGCACGACACATTGC TTCTGTGCGCGCAAGTGCCATCGAACGTACATGAGGCCCTCGGAGAGG CGGTACAGGGTAGTCCACGCTGCCGTGACACCTCGACGCACATGTGTT GCGTGCCCACTCGAGAGTACGTGAAAATAAAAAATATGTGTAGAAAGG TGCGAGAGTGCCCCCAGCTGGATCCTAATGCACGGGTGCCATCTACAC GGTGCGTATGTCTGTTTATCTCTTCGCACCCTCCACTATGTGTGATCC TACGAACACACCGTTCACTCTTTTGCCTTCCTGCCTTACTGCCTTCCT GCCTCCTCCCTTCTCCCTCCTCCCTTCGTTTGCCGCCATTCGGATCTC CACCCTTCATTGACGGTCAGCAACGCACGTGCTTACATCCGCATACAC GCGACAGAGGGCAGGGCATCATCTTCGAAAAAAACATCCGAAGAACGC ATAGTGCACCCTCCCTTTCCGTTAGAAAGCGAAGCATCAAACAAGTAA AAGGGGGCGTGTCTGACGAGGAAAGCACCTGACGAGTACAAGGACATT CACAGACGCCTCCGGCCAGCTGAACTCCCCTTCATTTTTCTCTGCGAG CCCCGTATGCTGGAGCCTGGGCGTTTGCCACGTGTCTGCCGTCTGTGT GATCCTGGTTGCTCTCTCGCATTGCTCATCCTCTCCCTTTTTCCCCTT CCCCCTCCCACGCACGTACACATACACGCTGCCGCGTCTCTGCCTTTG CGAGGTGCGTGTTGCTCTCTCTTTCATACTTGGCAAGTCCTTACTTGT ACTGGTGCGTGCTGACGCTCTCCTCGCTCGTATTGCTGACGTACGTCT GCGCGTGACTGCACCATATTGTGAGGTACGTGCGCTGTTCATTGACCA GCAGCAGGGCTGGTGCCCAACTCCATTCGTGTAAAGCGAACAGACAGT TGACACCACACCGGCGCACAGGTTCATACGCTAACGATGTACGGTGGC TATTACAGTATGAATGCTGGCATGCGCCAGGGCGGTGGCTACGGTGGC GGCCCTATGATACAGCAGCAGCAGCTATATCAGAATCCTCGACTGCAA CAAGTCCAGCAACTACCATCGCCACCGCCGCATATGCAGGCGCACCTA CGCGGCACTGGACAAGGTGGGATACCAAGCCACTTGCCGCCGGTAGGT GCTAGTGGAAATCCGGGCCAGCTAAGGCGCAACCCGAGTTTCATGATG ATGTACAACGACCGAGGTTTTGGCCAGCCGAATCCGATGATGCAGCGC ATGGGCTCCTTCAACTCGATGGGGTCGATGGGCATGATCCCTCGCTTT GACAGCTTTAGAGCGCACGGCGGTGGTGGCAACCAGCCACAGCGCCAT GGTAGTTTTTCTTCGTGCGGGACCGGAGCTGGCAGTTTGCGCCGCGTC AACAGCGGCATGAACTTCGACTACTCGTCAGTCTCGCAGGTCCACAGA GGAGGCTCGCTCGCACGCAACAACAGCTATGGCACCATGCGGCAGCCT GGTGGAAGCTTCTTCGGCGACACTTCAGCCCCGGGTGGTCGAGATCAG CCTCTTCAGCAGCTCAGTCGGCAGAACAGTGCCATCAGCTCCTACAAC TACGGTAGCTTCCGACAGCCGAGTTTTGCACAGGGTAGCGTTCACAAC GGCGCCACCGGTGTCGGCCCAGGCGTGTCGGCGAATAGTATAAACGGC ATGTTCAAGCTCGCTGACTCTGGCGGCAGCAGCACAGTCAGCCCCCCC CAAGCTCCTGTAAACTTCGGTGAGAGGGGGCCAACAGGTGCTATGGGC GCTTCCGGGGGGTTGCCCACGTTAGGCCTTTCTCGCCAGGACAGCGCC AGGTCGCTTCAGCGCAAGTACTCTATTGCTGGTCAGTTCTACAACTAC GGTGACAGCAATAACGGCGGTGGGGGTGTTGACCAGTGGGGGGCGCCC CCGGTACGGCAGCAACGTCTCTCACAGGCTATGCCGGGAGGCGGCTCC ATGATGGGTGGCGGTGGCATGATGGCACTAAACGCGAACACCGCTACG GTTCAGCAACGCGGCGGCATCGATCCCGTGATGCTGCAGAGGCAGCAG CAGATGAGGATGCAGCAGCAGTCACGCATGATGGCGGGCGGCGGTAGC AAAGGCGTCCCATCTTCGGACGCTCCATCGTCGAAGGGGACGTCGGAG

SEQ ID NO.	Description	Sequence
		AGCACGATGGTGCAGGAGGGTCAACCCCAGATGCTGGGGCGGAAGAAC AGTGTGCAGAACTTGACGCGTAAAAACAGTGAGAAGCGAGTTGGCATG TACTTCAAGAACAAGGAGACAGAGCAGGACGGCGTTCAGTACAAGAAG GATGGCGACCCGGGTACCTCCGGCAAGAACAGCTCTGGTGAACGGAAC TCGTCGCAGGCGAACACGGTGAAGGCCTCCCTCTTGCTGGACATCTTC AACGGCCGGAGTCCAGCAATCGAGGTGGACGGCCGCACCATCCGCGCC AGCAAGCCTGGTGCCGAGGAAGTACAGAAGTACGACATGCACGATGTT ATGTGCGTCAACCGCATCACCGACATTGAACTCTCGAGTGACTCGCTA GAAGAAATTCGAGACAACTTTCTGTACGGGTGCAATGCTGGCCTGATC ATGGCCGATTCCGGCTGCTCCGCTGCGCGGCCGACCGAGTGGTTTACG TGGCTGGCGTTGAAGTCCGTGGTGAAAGGCACCTTTGGCAGGCTGGCC TCTGCAACGTTCGAGTTCACTGTGTCGGTGTGCCTCCTGCAGGATGAT CAGGTGATGGACCTGCTTTCTGATTCGCCGCAACGCTTCGTGAACTTG ACCGTCGCAGAGAGCCCGTTGTTTGGTAATGTGGCCAATGGCATGGTG TACGTCTGCGTCGAGGATGCCGGTGAGTTCAACGATGTTCTGGAAGCG AGCCTGCAACGTGCGCAGGAGCACTGCAGTACCTTGGCCGAGGAGCAG GGTATTGTGCTGTGTACGTGTGTGCTGAAGCAGGTCAGGACCTCGCCA TCCTCCGGAAAGGAGGACGTCATCGTCTCGTCCATCTTCGCGAGCGGC GTCGGTGACGGTGTCATTCACTACAACCGTATCATCGACAAGAACCCG GCCGAGCCACGAGCGCTGTTCTACTCTGTAATGCACCGCTCAGTTCAC TCGACGGCACTGTTCTCGTGCGGCGTGAAAGATAGGGATATCTTCAAC TACCTTTCGACACTGCAGCGCTTCTCCAAGATCGAGACGCGCCGCCCA AAGGTGGGTAGTGCTCGGGCCTTCGTCGCCTACGGTACCAGCGCCATC CCAAGGATCCGCGAAGAACTCAAGGAGACTAAGGATTCCCGCCAGCGA ATGATGATGCAGCGGCAGTTGGAGAAGCTGGAGTTGATGGTGGCCGAT GCAGAGGACATGCTTCGGTCACCGGCCGATTGCGTACCCAAGACGTAT ATTTAAACGATCGAGTGTAGTGCGTCATGTAGATGGACGCGTGCGAGG CAAGCCTTCTCCTCTACCTCTCCAGACATTGATACGCGCGCCGTGGGC TGGCTCGATCATGGGAGATGCTGTCGCCCTTTTCTACCTTCGCTCTCC TTCCCGTGCCCGCATTTCCGGAGACAAACGAGCGTGCCGGTGTGCATG TGTGGAGGGGTACGCTTGCTTGCGGTGCCGCCATATGTGCTCACTGCG TCCATGACCATTTCCCCTGTGCCCCCCTCAGACGTGCCCCGCTGCGCA GCACAGGTGTTCGATTCTCTTTTGTGACCTCCTGTACTGATCCCTTCA TGCTTTCACTTGTTTCCCCCATCTCTCTCCCCTCTTCGTCCTTTATCA GACGTGTGTGTGTGTGGATGTGTGCTCTGCTCGGTGCTGTCTGTTGCC GTCGTCCAGACGGCCATCATACTCATCCCTTTTTCTACGCTTCTTTCA CTATGTATTCCTTTATTTTACCTCCCTCCCTCCGTGCGTGCGTGTGTG TGTGTGTGCATGTGCGTGCGCGTGAGCGACTCCGCTCTCCTATGTGTA TACGCCTTCCATGAATGTGTGACTGTGTACCTCCGGGCTGTGGCGTGT CTGCCGGCGTTGTTTCTCATTCGCGGCTGTTAGTGCTCCTCTTTTTAT TTACGCTGAATTCTGCTGTCGACGTGGTGGGGCAGGAGCGCGCGCACA CACAAACACACACGGACCCTTCTTTCGAACCCCTGTCGCCTCAGAGAC AGGCAGACGCTTACCAGCAAGGAAAAGGAAGGAGATGTACGAAAGGCA AGGGGAAAAAGCCGCTACGTTTCTGTGAGGCATATGCGTGCGCGCACA TGTGTGTGTGTGTGTGTGTGGATATGTGCCTGTGTGTACGTTCTTGGG CTCTATTTACACGGATTCACAATATTTATAATTTTTATCTTCTTGCCT GTCACATG

SEQ ID NO.	Description	Sequence
82	rna_Baya_228_0070-1-p1	MLGLASSTSNGMGAGARDPLEGFEMLFNASDPLWLADETGLARKQILR HLVHIDEWLQAIRAQLPSSEKLTLAEFASNNKDALNELRRRSRSVGDS HDDAWSRMIQDRTINNVNRPNELRFFSAVGDIPETESIQPFDDIQLLK YRHQLLLNAAEEDRRVSMLLSDTVAPLPYESKHRANELKRVLYNASSI FNRRFFYPARRYQRIRPHNTESAAQTDAWYTALVLEAKRLYAPSGQDR FANASSSHRIGLGDRPSLLRLPYLSEERRRQIERHFTSAQQALMPATD RGADTETIFVSMASYRDEQCSRTLVDMMRKAKHAHRVYVGIAQQNKKG EYACITQELFMPIPCYGDREGTAAKLNGDRGALALQLHHEADAAKRVW LNFTNWGQDHLDDFGRSVCFIADHVRIRRIDSSQAKGPTYGRFMAMLL YRGESMAMVIDSHNRFTPHWDTLAVHLYHKYNDDKVVLSHYPDGYEST KDFDLYRTSSAYLCGAKFLPDFGYIRLNGIIVGDPQPFWKNNQFNIPF VPPVTEPITKANNFRMPQPWVAGGFLFANASIMREVPFDPHLNYIFDG EEVLYSVRLWTHGYNIYSPERNLMYHFYLRSSSPKLWAESPHWNSGQQ RSRRRVQYLLRSRVKDLNQLHVSQDTDDPDVVVDANRYGMGPHRTVQQ WYQYAGADPVRYTLDNRWCST
83	CFAC1_160013000.1-p1	MSSLMPGPPPVPASGLNAVAPHRATSGPNPLARDVSLKHAEARASPTQ VELHPITIPVQESSVMSATTHQRHSQHSTLNTTASIAPGHRRRYLSWR VTSCFSGRVQACLRCVGFMRGDEEQRELTQRVVCACTGVAALLLLCLF LVVVLLLKVASTASTRVDGELETTRKSAGPEDDLRHLLTLDGVQRFLQ QGHRAEELHQQVAAASAQPAFKRLAAQLLQVSVYVQAVQAHDPSLGLV ELSDFLLNAKGRPAALERAAAAARREAAAAAGAAAGGGGAAAAGGAMV AAAAEWGAALKECLAGRGEAARVRAQLRGFVGVPAAQAERLARRPFDD VAMLQYRHAWTRSEVVPRLARVAGGGGEGGGAAVRAYDVASRAAEKAD VYEAASVLNHVHYYPLRRYAAMRAYAAETVADADAWYSEVAGGVQARF GAAVAARAGGGGGGAAAATTTAAGAAVRASPLSLLSVPYASAAREAE AAHLLTAADVGWMPEGLRAGAAVNTLTLFVSLASYRDAECPPTLLDLF RVARNPHRVYVGLAQQNRAGDTPCLLPEMYGALLCPSSGGDAVDAYAA AREAEARRRSLRGGVGADLRARHPGSGIALLDERVCFLSDHVRVRDID SRQAKGPTYGRYMAMLLYRGEDLTMVLDSHNRFRPMWDTLGASVLAKL DDPKAALSHYPGSYTPEETKFDLYPTTTVYLCKAIFNNFFSYVQLRAM VIGDTGEFVQNNKYNDPYVTVQSSTITKAQNFRLPQPWVAGGFLFSNA SIYRDVPFDPHLPYVFDGEEVLYSVRLWTHGYNIYSPPRGLCYHIYGR AKAPKLWDKNSLWYRTQDLVRPRIHFFLQSHRKKDTKLLVPADTTNAY VVVDSSRYGMGRQRTVGQWYDYAGADPVNYTLDGRWCGLALD
84	EMOLV88_020005500.1-p1	MDSDVDARVRLAPSQVVSGGSLCSLKTADPGAIGASVMRTSGGATHRR GELGHYAAGTVTTPVGDSDNVHVSLARAPQASPGSRCGGSSNAKRFGA AEERLDCLLAPSFSSSHNPYESSAAAAAAAAAAAGVTGVRGRGKSTVL QHLAFFPSQVYRLLHRLRFVKDENVKDASSMLECACAAVGVLWILLFL SLAALVGVVLVVRIAVRDGQRHVEKVAGQQLDLCSHGRSGATCSTSAH LAGIGRVLDGEGLKLFAEESRRAAEWRQRLQRNASLWAELRSTRGGGD TDRRGVVNLPKVAQTLPELEHLSLLLHEVSEHVRAIHEHDPVMGLVEL SNFLLHAKGRREALETAAERARAEAASAVTGTDGGAPVSGDSVAKWAA ALMESFVGHSEAARLRAQLRGFIRVSAHQTERVTEQPFDDLAMLQYRH AWMRSEVLPMIRDRSLRARDRGAQVGDANAAVPPDIVSTAHHQDTSSR RSSEALMARDLANRMAVKADLYDVASIFNHIYYYPLHRYSVCCSYSSE TVADTDAWYSAIAAVVQTRFGAPVTLNKVQEGEDASLPLTQRDSPLSS LALSPLGSRRVEEVGHLYTPEDRLLMPAALSSTHPVNTYSIFVSVASY RDVECAPTLLGLFRNARNPHRIHVGVVQQNRAGDIPCLLPEMYTPYLC

SEQ ID NO.	Description	Sequence
		PAEDLPGFSAENRAAGARESRARERTLYSKVLGSERLSPSSRFDARVC FLADQVRVREIDAHQAKGPTYGRYMAMLLYRGEDVTLILDSHNRFRPM WDTLGATMLRRMEDPKAVLSHYPEVHQSDTAEGNPYRTTTVYLCRARF LKDYGYLRLDGIVIASAAEYTSRNMYNDPYVSVKSSQIDQAHNFRLPQ PWVAGGFLLSYATIFRDVPFDPHLSYIFDGEEVLYSVRLWTHGYNIYS PPRGLCFHMYGRSSAPKIWNDSPLWYRIQSRARARVQFLLRAHTPGSP TVMVPANTTNSFALIDSSRYGMGTQRTVDEWYKYAGADPIKNKVDGRW CGVDPAT
85	LAEL147_000030200.1-p1	MDNHVTARVKRMLSPSPFGDGLDAVATAGTAVVGGPALCTAAGTECGR NERGRGPAGFAPTSMAFSSEGDGGLSGATQTSHSSNHRGPANVELRAV AEGRGYAPTHLMPKASASSSSAAAAAAVHGRGHLRPLKRLLCCASRAH RTLRALGFASDDDDPATMSQTLACSCAAVGVLLVLLLISFAALVVVLV VVMPDARQHLSQTIGPLLDSNTRRDGNTAGGGGGDAASRASALDLKI RRLLASEGLEAFFRETHRAAELRRRVLRNATLLAALRKANAARGKDGG HGANLVSLAQTLPELERLSFLLARVSAHVRAVQEHDPVMGLVELSDFL LNAVGREAALEKAAERARAEVADAATAARGASATRDAAAEWNAALKES FAGRSEAARLRAQLRGFVGVSSSETERLTEQPFDDLALLQYRHAWVKS EVLPIMRARLRRAGARADEEDPNAAVLRNNAASHTPQNRPGHESSAPL RPQDVASRMAMKADLYEVASIFNHIHYYPLRRYSALRPYGGDSVANTD AWYSAIAAVVQTRFGVPITSNTAQTAEAAALPLIQRDSPLSVLALPRL GLERADEVAHLYTREDRQLIPHALNSKAAENTHTIFVSVASYRDMECA PTLLNLFRTARNPHRLYVGVAQQNRAGDAPCLVPELYTPYLCPSDGVQ GAAGDGGVGAARELRARARTLHGKGVDLTTSTKGPEARYFDARVCLVA EHVRLREIDSSHAKGPTYGRYMAMLLYRGEDVTLVLDSHNRFRPMWDV LGATMLRRLEDPKAVLSHYPESYQGEEVDFQPYRRTTAYLCRARFLNN FGYLRLNGIVIGSTSEFAKNNVYNDPYVRVQSAEIDPATNHRLPQPWV AGGFLMSFATIFRDVPFDPHLPYIFDGEEVLYSMRLWTHGYNIYSPAR GLCFHIYTRSSAPKVWSESPQWYTMQARVRQRVQFFLQTHPLNKEDVL VPANTTNPHVIIDSSRYGMGKQRTVAQWYDYAGVDPIQYKLDGRWCGV DKPD
86	LAMA_000003590 00.1-p1	MHRASASSSAAAAVHGRSHLRPLVRLLCCASRVHRTLRALGLTSDGDD PASVSQALACSCAAVGVLLVLLVISLTALVVALVVVVPDARQHLSSRK GPLLDLDTKRGGHTAASGASAVDLTMRRLVASEGLEAFLRETDRVAAL RRRVQRNATLLAALRKANAARGKGGGHGLDFVGLAQTLPELEYLSFLL AQVGAHVRAVQEHDPVMGLVELSDFLLNTKGRREALEKAAERARGELA NATRAAGGASAIGDAATEWNAALKELFAGRSEAARLRAQLRGFVGVSS AATERLTEQPFDDLALLQYRHAWAQSEVLPIMRARLRRAGARGGEGGP TAAVLRNNAASHTLPNRTVHASSAPLRPQDVANRMAVKVDLYEVASIF NHIHYYPLRRYSALRPYGGDSVADTDAWYSAIAAVVQTRFGVPITSNT AQTAETAALPLIQRDSLLSVLALPRLGLERADEVEHLYTREDRRLMPH ALNSNAAENTHTIFVSVASYRDMECAPTLLSLFRTARNPHRLYAGVAQ QNRPGDSPCLVPELYTPYLCPSDGARGAAAADGGADAARELRARARTL YGKGVDMAKSAKGPEARSFDERVCFLAEQVRLRVIDAKQAMGPTYGRY MAMLLYRGEDLALVLDSHNRFRPMWDALGATMLKRMEDPKAVLSHYPE AYDGGKVAFQPYRTTTAYLCRAHFMKNFGYLRLNAIVIRAASEFAKNN GYNDPYVRPPSSAKDSATNHRLPQPWVAGGFLLSSGTIFRDVPFDPHL PYIFDGEEVLYSVRLWTHGYNIYSPMHGICFHIYTRSSAPKVWSESPQ

SEQ ID NO.	Description	Sequence
		WYAKQTHVRQRIQFFLQAHPLEKEDVLVPANTTNPYVIIDSSRYGMGK QRTVAQWYDYAGVDPIKYELDGRWCGTDKPD
87	LARLEM1108_0200071 00.1-p1	MDNHVTTRVKRMLSPSPFGDGLDAVATAGTAVVGGPALCTAASTMCGH NERGCGPAGFAPASMTLRNEGDGRLSGATQTSHSSNHRGPSNVELRAA AEGRGYVPTHLMPKASASSAAAAAVHGRGHLRPLKRLLCCAGRAHYTL RTLGFASDDDDPANMSQALACSCAAVGVLLVLLLISFAALVVVLVVVV PDARQHLSETIGPLLDSNTRRDGNTAGGGGGGDAASRASAFDRKIRRL LVSEGLEAFFRETHRAAELRRRVLRNATLLAALRKANVARGKDGGHGV NLVSLAQTLPELEYLSFLLAQVSAHVRAVQEHDPVMGLVELSDFLLNA MGRKEALEKAAERARAEVADARTAVRGASAIGDAAAEWNAALKESFAG RSEAARLRAQLRGFVGVSSFETERLTEQPFDDLALLQYRHAWAKSEVL PIMRARSRRADARADEEGPNAAVLRNNAARHTPQNRPGHESSAPLRPQ DVANRMAMKADLYEVASIFNHIHYYPLRRYSAIRPYGGDSVANTDAWY SAIAAVVQTRFGVPITSNTAQTAEAAALPLIQRDSPLSVLALPRLGLG RADEVAHLYTREDRQLMPHALDSKAAESTHTIFVSIASYRDMECAPTL LNLFHTARNPHRLYVGVAQQNRAGDTPCLVPELYTPYLCPSDGVQGAA GDGGVGAARELRARARTLHGKGVDLTTSTAGPEARYFDARVCLLAEQV RLREIDSSQAKGPTYGRYMAMLLYRGEDVTLVLDSHNRFRPMWDVLGA TMLRRLEDPKAVLSHYPESYRGEEADFQPYRTTTAYLCRAHFMNNFGY LRLNGIVIGSTSEFTKNNVYNDPYVRVQSAEIDPATNHRLPQPWVAGG FLMSFATIFRDVPFDPHLPYIFDGEEVLYSMRLWTHGYNIYSPARGLC FHIYTRLSAPKVWSETPQWYAMQTRVRQRIQFFLQSRPLNKEDVLVPA NTTNPHVIIDSSRYGMGKQRTVAQWYDYAGVDPIKYKLDGRWCGVDKP D
88	LbrM.02.0270:mRNA-p1	MLRLLGFVNDDDDPADVSQTLVCACTAVGALLVLLLINFAALVVVLVV MVPAAQRQLPQTAQSLLDFNHENKSGTADGAALASGLDIRRLLAGGGL ETFLREAHRAEELRRRVQGNATLLAALRKANEARNNDGGRGVDLVRLA QTLPELEYLSFLLYQVSAHVQAVQERDPVMGLVELSDFLLNAKGRREA LEKAAERARAEAVNATTAATVGGGARATGGGSVEKWNAALKESFAGRS EAARLRAQLRGFIGVASSEAERLTQQPFDDLALLQYRHAWMQSEVLPI MRSRSRRAGAQAVKEGPHAAVLRSNTASRPPENTSVRTSVEELRVYGV ANRMAMKAVLYEVASIFNHIYYYPLRRYEALRPYGGDSVADTDAWYSA ITAAVQTRFGVPIACNKAQTTEAAALPLVLRDSPLSVLALSRLGFRRA EEVAHLYSQEDRQLMPQALNPKAAVNVRSIFVSFASYRDAECASTLLD LFRAARNPHRLYVGIAQQNRAGDSPCLVPEMYTPYLCPSEGLQGAAAD GGVGAARESRARARALYGEGADLTKPPNGPEARHFDERVCFLAEQVRV REIDSGQAKGPTYGRYMAMLLYRGEGLALVLDSHNRFRPMWDALGATM LLRLEDAKAVLSHYPESYPGEKADLLPYRRTTAYLCRAHFLKPFGYIR LNGIVIDSTAEFAKNNVFNDPYVRVKSREIDPTTNYRLPQPWVAGGFL MAFGTIFRDVPFDPHLSYIFDGEEVLYSMRLWTHGYNLYSPPRGVCFH IYGRQEAPKVWSESALWYNLQNRVRSRIQFYVQAHLLHAEKVLVPANS TNPFVVMDSSRYGMGKQRTVAQWYDYAGIDPVKHQVDGRWCGEDVIH
89	LdCL_02000750 0-t42_1-p1	MPKASASSAAAAAAVHGRGHLRPLKRLLCCASRVHRTLRALGFASDDD DPANMSQMLACSCAAVGVLLVLLLINFAALVAVLVIVVPDARQHLSHT IGPLLDSNTRRDGNTAGGGGGDAASRASALDLKIRRLLASEGLEAFLR ETRRAAELRRRVRRNATLLAALRKASAARGKVGGHGVDLVSLAQTLPE LEHLSFLLAQVSVHVRAVQEHDPVMGLMELSDFLLNAKGRKEALEKAA ERARAEGADATTAARGASTIGDAAAEWNAALKESFAGRSEAARLRAQL

SEQ ID NO.	Description	Sequence
		RGFVGVSSFETERLTEQPFDDLALLQYRHAWTKSEVLPIMRARFRRAG ARADEEGPNAAVPRKNAASHTPQNRPGHESSAPLRPQDVANRVAMKAD LYEVASIFNHIHYYPLRRYSALRPYGGDSVADTDAWYSAIAAVVQTRF GVPITSNTAQTAEAAALPLIQRDSPLSVLALPRLGLERAKEVAHLYTR EDRQLIPHALNPKAAENTHTVFVSVASYRDMECAPTLLNLFRTARNPH RLYVGVAQQNRAGDSPCLVPELYTPYLCPSNGVQGAAGDGGVGAAREL RARARTLYGKGVDLTTSTTGPEAHYFDARVCLVAEQVRLREIDSSQAK GPAYGRYMAMLLYRGEDVTLVLDSHNRFRPMWDVLGTTMLRRLEDPKA VLSHYPEGYQGEGVDFQPYRTTTAYLCRAHFMNSFGYLRLNGIVIGST SEFAKNNVYNDPYVRVQSSEIDPATNHRLPQPWVAGGFLMSFGTIFRD VPFDPHLPYIFDGEEVLYSTRLWTHGYNIYSPARGLCFHIYTRSSAPK VWSESSQWYTMQTRVRQRIQFFLQTHPFSKEDVLVPANTTNPYVIIDS SRYGMGKQRTVAQWYEYAGVDPIKYKLDGRWCGVDKPD
90	LENLEM3045_00002960 0.1-p1	MDRHVTARVKRMLPLSPFGNDSGDVATSGISAAGGLVLRAAARTETDS SEHGHGPASFVPATMVVGDDCDGGLPGIAQTSHGGHPRGLANGERVTV PDSGGYVPAQSSHKAFAAGLHCHRKVRLMKRLASCAGSIHRALRALGL VDNDDDAANLSQTLACACAAIGVLVALLLISFAALVAVLVVVVPNAQL LPSQGIGPSVVRNENGGGTARGGAASGARGSDFDAGRLMADRDLSAFL RDARRAEEWRRRIRRNATLLAALRKANAARSMNGGRGADLLSLVQTLP ELERLSLLLYQVSAYVQALQVHDPVMGLVELSDFLLNAKGRKEALAKA AERARAEAADRTRATAAGGGVPTVEGSVAEWNAALKESFAGRSEAARL RAQLRGFIGVSSFETERLAEQPFDDLAVLQYRHAWAMSEVLPMMRAHS RRVVASAADKGSRAARLRNYGGIRPPQNASAGASAEALEARDIANRMA MKADLYEVASIFNHIYYYPLRRYTALRPYGGHSIADTDAWYSAIAAAV QARFGAPITCNKVGTTEAAALPLTQRDAPLSALTLPRLGFERAEEVAH MFSSRDRRLMPQALDLKASVNTNTIFVSLASYRDAECAPTLLSLFRTA RNPSRLYIGLAQQNRAGDSPCLVPEMYAAFLCPSGGLQGAAADDDVAA ARESRARARTLYGEGADFTKDTSNPEARHFDERACFLAEQVRIREIDS RQAKGPTYGRYMAMLLYRGEDLALVLDSHNRFRPMWDTFAATMLLRLE DPKAVLSHYPESYPGEGADLRPYRRTSAYLCRAHFLKDFGYVRLGAIV ILSSAQFAKNNVYNDPYVRVKSRDMDSTSNFRLPQPWVAGGLLMSYGT IFRDVPFDPHLPYIFDGEEVLYSMRLWTHGYNIYSPALGFCFHIYGRS SAPKVWSESPVWYSMQSRVRKRIQFFLQTHLLDKEEVMVPANSTNPFV VTDSSRYGMGKQRTVAQWYDYAGVDPIRYQVDGRWCGKDDTV
91	LGELEM452_02000680 0.1-p1	MDNHVTTRVKRMLSPSPFGDGLDAVATAGTAVVGGPALCTAASMMCGH NERGRGPAGFAPASMALSNEGDGGLSGATQTSHSSSHRGLSNVELRAA AEGRGYAPTHLMPKAPGSSSAAAAAVHGRGHLRPLKRLLCCASRAHYT LRALGFASDDDDPANMSQTLACSCAAVGVLLVLLLISFAALVVVLVVV VPDARQHLSQTIGPLLDSNTRRDGNTAGGGGGGDAASRASAFDRKIRR LLASEGLEAFFRETHRAAELRRRVLHNATLLAALRKANAARGKGGGHG VNLVSLAQTLPELEYLSFLLAQVSAHVRAVQEHDPVMGLVELSDFLLN TMGRKEALEKAAERARAEVADARTAARGASAIGDAAAEWNAALKESFA GRSEAARLRAQLRGFVGVSSFETERLTEQPFDDLALLQYRHAWAKSEV LPIMRARLRRAGARADEDGPNAAALRNNAASHTPQNRPGHESSAPLRP QDVANRMAMKADLYEAASIFNHIHYYPLRRYSAIRPYGGDSVANTDAW HSAIAAVVQTRFGVPITSNTAQTAEAAALPLIQRDSPLSVLALPRLGL ERADEVAHLYTREDRQLIPHALDSKAAESTHTIFVSIASYRDMECAPT LLNLFRTARNPHRLYVGVAQQNRAGDTPCLVPELYTPYLCPSDGVQDA

SEQ ID NO.	Description	Sequence
		AGDGGVGAARELRARARTLHGKGVDLTTSTAGPEARYFDARVCFVAEQ VRLREIDSSQAKGPTYGRYMAMLLYRGEDVTLVLDSHNRFRPMWDVLG ATMLRRLEDPKAVLSHYPESYRGEEVDFQPYRTTTAYLCRAHFMNNFG YLRLNGIVIGSTSEFAKNNVYNDPYVRVQSAEIDPATNHRLPQPWVAG GFLMSFATIFRDVPFDPHLPYIFDGEEVLYSMRLWTHGYNIYSPARGL CFHIYTRLSAPKVWSETPQWYATQTRVRQRIQFFLQTRPLNKEDVLVP ANTTNPHVIIDSSRYGMGKQRTVAQWYDYAGVDPIKYKLDGRWCGVDK PD
92	LINF_02000740-T1-p1	MPKASASSAAAAAAVHGRGHLRPLKRLLCCASRVHRTLRALGFASDDD DPANMSQMLACSCAAVGVLLVLLLINFAALVAVLVIVVPDARQHLSHT IGPLLDSNTRRDGNTAGGGGDAASCASALDLKIRRLLASEGLEAFLR ETRRAAELRRRVRRNATLLAALRKASAARGKDGGHGVDLVSLAQTLPE LEHLSFLLAQVSVHVRAVQEHDPVMGLMELSDFLLNAKGRKEALEKAA ERARAEGADATTAARGASTIGDAAAEWNAALKESFAGRSEAARLRAQL RGFVGVSSFETERLTEQPFDDLALLQYRHAWTKSEVLPIMRARFRRAG ARADEEGPNAVVPRKNAASHTPQNRPGHESSAPLRPQDVANRVAMKAD LYEVASIFNHIHYYPLRRYSALRPYGGDSVADTDAWYSAIAAVVQTRF GVPITSNTAQTAEAAALPLIQRDSPLSVLALPRLGLERAKEVAHLYTR EDRQLIPHALNPKAAENTHTVFVSVASYRDMECAPTLLNLFRTARNPH RLYVGVAQQNRAGDSPCLVPELYTPYLCPSNGVQGAAGDGGVGAAREL RARARTLYGKGVDLTTSTTGPEAHYFDARVCLVAEQVRLREIDSSQAK GPAYGRYMAMLLYRGEDVTLVLDSHNRFRPMWDVLGTTMLRRLEDPKA VLSHYPEGYQGEGVDFQPYRTTTAYLCRAHFMNSFGYLRLNGIVIGST SEFAKNNVYNDPYVRVQSSEIDPATNHRLPQPWVAGGFLMSFGTIFRD VPFDPHLPYIFDGEEVLYSTRLWTHGYNIYSPARGLCFHIYTRSSAPK VWSESSQWYTMQTRVRQRIQFFLQTHPFSKEDVLVPANTTNPYVIIDS SRYGMGKQRTVAQWYEYAGVDPIKYKLDGRWCGVDKPD
93	LmjF.02.0240:mRNA-p1	MDNHVTTRVKRMLSPSPFGDGLDAVATAGTAVVGGPALCTAVSTMCGH NERGRGPAGFAPASMSLSSEGDGRLSGATQTSHSGNHRGPSNVELRAT AEGRGYAPTHLMPKASASSSAAAATAVHGRGHLRPLKRLLCCASRAHY TLRALGFASDDDTPAKMSQTLACLCAAVGVLLVLLLISFAALVVVLVV VVPDARQHLSQTIGPLLDSNTRRDGNTAGGGGGDAASRASAFDRKIR RLLASEGLEAFFREAHRAAELRRRVLRNATLLAALRKANAARGKDGGH GVNLVSLAQTLPELEYLSFLLAQVSAHVRAVQEHDPVMGLVELSDFLL NATGRKEALEKAAERALAEVADARPAARGASTIGDAAAEWNAALKESF AGRSEAARLRAQLRGFVGVSSFETERLTEQPFDDLALLQYRHAWAKSE VLPIMRARLRRAGAQADEEGPNAAALRNNAVSHTPQNRPGHESSAPLR PQDVANRMAMKADLYEVASIFNHIHYYPLRRYSAIRPYGGDSVANTDA WYSAIAAVVQTRFGVPITSNTAQTAEAAALPLIQRDSPLSVLALPRLG LERVDEVAHLYTREDRQLMPHALNSKSAESTHTIFVSIASYRDMECAP TLLNLFRTARNPHRLYVGVAQQNRAGDTPCLVPELYTPYLCPSDGVQG AAGDGSVGAARELRARARTLYGKGVDLTTSTEGPEARYFDARVCLVAE QVRLREIDSSQAKGPTYGRYMAMLLYRGEDMTLVLDSHNRFRPMWDVL GATMLRRLEDPKAVLSHYPESYRGEEADFQPYRTTTAYLCRAHFMNKF GYLRLNGIVIRSASEFAKNNVYNDPYVRVQSAEIDPATNHRLPQPWVA GGFLMSFATIFRDVPFDPHLPYIFDGEEVLYSMRLWTHGYNIYTPARG LCFHIYTRSSAPKVWSETPQWYTTQTRVRQRIQFFLQTRPLNKEDVLV

SEQ ID NO.	Description	Sequence
		PANTTNPYVIIDSSRYGMGKQRTVAQWYDYAGVDPIKYKLDGRWCGVD KPD
94	LmxM.02.0240.1-p1	MHRASASSSSAAAVHGRSHLRPLARLLCCASRVHRTLRALGLTSDGDD PASVSQALACSCAAVGVLLVLLVISLAALVVVLVVVVPDARQHLSSRM GPLLDLDTKRGGHTAASGASAVDLTMRRLVASEGLEAFLRETDRVAAL RRRVQRNATLLAALRKANAARGKDGGHGLDLVSLAQTLPELEYLSFLL AQVGAHVRAVQEHDPVMGLVELSDFLLNAKGRREALEKAAERVRGELA NATPAAGGASAIGDAATEWNAALKELFAGRSEAARLRAQLRGFVGVSS AATERLTEQPFDDLALLQYRHAWVQSEVLPIMRARLRRAGARGGEGGP TAAVLRNNAASHTLPNRAVHASSAPLRPQDVANRMAVKVDLYEVASIF NHIHYYPLRRYSALRPYGGDSVADTDAWYSAIAAVVQTRFGVPITSNT AQTAEAAALPLIQRDSLLSVLALPRLGLERADEVEHLYTREDRRLMPH ALKSNAAENTHTIFVSVASYRDMECAPTLLSLFRTARNPHRLYAGVAQ QNRPGDSPCLAPELYTPYLCPSDGARGAAAADGGSDAAREVRARARTL YGKGVDMTKSAKGPEARSFDERVCFLAEQVRLRVIDAKQAKGPTYGRY MAMLLYRGEDLALVLDSHNRFRPMWDALGATMLRRMEDPKAVLSHYPE AYDGGKVAFQPYRTTTAYLCRAHFMMNFGYLRLNAIVIRAASEFAKNN GYNDPYVRPPSSAKDSATNHRLPQPWVAGGFLLSSGTIFRDVPFDPHL PYIFDGEEVLYSVRLWTHGYNIYSPMRGICFHIYTRSSAPKVWSESPQ WYAKQTHVRQRIQFFLQAHPLDKEDVLVPANTTNPHVIIDSSRYGMGK QRTVAQWYDYAGVDPIKYELDGRWCGTDKPD
95	LPMP_020160-t37_1-p1	MLRLLGFVNDDDDPADVSQTLVCACTAVGALLVLLLINFAALVVVLVV MVPAAQRQLPQTAQSLLDFNHKNKGGTADGAALASGLDIRRLLAGGGL ETFLREAHRVEELRRRVQGNATLLAALRKANEARNNDGGRGVDLVRLA QTLPELEYLSFLLYQVSAHVQAVQERDPVMGLVELSDFLLNAKGRREA LEKAAERARAEEVNVTTAATVGGGARATGGGSVEKWNAALKESFAGRS EAARLRAQLRGFIGVASSEAERLTQQPFDDLALLQYRHAWMQSEVLPI MRSRSRRAGAQAVKEGPHAAVLRSNTASRPPENTSVRTSVEELRVYGV ANRMAMKAVLYEVASIFNHIYYYPLRRYEALRPYGGDSVADTDAWYSA ITAAVQTRFGVPIACNKAQTTEAAALPLVLRDSPLSVLALSRLGFRRA EEVAHLYSQEDRQLMPQALNPKAAVNVRSIFVSFASYRDAECASTLLD LFRAARNPHRLYVGIAQQNRAGDSPCLLPEMYTPYLCPSEGLQGAAAD GGVGAARESRARARALYGEGADLTKPPNGPEARHFDERVCFLAEQVRV REIDSGQAKGPTYGRYMAMLLYRGEGLALVLDSHNRFRPMWDALGATM LLRLEDAKAVLSHYPESYPGEKADLLPYRRTTAYLCRAHFLKPFGYLR LNGIVIGSTAEFAKNNVFNDPYVRVKSREIDPTTNYRLPQPWVAGGFL MAFGTIFRDVPFDPHLSYIFDGEEVLYSMRLWTHGYNLYSPPRGVCFH IYGRQEAPKVWSESALWYNLQNRVRSRIQFYVQAHLLHAEKVLVPANS TNPFVVMDSSRYGMGKQRTVAQWYDYAGIDPVKHQVDGRWCGEDVTR
96	rna_LpyrH10_27_0530-p1	MSSAVRVSPPVLGECAVDAVPTTGAVLAGPVHRTFTDDNVRVREVAGA VSPSVFVDGSPNSAGGPLPHTRSGKYFASSHAAAAAPSLSSPASKERS SGGSGGSSRRRLLRRILCCPHRIQLCLRSAVPLKENRGAREASPLRVC AGTATAVLLALLFIGTVIFIVVLVVLLTGARQLPERQTLAPMRFETRS AGAAGVRHDSDGVIAASLDNVRHLLTAERLQHFLQRTPAAEEERRRAL RNDTLPAAARDVGDLVGLARTLPEQQRVSAQLARVRAYVAAVHAHDAG VGLAELSDFLRSVPGRGAALERAASKAAGSPGVAAALAGRAAGARVRA LLRGFVAAPAGQAERVGLRPFDDVAMLRYRHAWMLSEVVPRLAGRTRG GGGGGPVSAADVARGAARKAELYEAASVFNHVYYYPLRRYAAMQAFSP

SEQ ID NO.	Description	Sequence
		ATVADTDAWYTEVAAGVQARFGAAQAVAALSLPLLPAARAAEVAHLRE PDDMEWMPAGLRADAAVNRQTIFISLASYRDTECAPTVLDLFRAARNP YRVYVGLAQQNVAGDTPCLLPEMYGPFLCPSAGEALDAAAAAREAEAR RRSLGGGDGVDFRLVHPGSDAAHFDERVCFLADHVRVRDIDARQAKGP TYGRYMAMLLYRGEAVAMVLDSHNKFRPMWDTLGASLLRRYDDPKAAL SHYPQAYDPEKESKLDVYARTTAYLCKAVFHNIFAYLQLRAMVIGEAD EFANNMRYNAPYVATVEEKAPVRSYRLPQPWVAGGFLLTNSTIFRDVP FDPHLPYVFDGEEVLYSARLWTHGYNIYSPPRGLCFHIYGRPKAPKVW DVTALWYAVQDRVRPRIQFFLQSHLKGRPGLIVPADTTNAYAVVDASR YGMGRQRTVAQWYDYAGADAVNYTLDGRWCGVDTTT
97	rna_Lsey_0379_0030-1-p1	MPLALRALPSSQPDGEAEAAITADALHTSAAHHTLSEKAVRAGNLTHF ESLPVFVDGAPSGASVLLSTVASHTQTAKHRAFSHLRAALFSSSASGE RASSAGRLLRRMMCCTTRLRRCLRSFGFLKAEGNAHDLAQLLVCACTA VAVLLVLLLLAVGLLIVVFVVLVPGAQLQLQQTVKPSLDLNHPDMHTT NRSPAGKGGNQGDVSQLSYSDLHRVLEAAGLTQFLQQALDVEKLRRHL LRNEALLVSMRGMREKDGPAQGTDDLARLVQGRTELERLSGQLLQVAV YIGAVHAHDPRLGLVELSDFLLDVKGRGAALGRAAEQARRDAVTTAAT SGSGGRVMPAETGGPSVGWTAELKTVLADHTQSARLRAQLPGFVGVPA GQEERWTRQPFDDVAMLQYRHAWARSEVLPRLGRAGSSGRAGAGAVSA HDVAKRAALKADLYDVASIFNHVHYYPLRRYTAMQAFSPATVADTDAW YSEVVAGVQARFGAAVSGGGASGAAESIAVRDSPLSLLSLPRLPTARE DEVTRLLTREDAAWMPAGLRAGAAVNRQTIFVSLASFRDMECAPTVLD LYRTARNPHRVYVGLALQNHVGDMPCLLPEMYGPFLCPSSGDVLDAHA AAREVAARRRSLRGDGADFTKRSDSDVALFDKRVCFLPDQIRVRDIDA THAKGPTYGRFMAMLLYRGEELAMVLDSHNRFRPLWDTLGVSLLQRFG EPKTALSYYPEAYNPTDAHFNAFRTTTAYLCKAFFLSNFGYLRLNAMV ISSPAEFTQNNRYNDAFVAVQSNTIQQSQNFRLPQPWVAGGFLFTNAT IFRDVPFDPHLDYIFDGEEVLYSVRLWTHGYNIYSPPLGLCFHIYGRT KAPKIWSESAAWYSLQSRSRPRIQFYLQSHSKGNPNLLEPANTTNAYV VVDSSRYGMGRQRTVSQWYDYAGADPVNYTLDGRWCGIDQVTQ
98	LTRL590_020007500.1-p1	MDNHVTARVKRMLSPSPFGDGLDAVATAGTAVVGGPALCTAAGTECGR NERGRGPAGFAPTSMAFSNEGDGGLSGATQTSHSSNHRGPANVELRAV AEGRGYAPTHLMPKTSASSSAAAAAAAVHGRGHLRPLKRLLCCAGRAH RALRALGFASDDDDPASMSQTLACSCAAVGVLLVLLLISFAALVVVLA IVVPDARQHLSQTIGPLLDSNTRRDGNTAGGGGGDAASRASALDLKIR RLLASEGLEAFFRETHRAAELRRRVLRNATLLAALRKANAARGKGGGH GANLASLAQALPELEHLSFLLAQVSAHVRAVQEHDPVMGLVELSDFLL NAMGREAALEKAAERARAEVADAATAASGAPATGAAAAEWNAALKESL AGRSEAARLRAQLRGFVGVSSSETERLTEQPFDDLALLQYRHAWAKSE VLPIMRARLRRAGARADEEGSNAAVLRNNAASYTPQNRPGHESSAPLR PQDVANRMAMKADLYEAASIFNHIHYYPLRRYSALRPYGGDSVANTDA WYSAIAAVVQTRFGVPITSNTAQTAEAAALPLIQRDSPLSVLALPRLG LERADEVAHLYTREDRQLIPHALNSKAAENTHTIFVSVASYRDMECAP TLLNLFRTARNPHRLYVGVAQQNRAGDAPCLVPELYTPYLCPSDGVQG AAGDGGVGAARELRARARTLHGKGVDLTTSTKGPEARYFDARVCLVAE HVRLREIDSSQAKGPTYGRYMAMLLYRGEDLTLVLDSHNRFRPMWDVL GATMLRRLEDPKAVLSHYPESYRGEEADFQPYRRTTAYLCRARFMNNF GYLRLNGIVIGSTSEFAKNNVYNDPYVRVQSAEIDPATNHRLPQPWVA

SEQ ID NO.	Description	Sequence
		GGFLMSFATIFRDVPFDPHLPYIFDGEEVLYSMRLWTHGYNIYSPARG LCFHIYTRSSAPKVWLESPQWYTMQTRVRQRVQFFLQTHPLNKEDVLV PANTTNPHVIIDSSRYGMGKQRTVAQWYDYAGVDPIKYKLDGRWCGVD KPD
99	LTULEM423_02000660.1-p1	MDNHVTTRVKRMLSPSPFGDGLDTVATAGTAVVGGPALCTAASTMCGH SERGRGPAGFAPVSMALSSEGDGGLSGATQTSHSSNHRGLSNVELRAA AESRGYAPPTHLMPKASASSSTAAAAVHGRGRLRPLKRLLCCASRAHY TLRALGFASDDDDPANMSQTLACSCAAVGVLLVLLLMSFAALVVVLVV VVPDARQHLSQTIGPLLDSNTRRDGNTAGDGGGGDAASRASAFDRKIR RLLASEGLEAFFRETHRAAELRRRVLRNATLLAALRKANAARGKDGGH GVNLVSLAQTLPELEYLSFLLAQVSAHVRAVQEHDPVMGLVELSDFLL NAMGRKEALEKAAERARAEVADARTAARGASAIGDAVAEWNAALKESF AGRSEAARLRAQLRGFVGVSSFETERLTEQPFDDLALLQYRHAWAKSE VLPIMRARLRRAGARADEEGPNVAALRNNAARHTPQNQPGHESSAPLR PQDVANRMAMKADLYEAASIFNHIHYYPLRRYSAIRPYGGDSVANTDA WYSAIAAVVQTRFGVPITSNTAQTAEAAALPLIQRDSPLSLLALPRLG LERADEVAHLYTREDRQLIPHALDSKAAESTHTIFVSIASYRDMECAP TLLNLFRTARNPHRLYVGVAQQNRAGDTPCLVPELYTPYLCPSDGVQG AAGDGGVGAARELRARARTLHGKGVDLTTSTAGPEARYFDARVCLVAE QVRLREIDSSQAKGPTYGRYMAMLLYRGEDVTLVLDSHNRFRPMWDVL GATMLRRLEDPKAVLSHYPESYQGEEVDFQPYRTTTAYLCRAHFMNNF GYLRLNGIVIGSTSEFAKNNVYNDPYVRVQSAEIDPATNHRLPQPWVA GGFLMSFATIFRDVPFDPHLPYIFDGEEVLYSMRLWTHGYNIYSPARG LCFHIYTRSSAPKVWSETPQWYAMQTRVRQRVQFFLQTRPLNKEDVLV PANTTNPHVIIDSSRYGMGKQRTVAQWYDYAGVDPIKYKLDGRWCGVD KPD
100	Tbg.972.2.950:mRNA-p1	MHYASRGAKRQNQLRLPPAQKPGRLRVLARSFRGVNDAVGDFTQRNNE SPLLYALLFVVGLLILLFIVLFVVLLCILLRSDGWSTIDAFSSKTHIV EDPDKSALLEIRRLYDTMMRTGSDREATALLEFLSTYQRSMEARVSKS THGDDENAGDNGNVGDSGVPQGKSKYASEKPRVSNGTSLSQRSFAEVL ADVRETIQDIMTLDPDVGLDRAAFFVKEKFGASNDDRSQRTDSTGSHD IERGEVEAFEPFDDILYLQLLSFFAKEEPTRSISSADRLWWRRKRISA PSVMEGRFYYPLRRFHRMQSFSPDTISTVAAWFDTMALDYYGEEMEPF ESSLQQSYEGAQVSNHSGSSPENPEIKEHAVSFSPSHTASIFVSVASF RDVECQSTLQQVVHRATNMFRTYVGIAEQHNKSDPPCLSYDLFQPTLC PSAAIASDTASARAVFSDVLCFPMDNIRLRHIAPDAARGPTYGRYMTM LLYRGEDYVLILDSHTRFVYGWDSRVVAMHMYLRHPRIVLSHYPEGFE KELSNFTYERTTTVYLCRASFIESDGYVRLGGILVNEENVNKFSHQGR VLRYAAKGFGRKPDADVSRPLPQPWAAGGFLFARGSIMREVPLDPHLP NTFDGEEVLYSVRLWTHGYDIHSPNRTICYHVYTRNDQPKVWNNNPLW SSLRLRSRERIQCLLQTREKGQTVPKVPVNTTDPAVTIDVDRYGMGRV RTVENWYRFAGLDPVRYTFDGRWCGKGKI
101	TcIL3000_0_43290.1-p1	MPYGSLVERSRLRRAGRPGLTQLVPMEIKPPQSSGWRSILHPFFTCVR SMIEDLTRVNSGRLYFCRAFFSVVFLALLVITLILVAVVLMPSAPSPD VREPSTFMGEAVAKRVQSNTLWEVCKLFAAQVRANGAHVEESLKEFLL RCQQEPSDHTGNISTNSHMNNVEDAARNDSNVGHDTRSPPQFSEGSVT KPGANMTLMSDSPFAERRDISEVMDELRLTVNFIMAHDPDGGLEHLAN FMKKRLSPARVVDERGPETTAATSDWEETEAFQPFDEILYLQLSSFFA

SEQ ID NO.	Description	Sequence
		KHGNEGSITTRQARLWWRQKAVEVSSVVTGRFYYPLRRFHRAQQYSSE TADTVNAWLSAMMEDFCDEEMEPLVSPPSSSPKRTLRQAGGNEQLLSR GENILKGLKTNGYASIAPPNSKLHTASIFVNVASYRDEECWPTVRQSV ERAANMFRVYFGIAEQHLDTDLSCVSYDMLLPEPCTVPTDVPWAKNKG FDFDGAICFPVDNIRRRQIAPAAAYGPTYGRFVAMLLYRGEDYAFVLD SHTRFVFAWDSRITAMYMEMDHPRLVLSHYPEGYNTSDTHFNYERAST VYLCRASFVESDGYIRLDGIVISESEGSRIFRRRFVRPYASGGTSPEV YAGSRRPLPQPWAAGGFLFANASIMREVPFDPHLPNTFNGEEVLYSVR LWTHGYDIHSPKRSICYHIYTRKGQPKVWENNTHWEALRQKSRQRIQY LLQSRVKGTSTLLVPLNTTDPVVVVDKARYGMGRLRSVDAWYNFSGVN SVDYTVDGRWCGKK
102	TevSTIB805.2.1330-t26_1-p1	MHYASRGAKRQNQLRLPPAQKPGRLRVLARSFRGVNDAVGDFTQRNNE SPLLYALLFVVGLLILLFIVLFVVLLCILLRSDGWSTIDAFSSKTHIV EDPDKSALLEIRRLYDTMMRTGSDREATALLEFLSTYQRSMEARVSKS THGDDENAGDNGNVGDSGVPQGKSKYASEKPRVSNGTSLSQRSFAEVL ADVRETIQDIMTLDPDVGLDRAAFFVKEKFGASNDDRSQRTDSTGSHD IERGEVEAFEPFDDILYLQLLSFFAKEEPTRSISSADRLWWRRKRISA PSVMEGRFYYPLRRFHRMQSFSPDTISTVAAWFDTMALDYYGEEMEPF ESSLQQSYEGAQVSNHSGSSPENPEIKEHAVSFSPSHTASIFVSVASF RDVECQSTLQQVVHRATNMFRTYVGIAEQHNKSDPPCLSYDLFQPTLC PSAAIASDTASARAVFSDVLCFPMDNIRLRHIAPDAARGPTYGRYMTM LLYRGEDYVLILDSHTRFVYGWDSRVVAMHMYLRHPRIVLSHYPEGFE KELSNFTYERTTTVYLCRASFIESDGYVRLGGILVNEENVNKFSHQGR VLRYAAKGFGRKPDADVSRPLPQPWQRVGFSSLEVLLCVRFPSILISP IPSMVKKCCIPCGCGLMAMISTPPTVPSVIMCTPVMISRGVENPLWSS LRLRSRERIQCLLQTREKGQTVPKVPVNTTDPAVTIDVDRYGMGRVRT VENWYRFAGLDPVRYTFDGRWCGKGKI
103	DQ04_09771010-t26_1-p1	MPMNNDTPPQQSLLHRRGHDPALHNRHATAVPVDNTNTSSSKKRGLYR VYNDIQKWFRSDNNIICVLILNVVVLLVMCLALAGVCAWLLLYAPVYE PSPQMEKRFDDDAVLDVWRLYETASRTNDEYHKSALRRYLLQYKLTAE ARRRNSSRVAKAGAPRVPLDVPDVFDPKAAVLPKYTTEPQQNLTCVIE ALHAAISRIAAQQPNGGLDRAADFVEKEFRHGAENGGAPITAAAGRGT ISANAEESGHETEADAPFDDILYIQLRRFFIGTSKHAGEEDGGAFPAY GNSPADDPVLRAWWRRLQSAAPSVYVNRFYYPLRRYHRMRRFSPETPA ATAAWYDAVAYDYYHDYYSDSSNMSDRNVVKFTPPHVPEAYPASIADA VANSDAASLPLDTPAHTATIFVSVASYRDKECWPTVQHMMQRATNMFR VYIGIAEQHRATDPPCVSDTALQPLPCVGAQPSPASSGMTAARNAAEG IGGLGMLKRADYEGAVCFLGDNIRVRHIRPSASYGPTYGRYMAMLLYG GEDYTLVLDSHNRFVYAWDTRIVAMHAAMRHPKLVLSHYPESYVQEDS NFAWERTTTAYLCRAVFLDTAGYVRLNGIVVSSNEQHKANSRYLTPYT LAALRLEPGVVRLLPQPWAAGGFLFSTSSILREVPFDPHLPHIFDGEE VMYSVRLWTHGYDIHSPKRGICYHFYGRKGEPKVWTEARRWSAVQSES RKRIQYLLRARIRGVDVLRIAKGTPDPVVMVDVDRYGVGRLRGVDDWY KFAGVDPVNYTTDGRWCG
104	TRSC58_00083-t26_1-p1	MRLDESSVFRRHNSHRQRSVEAAETERYDGRSHRPGAKPARTLRQAVG AYLSSDARVINFLLVAIVILIVVCLGLIGLSAWLLLHGAGNASAFGSS RKFFDNNAVMDIWRLYDAAQRSGDEYHKTALHEYLTRYKNRVEERREA WNLQHNVTEIDIKDDTGGDEPILPPYTSSPTMRLPSLMASLRTIINRI

SEQ ID NO.	Description	Sequence
		ESRDPEKGLERAAAFVEEQMKEAVAISSDTGEVVEEGEAVEPLDDILY LQLRRLHESAKHDAAAPATPHRVWWECVKAAAPSVYTKRFYYPLRRFH RMRRFSVETQAVTAAWFDALVDDYYGDNVTHFSPPTLPTGFDALMAQA IADSEAASASLASPAHTGSLFVNIASFRDKECWPTVDHMIQRATNMFR VYWGIAQQNYYTDLPCVSVDALEPRPCLAAPITPGLVLSDAKYDGAIC FPADNIRIRRIHSHSAFGPTYGRYMAMLLYRGEDYALVLDSHNRFVYA WDTRIVAMQLALQHPKAVLSHYPESYDETKGTEFKWERTTTAYLCRAK FLESAGYLRLIGILIDDASSFKRNARFVNPYYLPRLNLDPDVERPLPQ PWAAGGFIFANASIMREVPFDLHLPHIFDGEEVMYSVRLWTHGYDIYS PKRGICYHFYGRPKEPKLWNEAKRWYTVQAHSRRRIQYFLRARVKGVD VLRVPKNTQDPVVMVDADRYGTGRLRSVEEWYEFAGADPVRYALAGRW CG
105	TM35_0 0039172 0-t36_1- p1	MPLESVAVPPQVIYRRSTDVFVSEHEQQAHGITTATPSVTRIPHVRDH NKNMRWRGRDHGWNNRNICSRIRDFYTDDQNVICTLFTVIVILLLLCI FLIGMCSWLLISKQEEIIVPKKASSSVKSIDKDALMDIWRLYETASRT KEEYHVRALREYLLRYKRMAEDRQREEDAGKTEKRIDVAPIDEPLAAV IPRFTAAPQQSLPEVLAALEKIMARVMEKDPMNGLEKAAVFLAKNFWR MEKTESYENKTQLTREKEALEPFDDILYLQLRRYFDTNEDDDDNDKKK KKKEFSSPWTPGEEGKIEEIINTDNKNEENEEKRKQCWHHIRSKAASV YTGRYYYPLRRFHRMRRFSVETADMTASWVNAMAYDYFEDNEEIINIT PFKPPEPPSQEYLTSMKNAWKKTLELSPIASSLLTTSPEAPVFTGTLF VNLASFRDKECWPSIENMFIRSGNMFRVYFGIAEQNHESDLSCLSYDV LLPRSCMSAPSSSLSTTTNTMTGVGEGITFNNNNNNNNNNNNNNNNN NNNNNNNNNNNNNNIDINSNDHRYGGAICFPIDNIRIRHVRSSAAFGP TYGRYISMLLYRGEDYTLVLDSHNRFVYGWDIRIIAMYVLQQHPKLVL SHYPESYIESEGDKFKFERETTAYLCKAQFLDTAGYIRLNGIVTNNPE EFNRNNQYAEPYKIEELHLNESIPRPLLQPWAAGGFLFANATIMREVP FDPHLPYIFDGEEVMYAVRLWTHGYDIHSPLRGICSHFYTRVGQPKVW FEAPRWTAVQGQSRKRIQYFLRARVKGVDVLRIPRNTQLPVVVMDADR YGVGRARSVEEWYSFAGVDPIHYTLDGRWCGN
106	TvY486 _020043 0:mRN A-p1	MSLESINPERQELRRQRSGVPLGSSTVQCSPLPVGVARSRRYIPGGLC NFIRFMIRPSNNREVNFLMVVILLFALICIVLIGMNMWLLHELGTRDK YTMPKPEVVVDVDAITGIWQLYETVLQTNKDSDKELLYQYLLKCRQKA APHGTSMQAGSGISFGGTATRTSRSEGAGGSPSDLPRVLDELQKTIGI IAAQEPNDGLEGAASFIHNLLSFAPGGNTAGQSGDDGTADSDGVPNYL LSTAGAQTETEANAPFDDILYWQLYLFFSSGESSGATKDAHAWWERIQ HTAPSVITARFYYPLRRYHNTHRFPSETPTTASLWYDAIAYDYFGNDA EPFTPPVGDAQVAGVLASNAELNTSLVSRTHSGTLFLNIASYRDPECW RTVQHAVGRAVNMFRVYVGIAEQHRSSDLSCIAYEALAPQACLAPGSS AETLAKSAGLNTAVCFPADNIRVRRITPAAANGPTYGRYMAMLLYRGE DYTLVLDSHIRFVYAWDSRLAALYIEMQHPRLVLTHYPESYNASSGSH FVYERKTTVYLCRATFIDSVGYVRLKGIVMDSADAVLYMHEEHVKDYP IPHLSLSPNVKRPLPQPWASGGFLFANGSIMREVPFDPHLPNLFDGEE VLYSVRLWTHGYDIHSPKNSTSFHIYTRGDQPKVWDNNPQWESTQRRT HKRVQFLLRSYLKGISVPRIPRETADPEVTVDVDRYGVGRARTVDDWY RFAGLDPVRYTVDGRWCGREMSRDAGG
107	rna_Bay a_014_0	MFSVRRQFRKVGRAKRLRRLVLIVVVLAVVLVSVLVVAVHSLRDIHTD ALVQDSGAAIVPDNPFVTATGTPPTPVWLDDKGVLHARSAKGKLEALS

SEQ ID NO.	Description	Sequence
	750-1-p1	PLTGAGSRLSALHTHRKVSAWARLYMPSEAFEVPQWAIPEERNTLNHA TIFVSIAAFRDRECAITIRNLFTQARSRHRIYVGVSDERSPTDVDCLS LLGLEDEQIARRLLWGNDAPAALYVERRSLTWADVMRDNRTIVTGGPG EAGVLHDNGTATGGAPAGVYLLPSYGEENITCLAGELETLRDEHLAKG FQRHGRGGPQQQLSSALVGCRVTSRVASPFGARGPTYGRYITSLFFSN QDYYMVIDSHSRFSLHWDAKMIVRTFLMPTRGILSHYPNGYEYGKSEG EFDKKDEMVMCKGVVLGNGMPKLGARWGPLGGRPVLQGFAAAGYMFGD AQFVLDVPFDPLLPYLFDGEEALYSARLWTAGWDHYAPGEANIFHNYA RSTAPRFWNVMPAEGDHMRALSEKRALYLLRRAQPWASLASATAEMGG TRKPKEEPSYIPPELRLIVPDSEAVAEPAISAHAEYYGMGKNRSLQEY WSFVGLSDDQIKTKDSEQRWEGSDALCLNS
108	BSAL_53670-t42_1-p1	MQPKRRPESATVQRNSAIIVAASFLVAVGVFLFVSKSSPLQDASEEQV RPLIRTGSKRHQSNNNDAVVAPHSAHDVTSAGNDDVLPLIAEVREHLQ SVRNRMQDRPGAPQVHTPLSPNSAQHLMMNQHLPIGGHNNGGEEVEDA HSTIFVSIAAFRDVECGPSLEDMFRKAKYPHRIFAGIVDQREPGEFNL CIPQSFRDCQNQPLNSSWAAAASSSDHNNNKDKTSAETWNSTKSTFCP MDNVRTRHTLPNEARGPTFGRFVAQLMYQGEQYYMMIDSHMRFVERWD VRLLSMYAKMPTRGVISHYPSGFEPGFVLESNHDIMFMCYAHFYDGVG ILRNGAKNVRNRQKRPVLQPFTAAGFLFGHSDYIFDVPFDPWLDYLFD GEEILYTVRLWTSGWDSYLPSHDIMYHFYGRPKAPKVWGTTNQWVAIQ RVSQRRVLHMLKMTKPNSTIPVVDPSTETETRIFNELETYGLGSVRRL EDFWPFAHVDPIKRTSDRGFCDRAN
109	CFAC1_090018200.1-p1	MQDFGSTPSLLKRPLRGPRRRVSGRRKALLACVGLVVLLVVFLLLGRS DETPFPPSPADNAGARGAAYTRHPAPPTDAHTTRPAAATGTKSTTTTP APAPQSDGDKPWVTAADGNTFNALVETHAHGTAWRDRRSNAIVALARS GTVALVTPTITVRHHRDDHQRWDSLYQPNDTYRVPAWAAPADRDSLRH ASIFTSLAAFRDHECATTLRDLFDMAVAPHRLYVGVSEERKPADTSCL ALLGLNDADTTETRRVLYGKDAPADMSVELRSLTWADVVSPRAIVDVD SVLSGAAAVPSAPHPEGIFLHPSYAAERLSCVAGELETLRDRLRLHED DARREAGGGTVFREGRGGPQQRPSRALAGCRVTTRVTAPELARGPTFG RYVTSLFFFDQDYFMVVDSHTRFSVHWDAKLMTRIFQLPTPGVLSYYP NGYREGHEREEYGKRDYMMMCTAQVLSNGMPKLGARWKPTGKHPVVQG FAAAGFMFGDAQYVLDTPFDPFLPYMFDGEEVLFSARMWTGGWDLYGP AESDVFHHYGRDNTPKYFGIIGGPEARRRLLAEQRTLHLLRRAHPWIQ ELVTRGYATPDGQVTLKPLPPVEAPETRLIVNDDMADRTREINVWKSY YGMGTQRTLAQYWEHTELSDSFVKKRDDENRWLGGESLCNGGF
110	EMOLV88_170014900.1-p1	MLPTAPLINSHSLEKPWVTADTDSYRLTTIIKGRVPGTAWRDTRFNAV VSLSKKGSLAYIHPPNRRRAVAKNSDAFREWDSIYQPNEKYTIPAWAT PEESLTLRHATIFTSLASFRDYECALTLRNLFSMAVAPHRLYVGISEE RKPSDASCLALIGARNLNMAEVRRVLYGEGAPIELSVELRNFSWEDVV HPRKLLDVDAEITLPLVNSSEKNASPPGVFVHPKHAAERLSCVAGELE TTRDAFLLAENDAQRAKNGTSIFRRGRGGPQQEPSRALAGCRITTRVA DSMSARGPTFGRYITSLFFFDQDYFMVIDSHTRFAVDWDVKLISRVFQ MPTRGVLSYYPNGYTEKNDRAEFDKTHTMLMCTAQVLANGMPKLGARW VPFTPHPVPQGFAAAGFMFGDAQFVLDSPFDPFLPYMFDGEEILFSAR MWTAGWDLYGPGQSVVFHNYDRPQTPKYFEILRMNENARRVLSELRTL YMLRRAQPWAEVLVRRGYTSPDGQSTVKPLPPVEAPETRLIVTDAAAF

SEQ ID NO.	Description	Sequence
		RKREISVWVGYYGMGSVRPISQYWEYTELTDRFVKRKDSEHRWMGGTG LCDKVTANLTQ
111	LAEL147_000253000.1-p1	MPDYVQVPSLLKRPLRVPRRRLSTRRRQALIAFIAILCLCALPFMYFF STSSATALSELSHPREKPWITFDENSTRFEHIVEGRTPGTAWRDSRLN MIVSFSKSGDVVHVTPTNYVRHRRGSDDSPGAFRKWESIYRPRDRYRI PAWATPADRDALHHASIFTSLAAFRDHECALTLRNLFDMAVAPHRLYV GVSEERSPSDASCLSSIGVDNLASGETRRVLYGAEAPRTLGVEVRSLT WADVVAPRQLLDVDAVLSVPADGAAEYGAQPAGVFLHPAYAGERLTCV AGELETARDRLLLAEDDARQGMNGGSVFRRGRGGPQQQPSRALAGCRV TTRVVEPAFARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSHYPNGYREGHDREEFDKKMVMLMCTAQVLSNGMPK LGARWMTLSPHPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEV LFSARMWTAGWDLYGPGQPDVFHHYGRPNTPKYFGIMTSKEAARRVLS EQRTLYMLRRAHPWIEELVRRGYVSANGQSTLKPLPLEEAPETRLIVT DEVAAETREISVWAKYYGMGTERSVSAYWQHTELSDEFVKAKDEENRW LGGFGLCQKGGAMA
112	LAMA_000268900.1-p1	MPDYDQVPSLLKRPLRMPRRRLSARRRQAFLVFAILCLCGPSFMYFFS TSSAKVRGELPDSREKPWITPSENSTRFAHIVDGHTPGTAWRDPRFNV IISFSKSGDVVHVTPTNHVLHRRASDDGSSVLRKWESIYHPSDKYRIP AWATPADRDTLHHASIFTSLAAFRDHECALTLRNLFDMAVAPHRLYVG VSEERSPSDASCLSSIGVDDLESGETRRVLYGAEAPRTIGVEVRSLTW ASVVAPRLLLDVDAALSVPTGSTAEYGARPAGVFLHPAHAGERVICIA GELETARDRLLLAEDDAKQDMDGGSVFRHGGGGPQQQPSRALAGCRVT TRVTEPRFARGPTFGRYITSLFFFNQDYYMVVDSHTRFSVDWDMKLIT RVFQLPTRGVLSHYPNGYREGNDREEFDRTIVMLMCTAQVLHNGMPKL GARWMKLSPRPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEVL YSARMWTAGWDLYGPGQSDVFHHYGRPNTPKYFGVMTPKEAARRVLSE QRTLYMLRRAHPWVEELVRRGYVSANGQTTLKPLPPKEAPETRLIVTD EVAAETREISVWAKYYGMGTERSVSAYWQHTELSDEFVKAKDEENRWV GGVGLCEKGGAMG
113	LARLEM1108_170015900.1-p1	MPDYGQVPSLLKRPLRVPRRRLSTRRRQALIAFIAILCLCGLLFMYFF PTSSASALSEFSDLREKPWITSDENSTRFKHIVEGRTPGTAWRDPRFN MIVSFSKSGDVVHVTPTNYVRHRRSSDDSPGAFRKWESIYQPSDKYRI PAWATPADRDALHHASIFTSLASFRDHECALTLRNLFDMAVAPHRLYI GVSEERSPSDASCLSSIGVDNLASGEARRVLYGVEAPRTLGVEVRSLT WADVIAPRQLLDVDAVLSVPTDGAAEYGARPAGVFLHPAYAGERVTCV AGELETARDSLLLAEDDARQGMDGGSVFRRGRGGPQQQPSRALAGCRV TTRVAEPAFARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSHYPNGYREGHDREEFDKKIVMLMCTAQVLSNGMPK LGARWMSLSPHPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEV LYSARMWTAGWDLYGPGQSDVFHHYGRPNTPKYFGIMTPKDAARRVLS EQRTLYMLRRAHPWIEELVRRGYVSANGQSTLKPLPLEEAPETRLIVT EEVAAETREISVWATYYGMGRERSLSAYWQHTELSDVFVKAKDEENRW LGGAGLCQKGGAMS
114	LbrM.17.1130:mRNA-p1	MRDYSQVPSVLKRPLRMPRRRLSVRRRQAILAVIAILCLCVLSFMYFL STSPVNEHRKFSDIPSKPWFTAEENATRFAQVVQGRTPGTTWRDATFN MILSLSKSGDTVYMTPTNYTRYRRTTDGNPGDFRKWESIYRPGDRYHV PAWATPADRATLHHASIFVSLASFRDHECALTLRNLFDMSASPHRLYV

SEQ ID NO.	Description	Sequence
		GVSEERRSSDASCLSRLGMDDLESGETRRVLYGAEAPASLGVEVRTLT WADVLAPRRLLDVDAVLSTPAVSAEGIGVEPDGVFVHPAHAAERVLCV AGELETARDTLLIGEEDAKSAIAGQSVFRKGRGGPQQQPSRALAGCRV TTRVTDASHARGPTFGRYITSLFFFNQDYFMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSNYPNGYREGHDREEFEKTDIMFMCTAQVLSNGMPK LGARWMPLSPRPVLQGFAAAGFMFGDAQFTLDTPFDPFLPYMFDGEEV LYSARMWTAGWDLYGPGQPDVFHHYSRPNTPKYFGIMTPKEAARRLLS EKRTLYLLRRAQPWMEELVHRGYVSPNGQSTLKPLPSAPPPETRLIVT DEVASATREINVWSKYYGMGAERSVSSYWQYTELSDEFVKTKDNENRW MGGIGLCEKGAALV
115	LdCL_17001720-t42_1-p1	MPDYGQVPNLLKRPLRMPRRRLSARRRQALIAFIAILCLCGLPFMYFF STSSATALGELPDPREKPWITSDENSTRFEHIVHGRTPGTAWRDPRFN MIFSFSKSGDVVHVTPTNYVRHRRGSDDSPGAYRKWESIYQPSDKYRI PAWATPADRDALHHASIFTSLAAFRDHECALTLRNLFDMAVAPHRLYV GVSEERSPSDASCFSSIGVDDLASGETRRVLYGAEAPRTLGLEVRSLT WADVVAPRQLLDVDAALSVPTDGAAEYGARPAGVFLHPAHAGERVTCV AGELETARDRLLLAEDDARQGMDGGSVFRRGRGGPQQQPSRALAGCRV TTRVAEPAFARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSHYPNGYREGHDREEFDKKIVMLMCTAQVLSNGMPK LGARWMKLSPHPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEV LYSARMWTAGWDLYGPGQPDVFHHYGRPNTPKYFGIMTPKEAARRVLS EQRTLYMLRRAHPWIEELVRRGYVSANGQSTLKPLPLEEAPETRLIVT DEVAAETREISVWAKYYGMGTERSVSAYWQHTELSDAFVKAKDEENRW LGGFGLCQKGGAMA
116	LENLEM3045_170016400.1-p1	MRDHSQVPSLLKRPLRVPRRRLSARRRQAILAAMAIVSLTVLSFTYIL ALSPSASAALGDPPATPWITADGNMLHFSGVIQGRTPGSAWRDASSSM IVSLSKAGDVVYTTPAKHIRHQRATDGGSGTFRKWESIYEPEVRYRIP DWATPSDRDTLQHASVFTSIAAYRDHECALTVRNLFDMAAAPHRLYVG VSEERSASDASCLSSIGIDNLASGETRRVLYGAGAPVTLAVEVRTLTW DAVLSPRPLLDVDAVTNMSAESAAEPGGVFLHPAHASERLFCVAGEVE TLRDTLLLEEDDMKRASSGGSVFRRGRGGAQNQPSHALAGCRVTTRVT EHLLARGPTFGRYITSLFFFNQDYFMVVDSHTRFSVDWDAKLITRVFQ LPTRGVLSNYPNGYREGHEREEFGKVDFMLMCTAQVLSNGMPKLGARW MPFSRHPVLQGFAAAGFMFGDAQFMLDAPFDPFLPYLFDGEEALYSAR MWTAGWDLYGPGQADVFHHYGRLNTPKFFAVLTEQKSARRVLSERRAL YLMRRAQPWIEELVRRGYVSAEGQSTSRPLPRIEAPETRLIVTDEVAA ATPEIGMWAKYYGMGAERSVSAYWQHTELADEFVKEKDKEHRWVGGDG LCKRAAIATE
117	LGELEM452_17001210 0.1-p1	MPDYGQVPSLLKRPLRVPRRRLSTRRRQALIAFIASLCLCGLLMYFFS TSSASALSELSDLREKPWITSDENSTRFKHIVEGRTPGTAWRDPRFNM IVSFSKSGDVVHVTPTNYVRHRRGSDDSPGAFRKWESIYKAGDKYRIP AWATPADRDALHHASIFTSLAAFRDHECAQTLRNLFDMAVAPHRLYIG VSEERSPSDASCLSSIGVDNLASGEARRVLYGVEAPRTLGVEVRSLTW ADVVAPRQLLDVDAVLSVPTDGAAEYGARPAGVFLHPAYAGERVTCVA GELETARDRLLLAEDDARQGMDSGSVFRRGRGGPQQQPSRALAGCRVT TRVAEPAFARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLIT RVFQLPTRGVLSHYPNGYREGHDREEFDRTIVMLMCTAQVLSNGMPKL GARWMSLSPHPVVQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEVL

SEQ ID NO.	Description	Sequence
		YSARMWTAGWDLYGPGQPDVFHHYGRPNTPKYFGIMTPKEAARRVLSE QRTLYMLRRAYPWIEELVRRGYVSANGQSTLKPLPLEEAPETRLIVTE EVAAETREISVWATYYGMGRERSLSAYWQHTELSDVFVKAKDEENRWL GGTGLCRKGGAIS
118	LINF_17001730 0-T1-p1	MPDYGQVPSLLKRPLRMPRRRLSARRRQALIAFIAILCLCGLPFMYFF STSSATALGELPDPREKPWITSDENSTRFEHIVHGRTPGTAWRDPRFN MIFSFSKSGDVVHVTPTNYVRHRRGSDDSPGTFRKWESIYQPSDKYRI PAWATPADRDALHHASIFTSLAAFRDRECALTLRNLFDMAVAPHRLYV GVSEERSPSDASCFSSIGVDDLASGETRRVLYGAEAPRTLGLEVRSLT WADVVAPRQLLDVDAALSVPTDGVAEYGARPAGVFLHPAHAGERVTCV AGELETARDRLLLAEDDARQDMDGGSVFRRGRGGPQQQPSRALAGCRV TTRVAEPAFARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSHYPNGYREGHDREEFDKKIVMLMCTAQVLSNGMPK LGARWMKLSPHPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEV LYSARMWTAGWDLYGPGQPDVFHHYGRPNTPKYFGIMTPKEAARRVLS EQRTLYMLRRAHPWIEELVRRGYVSANGQSTLKPLPLEEAPETRLIVT DEVAAETREISVWAKYYGMGTERSVSAYWQHTELSDAFVKAKDEENRW LGGFGLCQKGGAMA
119	LmjF.17.1020:mRNA-p1	MPDYGQVPSLLKRPLRVPRRRLSTRRRQILIAFVAILCLCGLLFMHFF STSSSTAPSELSDLRDKPWITSDENLTRFENIVEGRTPGTAWRDPRFN MIVSFSKSGNVVHVTPTNYVRHRRGSDDSPGAFRKWESIYQASDKYRI PAWATPADRDALHHASIFTSLAAFRDHECALTLRNLFDMAVAPHRLYI GVSEERSPSDASCLSSIGVDNLASGETRRVLYGLDAPRTLGVEVRSLT WADVVAPRQLLDVDAVLSVPTDSAAGYGAQPAGVFLHPAYAGERVTCV AGELETARDRLLLAEDDVRQGMDGGSVFRRGRGGPQQQPSRALAGCRV TTRVAEPASARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSHYPNGYREGHDREEFDKETVMLMCTAQVLSNGMPK LGARWMSLSPHPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEV LYSARMWTAGWDLYGPGQSDVFHHYGRPSTPKYFGIMTPKEAARRVLS EQRTLYMLRRAHPWIEVLVRRGYVSANGQLTLKPLPPVEAPETRLIVT EEVAAETREISVWATYYGMGRERSVSAYWQHTELSDVFVKVKDEENRW MGGVGLCHKGGALS
120	LmxM.17.1020.1-p1	MPDYGQVPSLLKRPLRMPRRRLSARRRQAFLVFAILCLCGLPFMYFFS TSSAKVRGELPDSREKPWITPSENSTRFAQIVDGRTPGTAWRDPRFNM IISFSKSGDVVHVTPTNHVLHRRASDDSSSAFRKWESIYQPSDKYRIP AWATPADRDTLHHASIFTSLAAFRDHECALTLRNLFDMAVAPHRLYVG VSEERSPSDASCLSSIGVDDLASGETRRVLYGAEAPRTIGVEVRSLTW ASVVAPRLLLDVDAALSVPTGSTAEYGARPAGVFLHPAHAGERVICIA GELETARDRLLLAEDDAKQDMDGGSVFRHGGGGPQQQPSRALAGCRVT TRVTEPRFARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLIT RVFQLPTRGVLSHYPNGYREGNDREEFDRTIVMLMCTAQVLHNGMPKL GARWMKLSPHPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEVL YSARMWTAGWDLYGPGQSDVFHHYGRPNTPKYFGVMTPKEAARRVLSE QRTLYMLRRAHPWVEELVRRGYVSANGQTTLKPLPPKEAPETRLIVTD EVAAETREISVWAKYYGMGTERSVSAYWQHTELSDEFVKAKDEENRWV GGVGLCEKGGAMG
121	LPMP_170990-	MRDYSQVPSVLKRPLRMPRRRLSVRRRQAILAVIAILCLCVLSFMYFL STSPVNEHRKFSDIPSKPWFTAEENATRFAQVVQGRTPGTTWRDATFN

SEQ ID NO.	Description	Sequence
	t37_1-p1	MILSLSKSGDTVYMTPTNYTRYRRTTDGNPGDFRKWESIYRPGDRYHV PAWATPADRATLHHASIFVSLASFRDHECALTLRNLFDMSASPHRLYV GVSEERRSSDASCLSRLGMDDLESGETRRVLYGAEAPASLGVEVRTLT WADVLAPRRLLDVDAVLSTPAVSAEGIGVEPDGVFVHPAHAAERVLCV AGELETARDTLLTGEEDAKSAIAGQSVFRKGRGGPQQQPSRALAGCRV TTRVTDASHARGPTFGRYITSLFFFNQDYFMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSNYPNGYREGHDREEFEKTDVMFMCTAQVLSNGMPK LGARWMPLSPRPVLQGFAAAGFMFGDAQFTLDTPFDPFLPYMFDGEEV LYSARMWTAGWDLYGPGQPDVFHHYSRPNTPKYFGIMTPKEAARRLLS EKRTLYLLRRAQPWIEELVHRGYVSPNGQSTLKPLPSAPPPETRLIVT DEVASATREINVWSKYYGMGAERSVSSYWQHTELSDEFVKTKDNENRW MGGIGLCEKGAALM
122	LMARLEM2494_170015500.1-p1	MRDPGQIPSLLKRPLRMPRRRLSARRRQAFLVVMAIMCVCMLSFIYVL RFSADAPDVVFDTQTKPWITADGNLTHFSQIVRGHTPGTAWRDPLSNR IVALSKLGDVVYMTPTKFIRHQSPMDGGPGTFHKWESLYQPDERYHIP DWATPSDRDTLQHASIFTSLAAFRDRECALTLRNLFDMAVAPHRLYVG VSEERNSSDASCLSSIGIDDLLSGEMRRVLYGSGAPAALGVEVRTLTW EAVLAPRSLLDADAAAGQPAGTAEEPDGIFLHPAHSSERLYCVAGEAE TLRDTLLLAEDDAQRTTSGGSVFRRGRGGLQQQRSRALAGCRVTTRVT EAAFARGPTFGRYITSLFFFDQDFFMVVDSHTRFSVDWDAKLITRVFQ LPTRGLLSNYPNGYREGHEREEYGKRDFMLMCTAQILDNGMPKLGARW MPFTRHPVLQGFAAAGFMFGDAQFVLDTPFDPFLPYLFDGEEALYSAR VWTAGWDLYGPGQPDVFHHYVRQNTPKYFDIVVAEKAARRVLSQKRAL YLMRRAQPWIEELVRRGYVTAEGRSTLKPLPQVEPPETRLIVTDEVAA ATPEIRVWAKYYGLGAARSVSAYWQHTELADEFVKAQDNEHRWMGGVG LCRRAGIDNA
123	LTRL590_000019100.1-p1	MPDYGQVPSLLKRPLRVPRRRLSTRRRQALIAFIAILCLCALPFMYFF STSSATALSELSDPREKPWITSDENSTRFEHIVEGHTPGTAWRDPRLN MIVSFSKSGDVVHVTPTNYVRHRRGSDDSPGAFRNWESIYQPRDKYRI PAWATPADRDALHHASIFTSLAAFRDHECALTLRNLFDMAVAPHRLYV GVSEERSPSDASCLSSIGVDDLASGETRRVLYGAEAPRTLGVEVRSMT WADVVAPRQLLDVDAVLSVPTDGAAEYGARPAGVFLHPAYAGERVTCV AGELETARDRLLLAEDDARQGMDGGSVFRRGRGGPQQQPSRALAGCRV TTRVAEPKFARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLI TRVFQLPTRGVLSHYPNGYREGHDREEFDKKMVMLMCTAQVLSNGMPK LGARWMTLSPHPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEV LYSARMWTAGWDLYGPGQPDVFHHYGRPNTPKYFGIMTPKEAARRVLS EQRTLYMLRRAHPWIEELVRRGYVSANGQLTLKPLPLEEVPETRLIVT DEVAAETREISVWAKYYGMGTERSVSAYWQHTELSDEFVKAKDEENRW LGGFGLCRKGGAMA
124	LTULEM423_17001570 0.1-p1	MPDYGQVPSLLKRPLRVPRRRLSTRRRQALIAFIAILCLCGLLFMYFF STSSESALSKLSDLSEKPWITSDENSTRFKHIVEGRTPGTAWRDPRFN MIVSFSKSGDVVHMTPTNYARHRRSSDDSPGAFRKWESIYQPSDKYRI PAWATPADRDALHHASIFTSLASFRDHECALTLRNLFDMAVAPHRLYI GVSEERSPSDASCLSSIGVDNLASGEARRVLYGVEAPHTLGVEVRSLT WADVIAPRQLLDVDAVLSVPTDGAAEHDARPAGVFLHPAYAGERVTCV AGELETARDRLLLAEDDARKGMDGGSVFRRGRGGPQQQPSRALAGCRV TTRVAEPGFARGPTFGRYITSLFFFDQDYYMVVDSHTRFSVDWDMKLI

SEQ ID NO.	Description	Sequence
		TRVFQLPTRGVLSHYPNGYREGHDREEFDKKLVMLMCTAQVLSNGMPK LGARWMSFSPHPVLQGFAAAGFMFGDAQFMLDTPFDPFLPYMFDGEEV LYSARMWTAGWDLYGPGQPDVFHHYGRPNTPKYFGIMTPKDAARRVLS EQRTLYMLRRAHPWIEELVRRGYVSANGQSTLKPLPLEEAPETRLIVT EEVAVETREISVWATYYGMGRERSLSAYWQHTELSDVFVKAKDEENRW LGGTGLCQKGGAIS
125	PCON_0046770.mRNA-p1	MPPGQFRSGIRAHGGILRRRRISVLLMLLCCSLLASFVAFRLLIRGES VDGSAVLVSLRTDGSSKAVRKPTVTVPRSQTPTAASTVVPSTVAATPT DGTVPPMDTATDAGTTGPPPSPEAEVETVMLKVHAAVKLPSKMFPNPI FKADPMQGTIFVLLASFRDVECVDTMENLFTTAKIPSRVFVGANEERF AKDELVPSCIPPRLLSQFRGTVHEFDWPEFVARNITPARVQCVVFEAF DKGTSTTSSPPSGSVETPLAAGGAVNGTPPATLPPFPLSRCQIVTRVA SPTGARGPTYSRYVSSHLFQQQDYAMVIDSHSQFIDSWDVEMITTAAL MPTKGVLSHYPNGYEPNATVNPDQGKHVMQMCRGQVLSNGIPKLGAHW IKAQAQPVLQSMVAAGYFFGSAQFIRDVPFDPHLPFLFDGEEILYTLR LWSHGWDSYCPGRELIRHHYGREKSPRFWGIMKPMDYQLRNQAEMRTK HFLQLRKINTTELLVPPEQQSEAVRVEENIYGMGSMRPVLEEYWVFAG LNHARLTTLDSEGRWIGGSELCLP
126	Tbg972.5.3320:mRNA-p1	MERGGKFAAIFVGHFVSRRHKVFLFLFSLLFFFTSVMLLSSCFLLSTP SFFSTGTSEGSSISRGIVSFSSGELPSSNVAADTATIFVSLASFRDNE CVTTLDRLLSAAKNPHRVFVGISEERFGSESGCTNSPTLLGFVGSQRD FNIRWRDVVPRAFDEATSDEFRPPPTTPLLHARRENDVLTCFLKPKIS RPSPLPQGKELLRNCQVVTRFGDPDDARGPTYARYITSLFYVDQDYYM VIDSHIRALLEWDEKMIKHARLMPTRGVLSHYPNGYTPQNPDKEVNYT HVMAMCKAVIPPTNIPKLGARWILKRQRPLLQSLVAAGYIFGDAQFVK DVPFDPYLPYLFEGEEMLYTARLWTNGWDSYCPGDSFVFHNYERASAP RFWSAIYKSNQSESRKRQEKIGVLRALYLMERKELNTTVPLVSRDVAQ IVCPAISIEEGRFGMGTVRPLDAFWEFAELTDAFLKEKDDEGRWMGGE GLCHQLEALSASIKHMASED
127	TcIL3000_5_2160.1-p1	MHKGRCASVTSALVSAPRRWRIYTFVLAIILSLTLVLTVLVYYTLSPK GFHIASPLQRVSDMPPYVTFPSSKLPSANVSIDLATIFVSIASFRDDE CASTVESILRNAKNASRVYIGISEERLQTDKSCLSAPVLSERIGVNQI LRFRWSDIVPSAFWGAEIVGKQPPPTPILHAGRDEDVLSCVLMPGISQ LAVHETGGDILHNCQIITRVGDPDDARGPTYARYLSSLLYGGQNYYMV IDSHTRVVPSWDVKMIERARLMPTRGVLSHYPNGYTPQNPDKELNYPN IMAMCKAVIPSTGVPKLGAHWILKSYRPLLQFFVAAGYIFGDAQFVKD VPFDPYLPYLFEGEEMLYTARLWTSGWDSYCPGDSFAFHNYERPGVPR FWTVIYDSDERQERAREEKIGTLRALYLMRRNVLNSTTPLVSHEVSHN LYPAISFEEERFGMGSERPLPLFWKLSQLSDEFVKAKDSEGRWVGGDQ WCSRLEAMSLSLKSKASKG
128	TevSTIB805.5.2740-t26_1-p1	MERGGKFAAIFVGHFVSRRHKVFLFLFSLLFFFTSVMLLSSCFLLSTP SFFSTGTSEGSSISRGIVSFSSGELPSSNVAADTATIFVSLASFRDNE CVTTLDRLLSAAKNPHRVFVGISEERFGSESGCTNSPTLLGFVGSQRD FNIRWRDVVPRAFDEATSDEFRPPPTTPLLHARRENDVLTCFLKPKIS RPSPLPQGKELLRNCQVVTRVGDPDDARGPTYARYITSLFYVDQDYYM VIDSHIRALLEWDEKMIKHARLMPTRGVLSHYPNGYTPQNPDKEVNYT HVMAMCKAVIPPTNIPKLGARWILKRQRPLLQSLVAAGYIFGDAQFVK DVPFDPYLPYLFEGEEMLYTARLWTNGWDSYCPGDSFVFHNYERASAP

SEQ ID NO.	Description	Sequence
		RFWSAIYKSNQSESRKRQEKIGVLRALYLMERKELNTTVPLVSRDVAQ IVCPAISIEEGRFGMGTVRPLDAFWEFAELTDAFLKEKDDEGRWMGGE GLCHQLEALSASIKHMASED
129	DQ04_01951010-t26_1-p1	MDRRRYHGPAGGHRTRARITIALICFASVGIISLVALMLSVLVPSPPP QAAQSPTDTKEGPQLRAVELPAAMVPVDEATIFVSIAAFRDNECVTTL ESLLTRSKNQHRVFLGISEERHPTDKSCLEAPHVLNRFALTHTRTMRW KDVVPAAFVSRDSHATPVYTPLLHARRDDDVITCIQSSDAAADESRQP GLHPLSGCRIVSRLGNPDDARGPTYGRYLTSLLYNNQDYYMVVDSHSR FVPGWDVKMIERARLMPTRGVMSHYPNGYVPENPDGEADKKFVMSMCK GVILPNNIPKLGARWIPLQSSPKLQGFVAAGYIFGDAQFVKDVPFDPY LPYLFDGEEILYSARLWTNGWDSYSPGDAFLYHNYARKDAPRFWSVMQ GGDVHGGRMLQQRTAIRRALYLLKRRELNTTRFIVSEEEAHSLKPEIG CDDQYFGAGKVRSLDDYWRFTQLSDEYVKEKDNEGRWMGGEGLCN
130	TRSC58_05317-t26_1-p1	MNRKRFERPWKFRRGGRESRRLMRACIFCVAFFILLVFGAGGYYATFE RETLIVPRGTVPVFSSENLPAARIPVDIATIFVSIAAFRDKECITTLE SLFTRAKYPRRVFLGISEERFETDVSCINSPKVLNSIDVNRSRTMRWK DLIPSAYDAASQQKHPKPTPVLHERRDEDIITCLLSADASDAPTSPGE SMLNGCQVVTRHGHPDDARGPTYGRYITSLFYNNQDYYMVIDSHSRFV PDWDVKMIERARLMPTRGVLSHYPNGYTPEAPDAEINKSDVMCMCKGV ILPDNIPKLGARWIAIRGHPVLQGFVAAGYIFGDAQFVRDVPFDPYLP FLFDGEEILYTVRLWTHGWDSYSPATALVYHNYMRVDAPRFFSVISRP GTKERRELERQTAIQRVLYFLKRRVLNTTQLVVTDDEAHRQNPAIVRE EAHFGMGSLRSLADYWEFVELSDAFVKEKDDEGRWMG
131	TM35_00020160 0-t36_1-p1	MKRFEKLGKIQRHRKRLVFLILLSLSIFICMALFLLISGMALQYNSEE GQSRMGKGSAVFGKMEGNVFSSHNLPSASKSVEEATIFLSIAAFRDVE CVTTVESALTRARFPHRVFIGISEERYENDESCINLTDTLQRMNMTRT RTLRWKDVVPSAFETEKNAESKSKPTPLLHPGRSNDLITCLLSPHAAS RTLDSTNTSVLDGCQIITRVGEPDDARGPTYARYITSLFFNNQDYYMV VDSHSRFIPDWDIKMIERARLMPTRGVMSHYPNGYTPENPDKEITKLD VMSMCKGVIMPNNIPKLGARWIPIQSKPVLQGFVAAGYIFGDSQFVRD VPFDPYLPYLFDGEEILYTARLYTSGWDSYCPGSALLYHNYERHKAPR YFAVIVRDEVRAHRLLQQRTAIRRVLYLLRRCQLNTTNRIVTDDEAHV LNPAIGQYEKFFGMGKVRSLHSYWHFTQLSDEFIKSKDNEGRWMGGEG LCEIK
132	TvY486_0501730:mRNA-p1	MRTEVYRRLRGGVAFRSSRFKRGLQLAYLLIGVLVAVLLLVLLLSNRV MATLAGGGRSKRDGGWSSSRYIPFPASKLPAANVPIGVATIFVSIASF RDVECLTTVESLLTQANNSHRIFLGISEERFGHEPSCVNAPLIFKAIG IERNRTLRWRDVVPSAFVERSKKHPPPPMPILHAGRDTDLLTCYVSKS ATMLHEGKQVGALKGCQIVTRVGDPDDARGPTYGRYLTSVMYTGQDYY LVVDSHTRVVPDWDSKMIRFARLMPTRGVLSHYPNGYTPQDPDKELSK DDIMSMCTGVIPPTNIPKLGAQWVKKRDHPFLQSFVAAGFIFGDAQFV KDVPFDPYLPYLFEGEEILYTTRLWTSGWDSYCPGDAFLYHNYDRPKA PRFWSVVYNSKMKEQRMYEERIASMRVLYLTRRHKLNSTVLEVSHADA HKTHPAVGYEEERFGMGHLRPIHEYWKFAELSDEFTVAKDNEGRWTGG RGLCNRAV
133	rna_Baya_228_0	MYADLHGVVLNETDLAYRLHSIGRDPLEGSILLDEHLQYNEHALPFSN TTPPQNVLSSYYGNNNGYLARLNHLAENRLESDGYTNRTMFSEAFWDP IHLTRRGYGLEGSIFVGLIHNHRNIGFWIQELTNASNINLDEDGINPY

SEQ ID NO.	Description	Sequence
	080-1-p1	EMCSATIESIFKNAQWPVGVFVGVVELLIVPPDSTSNSLDNVHTSSYS CVPPEFESARQQESLGFSYADNLRVRRVPFSMNVDIPGATKPGNPWYL PYSSASAVRAATLNLYNGESYIMFLETGSHMVPDWDWRLRLMYLQLPS AERAIISTKPLQNISIVWSSLVHVAVNAHGNPNIKVSDGEQRIILPSG TLPPDPERQNDDTLLGAEASLRFSAVVKLLKVDPWSAIRFALPFWLHP LLGKCCEGSETAPFASAGSVLQELRRSLMMNETEHNFYQSSLFAMSRE SLSKTEVLSLLYLSRLSSNDQPVTTSEERQTLLVQCEKFMDEARQLLL KKEYEKCWLLEHRDVIRKAVSMGFGATLEVPLLSIAPLDMANGVTGAL NQSFRVSTHTSARLTDTLQDAKFMRADVQSLLTESSANKLPDEAEFGN SPYSNGNGVPFLLQGVASAAFMFSRAEVFFDIPPELQLRVSAEHTNNF CPSPLHLDPYYSFLTDDEADLHLSASLWGRGWNIFAPVEPVLFSVDSA ISANRNLSHSIPKPILQFRRATVSRLQKVFSSNTQETDAEGCGKGGVY GLGTVRDFGEFCSRTGFSLGDQLNLWRLEEEELRRSLG
134	CFAC1_160013300.1-p1	MRLKASLLPGHRSRTSRVARRVMIAVLFLIVLLVACLGYMVYHSLGDG NGIFPLETLPVTDPSQPNRGGAHGGLTFPPSPERDAHAEGAMPYSESL NELVQLLKLYTATRGVAVNTTQLRLPTPSGGGAGGDDLPAELQLAGLR ELYANASMIPPAGAGRTWMLDDPAVIQTEQEDYVERFIAPVQSDESLT PLRVLSAYYDPQSPRSLHHLAAATEKSANDDGYAAYIQRSPTFYDPAH AARRGYGAEGSIFVGVPFTLSDITADMIAAITARATAPFVKKEEPAVE ADARRSPLDGGDDAASVRDTDGFREVHRTAARCAVTVESLLRHAHHAS AITVGTIDVVVVSGVTSAEETDLAMPADVRLPITLEERQNLTAKPTRH YDRITCEPPDFRSGWGDASYGFYWRDNMRQRRVTVPLMQLASADARTG VPRPSFLDGAQVGRYAVLQLYRGESYVFLLRPGSLALPRWDLKLRLLY LRTPQHQRAVLSSRPTPAVLPQALAAVTIKTWAAHPVLPFGLLTSAAA EGAGGGAGIVTDPAAAAAATTNTPATDWMYQRLLATLPTDVAAWLGEA HAEAPLALWLVTPRWLWPTVLSALSEWRKMTNNTAASPPLRPSLQDLF GEEAVQTFLGPATSGTAVLDVASSVTVADAPVSATEPNAPAKVLLSGV GAQTRTPQSVLETSLTPAEVAKLVFLHEKRAPLPNEPIVDMKELLVEN ASVETVSPAAAAAAVTGGPIPCGTTGTPLAFYSTAHKALVKRAFEFCW LQRHRDKLRPLAVRLARSARPLTVLTTSATTGEAAPPPAGDVKCGGNE DANGLAWYATTVADRVKASHCLSDMRYLDPSDPPLLDADGTAPVSLKS WFVASGNAGQVRGSSALPARLNAAAAEVNADARATAIATNTAAGGEPQ TAATAATPYVLQSAASADLLFAPAEAFFPISPEDRLRTRAQSLEAQLR QRKAANGTGTNGTSAAQSDYAETPEPIVLDPSLHYLDSGSLDLYVTTA LWTRGWNVFGLTEAVIAGDAVPTSTTTTEAEVCKIGGGGAAASVVVPE VVAAAQAFGQEKLWAVLAAHRAAGTPVGPLMASENELNTTAMVARFPL RRTLSDFEAFARVKLDDLRPK
135	EMOLV88_020005600.1-p1	MRLWSLSSRRCRTRRLKRFIFIFIFVFILLLTFWLSTFEVTVSHKNAV GGPSANFPSSDRPNRSGGAGENGDAQALPEKSIEVPYGESLEELLQLL RVYAAYRGVRVNHTYLAPTKATAAADAGYKVDNSTRESKGRGLSLELS GMELLHGLLGDHDHLWANWSLEAPEKIMDEHEVYVEQFIAPTRVDDEI TPLRVISSHYSTQSIQGGLDGIAANTEKAMNDDGYAEHTQRSPGFFDV SHAARRGYGQEGSIFVAVPFSLADITAEMIDTIRQRSTTSGNVSQAPK ATATERPPNADDFVGDDGFTEWRFTAARCAMTVSSLFSQAHRGVAVTV GTIDVVVVSGVASLREVEWDRPADALFPLRATERSSLTPSRHRRYSRI TCEPPEFAGGLGDASEGFHWKDNLRRRRVVVPLPRLESASPAAAAALE QSFAFPYVGRYAALRLYRGESYIFFLRTGALALPNWDLMLRLLYLRTP ARNRGVLTSRPTPGVVWRALAAALAKTWITEPLLPLSLTTAVRGRGGE

SEQ ID NO.	Description	Sequence
		GKVGAPATTPDEAGNRLLAALPAEVSSWLSAARVEAELVLWLVTPGWL WPTMLETLEDWRHLAAAPTSSPPATAPPALSSLFSRSAVRDLLGEKPT APPDVDVGTLRVDHVMGAHGGAAAAASRKGQPVVQVRGGKGAATGGVS QSFLSASLTASEVYESVFLPTSGRSTPSYPTVDMAHAASTRSAAPSRG FDGAAKTLCGEQRSAAPYYSAADKMLLKRSFEYCWLMRHIQVVRQHVH RLLNATEATTLLRVFSGTQAAANFSTEVQFAESVLRPRSSSCLADMRY LEPVEGFGLAGIGRGAGKDDKNTLSDQHALDPQSTPRETDWLVSAVDV GKVHGVPTAERLKRTAGDDRLLRVNATQPTEDTLSSLTQPTPYIVQAA ASADLLFGPAEAFFHFRPEHQLRTRARSLSEHLEDRRLYREKVSSTAT HARVPEAVELDASLQFLDGDAEDIYMTQALWTRGWNLFGLTEPVAVNI GEDGLHTPSSTAPPPAGDGGQRRLRTSVRDVPSVLQKARAFTDHKLWA LLMSHRNAGTVLGATEGSSETATPYSFRRTIKDWELFARVQLTILNET LRRWQ
136	LAEL147_000030300.1-p1	MWRTVRDRGEGAKVGGKATEHPSAPGNPTVSLVPGAGADGDAPLLGGD RGAAPYTESLEDLVRLLRIYAEHRGVRVNHTYDALPAAIAAAAGLTDS GENSQTGAGARVGGLQLPGAELLHGLYGDGGQAGGHLSANWVLDEPEM ITAEQETYVERYLVPTQAEVELTPLRVISSYYDTQGSRSLHRMAAETE KAMNGDGYATYIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITA EMVATIRRRASTVPTSSQAQKPASSSPLEGRDDGFHELRFTAARCAMT VESLFRQAHRGVAVTVGTLDVVTVSGVSSAAELDFSKPADVTFPLRAE DRAGLPHTRRYSRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLT QLDAASAAQADLLHGDGAAAALERYFAFPHVGHYATLQLYRGESYVFF LRTGSLALPNWDLTLRLLYLRTPARDRAVLSSRPTPRVAWTALAASVA KMWDTEPFLRLSLATASRQRNGEDATGDDMGVVATAPPPDKMGRRLLA ALPADVSSWLIAARTEAELVLWLVTPSWLWPTMVETLADVRQLAASPD SPPPATASSALRLLFASDAVRGVLGNGLSTLMQADLNTVQVDPVRRSE GAAAAAASPRGQRVVSLRGGKSPTTNSTSQALLSASLTASEVYELLLL AEKRPPMQEQPVVRVPQSDPTIKWVPSSDSGAAAERLCGEATSEAPYY SAADKALLKRSFEYCWLKGHRRAVRQQLNRLVHATTAATVLKATPGTK ASAAGAAAAAKCSRKRGFVEAEVVPRSSVCLADMRYLEPMEATWLTGA GGGALGDGDSANREWHATDPRSPGHENAWFTSAASVGKVHGVATASSL VSQAADGTEEPQLNSPRSPKDAASTPVESTPYVLQAVASSDLLFGPAE VFFEFDTEHQLRTGARSLSEQLAERRLHRQGLTATAAHARVPEAVELD PSLQFMDSDLEDVYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSASA TAPTSSSARDDGPCTVDEAADGVPSELRNARTFTQDKFWALVMAHRDA GTLLGATAVTNHSSTPPESSPPLYPLRRTMKEWELFAGMQLTTLRDAL RSP
137	LAMA_000003620 00.1-p1	MRDGGEDAKAGGKATQHPSTPGTPTVSLLPGAGAEGDARSFGGDGGVA PYTESLEELVQLLRIYAEHRGVRVNHTYDALPAGLTDSGESSQRGAGA KVAGLQLPGAELLHGLYGDDGQAGGHLSANWVLDEPETIMAEQEAYVE RYLVPTQAEVEVTPLGVISSYYDMQGSRSLHRMAAETEKAMNDDGYAT YILRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITAEMVDTIRRRA SAVPTSSPAQRSTSSSPLEERDDGFHELRLTAARCAMTVGSLFRQAHR GVAVTVGTLDVVTVSGVSSAAELDFAKASDVVFPLRPEDRAGVPYTRR YSRITCEPPDFASGWDDASYGFHWKDNLRRRRVVVPLTRLADASAAHA GLLRGDGAAATLERHFDFPYVGRYATLQLYRGESYVFFLRTGSLVLPN WDLTLRLLYLRTPARDRAVLSSRPTPRVAWTALSASIAKVCDTKPFLP LSLTLTSRQRNRENATGGDTDVVTTAPPPEKMGMDLLAALPADVSSWL

SEQ ID NO.	Description	Sequence
		TAARSEAELVLWLVTPRWLWPTMVETLADWRQLASSPDSPPPASASSA LRVLFASDAVRDVLGNEPSTLMQADLSTVQVSPVRRSDGATAVAASPH GQRVVSLRGGRSPTTNSTSQAVLSASLTASEVYELLFLDEKRGPMPGQ PIVHMPQSEPTIGQVPSRDSGAAAVRLCGEATSETPYYSAADKALRKR SFEYCWLRAHRGAVREQLNRLVHSTKAVTVLKAAAGTKAPAAGAAAQC SSKRRLLEAAMVPRSSVCLADMRYLEPMEETRLTGAGGGTLGHGDSAH QEWHAADQRSLREENAWLTSAANVGKVHGVATSSLLVSQGADGTEKPQ LNSPRSPKDAPPIPVESTPYVLQAVASSDLLFGPAEAFFEFGTEHQLR TGARSLSEQLAERRLHRQGLTATAAHARVPEAVELDPSLQFMDSDLED VYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSATEAAPRSSPARDDG KCAVDGATDGVPSELRNAHTFTQDKFWGLVMAHRDAGTLLGATDARNY TTTPRGSSPPLYPLRRTMKEWELFAGMQLTTLRDALRSP
138	LARLEM1108_0200072 00.1-p1	MWRTMHGRDEDAKVGGKATQHPSTPGNPTVSPAPGAGADGDAPPLGGD RGADPYTGSLEELVWLLRIYAAHRGVRVNHTYDALPAGIAAAAGLSDS GKNSQRGVGARVAGLQFPGVELLHGLYGDGGQAGGHLSANWVLDEPEM ITAEQEAYVERYLVPAQAEVELTPLRVISSYYSMQGSRSLHRMAADTE RAMNSDGYATYIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITA EMVDTIRRRASTVRTSSQAQKPASSSPLEGKDVGFHELRFTAARCAMT VESLFRQAHRGVAVTVGTLDVVTVSGVSSAAELDFPKPSDVTFPLRAE DRAGLPHTRRYSRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLA QLDAASAAQADLLHVDGAAAALERYFAFPYVGHYATLQLYRGESYVFF LRTGSLALPNWDLKLRLLYLRTPARNRAVLSSRPTPRVAWTALAASVA KMWDTEPFLRLSLATASRQRNGEDATGDDMDVVTTTPPPDKMGRRLLA ALPADVSSWLNAARTEAELVLWLVTPSWLWPTMVEALADMRQLAASPD SPPPATASSALRLLFASDAVRGVLGNGLSTLMRADLNTVQVDPVRRSE GAAAAVASPRGQRVVSLRGGKSPTTNSTSQAVLSASLTASEVYELLFL AEKRPPMQEQPVVRMSQSEPTIKWVPSSDSGAAAERLCGETTSEAPYY SAADKALLKRSFEYCWLKRHRRAVRQQLNRLVHATTAATVLKATPGTK ASAAGAAAAAKCSKKRGFVEAEVVPRSSVCLADMRYLEPMEATWLRGA GGGTLGDGDSANREWHAADPRSPRQENSWFTSAANVGKAHGVATASSL VSQAADGIEEPQLNSPRSPKDAASTPVEPTPYVLQAVASSDLLFGPAE VFFEFDTEHQLRTGARSLSEQLAERRLHRQGLTATAAHARVPEAVELD PSLQFMDSDLEDVYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSASA TAPTSSSARDDGPCTVDKAADGVPSELSNARTFTQDKFWALVMAHRDA GTLLGATAARNHSFTPPESSPSLYPLRRTMKEWEMFAGMQLTTLRDAL RTP
139	LbrM.02.0280:mRNA-p1	MRSRLLPSRRSRPARFARCIALCLALSIGALVLFSGLFLWKMFSDEVE GARTGSKMPQRPSMPGHPAGSSVPDAGADGVVQPLADNREAAPYTESL EELLRLLRIYAEHRGVRVNSTYHVPLEALTAALGLRGGGDSSQRGAEA RGADLQLPGAELLHSLYGNGGQAGDHLFANWVLDDPETITTEQEAYVE RYLVPTQAEVDLTTLRVISSYYNTQSSRGLDRMAAETEKAMNDDGYAT YVQHSPSFYDVSHASRRGYGQEGSIFVAVPFTLSDITEEMIDTIRRRA SAASALSQTPATPSSAPLQGRVESVGGGGFEELRLTAARCAMTVESLF RQAHRGVAVTIGTIDVVAVSGVSSATELNIEKPADVLFPLRTADRAKL TPSHKRRYSRITCEPPDFASGWDDADYGFRWKDNLRRRRVVVPLAGLD DAAAAHSSLPRRADTAAALERGFALRHVGRYATLQLYRGESYIFFLRA GSLALPNWDLTLRLLYLRTPARDRAVLSSRPTPGVTWRALAASVANVW STEPLLRLSLTTAPRGRHSEDGFGGEREAAASVPPPDKVGERLLAALP

SEQ ID NO.	Description	Sequence
		ADVSSWLSAARAEAELVLWLVTPSWLWPTMVETLADWRQLAASPDLPA SATASSVLGLLFTSAAVRGVLGDAILDLSDADLRAVQVDTLANCDGDA PTKASPCGQGMVYVRSGKNSSTSRTPQAVLSASLTASEVYELLFLAEK RPPMPAQPIVHMPPSASTTTPAPFRESGAAAGRLCGEEESEAPYYSAA DKALRKRSFEHCWLKEHRGAVRQQVRRLVHSTNASTVLQASSGMQAPA AGAAAAAKCHAKGSFVKAEVMPRSSVCLADMRYLEPMEGTWLTSADGG TLGSGDRAPQAHHAADEHSPLQESAWLASGANVGKVKGVATSARNAQA SGRVDELQFNSPQSPGDAASATVEPTPYVLQAVASADLLFGPAEVFFE FDREHQLQTRVRSLSEQLEERRLHHQGLTATAAHARVPEAVELDPSLQ FMDSDLEDMHTTLALWTRGWNVFGLTEPVAVGTGESELPTSMPATAPA ASGAGHDGQCLVDEAADGVPTELSNARTFTQDKFWALVMSHRDAGTPL GSTKERNQTPTPRASSPSPYPLRRTMKEWELFAGVDLTVLHDALRSP
140	LdCL_02000760-t42_1-p1	MRPRLLPSRRSRTARSAHRTLLCLVLSVGALVLLSGVVVWRTMRDGGE GAKVGGKATQHPSTPGNPTVSLVPGAGADGDAPPLGGDREAAPYTESL EELVRLLRIYAEHRGVRVNHTHDALLAGIAAAAGLTDSGENSQRGAGT RVAGLQLPGVELLHGLYGDGDQAGGHLSVNWVLDEPEAITAEQETYVE RYLVPTQAEVELTPLRVISSYYNMQGSRSLHRMAAETEKAMNDDGYAT YIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITAEMVGTIRRRA SAVPTSSQAQKPASNSPLEGRDDGFHELRLTAVRCAMTVESLFRQAHR GVAVTVGTIDVVTVSGVSSAAELDFSKPSDVTFPLRAEDRAGLPHTRR YSRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLTQLDAASAAHA DLLHGDGAAAALERYFAFPYVGHYATLQLYRGESYVFFLRTGSLALPN WDLTLRLLYLRTPTRDRAVLSSRPTPRVAWTALAASVAKMWDTEPFLR LSLATASRQRNGEDATGDDMDVVTTAPPPDKMGRRLLAALPAEVSSWL IAARKEAELVLWLVTPSWLWPTMVETLADGRQLAASPDSPPPATAPSA LRLLFTSDAVSGVLGNGLPTLMQADLNTVQVDPVRRSEGAAAAAASPR EQRVVSLRGGKSPTTNSTPQAVLSASLTASEVYELLFLAEKRPPMPEQ PVAHMPQSEPMIKWVPSSDSGAAAERLCGEATSEAPYYSAADKALLKR SFEYCWLKRHRRAVRQQLNRLVHATMAATVLKATPGTKASAAAGAAAA KCSTKRGFVEAEVVPRSSVCLADMRYLEPMEGTWLTGAGGGTLGSGDS AHQEWHATDPRSLPEEDAWFTSPANVGKVHGVATASLLAAQTADGTEE PQLNSPRSPKDAASTPVEPTPYVLQAVASSDLLFGPAEAFFEFDTEHQ LRTGARSLSEQLAERRLHRQGQAATAAHARVPEAVELDPSLQFMDSDL EDVYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSPPATAPTSSSARD DGPCTVDEAAAGVPSELNDARTFTQDKFWALVMAHRDAGTLFGATAAR NHSSTPPESSPPLYPLRRTMKEWELFAGMQLTTLRDALRSP
141	LGELEM452_02000690 0.1-p1	MHGRGEDAKVDGKATQHPSTPGNPTVSLAPGAGADGDAPPLGGDRGAD PYTGSLEELVRLLRIYAAHRGVRVNHTYDALPAGIAAAAGLSDSGKNS QRGAGARVADLQLPGVELLHGLYGDGGQAGGHLSANWVLDEPEMITAE QEAYVERYLVPTQAEVELTPLRVISSYYSMQGSRSLHRMAADTEKAMN GDGYATYIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITAEMVD TIRRRASTVRTSSQAQKPASSSPLEGRDDGFHELRFTAARCAMTVESL FRQAHRGVAVTVGTLDVVTVSGVSSAAELDFSKPSDVTFPLRAEDRAG LPHTRRYSRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLTQLDA ASAAQADLLHVDGAAAALERYFAFPYVGHYATLQLYRGESYVFFLRTG SLALPNWDLKLRLLYLRTPARNRAVLSSRPTPRVAWTALAASVAKMWD TEPFLRLSLATASRQRNGEDATGDDMDVVTTAPPPDKMGRRLLAALPA DVSSWLIAARTEAELVLWLVTPSWLWPTMVETLADVRQLAASPDSPPP

SEQ ID NO.	Description	Sequence
		ATASSALRLLFASDAVRGVLGNGLSTLMRADLNTVQVDPVRRSEGAAA AAASPCGQRVVSLRGGKSPTTNSTSQAVLSASLTASEVYELLFLAEKR PPMQEQPVIRTPQSEPTIKWVPSSDSGAAAERLCGEATSEAPYYSAAD KALLKRSFEYCWLKGHRRAVRQQLNRLVHATTAATVLKATPGTKASAA GAAAAAKCSRKRGFVEAEVVPRSSVCLADMRYLEPMEATWLTGAGGGT LGNGDSANREWHAADPRSPRQENSWFTSAANVGKVHGVATASSLVSQA AGGTEEPQLNSPRSPKDAASTPVEPTPYVLQAVASSDLLFGPAEVFFE FDTEHQLRTGARSLSEQLAERRLHRQGLTATAAHARVPEAVELDPSLQ FMDSDLEDVYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSASAAAPT SSSARDDGPCTVDEAADGVPSELSNARNFTQDKFWALVMAHRDAGTLL GATAARNHSSTPPESSPPLYPLRRTMKEWELFAGMQLTTLRDALRTP
142	LINF_02000750-T1-p1	MRPRLLPSRRSRTARSAHRTLLCLVLSVGALVLLSGVVVWRTMRDRGE GAKVGGKATQHPSTPGNPTVSLVPGAGADGDAPPLGGDRGAAPYTESL EELVRLLRIYAEHRGVRVNHTHDALLAGIAAAAGLTDSGENSQRGAGT RVAGLQLPGVELLHGLYGDGDQAGGHLSVNWVLDEPEAITAEQETYVE RYLVPTQAEVELTPLRVISSYYNMQGSRSLHRMAAETEKAMNDDGYAT YIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITAEMVGTIRRRA SAVPTSSQAQKPASNSPLEGRDDGFHELRLTAVRCAMTVESLFRQAHR GVAVTVGTIDVVTVSGVSSAAELDFSKPSDVTFPLRAEDRAGLPHTRR YSRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLTQLDAASAAHA DLLHGDGAAAALERHFAFPYVGHYATLQLYRGESYVFFLRTGSLALPN WDLTLRLLYLRTPTRDRAVLSSRPTPRVAWTALAASVAKMWDTEPFLR LSLATASRQRNGEDATGDDMDVVTTAPPPDKMGRRLLAALPAEVSSWL IAARKEAELVLWLVTPSWLWPTMVETLADGRQLAASPDSPPPATAPSA LRLLFTSDAVSGVLGNGLPTLMQADLNTVQVDPVRRSEGAAAAAASPR EQRVVSLRGGKSPTTNSTPQAVLSGSLTASEVYELLFLAEKRPPMPEQ PVAHMPQSEPMIKWMPSSDSGAAAERLCGEATSEAPYYSAADKALLKR SFEYCWLKRHRRAVRQQLNRLVHATMAATVLKATPGTKASAAAAPAAA AKCSTKRGFVEAEVVPRSSVCLADMRYLEPMEGTWLTGAGGGTLGSGD SAHQEWHATDPRSLREEDAWFTSPANVGKVHGVATASLLAAQTADGTE EPQLNSPRSLKDAASTPVEPTPYVLQAVASSDLLFGPAEAFFEFDTEH QLRTGARSLSEQLAERRLHRQGQAATAAHARVPEAVELDPSLQFMDSD LEDVYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSPPATAPTSSSAR DDGPCTVDEAAAGVPSELSDARTFTQDKFWALVMAHRDAGTLLGATAA RNHSSTPPESSPPLCPLRRTMKEWELFAGMQLTTLRDALRSP
143	LmjF.02.0250:mRNA-p1	MPVRLLPSRRSRTARSVHRTLLCLVLSLGTLVLLSGVVMWRTMHGRGE DAQVGGKATRHPLTPGNPTVSLVPGAGADGDAPPSGSDRGADPYTGSL EELVRLLRIYAAHRGVRVNHTYDTLPAGIAAAAGLTDSGNNSQRDAGA RVAGLQLPGVELLHGLYGDGGEAGGHLSANWVLDEPEMITAEQETYVE RYLVPTQAEVELTPLRVISSYYSMQGSRSLHRMAADTEKAMNGDGYAK YIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITAAMVDTIRRRA STVETSSQAQQPASSSPLEARDDGFHELRFTAARCAMTVESLFRQAHR GVAVTVGTLDVVTVSGVSSAAELDFSKPSNVTFPLRAEDRAGLPHTRR YSRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLTQLDAASAAQA DLPHVDGAAAALERYFAFPYVGNYATLQLYRGESYVFFLRTGSLALPN WDLKLRLLYLRTPARNRAVLSSRPTPRVAWTALAASVAKMWDTEPFLR LSLATASRQRNGEDATGDDMAVVATAPPPDKMGSRLLAALPADVSSWL IAARTEAELVLWLVTPSWLWPTMVETLAAVRQLAASPDSPPPATASSA

SEQ ID NO.	Description	Sequence
		LRLLFASDAVRGVLGDGLSTLMQADLNTVQVDPVRRSEGAAAAAASPR GQRVVNLRGGKSPTTNNTSQAVLSASLTASEVYELLFLAEKRPPMQEQ PVVRMPQSESTIKWVPSSDSGAAAERLCGEATSEAPYYSVADKALLKR SFEYCWLKRHRKAVRQRLNRLVHATTAATVLKATPGTKASAAGAAAAA KCSRKRGFVEAEVVPRSSVCLADMRYLEPMETTWLAGAGGGTLGDGDS ADREWHAADLRSPRQENSWFTSAVNAGKVHGVATAASLVSQAADGTEE PQLNSPRSPKDAASTPVEPTPYVLQAVASSDLLFGPAEVFFEFDTEHQ LRTGARSLSEQLAERRLHRQGLTATAAHARVPEAVELDPSLQFMDSDL EDVYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSASATAPTSSSARD DGPCTVDEAADGVPSELSNARTFTQDKFWALVMAHRDAGTLLGATAAR NHSSTPPGSSPPLYPLRRTMKEWELFADMQLTTLRDALRSP
144	LmxM.02.0250.1-p1	MRDGGEGAKAGGKAMQHPSTPGTPTVSLVPGAGAEGDARSFGGGGGVA PYTESLEELVRLLRIYAEHRGVRVNHTYDALPAGIAAAAGLTDSGESF QRGAGAKVAGLQLPGAELLHGLYGDDGQAGGHLSANWVLDEPETIMAE QEAYVERYLVPTQAEVEVTPLGVISSYYDMQGSRSLHRMAAETEKAMN DDGYATYIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITAEMVD TIRRRASAVPTSSQAQRSTSSSPLEERDDGFHELRLTAARCAMTVGSL FRQAHRGVAVTVGTLDVVTVSGVSSAAELDFAKASDVVFPLRPEDRAG VPYTRRYSRITCEPPDFASGWDDASYGFHWKDNLRRRRVVVPLTRLAD ASAAHAGLLRGDGAAATLERHFDFPYVGRYATLQLYRGESYVFFLRTG SLVLPNWDLTLRLLYLRTPARDRAVLSSRPTPRVAWTALAASIAKVCD TKPFLPLSLTLTSRQRNRENATGGDTDVVTTAPPPEKMGMRLLAALPA DVSSWLTAARSEAELVLWLVTPRWLWPTMVETLADWRQLASSPDSPPP ASASSALHVLFASDAVRDVLGNEPSTLMQADLNTVQVSPVRRSDGATA AAASPRGQRVVSLRGGRSPTTNSTPQAVLSASLTASEVYELLFLDEKR RPMPGQPIVHMPQSEPTIGRVPSRDSGAAAVRLCGEATSETPYYSAAD KALRKRSFEYCWLRAHRGAVRQQLNRLVHSTKAVTVLKAAAGTKAPAA GAAAQCSSKRRLLEAAMVPRSSVCLADMRYLEPMEETRLTGAGGGTLG RGDSAHQEWHAADQRSLREENAWFTSAANVGKVHGVATSSLLVSQGAD GTEKPQLNSPRSPKDAPPIPVEPTPYVLQAVASSDLLFGPAEAFFEFG TEHQLRTGARSLSEQLAERRLHRQGLTATAAHARVPEAVELDPSLQFM DSDLEDVYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSASAAAPRSS PARDDGKCAVDGATDGVPSELRNARTFTQDKFWGLVMAHRDAGTLLGA TDARNYTTTPRESSPPLYPLRRTMKEWELFAGIQLTTLRDALRSP
145	LPMP_020170-t37_1-p1	MRSRLLPSRRSRPARFARCIALCLALSIGALVLFSGLFLWKMFSDEVE GAKTGSKMPQRPSMPGHPAGSSVPDAGADGVVQPLTGNREAAPYTESL EELLRLLRIYAEHRGVRVNSTYHVPLEALTAALGLRGGGDSSQRGAEA RGADLQLPGAELLHSLYGNGGQAGDHLFANWVLDDPETITAEQEAYVE RYLVPTQAEVDLTTLRVISSYYNTQSSRGLDRMAAETEKAMNDDGYAT YVQHSPSFYDVSHASRRGYGQEGSIFVAVPFTLSDITEEMIDTIRRRA SAASALSQTPATSSSAPLQGRVESVGGGDFEELRLTAARCAMTVESLF RQAHRGVAVTIGTIDVVAVSGISSATELNIEKPADVLFPLRTADRAKL TPSHKRRYSRITCEPPDFTSGWDDAEYGFRWKDNLRRRRVVVPLAGLD DAAAAHSALPRRADTAATLEQDFALRHVGRYATLQLYRGESYIFFLRA GSLALPNWDLTLRLLYLRTPARDRAVLSSRPTPGVTWRALAASVANVW STEPLVRLSLTTAPGGRHSEDGLGGEREAAASVPPPDKVGERLLAALP ADVSSWLSAARAEAELVLWLVTPSWLWPTMVETLVDWRQLAASPDLPA SATASSVLGLLFTSAAVRGVLGDAILDLSDADLKAVQVDTLANCDGDA

SEQ ID NO.	Description	Sequence
		PTKASPCGQGMVYVRSGKNSSTSRTPQAVLSASLTASEVYELLFLDEK RPPMPAQPIVHMPPSASTTTPAPFRESGAAAGRLCGEEESEAPYYSAA NKALRKRSFEHCWLKEHRGAVRQQVRRLVHSTNASTVLQASPGMQAPA AGAAAAAKCRAKDSFVKAEVMPRSSVCLADMRYLAPMEGTWLTNADGG TLGSGDRAPQAHHAADEHSPLQESAWLASGANVGKVKGVATSARNAQA SGRVDELQFNSPQSPGDAASATVEPTPYVLQAVASADLLFGPAEVFFE FDREHQLQTRLRSLSEQLEERRLHYQGLTAAAAHARVPEAVELDPSLQ FMDSDLEDMHTTLALWTRGWNVFGLTEPVAVGTGESELPTSMPATAPA ASGAGHDGQCFVDEAADGVPTELSNARTFTQDKFWALVMSHRDAGTPL GSTKERNQTPTPQASSPSPYPLRRTVKEWELFAGVDLTALHDALRSP
146	rna_LpyrH10_27_0550-p1	MRSKVSQLLPGRRSRTNRAARRVLTVTALLLFGLVGFFSYRMYSSSLS PSSATEQIDLLGAKRQTTPPGEGETSAAATPAAGGDGGVAVTAGAGVA SLSESLDDLVGLLRLYTAAHRIRVNRSLVEGNAAHNKTAEGMSDVPKE LLLEGVSEMPFIGDDTDLLDDPAVIQAEQESYVERYIAPTQSGAALTP LRVLSAYYDPQNSRGLDHLAAAVEKRMNDDGYATHNRPSPTFYDASHA ARRGYGAEGSVFVAIPFALSDITPDIVDAIAARATAPLAKSANRPPTT ADAGAAAAEAADALHNPLDGADDAGAALDGDGYREIIRTAARCAVTVE SVFRQAHRGISVTVGTIDVVVVSGVQSAADVHLAYPADVRRPITAEER VKAGSVPSRRYDRLTCEPPNFRSGWEDASYGFSWKDNLRQRRVLVPLT TLATTPAVKGAGAKATLSSSSPLALPHVGRYAALQLYRGESYVLFLRP GSVALPNWDLKLRLLYLRTPQRERAVLSSRPTPAVVPHALAAAVMKAW TQQPYLLFSSLTDGAAKNTGRSSTVAHGAGAQKDRAGVTNAPALDWTG RRLLQAFPDGVAAWLAEARGESALALWLVTPRWLWPTLVDALRAWREL SNGTATSTTPPTTPPQTPPMRDVFRESVLREVLGDFTAAAEHLNLTSV AVTAATTAAANEEADTAQLHGTGAVTATSQPVLTTSLTEAEVYQILIL TPKRGPLPKEPITDTALFMTHNGGAASTTGEATAAGGTGTGVGAGLVA CGTATTPLPYYSNEHGALVKRAFEYCWIMHHRAALRALAERLTHATDA APILISASSKAAKNPAGGLAGKPIIAAAAAAATVMCGRNPASTVPWYD TALLVHNHTSRCLADMRYLDPSETPLLDETNKIAVGEEEERATVASWF ASSQNAGQLRGSSAVPAHPPTLVDGETPAGGAAAAAAGTTTPYVLQSA ASADLLFGPAEAFFDIAPEGRLRTRADARTAQLDERRGGGGGGTTLRY AETPEAAPLDPSLHYLDSGALDLYLTAALWTRGWNIFGITEAVVAGDD APTAAPAVKTGNAGSAPMCGLTKGGNDEAEKLLSAAMKTAKSIGEEKL WALMEAHRTAGTPLGPASAPATPDTLPLSAARFPLRRTLRDYEKFANL TLAELQRK
147	rna_Lsey_0379_0020-1-p1	MWYRALLLQLRRSRSSRVVHRTAIAVAVSTLVLASILCALSFTSLGNG DRFFPLNSNFAGNPAHWSGDRRSTAPNGGASAGVAVTTSPDAIPYSET IDELLKLLYIYTAARGIVVNTSVLDALNLTPMDGSPAGTVPASTPALP EHLQMAGVDELRFNGADVGRYAAQLLDDPFVIQAEQEDYVERYIAPTQ FGVPLTPLRVLSSYYDPQSARGVDQLAEAVEKSMNDNGYAKYIRRSPT FFDPSHAARRGYGLEGSIFVVIPFVLSDITPDIVAAITARARAPPSAA NSATAAPREAAALRNPLDGADEASAAQAGDAFYEVRRTAARCAMTVES VFRQAHHAIGVTVGTIDVVVVSEVDSPSDIDLAFPADVRRPITEAERV KDAALRKRRYDRITCEPPSFRSGRDDVSYGFSWKDNLRQRRVLVPLAK LASTAHTGAAARGGPSTFELPHVGRYAALQLHRGESYIFFLRPGSAAL PNWDVKLRLLYLRTPQHQRAVLSSRPTPAVVWKSLAAAVAKVWTQHPY LLFSSLAGGEAQSTGLAGTAGQSPAGMEKGSHSARNAGAGAAAAPALD WTGRRLLEAFPFEMATWLVEARTESALALWIVTPRWLWPTLVDVVQEW

SEQ ID NO.	Description	Sequence
		RALSTGTAPAAAAPSQTPSLRDLFSEATLKAILGDGAAATANWTLASV TAAASSVAGTALLHGTGAATAASRPILTASLTEAEVYAMLLLEEKRMP PPAEPISGMSQLSKRNVNAGVNDAAGATGAAAVGVGTGAGMVACGTLG TPLSYYSAKDNALVKRAFEYCWIHHHRAALSTLAERLIHTTKASAILT SPSPHSARHGAGADGAAVRCRGDGQSTFKWYDTKLLPHNRASQCLADM RYLDPSEVPLLGVAKEGTVEEQRVAAAQWFVSPSNAGQLSGDSAVPPQ PANVAEREAAATATTTTTTPYVLQSVASADLLFGPAEAFVDIAPEDRL RTRAYTLAEQLSRKQRSATSGPTAAATPEASRYADTPEAVALDPTLHY LDSDALDLYLTTALWTRGWNLFGLTEAVAAGDAAPNPVTAPVTAPVNT TAAPAADAVGSVMTQACGLAEKGNDAWESLPAEVRAAQTFAEEKLQAL MAAHHAAGTPLGPVGNLTAQGTPATTRFPLRRTLQAYENFASFKLADL LKK
148	LMARLEM2494_020006500.1-p1	MRLRTFLGRRLRTARFARSTFLFGALSIGALVLLSGVFMWTVADNWAG GATARSNGAPPFSTPGNPAGSLVSGASADGPEGSVQPLTGYREAAPYT ESLEELLRLLRIYAEHRGVRVNSTYHAQLEAIAAVAGLSNGADDSKRG AGGGVADLQLPGVNLLHHFYSGIGHVVGHLSADWALDDPKAIVTEQEA YVEQYLVPTQAEVRLTPLRVIASYYNARGSRSLDRMAAETEKAMNDDG YATYMHRSPTFYDVSHAARRGYGQEGSIFVAVPFTLADITAEMVDTIR HRATAASMPQKTTPNASSGAAPQEGDDLVGDDGFQEWRHTAARCAVTV ESIFRNAHRGVSVAVGTIDVVVVSGITTAAELPFATPADVSVPLRAAD RAPLSLARKRRYSRITCEPPDFASGWDDANYGFRWKDNLRRRRVVVPL TRLDSEAANDATLLQREDIAALLGQYLDIAYVGRLATLQLYRGESYIL LLRTGAVTLPKWDLALRLLYLRTPVRDRAVLSGRPTPGVVWTALAASI ARVWASRPYLRLSLETASSRRSAAGEPSGGRRNRTAVPPPDEFGERLL AALPVDVSAWLSAARAEAALVLWLVTPGWLWPTLVETLADWRQIAAAP ELPPSTTAPSALRLLFGNATFGDATVDELLTLREVDVKTVQVDVVRRS DSANATNASPLRNRRVHVRGGENSAVSSVPQAVLSASLTESEVYKAVL LTEKRPPMPAELTTLMAQAASTKAPAQPRTPRAAMRLLCGEETSGAPY YSALDRALVKRSFEDCWLKEHRGAVQQQVRRILRSTQATTVLKAAPGT KPPPAGAVAAAKCRPKKGFSKVEVVPRSSVCLEDMRYLVPLETPTCTG AGGGLYGRENSTHQELNAANQRLPLREEAWLTSAADVGTVHGVPTSTC VSETADGADEPTPYVLQSVASAELLFGPAEVFFNFAPEHRLRTRARSL SEQLAERRRRHPGAEAATAHAQVPEAVELDPSLPFMDSDQEDVYMTQA LWTRGWNIFGLTEPVAVGLGESELLSSAAAKAPVICAGEDTEQQRIEQ EADDVPPELRHARTFTHDKFWALLTDHREAGTPLGVAQARNGTTPQRA ASQSLHPLRRTIKEWEVFSGVPWPALREAFHGP
149	LTRL590_020007600.1-p1	MWRTMRDRGEGAKVGGKATQHPSTPGNPTVSLVPGAGADGNAPPLGGD RGAAPYTERLEDLVRLLRIYAEHRGVRVNHTYDALPAGIAAAAGLTDS GENSQRGAGARVGGLQLPGAEPLHGLYGDGGQAGGHLSANWVLDEPEV ITAEQETYVERYLVPTQAEVELTPLRVISSYYDMQGSRSLHRMAAETE KAMNGDGYATYIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITA EMVDKIRRRASTVPTSSQARKPASNSPLEGRDDGFHELRFTAARCAMT VESLFRQAHRGVAVTVGTLDVVTVSGVSSAAELDFPKPSDVTFPLRAE DRAGLPHTRRYSRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLT QLDAASAAQGDLLHGDGAAAALERYFAFPYVGHYATLQLYRGESYVFF LRTGSLALPNWDLTLRLLYLRTPTRDRAVLSSRPTPRVAWTALAASVA KMWDTEPFLRLSLATASRQRNGEDATGDDMDVVATAPPPDNMGRRLLA ALPADVSSWLIAARTEAELVLWLVTPSWLWPTMVETLADVRQLAASPD

SEQ ID NO.	Description	Sequence
		SPPPATASSALRLLFASDAVRGVLGNGLSTLMQADLNTVQVDPVRRSE GAAAAAASPRGQRVVSLRGGKSPTTNSTSQAVLSASLTASEVYELLLL AEKRPPMQEQPIVRMPQSETTIKWVPSSDSGAEAERLCGEATSEAPYY SAADKALLKRSFEYCWLKGHRRAVRQQLNRLVHATTAATVLKATPGTK ASAAGAAAAAKCSRKRGFVEAEVVPRSSVCLADMRYLEPMEATWLTGA GGGTLGDGDSASREWHATDPRSSGQENAWFTSAANVGKVHGVATASSL VSQAADGTEEPQLNSPRSPKDAASTPIEPTPYVLQAVASSDLLFGPAE VFFEFDTEHQLRTGARSLSEQLAERRLHRQGLTATAAHARVPEAVELD PSLQFMDSGLEDVYMTQALWTRGWNIFGLTEPVAVGTGEEELSSSASA TAPTSSSARDDGPCTVDEAADGVPSELRNARTFTQDKFWALVMAHRDA GTLLGATAVRNHSSTPPESSPPLYPLRRTMKEWELFAGMQLTTLRDAL RSP
150	LTULEM423_02000670.1-p1	MWRTMHGRGEDAKVGGKAAQHPSTPGNPTVSLAPGAGADGDAPPLGGD RGADPYTGSLEELVRLLRIYAAHRGVRVNHTYDALPAGIAAAAGLSDS GKNSQRGAGARVAGLQLPGVELLRGLYGDGGQAGGHLSANWVLDEPEM ITAEQEAYVERYLVPTQAEVELTPLRVISSYYSMQGSRSLHRMAADTE KAMNSDGYATYIQRSRTFYDVSHAARRGYGQEGSIFVAVPFTLTDITA EMVDTIRRRASTVRTSSQAQKPASSSPLEGRGDGFHELRFTAARCAMT VEALFRQAHRGVAVTVGTLDVVTVSGVSSAAELDFSKPSNVTFPLRAE DRAGLPHTRRYSRITCEPPDFASGWDDASYGFRWKDNLRRRRVVVPLT QLDAASTAQADLPHVDGAAAALEKYFAFPYVGHYATLQLYRGESYVFF LRTGSLALPNWDLKLRLLYLRTPARNRAVLSSRPTPRVAWTALAASVA KMWDTEPFLRLSLATASRQRNGEDATGDDMDVVTTAPPPDKMGRRLLA ALPADVSSWLTAARTEAELVLWLVTPSWLWPTMVETLADVRQLAASPD SPPPATASSALRLLFASDAVRGVLGNGLSTLMRADLNTVQVDPVKRSE GAAAAAASPRGQRVVSLRGGKSPTTNSTSQAVLSASLTASEVYELLFL AGRRPPIQEQPVARTPQSEPTTKWVPPSDSGAAAERLCGEATSEAPYY SAADKALLKRSFEYCWLKGHRRAVRQQLNRLVHATTAATVLKATPGTK ASAAAGAAAAAKCSRKKGFVEAEVVPRSSVCLADMRYLEPMEATWLTG AGGGAWGDGDSANREWHAADPRSPRPGSSWFTSAANVGKVRGVATASS LVSQTAGGTEEPQLNSPRSPKDAASTPAEPTPYVLQAAASSDLLFGPA EVFFEFDTEHQLRTGARSLSEQLAERRLHRQGLTATAAHARVPEAVEL DPSLQFMDRDLEDVYMTQALWARGWNIFGLTEPVAVGTGEEELSSSAS ATAPTSSSARDDGPCTVDEAADGVPSELSNARTFTQDKFWALVMAHRD AGTLLGATAARNHSSTPPESSPPLYPLRRTMKEWELFAGMQLTTLRDA LRTP
151	Tbg.972.2.930:mRNA-p1	MRSETRRRGRRCITVPMYMVLPALVMLTFLLWNNMSREHENRMRGGHI GEGSHAVRGGLPGVENLRASPAVFSFTTKLLSVLTAFVDQETDGMPAS VAAAGGATDMFGLPPNATPAAILLEYYETQLPKFNNELEKRLDNGSIK NVTHSDTYWSPTHVARRGYGLEGSIFVGLLHHETPLVRMRRSVSLESV CAMTVHNLYESALWSVAIFTGIVEFLPDVMTAEESGGRGGHNSSRWPF PPSSPCIPAAYQSHTCAERYGFCPRDNIRLRQLRVSAKSRRHGKGSNM GGGEGNVKVSEKKENPRSRRAEDDYEHAGYRDGDASSGSDASGGPSDF TSIASQRYATLALYRGETYVMFLNAGVLLVPSWDVTARLMLLRLPSRR PILSQMANIIQRDVVHRAWEEVVVRHVSNEGHRHEGVKDHGDQQFRDD QRGKERGGTEDYFNVAHERNPSKKRSGSTLYDLEGLRLHSSDGMEDKE KGDGNGESAAEGARGFGSEDVVEFLFRLPTEEDGGEATSGAEPLNYPR NGASIPNVRTRMPNSAQLYWMKKLREPLRKKLLTSMSEQNTTSYVCGV

SEQ ID NO.	Description	Sequence
		AVKMQHSEEGCRKVCDAKSDGGSSGCGNVENGEDVSAAVSGGEGAKFK LRYESRRRLTYVLRDRRYMEPLPIHWCNEKNDAVCLGSRRQESFPSSL SQPWLSTDFLFTRAGAFFDFSHDAADHQNSHNNSSSGNAGNHVPLDPY MGFLTPDEEAVLLAGRLWTHGWDFYAPTEPIAFAAAVHAEGAGNGTSG NNKVANMSSKVRDARLRGLVRLNFVLFGQSNAARGLRSDGEAALKHVE KYGLGSRRSRESFLQHVGLRSSRSGRMICTQEDDFDCVQKNAKNPWKW YHCGEVCSGL
152	TcIL3000_2_200.1-p1	MHSRATRQGQLRRVLRFLVLLAVFVALNVAYILVMFASRYATVEGKSD FGNGGNLTAGFEGVEMPHRPGAAVSYAAHLLLLLETYLGKGSGGLLRG SDTWTPAFPSNATPHSVLSGYYSEGLPKLNSRLERRLDGGSMMDGVHS DSFWSTPHIVRRGYGLEGSIFVALMHREVPSSRERRPVQFESRCAMTI YDMYETAQWPVAIFTGIVEVVHDAVSGKEPKGRDGEGSPRWRALPPSR CLPAAYQSHSCAQRRGFCPRDNIRLRQIRGPTKSESEKRARGMKEKGG RSQRVDGNGYNGGSKGQTSDSDGEDNYRRDFTSSAAHRYATLSLYRGE TYVLFLNDGLLLVPSWDVKTRLMLLQLPSRYPVLTQKANIIARGIVRQ AWKGSVLCNATITSSNNGKAAEDMDTYNCDPNQKRKRDKSTDTSKRAP LRSRLDHGCAAGTLDLNSGSDNGQCSRGLWEEDVVEFLFRLPSDDVET SGSYGVDDHMDEAEPVSPKTVGDHPSFRQSRQPNRIQLYWMRKLRETL RTELKKRMSEWDTTTFICGVMVKVLDELRVKNVCTEGNRHCGAGMGNT SSSEEGGGILRLRTNSVRRLSDTLHDPQYMHPSPLHRCVTNGLTPRAS TPVSKIVPASFLHNRG
153	TevSTIB805.2.1310-t26_1-p1	MRSETRRRGRRCITVPMYMVLPALVMLTFLLWNNMSREHENRMRGGHI GEGSHAVRGGLPGVENLRASPAVFSFTTKLLSVLTAFVDQETDGMPAS VAAAGGATDMFGLPPNATPAAILLEYYETQLPKFNNELEKRLDNGSIK NVTHSDTYWSPTHVARRGYGLEGSIFVGLLHHETPLVRMRRSVSLESV CAMTVHNLYESALWSVAIFTGIVEFLPDVMTAEESGGRGGHNSSRWPF PPSSPCIPAAYQSHTCAERYGFCPRDNIRLRQLRVSAKSRRHGKGSNM GGGEGNVKVSEKKENPRSRRAEDDYEHAGYRDGDASSGSDASGGPSDF TSIASQRYATLALYRGETYVMFLNAGVLLVPSWDVTARLMLLRLPSRR PILSQRANIIQRDVVHRAWEEVVVRHVSNEGHRHEGVKDHGDQQFRDD QRGKERGWTEDYFNVAHERNPSKKRSGSTLYDLEGLRLHSSDGMEDKE KGDGNGESAAEGARGFGSEDVVEFLFRLPTEEDGGEATSGAEPLNYPR NGASIPNVRTRMPNSAQLYWMKKLREPLRKKLLTSMSEQNTTSYVCGV AVKMQHSEEGCRKVCDAKSDGGSSGCGNVENGEDVSAAVSGGEGAKFK LRYESRRRLTYVLRDRRYMKPLPIHWCNEKNDAVCLGSRRQESFPSSL SQPWLSTDFLFTRAGAFFDFSHDAADHQNSHNNSSSGNAGNHVPLDPY MGFLTPDEEAVLLAGRLWTHGWDFYAPTEPIAFAAAVHAEGAGNGTSG NNKVANMSSKVRDARLRGLVRLNFVLFGQSNAARGLRSDGEAALKHVE KYGLGSRRSRESFLQHVGLRSSRSGRMICTQEDDFDCVQKNAKNPWKW YHCGEVCSGL
154	DQ04_04291000-t26_1-p1	MVAVRRGAGVLGRLRLRRGAAWSALTLVVLAVVCYMVMLPVLLNNMSI PATTTAEIRLNNERQQQPQREALSYVTQLLTLLKRFELMHNESTKAIA EAGAAAKSTIETPESMLSAYYEEDLVRLNNALEKSLDSGYAEHVVHSD AYWSPYHAVRRGYGLEGSIFVGLLHHEASYTTRRTTPPREGKCAMTLK NIYDNARWPIGVFTGVVEVVLDSAARAKTTATGGDQSGNSTWSPLPPS VCVPESYLSMDCEERYVFCPADNIRVRQLRFPLPSEGVDSTAAATPRR RTTRTPFSSVAAQRYATLTLYRGETYVLFLRDGLLLVPQWDAVTRLLL LQLPSRHSVLSQAPNTVSDEAVRAAWTGAVISSVNGLVLASTQLYRNI

SEQ ID NO.	Description	Sequence
		SGAAQPPTLRPMDKIEKWMMTFDWALDTNAVRLHTSGGAERTGSVSGT RGGDLGITEAEVVDHVFGSSSLTEAPYTSRSRLDGSHASSGGIDIRSN ANKDRTPNTRRRRDIQLYWLYRFREALQRLLILEAAKQNTTSYIAGFR PEKLDESLPSQQQQQQQKQQAMPLFFHITNVNRLSHVIQDKRYMQPSP THWCTEYGEQGCPDVMSKDRKSNTKLPFQLLSWITTDFLFARAEAFFD YTRGDESHTSIHSEGSTAKRGSDHVPLDPFIQFVTPDEEAVLLSARLW THGWDLFSPTEPIVFFSASNTEATSRATEKTHSPTTTRLRWRSVARLC HILFGARRDGNGEDAFAETEYAEALREVGRYGLGERRSREQMLRFLDL DGGATQPQQRFAAWCKDHGMR
155	TRSC58_03864-t26_1-p1	MKRSVRLFVLLTIVVLLVLLSIVMSGPAVDEMGADYMDVEDDAHELEH QTRLTHHDMVGMQRQIERSKQSVLLHAKGLLSLLQRFSDEITIDATNA RPGEVARSVTNSLKTPEAILSQYYGTELLRLNNLHEKDLDAGYAENVV HSDTYWSPSHVTRRGYGLEGSIFVGVTHSQEAASSSEVETACAATVRS LYEAARWPAAVFTGVVDVTLLTTPTPRGTTASTASSKKTETQSPEETP AWTPTPPPTSVCVPRAYLLPSCAERASFCPADNIGVRQVQVGPTSAGT VGAAGNARRRRMHPLFSSVAAQRYATLALYRGETYVMFIAAGLQLVFK WDVLTRILWLQLPSRHAVLSQTPVPISRQAVRAAWDAVVVKHVEGIIA ATKQFPNVTAEGAPRSNLSEEKLGNGVDRWLESIRWTLNLKAVQLQLA KDAAAGSGEKEPTGNEKDTGMREEDVVSYIFHHDAAVFRHTKEQAPTT GGATPMKEGLTPGAASRRDIQLYWLRQFYETLRGALMNEVVEQNTTSC LSGLQMKEPKSRQYGESVFRLHATRVKRLSHAMEDPRYMRPSPFHACG RKGASACPDLSEAKDVCHTDAMLPYLRQSWVTTDFLFTRAEAFVDLPR EGGDDYGGPTNADTVRLDPYLSFVGADEEAVLLSARLWTHGWDLFSAT EPVAFVVAQPRTEAASDVNAYTLSPTQQRLREQSVARLRHILFGKTGT AGAAPNVEAAALRDVEHYGLGERRSKEKLFYFSGLQEATQREGLVEPD TAAQHAEESICPAFFCRGSQS
156	TM35_00039174 0-t36_1-p1	MTHSSRRCCLYTSLFLRKRAVVSLLFLLILFAVVCTTLLWTQLMEDII ITTTSSSPALQKNSNDNSQQQEGKLKEQLLQLEKIQNLDLVSYVSRML SVLSSFLNEQESHHVDHKILNISYTPRKENTPESILSDYYEKELAQRN NFFERTIDSDYSENILHSDSYWDPIHTVRRGYGMEGSIFVALLHQEMS IFTRKEEEEKEEERKESESACAMTVQNMYETARWPIAIYTGIVEVILD TTTTTTTTTIPTTNENTGKEAEEEQKKKQQQQQQSKWPKQPISACIPR LYRQPTCAEGFVFCPLDNIRLRQVRVNGESNQTTTTLSSSKQRNRKHL FSSIAAQRYATLTLYRGETYVMFLRAGLLLRPHWDILTRLLWLQLPSN YAVLSQSPLHVNKAILRSAWNETIVKSVKSIILATQRMQMDRNKNNNN TNNTNTTNSDNNNNNNNNNNNNERKSGVYKWLENARWALHEDLVRLDD HPTTPRGLTEEDILRYLFTTTSSSNSNSNSDKNKKKEKEGNTSNVNGE EIREEVQLYWLNHFRNVLYPIVLSALSNHSVTPYLCGLEMRKGMESQQ QEKEEEEKEKEKEEVKENENTLLLKLHSVNVKRLSHALQDLKYMQPSS THYCEGESHPACTDVKMMTMMEDEKEKKLREKPPFSSSFQRNNNNNNN NNNNNNKSLPYLLQPWITTDFLFTRAEAFFDFSQTPMDNSPPPPNNNN NNNNNNNNKENKNNKNIDEKSNEKKTKGRSVPLDPYLHSLMRDEESVL LSARLWTHGWDLFSPNEPIVFLGPHQQQQQQEEEEEKEKREKESLSLG EKKNKIKVSEKLKRMRELSLIRLRFILFGIRESTGETEKEKKKKISLL ELETEALQDVGRYGLGIHQSREDLFRFAGIEKENERKEEKEEREEGNE SRKSMKDYLSWCSDYE
157	human O-	MASSVGNVADSTEPTKRMLSFQGLAELAHREYQAGDFEAAERHCMQLW RQEPDNTGVLLLLSSIHFQCRRLDRSAHFSTLAIKQNPLLAEAYSNLG

SEQ ID NO.	Description	Sequence
	GlcNAc enzyme OGT (Uniprot: O15294)	NVYKERGQLQEAIEHYRHALRLKPDFIDGYINLAAALVAAGDMEGAVQ AYVSALQYNPDLYCVRSDLGNLLKALGRLEEAKACYLKAIETQPNFAV AWSNLGCVFNAQGEIWLAIHHFEKAVTLDPNFLDAYINLGNVLKEARI FDRAVAAYLRALSLSPNHAVVHGNLACVYYEQGLIDLAIDTYRRAIEL QPHFPDAYCNLANALKEKGSVAEAEDCYNTALRLCPTHADSLNNLANI KREQGNIEEAVRLYRKALEVFPEFAAAHSNLASVLQQQGKLQEALMHY KEAIRISPTFADAYSNMGNTLKEMQDVQGALQCYTRAIQINPAFADAH SNLASIHKDSGNIPEAIASYRTALKLKPDFPDAYCNLAHCLQIVCDWT DYDERMKKLVSIVADQLEKNRLPSVHPHHSMLYPLSHGFRKAIAERHG NLCLDKINVLHKPPYEHPKDLKLSDGRLRVGYVSSDFGNHPTSHLMQS IPGMHNPDKFEVFCYALSPDDGTNFRVKVMAEANHFIDLSQIPCNGKA ADRIHQDGIHILVNMNGYTKGARNELFALRPAPIQAMWLGYPGTSGAL FMDYIITDQETSPAEVAEQYSEKLAYMPHTFFIGDHANMFPHLKKKAV IDFKSNGHIYDNRIVLNGIDLKAFLDSLPDVKIVKMKCPDGGDNADSS NTALNMPVIPMNTIAEAVIEMINRGQIQITINGFSISNGLATTQINNK AATGEEVPRTIIVTTRSQYGLPEDAIVYCNFNQLYKIDPSTLQMWANI LKRVPNSVLWLLRFPAVGEPNIQQYAQNMGLPQNRIIFSPVAPKEEHV RRGQLADVCLDTPLCNGHTTGMDVLWAGTPMVTMPGETLASRVAASQL TCLGCLELIAKNRQEYEDIAVKLGTDLEYLKKVRGKVWKQRISSPLFN TKQYTMELERLYLQMWEHYAAGNKPDHMIKPVEVTESA
158	human EOGT (Uniprot: Q5NDL2)	MLMLFVFGVLLHEVSLSGQNEAPPNTHSIPGEPLYNYASIRLPEEHIP FFLHNNRHIATVCRKDSLCPYKKHLEKLKYCWGYEKSCKPEFRFGYPV CSYVDMGWTDTLESAEDIFWKQADFGYARERLEEMHVLCQPKETSDSS LVCSRYLQYCRATNLYLDLRNIKRNHDRFKEDFFQSGEIGGHCKLDIR TLTSEGQRKSPLQSWFAELQSYTQLNFRPIEDAKCDIVIEKPTYFMKL DAGVNMYHHFCDFINLYITQHVNNSFSTDVYIVMWDTSSYGYGDLFSD TWNAFTDYDVIHLKTYDSKRVCFKEAVFSLLPRMRYGLFYNTPLISGC QNTGLFRAFAQHVLHRLNITQEGPKDGKIRVTILARSTEYRKILNQNE LVNALKTVSTFEVQIVDYKYRELGFLDQLRITHNTDIFIGMHGAGLTH LLFLPDWAAVFELYNCEDERCYLDLARLRGVHYITWRRQNKVFPQDKG HHPTLGEHPKFTNYSFDVEEFMYLVLQAADHVLQHPKWPFKKKHDEL
159	pLMTB6681	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCGGC CGAGCCGCATACGTCTCTCGCACGGTCTCGTTTATTTGATCATGTAGT TGAGTATTAAATTGGGAAGACAAAAACATAATAGCACGAAGAGTCGGG CACGAAAAGCCCGATCTCTCTCTCTCTCTCTCGTGCGCGCAGGGGCGT GTGGGTGCACGACGACGAGGACGGAGGGGGGAAGGGAGGCATAAACGG ATCGATCCCCCATCGCACATGCGGGTACGAGCATTATCTGCTGTGTCT GGTCCTTTATCATATCGCTACCCGCCCGCCCCCCGCCCCCCTCCCCCC CCCCCCCCCGCGGCTCCTGTCACTGTCGTTCCTGCGACTCCCCACACA CCCGCGCAACGCTCATGTCACGAAGAGAAAAGTAGAAGGCGTGGCGAT

SEQ ID NO.	Description	Sequence
		GCGTTGCGCGGCCCCCTGTCCGCTGGCATGCAGACGTCGAGCCGTGGA ACGGATGGTAGCGAGAGACAACGCGGCGATGCAGGAAAGGAGATTTAC TGCAGGACGTCTACACACGCGCGCACACCACTGCGAATGGCACCGTGC TGAGGAAAATTGGGGGGGAGGGCGCACGGGGGCGGGGCAGGAAACGGT TGGATCAGCAGCACTCTCAACTTGTGTCCGTATTGCGAAGGAGGGAGA GGAGCCTGCCCGTATTATGGGCGCTGAAACGTCGGAACCACCTATGAA TCCCACTTCTGCGTCGCGGAGGCGTACTGCTTCCGACCACCTCCGCAG CTCACGCGCGTCGAGCTCCCTCCCTTTCCCCTTCTTTCCGTTGTGTGT GTGTGTGTGTGTGTGTCTTGTCACGATGCATGGCCATCTCTCCTCCAA CCCTCCACGCCTTCCTCTCCCCCGCCCATCAAACGCGCTACGGCCACA ACCATTTCTTCAAGTATCACATCCACCACCACTCTTACCCACCTACCC TCTTCGACTCTGACACAGCCACTGACGCCCTCTCCGCCTCTCTCGCTC GCTGCACATTGACTCTCCACAGCCCCCCCTCCCTCGCACAGCCAGCCC CACCCACCCACCCACCCACCCACCGCTCTACACACCTCCACAGCAGCC ATGAAGATTTCGGTGATCCCTGAGCAGGTGGCGGAAACATTGGATGCT GAGAACCATTTCATTGTTCGTGAAGTGTTCGATGTGCACCTATCCGAC CAAGGCTTTGAACTATCTACCAGAAGTGTGAGCCCCTACCGGAAGGAT TACATCTCGGATGATGACTCTGATGAAGACTCTGCTTGCTATGGCGCA TTCATCGACCAAGAGCTTGTCGGGAAGATTGAACTCAACTCAACATGG AACGATCTAGCCTCTATCGAACACATTGTTGTGTCGCACACGCACCGA GGCAGGTACCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAG CATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTC CACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCT AATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTT TCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAAC GCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGC TCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAG CTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACG CAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTA AAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACG AGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAG GACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCT CTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCC CTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCA GTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCC CCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGT CCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTA ACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGA AGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCT GCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTT GATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCA AGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGA TCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAG GGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTT TAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAA CTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCA ATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTT TCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAA

SEQ ID NO.	Description	Sequence
		GATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAAC CTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCAC CATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTT CTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAAT CACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGA GACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCG AATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCAC CTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGA TCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCT TGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCA TCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAA ACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCAC CTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAG CATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTT GAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATC AGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAA ATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTG ACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGC GTATCACGAGGCCCTTTCGTC
160	pLMTB6683	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCCCG ACCAAGGCTTTGAACTATCTACCAGAAGTGTGAGCCCCTACCGGAAGG ATTACATCTCGGATGATGACTCTGATGAAGACTCTGCTTGCTATGGCG CATTCATCGACCAAGAGCTTGTCGGGAAGATTGAACTCAACTCAACAT GGAACGATCTAGCCTCTATCGAACACATTGTTGTGTCGCACACGCACC GAGGCAAAGGAGTCGCGCACAGTCTCATCGAATTTGCGAAAAAGTGGG CACTAAGCAGACAGCTCCTTGGCATACGATTAGAGACACAAACGAACA ATGTACCTGCCTGCAATTTGTACGCAAAATGTGGCTTTACTCTCGGCG GCATTGACCTGTTCACGTATAAAACTAGACCTCAAGTCTCGAACGAAA CAGCGATGTACTGGTACTGGTTCTCGGGAGCACAGGATGACGCCTAAC TAGCCTCGGAGATCCACTAGTTCTAGTTCTAGGGGCCGAATTCAGATC CTCGTGTGAGCGTTCGCGGAATCGGTCGCTCGTGTTTATGCCCGTCTT GGTGTTGTGCTCGCAAGGCGGTGCAGCAGGATACCGTCGCCCTCCTCT CTCCTTGCTTCTCTGTTCTTCAATTCGCGATCTCACAGAGGCCGGCTG TGCACGCCCTTCCTCACCCTCCTTTTCCCACCTCTCGGCCACCGGTCG GCTCCGTTCCGTCTGCCGTCGAGAAGGGACGGGCATGTGCAGCTCCTC CCTTTCTCTCGCGCGCGCATCTTCTCTTGCTTGTGGCACTCACGCTCA TGCGTCAAGGCGGCCCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTG CGCATCCGTAGCGCGGATGCCGTCGATGCGCAAGGCCGGCATGAAGGA GCGCGTGCCCTCAAGAGGGCACACTATCATGCCCTACGTGGGCCACGC AGCGATGAGGCCGGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		AAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATC AATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTC ATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAAT ACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACC GAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCC GACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAAT AAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGA GAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATT CATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAA AGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGC CAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATAC CTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATC ATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTC CGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAAC GCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCC ATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGC CCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGG CCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTT TCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATA CATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCAC ATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCAT GACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
161	pLMTB6948	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCAAC ACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTGTGTGCGA GCGCACACACACATGCACACGACTCACGTTGTCACACAATTGAGAGCT CTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTCT CTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTCGAG CCACCATGGTCCGGAAGAAGGGCTCCCTGATCCTGTGCGGCGCCTTCC TGTTCGTCGCCTGGAACGCCCTGCTGCTGCTGTTCCTGTGGGGCCGGC CCCCCATCGGCCGGCTGGGCGAGGGCGGCGGCGCCGAGCCCGGCGCCG GCGAGGAGTGGGGCGCCGGCAAGTCCAAGGTCGGCGGCGCCAACGGCC TGGCCGGCGAGGTCATCCGGCTGGCCGAGGAGGTCGAGTCCGAGCTGG AGACCCAGAAGAAGCTGCTGAAGCAGATCCAGTCCCACCGGGAGCTGT GGGAGCAGCGGAAGGAGCTGGAGAAGCGGGAGTCCGAGGACACCAAGG ACGAGAAGATCGACGTCGAGCCCAAGAAGCCCCGGCAGATCCCCGCCG TCCACCTGTCCCACAAGGTCGTCGAGGACGCCCAGACCGTCACCAAGA AGATGCAGACCCTGATGGTCACCCCCCCCCAGCTGGTCATGAAGGAGC AGGAGACCGACCAGAAGAACAAGCAGATGATGGAGGACCAGCTGGGCC TGACCACCCCCTCCCCCCAGATCATCATCCCCATCCTGGTCATCGCCT

SEQ ID NO.	Description	Sequence
		GCGACCGGGTCACCGTCAAGCGGTCCCTGGACCGGCTGATCCAGTATC GGCCCTCCGCCGAGCTGTATCCCATCATCGTCTCCCAGGACTGCGGCC ACGCCGACACCGCCCGGGTCATCGGCTCCTATGGCTCCCAGATCACCC ACATCTCCCAGCCCGACCTGGCCGACATCCCCGTCCGGCCCGACCACC GGAAGTTCCAGGGCTATTATAAGATCGCCCGGCACTATCGGTGGGCCC TGAACCAGGTCTTCAACGTCTTCGCCTATTCCACCGTCGTCATCGTCG AGGACGACCTGGAGGTCGCCCCCGACTTCTTCGAGTATTTCCGGGCCC TGTATCCCATCCTGCGGTCCGACCCCACCCTGTGGTGCATCTCCGCCT GGAACGACAACGGCCGGGACGGCCTGGTCGACCCCGGCAAGGCCGAGC TGCTGTATCGGACCGACTTCTTCCCCGGCCTGGGCTGGATGCTGCTGA AGGAGGTCTGGGCCGAGCTGGAGCCCAAGTGGCCCAAGGCCTTCTGGG ACGACTGGATGCGGCACCCCGAGCAGCGGAAGAACCGGTCCTGCATCC GGCCCGAAATTTCTCGGACCATCACCTTCGGCCGGAAGGGCGTCTCCC TGGGCCAGTTCTTCGACCAGTATCTGCGGTATATCAAGCTGAACACCG AGTTCGTCCCCTTCACCAAGCACGACCTGTCCTATCTGGTCCGGGAGA AGTATGACGTCTCCTTCGAGAAGGACGTCTATTCCGCCCCCCTGGTCA AGGTCGAGGAGCTGCAGCACGGCGGCTCCCTGAAGGGCTCCGGCCCCT TCCGGGTCCAGTATTCCTCCCGGGACTCCTTCAAGGTCCTGGCCCGGA ACCTGGGCGTCATGGACGACCTGAAGTCCGGCGTCCCCCGGGCCGGCT ATCGGGGCGTCGTCTCCTTCATCTCCCGGGGCCGGCGGATCTATCTGG CCCCCCCCGAGGGCTGGACCAAGTATGACGTCTCCTGGTCCTAAGGTA CCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCA TAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG GGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGG AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGAC TCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA AGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTG TAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCG GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTG CTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAG ATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT ACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTG GTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAA AAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCT GACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTC ATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAAT

SEQ ID NO.	Description	Sequence
		GAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGG TATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAAT TTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTG ACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAG ACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCA TCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAAT ACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAAC CGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCA GGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTG GTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTC GGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCT GTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCT GGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGC CCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATG TTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGG CTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTAT TGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAA ATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAA GAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACG AGGCCCTTTCGTC
162	pLMTB 7084	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCTGG AACAGCGGCGCGCTGACGAGCGGCGTGCACACGTTCCCGGCGGTGCTG CAGAGCAGCGGCCTGTACAGCCTGAGCAGCGTGGTGACGGTGCCGAGC AGCAGCCTGGGCACGCAGACGTACATCTGCAACGTGAACCACAAGCCG AGCAACACGAAGGTGGACAAGAAGGTGGAGCCGAAGAGCTGCGACAAG ACGCACACGTGCCCGCCGTGCCCGGCGCCGGAGCTGCTGGGCGGCCCG AGCGTGTTCCTGTTCCCGCCGAAGCCGAAGGACACGCTGATGATCAGC CGCACGCCGGAGGTGACGTGCGTGGTGGTGGACGTGAGCCACGAGGAC CCGGAGGTGAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCACAAC GCGAAGACGAAGCCGCGCGAGGAGCAGTACAACAGCACGTACCGCGTG GTGAGCGTGCTGACGGTGCTGCACCAGGACTGGCTGAACGGCAAGGAG TACAAGTGCAAGGTGAGCAACAAGGCGCTGCCGGCGCCGATCGAGAAG ACGATCAGCAAGGCGAAGGGCCAGCCGCGCGAGCCGCAGGTGTACACG CTGCCGCCGAGCCGCGACGAGCTGACGAAGAACCAGGTGAGCCTGACG TGCCTGGTGAAGGGCTTCTACCCGAGCGACATCGCGGTGGAGTGGGAG AGCAACGGCCAGCCGGAGAACAACTACAAGACGACGCCGCCGGTGCTG GACAGCGACGGCAGCTTCTTCCTGTACAGCAAGCTGACGGTGGACAAG AGCCGCTGGCAGCAGGGCAACGTGTTCAGCTGCAGCGTGATGCACGAG GCGCTGCACAACCACTACACGCAGAAGAGCCTGAGCCTGAGCCCGGGC AAGTAACCTCCTCCTCCTTTCTTGTTCCTTTCACGTCGCCTTCTCGGT

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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163	pLMTB 7805	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGTGAAATGGTGTATCCCATGACACGTCTTACGTCATGTTCCTCC CTCCTTCGTATGCGTACGACTCTCCTCCGCCTCCGCCTCCGCCTCCGC CTCCGCCTCCGCCTCCGCCTTCTCTGCGCCGGTTTCCTGGAGGATGGA GAGCTCTTGCTCATAGATTGAAGAAAGACCAGGCAAGCCACGGAAAAC TCCGAACAAAAGCGGACTCACGCGGCCGTCTGCATTTGACGTGCTTGC ATACATATACGCACCAACCTTGTGCACGTCTTGTTGACATCCGTAACA CTTGCCTCATTTTTTCCGTGCTGCTCGGATGCACACTCCTGGTGTGGG GCGTAGTCACTATTCGTCTCTCACCAACACACACACACACACACACAC ACACCTGTACATCTCTCTCTCTCTCCTTTTCTGTGTGCCCCGGCGGAC GTGCGTGCGTGTCTAATCACTGAAATTCTTCACATTGCATAGAACGTA GCGTCAGGACGCAGCCTCGAACGGCGATGAAGCCAGAACTCGAGAGTA TGGGATCGGCCATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCG CTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCG GCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGG TTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAGG ACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCG CAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGTTGCTAT TGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTG CCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGC TTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCG AGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATC TGGATTCGAAATTTAAATGGTACCATCCCAATGGCGCGCCGAGCTTGG TCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCAC AATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGG TGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCC CGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGG CCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTC CTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGT ATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGA TAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAA CCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCC

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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165	pLMTB 7810	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAAACCGAACTGCCCGCTGTTCTGCAGCCGGTCGCGGAGGCGATGG ATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGCGGGTTCGGCCCAT TCGGACCGCAAGGAATCGGTCAATACACTACATGGCGTGATTTCATAT GCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACG ACACCGTCAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTT GGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCG GCTCCAACAATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTG ACTGGAGCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACA TCTTCTTCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGCT ACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCGGG CGTATATGCTCCGCATTGGTCTTGACCAACTCTATCAGAGCTTGGTTG ACGGCAATTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCAA TCGTCCGATCCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGCA GAAGCGCGGCCGTCTGGACCGATGGCTGTGTAGAAGTACTCGCCGATA GTGGAAACCGACGCCCCAGCACTCGTCCGAGGGCAAAGGAATAGCCTC GGAGATCCATGGAGGGAGAATGATGATGTGACCGAGGTGGCGCGCTCG CACGTGTCCTCCTCCTCCCCCTCCTCCTCCTCTTCTTCTTCCTCCTCA TGGCCGCCCTCTGCGGTGGTCCTCTCTCACCTTTTCATGTGTTCCTGT

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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167	pLMTB 7812	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT

SEQ ID NO.	Description	Sequence
		GCAGGCTCTCTCGTGCTGGACGCCTCTGCACCACTGCGTCGCACACGA ATCGCCGGTAGTGATGGTGCTTTTTCGTACACCGATGCGCGCGAGCAC CTCCGCTCTTGCCGCGTCCTTCTGAGCTTTGCTGCTACGCGTCGCCGT GGCGTCCTTCCATCGTGTTGCTTTTCTTTCAACGTTCCTTCTGCAGCG ATGCGACTGGCATCCCCTTCGTATTAGCACCAGCACCAACAACACGGC AGCTGCGCGCACTTTTGTCGCACGTGACTGCGCGACCGCGATATCTGC TTTCCATTCTGCAGTTCTCTACACACTTCTTTGTGTCTTTCCTTCCCC CCTTTCGAGCGCACACACGCGGGCGCGCTCAGAATCCGCCTCGCCTGC TGTCCTCCTGTGGGCGCGCGCGTAATCGGGCACGCGTCAGGCAGCGCC ACAGAGGCCTGCCCAGACAGCGAACGGGTCCATCGGACACCCTCGGTC CCCGGCATTCGCAGGACTGTGGGTCCTCGAGAGTATGGGATCGGCCAT TGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAG GCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGC CGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAA GACCGACCTGTCCGGTGCCCTGAATGAACTGCAGGACGAGGCAGCGCG GCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGA CGTTGTCACTGAAGCGGGAAGGGACTGGTTGCTATTGGGCGAAGTGCC GGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATC CATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTAC CTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAC TCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGATTCGAAATT TAAATGGTACCATCCCAATGGCGCGCCGAGCTTGGTCGAGCATGGTCA TAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAAC ATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTG AGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCG GGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGG AGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGAC TCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCA AAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAG AACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCC GCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCAC AAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAA AGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTT CCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGA AGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTG TAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAG CCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCG GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATT AGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGG CCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTG CTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGC AAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAG ATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCT ACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTG GTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAA AAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCT GACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTC ATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAAT

SEQ ID NO.	Description	Sequence
		GAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGG TATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAAT TTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTG ACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAG ACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCA TCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAAT ACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAAC CGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCA GGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTG GTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTC GGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCT GTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCT GGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGC CCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATG TTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGG CTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTAT TGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAA ATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAA GAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACG AGGCCCTTTCGTC
168	pLMTB 7813	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGCTCTCTCGTGCTGGACGCCTCTGCACCACTGCGTCGCACACGA ATCGCCGGTAGTGATGGTGCTTTTTCGTACACCGATGCGCGCGAGCAC CTCCGCTCTTGCCGCGTCCTTCTGAGCTTTGCTGCTACGCGTCGCCGT GGCGTCCTTCCATCGTGTTGCTTTTCTTTCAACGTTCCTTCTGCAGCG ATGCGACTGGCATCCCCTTCGTATTAGCACCAGCACCAACAACACGGC AGCTGCGCGCACTTTTGTCGCACGTGACTGCGCGACCGCGATATCTGC TTTCCATTCTGCAGTTCTCTACACACTTCTTTGTGTCTTTCCTTCCCC CCTTTCGAGCGCACACACGCGGGCGCGCTCAGAATCCGCCTCGCCTGC TGTCCTCCTGTGGGCGCGCGCGTAATCGGGCACGCGTCAGGCAGCGCC ACAGAGGCCTGCCCAGACAGCGAACGGGTCCATCGGACACCCTCGGTC CCCGGCATTCGCAGGACTGTGGGTCCTCGAGAGTATGAAAAAGCCTGA ACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCGAAAAGTTCGACAG CGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAGAATCTCGTGCTTT CAGCTTCGATGTAGGAGGGCGTGGATATGTCCTGCGGGTAAATAGCTG CGCCGATGGTTTCTACAAAGATCGTTATGTTTATCGGCACTTTGCATC GGCCGCGCTCCCGATTCCGGAAGTGCTTGACATTGGGGAATTCAGCGA GAGCCTGACCTATTGCATCTCCCGCCGTGCACAGGGTGTCACGTTGCA AGACCTGCCTGAAACCGAACTGCCCGCTGTTCTGCAGCCGGTCGCGGA GGCGATGGATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGCGGGTT

SEQ ID NO.	Description	Sequence
		CGGCCCATTCGGACCGCAAGGAATCGGTCAATACACTACATGGCGTGA TTTCATATGCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACTGT GATGGACGACACCGTCAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCT GATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGTTCGA AATTTAAATGGTACCATCCCAATGGCGCGCCGAGCTTGGTCGAGCATG GTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACA CAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATG AGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCA GTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGC GGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCAC TGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCA CTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGG AAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAA GGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCA TCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACT ATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCC TGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTC GGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTC GGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGT TCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAA CCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAG GATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTG GTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGC TCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATC CGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCA GCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTT TTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGAT TTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAA TTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTG GTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTT ATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTG TAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATC CTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTAT TAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATG AGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTT CCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACT CGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACG AAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATG CAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGA ATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGC AGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGAT GGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTC ATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAA CTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGA TTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATC CATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAAT ATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGG TTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAA

SEQ ID NO.	Description	Sequence
		ACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGT CTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTAT CACGAGGCCCTTTCGTC
169	pLMTB8223	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATCCACACAAT ACCACCGTGCACACGCACAGCTTCTCTCTCCCCCCCCCACCTATACAC ACATACTCACACAGAGAGAGAGACAGAGACAGAGAGGGGAGGAGAGGG GCACAGAGAGCGACGCACAGGGTGACGAGGAAAGCAGTATCGAAACAG TGACCAGCAGGAACGTTCCTGCCGGTGTCCACTTGTGCCCGTGCTCCA CTACGGGCCGGTCAACCAACGGACACCCGCACCGCCCCCCACGCCAAG AGTCCAACCAGCCATCACCTCGAGAGCCTGCTGCCGCGCCCGCACGCC CCACGCCCCAGTGGCCGGCATCCCCCCCCCCCCACACACACACGGGAAT CCCCTGAGCGACACGCACGCCACACAGGAACACATGAAAAGGTGAGAG AGGACCACCGCAGAGGGCGGCCATGGGGAGGAAGAAGAAGAGGAGGAG GAGGGGGAGGAGGAGGACACGTGCGAGCGCGCCACCTCGGTCACATCA TCATTCTCCCTGCGTGGGGATGGATCGCGAGGGACGCGGGGTTTGAGG GCCGTGGGTGGTGTGGAGAGTGTGGTTGATTATTGTATGGTGGTGAGG GTGGAAGGTGTGGCGGGGATGGTGGTGCGGTGGTGTCGGAAGGGGTGT GTGAGAGGGCGCGGGTCCTTGAGGGAGGGTGGGTGTGTTGTTGTTTTG CGGGTGTTATCCGGGGCTTGGGTGTTGGTGTGATTGGTGACTATGTAG GGGTGAAGGGTGAGTGGAGGGGGTCGCCAGAGGCGTTCCGTTCTACGA AGCTTCATTCCTATGTCCGACTCCGAAGCATGCCTGCAGTTCTGCTGG CTATGTGGGCGTGTCTGGGCAACGACTGAATTGAGAAGGGGAGTCGAA ACGGTGCGTGGATGCTGTGTTTGTGCTACACACAAGCAAAGGCAACAA CACAAGCGCATCGAGCCAGACGAACCAACCCAATATTCACACAACTGT ACGTGGCCGCGCGCTGTATCTCCGATGGGATGATGCGTGTGCGTGTGC CACCACCACGTACTAGTTTCCAGCCTTACTGCTTGTATACCTTGTCTT TTGCGTTGTGCTTGCGCGTGCTGTGTACCTCTGCTCGTGCGTTCCGTA TCCCGGGACCTGCGGGCGGTGGGTGCCACACAACCCGTCACATTCAAC ATCACTCATACATCTCACCGATGTGTGCGTGTGCTTGCTGTGTGCGTG TGTTGTGTGGCGTCAAACCTGTTTGAAAACACACCCCTAGCACTATTC GACCGCGAAAGCGCCCCCCCCAAAGGGGCCGGTGTGCAATGCGAGCTAC ATGTATGTGTAGAGAGCGCTGCGCCGAACTAGTCGTGCGTGCTGAACA TGTTTTGTGTGTGCTGCCGTGTCTACACGTTTGCAGCGGAAACTCGGT TGAACCAGAAACAGAACTTGATTGTTGCTGCATTTCGAGGAATTTCAG CCAAACAAGAGGTCAACAACCAAGCCGCGTGTACACATATACACACAC CGCGTGTATGTATATATGCGTTTGTTTTGTTACCACAAATACTGAGTT GTCTGATGTGAGCTTCTGCTACAGACGCAATTCAGGAAATACAACAAA ATACAACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTG TGTGCGAGCGCACACACACATGCACACGACTCACGTTGTCACACAATT GAGAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCA

SEQ ID NO.	Description	Sequence
		GAGCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGA GCTCGAGCCACCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCG AGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAAT TCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGC CTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGC TTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCA ACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTC GCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATC AGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAA CGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCG TAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGA CGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGAC AGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCG CTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCT CCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCT CAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACC CCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGA GTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGG TAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTT GAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTAT CTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTC TTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTG CAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTT GATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTA AGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCT TTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTA AACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTG CAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCG TTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGC AAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACA ACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATC ACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCAT TTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAA ATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGC GAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAAT CGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTC ACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGG GATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATG CTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGAC CATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAG AAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGC ACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATC AGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCG TTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTA TCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAA AAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACC TGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAG GCGTATCACGAGGCCCTTTCGTC

SEQ ID NO.	Description	Sequence
170	pLMTB8234	ATGCGGTTCCGGATTTACAAGCGCAAAGTGGTCATCTTGACCCTCGTC GTGATTATATGCGGTTTTGCAGTGTGGAACAGTGGCAAACCGAAGAAG GCCAGCACGGTGTTTCCGAAAGAGGTGGAGACAGTGAAGCGCAGTAGT GTGGGCAGCCAAATCCAGGCGACCATTCCTGTCACGCGGAAGCCGATC AACGAGTCGATCCCAGAGAAGCAGCAGCAGCAACAGCCTGTGGCAAAG TCTGAAGCAGACAACACGACACTTGTCTACCGGGGCATCGTGTTCCAG TTGAACTTTGACCAGAACCTCAAAAACGAGGAGAAGTTTCGAGCGGTT CGCCAGAAGGACGACCTGGTTATCGTCGTCCAGGTGCACAACCGCCCG GAGTATCTGCGTCTTCTGGTGGATAGCTTGCGAAAGAGCAAGGGTATT GAGAACATACTCCTTATTTTCAGCCACGACTTCTGGTCGCCTGAGATC AATCAAATCGTAGCTTCGGTAGATTTCTGCCTCGTGCTGCAAATCTTC TTTCCATTCTCCATCCAGTTGTATCCCCAAGAGTTTCCCGGCAACGAC CCCCGAGACTGCCCCCGCGACATCCCTAAAAAGGAGGCACTGACACTT GGCTGCATCAACGCAGAATACCCGGATTCATTTGGCCACTACCGCGAG GCCAAATTTAGTCAGACGAAGCACCATTGGTGGTGGAAGCTGCATTTT GTGTGGGACCGGGTGCGGGTGCTGAAGGACCATAAGGGGCTGGTGCTG CTGATCGAGGAGGACCACTACCTCGCTCCCGATTTCTACCACCTTCTG AAGCTGATGGCAAGTCTCAAGAAGGAGCAGTGCCCTGACTGTGATATA CTCTCTCTGGGGTCGTATGGCCACATCGGCTACTCATCAAAGGCAAAT AAGGTTGAGGTCAAGGCCTGGAAGTCCACGGAGCACAACATGGGCATG GCCCTCAACCGCGATGCCTACCAGAAACTCCTCCGCTGCACGGACGCG TTTTGCACCTATGATGACTATAACTGGGACTGGAGCCTGCAGCATCTG ACAGTCACGTGTCTGCCCGCGTTTCTCAAGGTGATGGTTTCGGAGGCA CCACGGATATTTCACGCTGGCGACTGCGGGATGCACCACAAGAAGTCT GCCTGCATGCCGAGCGGCCAGAAGACAAAGATTGAGAACGTGCTCCAG AATAGCGGTAATCAGCTCTTCCCTAAGCAGCTCTTGATCACGAAGCGA CTGCCCGCGTCGGGGGCGAAGGGCGTAGCCCCCCATGTGAAGAACGGC GGTTGGGGCGACATCCGGGACCACGAACTGTGCAAGTCTTACCTGCGC CTTCAGTAGATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGC ATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTA ATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTT CCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCT CACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGC AGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAA AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG ACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCC TTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAG TTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAA GTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG CGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG

SEQ ID NO.	Description	Sequence
		ATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAA GCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGG GATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAAC TTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAA TTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTT CTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAG ATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACC TATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACC ATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTC TTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATC ACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAG ACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGA ATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACC TGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGAT CGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTT GATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCAT CTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAA CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACC TGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGC ATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTG AATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCA GGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAA TAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGA CGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCG TATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAA CCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGC GGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGG CGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACT GAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAG AAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTG GGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAA AGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTC CCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGACGCGTATTGG GATATTTAAAT
171	pLMTB 8235	ATGCTGAAGAAGCAGTCCGCCGGGTTGGTGCTGTGGGGCGCAATAATC TTTGTTGGCTGGAACGCGCTCCTTCTGCTTTTTTTCTGGACCCGCCCT GCCCCCGGACGCCTCCCTTCGGACAGCGCTCTCGGGGACGACCCCGCA AGCCTTACGCGTGAAGTCATTCACCTGGCAGAGGATGCTGAGGCGGAG CTTGAGCGCCAACGTGGCTTGCTTCAACAGATTAAGGAACACTACAGC CTGTGGCGCCAGCGCTGGCGGGTGCCAACAGTCGCTCCACCGGCCTGG CCACGCGTACCAGGAACACCGAGCCCCGCTGTAATTCCTATATTGGTG ATTGCGTGCGATCGATCTACAGTCCGCCGCTGCCTTGATAAGTTGCTC CACTATCGTCCATCCGCCGAGCACTTCCCCATCATCGTCTCGCAAGAC TGCGGTCATGAGGAGACGGCCCAGGTCATTGCAAGCTACGGCACTGCG GTTACGCATATCCGTCAACCCGACCTCTCCAATATCGCTGTCCAACCC GACCACCGAAAGTTTCAGGGATACTACAAGATTGCACGACATTACCGG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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172	pLMTB 8236	ATGTTGAAGAAGCAGTCAGCGGGGCTTGTGCTCTGGGGAGCGATCCTC TTCGTGGCCTGGAACGCTCTTCTGCTCCTGTTTTTCTGGACCCGTCCG GCCCCGGGCCGCCCGCCGTCGGTCTCCGCACTGGACGGCGATCCTGCT TCTCTCACCCGGGAGGTAATTCGCTTGGCTCAGGATGCGGAGGTGGAA TTGGAGCGTCAGCGGGGCCTCCTCCAGCAGATTGGCGACGCACTTAGC TCGCAGCGGGGGCGTGTGCCAACGGCGGCCCCTCCAGCGCAGCCCCGC GTGCCCGTGACCCCGGCACCGGCAGTCATCCCGATCCTCGTGATTGCG TGCGACCGTAGCACGGTCCGCCGCTGTTTGGATAAGCTTTTGCACTAT CGGCCGTCAGCGGAGCTTTTCCCAATCATCGTGTCCCAGGATTGCGGA CATGAGGAAACAGCGCAAGCTATCGCGTCTTACGGCAGCGCAGTGACG CATATTCGACAGCCGGATCTGAGTTCTATCGCCGTCCCTCCTGATCAT CGAAAGTTCCAGGGATACTATAAGATTGCCCGTCATTATCGATGGGCC CTTGGCCAGGTATTCCGCCAGTTCCGTTTCCCTGCCGCCGTCGTAGTT GAAGACGACCTCGAGGTGGCGCCGGATTTCTTCGAGTACTTTCGTGCC ACGTATCCTCTGCTTAAGGCAGACCCGTCGCTGTGGTGCGTGTCTGCG TGGAATGACAATGGGAAGGAGCAGATGGTGGATGCCTCACGTCCGGAG TTGCTTTATCGAACCGACTTTTTCCCCGGCCTCGGTTGGTTGCTTCTC GCCGAACTGTGGGCGGAGCTTGAACCTAAATGGCCGAAGGCGTTCTGG GACGACTGGATGCGCCGTCCGGAGCAGCGTCAGGGTCGCGCCTGCATC CGGCCCGAGATCTCGCGTACAATGACCTTCGGGCGAAAAGGGGTATCC CATGGCCAGTTTTTTGATCAGCATCTCAAGTTCATTAAGCTGAACCAA CAATTTGTGCATTTTACGCAACTCGACCTGAGCTATCTGCAGCGCGAG GCCTACGATCGCGACTTTCTGGCACGGGTGTACGGTGCCCCTCAGCTG CAGGTGGAGAAGGTCCGCACGAATGACCGCAAGGAGCTCGGTGAGGTG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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173	pLMTB8281	GGTAGACTCGTGCCGCGCGCTGATGATGTAGGTGCACGCGTGCGTGTG CTGCAGCGGAGCCGCCGCCACCGCGACTGTGTGTGTGTGCGCGCGTGA CGACCGGCTCGAGGAAGGAGGAGCGCGCGTGTGCGTGCGATGCGCCTC CTCTTTTTTTTTCGCCCTCGTCGGTTTTTTTTTTTCTGAGAGGACGGC GGCGGCGGATGGCGGGGCGGCGGCGCTGACGGAGCGGCCACGCTCTGC ACCTCCCCGCCCTCCGCCGTCTCTCCGTTCGCCGTCCTCTCCTTCCTC GTGCGTGCGTCTGCCGCGCATGCACACGCGCGCGCGTTGCCGTAGCGC TGTGTATCTGTGGAGGAGGGCCTTGTCTCTCCCTCCCCGTCGCTGAGA GATGAAGGGGCAAAAAGAGAGAGCAGTGCGCATGTGTGCCTCCGCTCC CTGGAGCTCCCCACGAGCCCCCTGCGCCACGCACCTGCGAACCTGCAC AGCGGCCCACCTGCCCGCACACGTGAGCAGAAATGGGTGTGTGGAGCG GGTGATGTCGGCGCGCACACGCGCGCGCGCTGACCACTCCGACGTGAA AACACGGAAGAGCGAGGCTGGCAAGGCAGGGCAGGAACCTGATCACGT GCGCGCGCACAAACGGAATGAGCAGCTCCTGAAGAGGAGATGGGGCTC ATGCACGCAGACACGCACGTGCACACTCCTCCGTCTTCACGGAGCGCG GCCCTGCTGCTGCTGCCATGTGCCGGACGTCTGCCACGCGTCTCTTCC CCACACCTTGCTCTTCCCCCCCCCCCTTCCCTCCCGGCGAACACAAAA CACGCGCACGCCCACCGAAACAACAACGCGCAGCTCTTCGCTCTCGTT CTTCGAACAAACACCTTTAAACCGCCTTCCAACCCCTCTTTCTTCTTT TTCAGCCATGGCCAAGCCTTTGTCTCAAGAAGAATCCACCCTCATTGA AAGAGCAACGGCTACAATCAACAGCATCCCCATCTCTGAAGACTACAG CGTCGCCAGCGCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGT CAATGTATATCATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCT GGGCACTGCTGCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGC GATCGGAAATGAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCG ACAGGTGCTTCTCGATCTGATTTAAATATCCCAATGGCGCGCCGAGCT TGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGC TCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCT GGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCAC TGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAA TCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCG CTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAG CGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAG GGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA GGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCC CCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCC

SEQ ID NO.	Description	Sequence
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174	pLMTB 8297	TCAGCGTTCCGTAGCGCGCTGCACATCCGGTACTGCGTTCCAGCGCAT CACGCGACGCACAGCAACACAAATTTTCGTTTTGTTTCTCTTCCATTC GAAAAAAAAAAGATAACACCCACCCCACTTAACCTCCATAACAAGAGA GCGTGAGAGGAGAGTCTGCTCTTGGCCTTCACACCGCAAATGCAGCAA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		TAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATC CTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTAT TAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATG AGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTT CCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACT CGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACG AAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATG CAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGA ATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGC AGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGAT GGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTC ATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAA CTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGA TTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATC CATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAAT ATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGG TTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAA ACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGT CTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTAT CACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCT CTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGA TGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGG GTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAG AGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAA ATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGA AGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGG GGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCA GTCACGACGTTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGAT ATTTAAAT
175	pLMTB8310	GCAGCGGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCAAGG TCCTTGCCCGCAACCTCGGGGTGATGGATGACCTGAAGTCAGGCGTGC CACGCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCCGGC GCATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATACGACGTGAGCT GGAGCTAAATTGCACGGCTCTTATTTGTCCTTTGAAGTATATATATAT ATATATATATTCTGTTTTCGACTTCACTGAGAAGCGGAGAAATATCAT TAAAAAATTTCAGTGGGCTTGAATGTCGCTGACTAAATGTGATGCACA TCTCGAAAGAGATGCGTAGGAGATCGAGTGGCTGACAGTTTTTGTGTT CAACCACTTCCCCTCCGTTACAAATGTGCGGATAACTCCGTATTTTCC GGATGTGGCACAATGAAAACGATATGTGGATATAGAGCTGTTTTCCTT GCCTGTGCTCGTTATGTTTGTTTTCTTGTCTCTCTTCTGTCTTCCTCT CGAGATTACTGTGAGGAGGAAAGCTATCATCTGTGATCTTACATACCT AGCCTCTTTTTCGCGATTACAAAGGTACTGCAGGCTCAGCGCACATAGA TTTACTCTCTGAAGGGACTGTGCTCAGTCCATTTTTAGACTAACTGAG GAGCACTGACGACAACAAGGATACATAAACATGCGGTTCCGGATTTAC AAGCGCAAAGTGGTCATCTTGACCCTCGTCGTGATTATATGCGGTTTT GCAGTGTGGAACAGTGGCAAACCGAAGAAGGCCAGCACGGTGTTTCCG AAAGAGGTGGAGACAGTGAAGCGCAGTAGTGTGGGCAGCCAAATCCAG GCGACCATTCCTGTCACGCGGAAGCCGATCAACGAGTCATTTAAATAT

SEQ ID NO.	Description	Sequence
		CCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCT GTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGA AGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACA TTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCG TGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTG CGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCG GTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATA CGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCA AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCG TTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGC TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCG TTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCG CTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTT TCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGC TCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGC GCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGAC TTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGG TATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGC TACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACC GCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGA AAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGAC GCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTA TCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTT AAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAA AACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTA TCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAAC TCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCG ATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCA AAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCC GGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACA GGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCG TTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTG TTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAAC ACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCT AATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCAT GCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATA AATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTG GCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGC TTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCG CGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAAT CGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTC CTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGC GGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCG CGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATT ATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGT CTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTC CCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAA

SEQ ID NO.	Description	Sequence
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176	pLMTB8311	CTGCATGCCGAGCGGCCAGAAGACAAAGATTGAGAACGTGCTCCAGAA TAGCGGTAATCAGCTCTTCCCTAAGCAGCTCTTGATCACGAAGCGACT GCCCGCGTCGGGGGCGAAGGGCGTAGCCCCCCATGTGAAGAACGGCGG TTGGGGCGACATCCGGGACCACGAACTGTGCAAGTCTTACCTGCGCCT TCAGTAGGTCCTCCGGCCTGACAGCGCGCGCCGCTGTATGTGCGCG TGTGCGCGGCTTCCCACTGGGGCCAGCGATGAGGCGCATCATACCTCC ATAGAGACCCTATCTTTTGTTTTCTGGGCTTCCCAGATGACCACTTGA TTCCTTCCTTCCTTTGATTTGTTTCTCTCCTCCCCTCCGCAGAGGGTA CGAGTCAGGGTAGGCTCGGAGAAAGCTTGCCGCATCCACGATGAGCCA CGGCTGTCTCTCTCTCTCTCTTGACCGGGACAGGCTGTTGCCCAGTCA CGCGTATCGGCGTGCACACCCGCTCTTGCGCCCTGCCCCACTATTCGT CGAATGATGCGCTACGCGCATGACAGGCGCTGCTGCAGCGCTGCTCCC TGCGGTTGCTGAGTGCGTACATGCCGTTGCTACTGATGTGTTTGCACT GCATCTCACCTCGCTCTCTTTGCGCATGCGCTTGCCCTTCCTCCCTCC TCGCGACCGTGTCGGTCCTCTCGCGCCGCTGTGGCGCAGCTCGCCGCC TTCCACTCCCCCAAACACACACGCTCATACGCTCATATAGCACTCGTG CGCACCGACACACCCACACCCCCTCCTCTCTCTCTTCTCCCCAACCTA CCCATCGCAGCCATGCTGAAGAAGCAGTCCGCCGGGTTGGTGCTGTGG GGCGCAATAATCTTTGTTGGCTGGAACGCGCTCCTTCTGCTTTTTTTC TGGACCCGCCCTGCCCCCGGACGCCTCCCTTCGGACAGCGCTCTCGGG GACGACCCCGCAAGCCTTACGCGTGAAGTCATTCACCTGGCAGAGGAT GCTGAGGCGGAGCTTGAGCGATTTAAATATCCCAATGGCGCGCCGAGC TTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCG CTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCC TGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCA CTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGA ATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCC GCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGA GCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCA GGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCC AGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGC CCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGA AACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCC CTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCC GCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGT AGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTG CACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTAT CGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCA GCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA GAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTT

SEQ ID NO.	Description	Sequence
		GGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTT TTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAA GATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAAC TCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACC TAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATA TATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAA TGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGA AAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCAT AGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACA TCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGT GAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGT TTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCG TCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGC GCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAA ACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACA ATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTT TTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGG ATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTT AGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCA TGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAG ATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCA TATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGAC GTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGA AGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGT ATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAA GTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTAT AAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGAT GACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCT TGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCA GCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAG CAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGA TGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTG CGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGC CAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACG CCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTG ACGCGTATTGGGATATTTAAAT
177	pLMTB 8313	ACAAGAAGACGTGCCGCCCTTCCACTCAGTCAGCCCAGATCGAAAGCC TGCTCAATAACAACAAACAGTACCTCTTCCCAGAAACCCTCGTGATCG GCGAGAAGTTCCCTATGGCGGCGATCTCCCCGCCCCGTAAGAACGGGG GGTGGGGCGACATACGTGATCATGAGCTCTGTAAGTCGTATCGCCGCC TCCAATAGAGTCGTAGGCCGATGCTCATATCTTCCCCTTTTTTCACGG TGCCGTTCCTTTTCTTCTTTCATTTCTTCCCTTCCGAGACAACAAATA AACGCAACACATAGAAGTATAGACAGGAACTGCGCCAAGCTGTGTATT GCCCTTCTCCCCCCTCCCACAACGACACAGTGTGTGCGCTGTTCATGG ACGCTTCATGTGAGGAGGAACGCGACGAGAGACGGACAGGGATGGAGA GCCGCGCTGAACACGCAAAGCGCCCGCCCACAGGGACACAAACAGAGG CACAGATGGCCCGCTACTGGCTTCCTTTTCGCCGCCAAGAGGGCGCTG TGCATGCGCACGTGTGGGGTGGCGGTGGCCCAATAGCACAAGCGTGCC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		AATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCG CAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGA TGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCT CATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACA ACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTG ATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCAT CCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAA TATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGG GTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATA AACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACG TCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTA TCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACC TCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGG ATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCG GGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGA GAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAA AATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGG AAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAG GGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCC AGTCACGACGTTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGA TATTTAAAT
178	pLMTB8314	AGCTCGGTGAGGTGCGGGTTCAGTACACCGGTCGCGACAGTTTTAAGG CATTCGCGAAGGCACTGGGGGTGATGGACGACCTGAAGTCCGGCGTGC CCCGCGCGGGTTACCGCGGAATCGTGACGTTCCAGTTCCGCGGCCGCC GAGTGCACCTGGCGCCGCCACTTACGTGGGAAGGCTACGACCCTTCAT GGAACTAGGGTCCTTGTGACCGCGCGTTTGGCGGACTGCTCAACAGAG CGGGCTAACGCTGACGAAGATATGCTGGTTTCCCTGTGTTTGTGATTT GCCATCCTTTCGTGTCAAAAAGAAACAACAACAACAGCAACCCGTTTA GGCCAAGAAGCGGGCGCTCGGACTCTTTCCCTGCCTGCCCCATCCCCA TGAAGCACGCCGGCTGTCGCACTGGGCACCTCATGACCCTGTTGATAG CGCTGGAGGCCTTCATTGCGTGCTGGTTGTGGGGGGGGGTGGAAGGGG GAGAGGCGTGTTGTATTCATGTGAGGTGGTGGTGGCATTGCGCAGCGG TGGGAAAAGCAGGGTCTTTTCCGTACTCCGTGACAGAGCTGCCGTGCT CATCTTTTCCCGGTTCACTGCTTGCACTGTTGGCTGCCTCGCCTTCTC CCCTCCCCCTGCCCCCACGAAACGCGGTTACCGCGTCTCCTTCGTGGG AGAAGTGGAGTGGCACAGTTAAGGCGACTACAAGGAGTTCCCCCTACC CTGGAGGGAGACTTGCGGGCGCGGGACGCCTTGTCTACGTGAGCGTCT CTTCCCAAGTAGACGACTCCCTCGACTTTGTCCCCTCCGTCGCATTCC GCCCCTCTCCGCCCTCCTTTCGTGTACGTCTCTGCATTGTACACTTCC TTTCGCCTGCTTTCCCACGCTCGCGCGCAACAACGTGGACGCACCACA TCGCTCGCTGGAGAAGAGAGAAAAGTGGTGAGTACGTGTTCCGCTCTT TCCCTTCTCCCCTCCGCTCGCGTCGCACCTCTCCGCAGCTTTACCGCT CTCTTCCCTTCCATCATCCGCGTCGTGCACCACTTCCCTCATTTTCCG TGCGGCAGTAGAAAATGCGGTTCCGCATTTATAAGCGCAAGGTCTTGA TCCTGACGCTGGTCGTCGCCGCATGCGGATTTGTGCTGTGGAGCTCGA ACGGTCGCCAGCGCAAGAACGAAGCGCTCGCCCCGCCGCTGCTTGACG CGGAGCCTGCACGAGGCGCGGGTGGCCGTGGCGGCGACCACCCGAGCG TGGCGGTGGGTATCCGCCGCGTATTTAAATATCCCAATGGCGCGCCGA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		CAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAG AGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACA GATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGC TGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTAC GCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAA CGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAAT TGACGCGTATTGGGATATTTAAAT
179	pLMTB8389	GGCGTGTGCGCACCGGCGTGTGCCAACGCCCAGGTACTGTGCGCACGT TCGTATCTCCATACGCTAGCTGACCGAGACGCATGCCCTCCGCCACCC TCAGTGGCGCGCACCTTCTCTCGTTTGAGCTCTTTATGCTCTCGTGAA TGGCACACAACATCCCGTGACTATCACGATGATCCTTCTCAAGCCACA CCGCTTGCCTTTTCTACAGCTCTGCGTTCTCTGGCCCATCCTCCTCTT GTTTGCTTTCCCTCTTTGCACATCCGTGTGCGCGTCCTTGTTCTTCTC TTCTGCGCACACTATTCTGCGCCCGCGACCCGCGCTTCGACTGCTGTC GGGTCATGCCTTGTGCTGCGCGTTCAGCTCTTCATTGCCCCTCGGCCT TGTACATAGCGGCTCTCCGTCATCGACGTTTTCCTCTCTCTTCAGCTC TATACACTCCCTCCCTTGTCAACACACTACACTGTGTCTCCCCCTTTC ATCTCTCCTCCCCTGTCACAATGGTCCGCAAGAAGGGATCTCTGATCC TGTGTGGGGCGTTTCTGTTCGTGGCCTGGAACGCGCTCTTGCTCCTTT TTTTGTGGGGCCGCCCGCCCATTGGTCGACTCGGCGAGGGTGGGGGGG CGGAGCCGGGCGCGGGCGAGGAGTGGGGTGCGGGGAAGAGCAAAGTGG GTGGCGCTAACGGCCTGGCGGGTGAGGTTATCCGCCTGGCGGAGGAGG TCGAGAGTGAGCTGGAGACGCAGAAGAAGCTTCTGAAACAGATACAGT CGCACCGCGAGCTTTGGGAACAGCGTAAGGAACTGGAGAAGCGTGAAA GCGAGGATACCAAGGACGAGAAGATTGACGTTGAGCCTAAGAAGCCCC GCCAGATCCCGGCCGTGCACCTGTCCCACAAGGTGGTGGAAGACGCCC AGACAGTAACCAAGAAAATGCAAACGCTGATGGTGACACCGCCTCAGC TGGTGATGAAGGAGCAGGAGACAGATCAGAAGAATAAGCAGATGATGG AGGACCAGCTGGGGCTCACCACGCCATCTCCGCAAATCATCATCCCGA TTCTCGTGATCGCGTGCGATCGCGTGACCGTGAAGCGGTCCCTCGACC GTCTGATCCAGTACCGGCCAAGCGCAGAGTTGTACCCAATTATCGTCA GCCAGGATTGTGGCCACGCTGACACAGCCCGCGTGATCGGGTCCTATG GCAGCCAGATCACGCACATAAGCCAGCCTGACCTTGCAGATATACCGG TGCGGCCAGATCATCGCAAGTTTCAGGGGTACTACAAGATCGCCCGCC ATTACCGTTGGGCGCTCAACCAGGTGTTCAACGTGTTTGCCTACTCAA CGGTGGTGATAGTCGAGGACGACCTGGAGGTGGCGCCTGACTTCTTCG AGTACTTTCGAGCTCTCTATCCGATCTTGCGCTCAGATCCTACCTTGT GGTGCATTTCGGCTTGGAACGATAACGGGCGTGATGGTCTCGTGGATC CCGGGAAGGCCGAGCTCCTCTACCGCACGGACTTCTTTCCTGGACTGG GTTGGATGTTGCTTAAGGAGGTGTGGGCGGAACTCGAACCCAAGTGGC CAAAGGCGTTCTGGGACGACTGGATGCGACACCCGGAGCAGCGTAAAA ATCGCTCTTGCATCCGACCGGAAATTAGTCGGACGATCACATTCGGTC GTAAAGGTGTGTCCTTGGGGCAGTTCTTCGACCAGTATCTCCGTTACA TTAAGCTCAACACTGAATTCGTCCCTTTCACGAAGCACGACCTCAGCT ATCTTGTGCGAGAGAAGTACGATGTTAGCTTTGAAAAAGATGTATACT CGGCTCCCCTCGTAAAGGTAGAGGAGCTGCAGCACGGCGGCAGCCTTA AGGGCAGCGGCCCCTTCCGAGTACAGTACTCGAGCCGAGACAGTTTCA AGGTCCTTGCCCGCAACCTCGGGGTGATGGATGACCTGAAGTCAGGCG

SEQ ID NO.	Description	Sequence
		TGCCACGCGCCGGTTACCGCGGCGTGGTCTCGTTCATATCTCGCGGCC GGCGCATCTACCTCGCGCCCCCTGAGGGTTGGACGAAATACGACGTGA GCTGGAGCTAAATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGA GCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCC TAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCT TTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCG CTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAAC GCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGT AAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACA GGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTC CCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTC AGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAG TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATC TGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGC AAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG ATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAA GGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTT TTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAA ACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGC AATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGT TTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCA AGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAA CCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCA CCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATT TCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAA TCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCG AGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATC GAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCA CCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGG ATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGC TTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACC ATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGA AACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCA CCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCA GCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGT TGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTAT CAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAA AATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT GACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGG

SEQ ID NO.	Description	Sequence
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180	pLMTB 8391	GGCGTGTGCGCACCGGCGTGTGCCAACGCCCAGGTACTGTGCGCACGT TCGTATCTCCATACGCTAGCTGACCGAGACGCATGCCCTCCGCCACCC TCAGTGGCGCGCACCTTCTCTCGTTTGAGCTCTTTATGCTCTCGTGAA TGGCACACAACATCCCGTGACTATCACGATGATCCTTCTCAAGCCACA CCGCTTGCCTTTTCTACAGCTCTGCGTTCTCTGGCCCATCCTCCTCTT GTTTGCTTTCCCTCTTTGCACATCCGTGTGCGCGTCCTTGTTCTTCTC TTCTGCGCACACTATTCTGCGCCCGCGACCCGCGCTTCGACTGCTGTC GGGTCATGCCTTGTGCTGCGCGTTCAGCTCTTCATTGCCCCTCGGCCT TGTACATAGCGGCTCTCCGTCATCGACGTTTTCCTCTCTCTTCAGCTC TATACACTCCCTCCCTTGTCAACACACTACACTGTGTCTCCCCCTTTC ATCTCTCCTCCCCTGTCACAATGCGCCTCCGCGAACCCCTCCTGAGCG GCTCCGCAGCGATGCCTGGGGCTTCGCTGCAGCGCGCCTGTCGGCTGC TCGTAGCGGTCTGCGCACTCCACCTTGGCGTGACTCTCGTCTACTATC TGGCGGGACGAGATCTGTCGCGCCTCCCACAGCTCGTGGGTGTGTCGA CGCCGCTGCAAGGAGGCTCAAATTCGGCCGCGGCCATCGGTCAGAGCT CCGGCGAGCTGCGCACGGGAGGAGCACGCCCGCCACCTCCGCTGGGTG CATCGTCTCAGCCCCGTCCGGGCGGCGACAGTTCACCGGTTGTGGACT CGGGTCCAGGACCTGCATCTAACCTTACGTCCGTGCCCGTACCACACA CGACGGCTCTTTCGCTTCCAGCCTGTCCCGAAGAGTCCCCTCTGCTTG TTGGTCCGATGTTGATCGAGTTCAACATGCCTGTTGATCTCGAATTGG TGGCAAAACAAAACCCAAACGTGAAAATGGGAGGCCGGTACGCCCCGC GAGATTGCGTGTCGCCTCACAAGGTTGCGATCATCATCCCCTTTCGGA ATCGCCAGGAACACCTTAAGTACTGGTTGTACTACCTCCACCCCGTTT TGCAGCGCCAGCAGTTGGATTATGGCATCTACGTCATTAACCAGGCCG GTGATACGATTTTTAACCGCGCCAAGCTGCTCAACGTGGGTTTTCAGG AGGCGCTCAAGGACTACGATTACACGTGCTTCGTCTTTTCCGACGTTG ATTTGATTCCTATGAACGACCACAATGCGTATCGGTGTTTCAGCCAGC CGCGCCACATTTCGGTAGCCATGGATAAGTTTGGATTCTCCCTGCCTT ACGTACAATACTTCGGCGGCGTGAGCGCATTGTCGAAGCAACAGTTCC TGACGATCAACGGCTTTCCAAACAATTACTGGGGTTGGGGCGGGGAAG ACGACGACATCTTCAATCGTCTGGTGTTTCGTGGGATGTCTATTTCCC GCCCGAACGCAGTCGTCGGTCGCTGCCGTATGATCCGACATTCTCGTG ATAAGAAGAACGAGCCTAACCCACAGCGCTTCGACCGAATCGCTCATA CTAAGGAAACGATGCTCTCCGACGGGCTCAACTCTCTCACATACCAGG TCCTCGACGTGCAGCGCTATCCACTTTACACGCAGATTACGGTCGACA TCGGCACCCCGTCGTGAATTTAAATATCCCAATGGCGCGCCGAGCTTG GCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTC ACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGG

SEQ ID NO.	Description	Sequence
		GGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTG CCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATC GGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT TCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCG GTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGG GATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG AACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCC CCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAC CCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTC GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC TTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGG TATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCAC GAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGT CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTT GGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGT AGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTT GTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGAT CCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCA CGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAG ATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATAT GAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGA AACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAA AGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGG ATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCA ATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAG AAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTA TGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCC TGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACA GGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATA TTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTC CCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATA AAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGT CTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGT TTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATT GTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATAT AAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTT TCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGC ATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATT TAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG CCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAA AATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGAC GGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGT CTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCG GGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAG ATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGC

SEQ ID NO.	Description	Sequence
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181	pLMTB8392	CGCAAGGAATCGGTCAATACACTACATGGCGTGATTTCATATGCGCGA TTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACGACACCG TCAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTTGGGCCG AGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCGGCTCCA ACAATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTGACTGGA GCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACATCTTCT TCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGCTACTTCG AGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCGGGCGTATA TGCTCCGCATTGGTCTTGACCAACTCTATCAGAGCTTGGTTGACGGCA ATTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCAATCGTCC GATCCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGCAGAAGCG CGGCCGTCTGGACCGATGGCTGTGTAGAAGTACTCGCCGATAGTGGAA ACCGACGCCCCAGCACTCGTCCGAGGGCAAAGGAATAGCTAGCCTCGG AGATCCACTAGTTCTAGTTCTAGGGGCCGAATTCAGATCCTCGTGTGA GCGTTCGCGGAATCGGTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTG CTCGCAAGGCGGTGCAGCAGGATACCGTCGCCCTCCTCTCTCCTTGCT TCTCTGTTCTTCAATTCGCGATCTCACAGAGGCCGGCTGTGCACGCCC TTCCTCACCCTCCTTTTCCCACCTCTCGGCCACCGGTCGGCTCCGTTC CGTCTGCCGTCGAGAAGGGACGGGCATGTGCAGCTCCTCCCTTTCTCT CGCGCGCGCATCTTCTCTTGCTTGTGGCACTCACGCTCATGCGTCAAG GCGGCCCCACGCCGAGCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGT AGCGCGGATGCCGTCGATGCGCAAGGCCGGCATGAAGGAGCGCGTGCC CTCAAGAGGGCACACTATCATGCCCTACGTGGGCCACGCAGCGATGAG GCCGGCTTCGGCGGAGATGCGTCACGCACGTGCCAGATGATGCGCTAC GCCTTCCTTGACTTGCGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCT CTCTCTCACACACACACACACACACACACACACACACAAATGATGTCCCC TGAAGATGCGACCGGGCTGGAGGCTGCACGCAAGCAGAAGATCCATAA CCTGAAGCTGAAGACGGCGTGCCTAGAGAATGAGGAGCTTGTGCAGGA GCTGCACATCTCTGACTGGTCAGAGACGCAGCGACAGAAGCTGCGCGG CGCCCATGAGAAGGGCGAGGAGCTGCTTGCGTCCGTGGAGGTTGGGAC GAAGTGGAACCTGATGGAGGCGTACGACCTGGCGAAGCTGATGCGCGT GTGCGGGCTGGAGATGAGTCAGCGCGAGCTGTACCGCCCGGAGGACAA GCCGCAGTTCATGGACATCATTGGCGTGAAGAAGGTGCTACAGGACCT TCGACAGAACCGGAACAAGACGCGCGTTGTGAGCTTCACGCAGCTGAT CGACAACAGCATCGCGAAGATGGAGAAGGTGGAGGAGGAGCTGCGGCG GTCGCAGCTGGACGCGACGCAGCTCGCGCAGGTGCCGTCTCGGACGGT GAAGATGATATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGC ATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCC ACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTA ATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTT CCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACG CGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCT CACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGC

SEQ ID NO.	Description	Sequence
		TCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGC AGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAA AAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGA GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGG ACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTC TCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCC TTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAG TTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCC CGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTC CAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAA CAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAA GTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG CGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTG ATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAA GCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGAT CTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGG GATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTT AAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAAC TTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAA TTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTT CTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAG ATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACC TATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACC ATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTC TTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATC ACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAG ACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGA ATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACC TGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGAT CGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTT GATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCAT CTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAA CAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACC TGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGC ATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTG AATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCA GGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAA TAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGA CGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCG TATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAA CCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGC GGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGG CGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACT GAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAG AAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTG GGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAA AGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTC

SEQ ID NO.	Description	Sequence
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182	pLMTB 8564	AACACTTGATCATCAATGCGCAATGTGCGCGTGTTGTGTGTGTGTGTG CGAGCGCACACACACATGCACACGACTCACGTTGTCACACAATTGAGA GCTCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGC TCTCTCTTCTCCTTCCCCTCTCTCTCCTCTCTCCTCTCTCCAGAGCTC GAGCCACCATGCGCCTGAATGTTAAGAAGGCGCTTATATTTGTTGGAT GCGTCGTGTTCCTCTGGGTCCTTCTGAGCTACGCGAGCGTCATTGAAG TGCCTCGTGCAGTCCCCCAGAAAGACCCGGCCGTCGAAATCGAAAAGA AGATCATCAAGCTTCAAAAGCAGGTCGATGCACAAATGGCGGAGTCCA AGAGCTTGCTCGCCAAGGTGAAGAAACTGAAGAAGATCAGTGAGGGAG AGAACGTTGGCGGCGAGGAGGACTCGCTGAAGGACAGTGAGGTTATGC AGCACCTGTCTCAGCCGATCCTCCCCGTTCTGGTGATTGCCTGCGACC GCGTCACTGTGCAGCGTTGTTTGGACAACCTGGTGAAGTTCCGCCCCT CGAAGGAAACGTTCCCCATCATTGTTTCGCAAGATTGTGGCCACAACG CGACCTATGAAGTCATTACGTCATACACGGCCTCCGACCCGACTATCT CTGTGGTGCGTCAGCCTGATTTGAGCGAAATCGTCCTCCCCCGCGTGA AGGTGAAGTTCCGCGGCTATTACAAGATTGCTCGGCACTACAAATTTG CCCTTAACCACGTTTTTGAGACCCTTGGCCACGAGGCGGTGATCATCG TGGAAGACGACCTGGATATCAGTCCAGATTTCTTTGAGTACTTCCTGG GGACGTACCCGCTGCTTTTGAAAGACCCGTCCTTGTGGTGCATCTCGG CGTGGAACGACAACGGTAAGATGGAGGTCATCGACATGTCGCGCCCGG ACCTGCTGCACCGCACCGACTTCTTTCCGGGCCTTGGCTGGGTCCTGC GCCGCGAAATGTGGCGTAAGCTTGCTCCAAAATGGCCCACCGCGTTTT TTGACGACTGGCTGCGAAACCCGGTTAACATCGACGGCAAGGCCTGCA TCCGCCCAGAGATATCTCGTACCTATAGTTTCGGGAAGGTGGGTGTGT CTAAGGGACTGTTCTTCGATCTTCACCTCCGCAACATTCAGCTCAATA TGGAATACGTCGAATTTACGAAACTGAACCTCACATACCTGCTTAAGG AACACTACGACGATGCCCTCGTCTCCACCGTTTACAATCTGCCGGAGA TGAGTGCATCCGAGGTGGTTGCAGGCAGCGATCTCAGCGCAGACCCGG TGCGTGTTATGTACTCCAATGCCAAGACATATCAGCGCGCCGCGAAAA AGCTCGGCCTGATGGACGACTTCCGCTCCGGGGTACCGCGCACGGCCT ACCGCGGCATCGTGACGTGTTTCATTCGGGGCCGACGAGTATACCTTG CCCCGTCGTTTGAGTGGAACAAGTACGACCCGACCTGGGGATAGATTT AAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTG TTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGA GCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAA CTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAAC CTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGC GGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTG CGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCG GTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATG TGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTG CTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAAT CGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAC CAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACC CTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTG GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTC

SEQ ID NO.	Description	Sequence
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183	pLMTB 8568	ATGGTGCGGAAGAAAGGGAGCCTGATCCTTTGCGGCGCGTTCCTCTTT GTGGCATGGAATGCCTTGCTGCTGTTGTTCCTTTGGGGCCGCCCCCCG ATCGGGCGCCTCGGTGAGGGCGGGGGCGCCGAACCGGGCGCCGGAGAA GAGTGGGGCGCTGGAAAATCAAAGGTGGGCGGCGCCAATGGTCTGGCA GGGGAAGTCATCCGGCTGGCGGAAGAAGTGGAGAGTGAACTCGAAACG CAGAAGAAGCTGCTGAAGCAGATTCAGTCGCATCGCGAGTTGTGGGAG CAGCGCAAAGAGCTGGAGAAGCGCGAGAGCGAGGACACAAAAGACGAA

SEQ ID NO.	Description	Sequence
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184	pLMTB 8582	ATGCTCAAGAAGAGCAGCCTCGTTCTTTGGGGAGTTGTATTGTTTGTG GCATGGAATGCTCTGATACTGTTTTTCCTGTGGACGCGTCCTCAGAGC CTGTCCGACCACTCGCACCTGACCGAGGAGGTGATCCGCTTGGCCCAG GATGCGGAATCGGAGCTGGAGCGTCAGAAGGATCTGCTTCAGCAGATC TACCGATACAGCGCGCTCTGGTCACGGCGTAAGGCCTCTGAGGCGAAG CTGCACCCGCCAGTGGCAGCTTCCGCTCAGCCTAGCACGGCCGCCCCG CTTTCACACCACTCGCAAATTTCCCCTGACGCTGTTCTGCCTGTTCTT GTGATAGCATGTGATCGGAGTACAGTGCGCCGGTGCCTGGACAAACTG CTGCACTATCGGCCGAGCCAGGAGCGCTTCCCCATTATTGTGTCGCAA GACTGCGGTCACGACGAGACGGCCCGAGTGATCGCATCATACGGCGAT GCTATTATGCATATCAAGCAGCCGAACTTGAGCGACATTCCCGTGCCA ACCGATCACCGCAAGTTTCAGGGTTACTACAAAATTGCCCGTCACTAT CATTGGGCCCTTTCTCAGGTCTTCCGTACATTCCAGTATCAGGCGGCA ATCGTGGTTGAGGATGACCTTGAGGTGGCTCCGGATTTCTTTGAATAC TTTCAGGCGGCCTTTCCTCTGCTGCTGGCCGACCCGACATTGTGGTGC

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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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186	pLMTB 8631	GCTTGGCGAGGTGCGTGTCCAGTATACGTCCCGCGACAGCTTTAAGGC ATTTGCTAAAGCCTTGGGTGTCATGGATGATCTGAAGTCTGGCGTGCC CCGTGCAGGCTACCGTGGAATCGTGACCTTCCAGTTCCGGGGTCGCCG GGTCCACCTCGCCCCGCCGGAGACCTGGAACGGCTACGACCCGTCCTG GAATTGAGTGACTATAAAGTGCTATTGAATTTTTTTTTCTTTTCCTTT CACGAAACAAAAATCTGTGTGTGCGCATTTTCTTACTCTCCATTTGGT GCGCACCCTTCTGGGGGTATGACCTTCAGCACACACAAAGAACGTGTG CTGCGCATATGTGTTCAATGCATGTGCTTTTCCTCTCTTTGTTTCTAT CAAGGAGGTTCATATGAGAGGGCATGCTCACAGCAGCTTCCCTTATGC ATATGTAGCCTTCTGAGTTCAGATGTGATACTGCTCCCTTGATCTCCC TTTTGTGTTTTTGTTCGAAACAACAATGACGCTCTTACATTCTCTCTA CCTATTATCGTTTCTTTCGCATCTGAAAGCGTGGTACTAGTTAGCTTT ATCTTAGTAAAACAGTTACCATTCACTGCCACCAAAAATGCGGTTTCG GATCTACAAGCGCAAGGTATTGATTCTTACTCTCGTGGTGGCGGCGTG CGGCTTTGTGCTGTGGTCTAGCAATGGCCGGCAGCGTAAGAATGACGC GTTGGCTCCGCCGCTGTTGGACAGCGAGCCGCTTCGCGGGGCGGGCCA TTTTGCCGCTTCGGTGGGCATCCGTCGTGTGTCTAACGATTCAGCATT TAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCT GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACG AGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAA CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGG CGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGC GGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTT GCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAA TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGAC CCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT CGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGA CCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACA AACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTAC GCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG

SEQ ID NO.	Description	Sequence
		GTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT GAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATG AAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAG TTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATC AGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGG AGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCG GTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCC CTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC TGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTG TTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAAC CAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCG ATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCG CAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATA TTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAG TAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAG AGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAAC ATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGC ATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGA ATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCAT ACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGG GGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAAC CATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCC CTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACAT GCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAG CAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGG CTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCA TATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCAT CAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATC GGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGC TGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT
187	pLMTB 8632	ATGCGGTTTCGGATCTACAAGCGCAAGGTATTGATTCTTACTCTCGTG GTGGCGGCGTGCGGCTTTGTGCTGTGGTCTAGCAATGGCCGGCAGCGT AAGAATGACGCGTTGGCTCCGCCGCTGTTGGACAGCGAGCCGCTTCGC GGGGCGGGCCATTTTGCCGCTTCGGTGGGCATCCGTCGTGTGTCTAAC GATTCAGCCGCGCCGCTCGTGCCGGCCGTCCCTCGTCCGGAGGTGGAC AACCTCACCTTGCGATACCGCAGCCTGGTCTACCAACTCAATTTCGAC CAGATGCTGCGCAACGTAGATAAGGACGGGACATGGTCGCCCGGCGAG CTGGTACTGGTCGTGCAGGTGCACAATCGTCCAGAGTACCTGCGGCTC CTGATCGACTCACTGCGCAAGGCTCAGGGCATCCGGGAGGTGCTGGTG ATCTTTTCTCACGACTTCTGGTCCGCTGAGATTAACAGCCTGATAAGC TCTGTGGACTTTTGCCCAGTACTTCAGGTATTCTTTCCATTCAGCATT CAGCTGTACCCCTCCGAGTTTCCGGGTAGTGACCCGCGCGATTGCCCG CGCGATCTCAAAAAGAATGCCGCATTGAAGTTGGGCTGCATCAATGCG GAGTATCCAGACAGCTTCGGCCACTACCGTGAGGCCAAGTTCTCTCAG ACGAAACACCATTGGTGGTGGAAGTTGCATTTCGTCTGGGAGCGCGTG

SEQ ID NO.	Description	Sequence
		AAGGTCCTGCAGGATTACACAGGCCTGATTCTGTTCCTTGAGGAGGAT CACTACCTGGCGCCCGACTTCTACCATGTGTTCAAGAAGATGTGGAAG CTGAAACAACAAGAGTGCCCTGGTTGTGATGTGCTCAGTCTCGGGACC TACACCACCATTCGTAGTTTCTACGGCATCGCTGACAAGGTGGACGTG AAGACATGGAAATCGACAGAGCACAACATGGGTCTGGCATTGACACGG GATGCGTATCAGAAGCTGATTGAGTGCACCGACACATTCTGCACGTAC GACGATTATAACTGGGACTGGACGCTGCAGTACCTTACGCTGGCGTGC CTTCCGAAGGTATGGAAGGTCCTGGTGCCGCAGGCCCCGCGAATCTTC CACGCGGGTGATTGCGGCATGCACCACAAGAAGACGTGCCGCCCTTCC ACTCAGTCAGCCCAGATCGAAAGCCTGCTCAATAACAACAAACAGTAC CTCTTCCCAGAAACCCTCGTGATCGGCGAGAAGTTCCCTATGGCGGCG ATCTCCCCGCCCCGTAAGAACGGGGGGTGGGGCGACATACGTGATCAT GAGCTCTGTAAGTCGTATCGCCGCCTCCAATAGATTTAAATATCCCAA TGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTG AAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCAT AAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAAT TGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA GCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTAT TGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGT TCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTT ATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGG CCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTT CCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG TCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCC CCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTAC CGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCA TAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAA GCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTT ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATC GCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACAC TAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTT CGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGG TAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAA AGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCA GTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAA AAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATC AATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTC ATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAAT ACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACC GAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCC GACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAAT AAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGA GAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCA GCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATT CATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAA AGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGC CAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATAC

SEQ ID NO.	Description	Sequence
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188	pLMTB8633	ATGCGGTTCCGCATTTATAAGCGCAAGGTCTTGATCCTGACGCTGGTC GTCGCCGCATGCGGATTTGTGCTGTGGAGCTCGAACGGTCGCCAGCGC AAGAACGAAGCGCTCGCCCCGCCGCTGCTTGACGCGGAGCCTGCACGA GGCGCGGGTGGCCGTGGCGGCGACCACCCGAGCGTGGCGGTGGGTATC CGCCGCGTGTCAAACGTCTCAGCCGCATCATTGGTGCCAGCCGTGCCC CAGCCAGAGGCGGACAACCTCACATTGCGCTACCGATCCTTGGTCTAC CAACTTAACTTTGACCAAACGTTGCGCAACGTCGACAAGGCAGGTACT TGGGCTCCACGCGAGCTTGTGTTGGTCGTCCAGGTGCATAATCGTCCG GAGTACCTTCGCCTCCTGCTGGACTCCCTTCGCAAGGCACAAGGCATC GACAACGTGCTGGTTATTTTCAGCCACGACTTTTGGTCCACCGAGATC AATCAACTTATCGCGGGCGTGAACTTCTGTCCAGTGCTCCAGGTTTTC TTCCCGTTCTCCATCCAGCTGTACCCCAACGAATTCCCAGGATCCGAC CCGCGAGACTGTCCACGGGACCTCCCGAAGAACGCCGCTTTGAAGCTT GGTTGCATTAACGCGGAATACCCGGATAGCTTCGGTCACTACCGAGAG GCCAAATTCTCTCAGACGAAGCACCACTGGTGGTGGAAATTGCACTTC GTGTGGGAACGTGTTAAGATCCTGCGTGACTACGCCGGCCTCATATTG TTCTTGGAGGAGGACCACTACCTCGCCCCCGATTTTTACCACGTGTTC AAGAAAATGTGGAAACTGAAGCAGCAGGAGTGTCCTGAGTGTGATGTG CTGAGTCTCGGAACCTACTCAGCCAGCCGCTCTTTCTACGGCATGGCC GACAAGGTTGACGTGAAAACCTGGAAGAGCACTGAGCACAATATGGGT CTGGCACTTACGCGCAACGCGTACCAGAAGTTGATAGAGTGCACCGAC ACGTTCTGTACGTACGACGATTATAACTGGGACTGGACGCTCCAGTAC CTGACCGTGAGCTGCCTCCCTAAGTTTTGGAAAGTGCTGGTTCCGCAG ATCCCACGTATCTTCCACGCAGGGGACTGCGGCATGCACCACAAAAAG ACGTGTCGTCCATCGACGCAATCTGCCCAAATCGAGTCGCTTCTGAAC AATAACAAGCAGTACATGTTTCCCGAAACGCTCACTATCTCGGAGAAG TTTACCGTCGTGGCCATATCACCGCCACGCAAGAATGGCGGCTGGGGC GACATACGCGATCATGAATTGTGTAAGTCGTATCGCCGCCTGCAGTGA

SEQ ID NO.	Description	Sequence
		TCAGCGTTCCGTAGCGCGCTGCACATCCGGTACTGCGTTCCAGCGCAT CACGCGACGCACAGCAACACAAATTTTCGTTTTGTTTCTCTTCCATTC GAAAAAAAAAAGATAACACCCACCCCACTTAACCTCCATAACAAGAGA GCGTGAGAGGAGAGTCTGCTCTTGGCCTTCACACCGCAAATGCAGCAA AACGCGGCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCA TGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCA CACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAA TGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTC CAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGC GCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTC ACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCT CACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCA GGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAA AAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAG CATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA CTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCT CCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCT TCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGT TCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCC GTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCC AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAAC AGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAG TGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGC GCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGA TCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAG CAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATC TTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGG ATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTA AATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACT TGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAAT TTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTC TGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGA TCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCT ATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCA TGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCT TTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCA CTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGA CGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAA TGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCT GAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATC GCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTG ATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATC TCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAAC AACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCT GATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCA TCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGA ATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAG GGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAAT

SEQ ID NO.	Description	Sequence
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189	pLMTB8698	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCCGG GGGCAGCGGTGTTGGCGGAACGGCCAACGCCCTGCCCCCTCCCCGCCC TGCGACGTTTCTGCGCACCCGTTCTCTCCTTCCTGCGTGCGTGTCTGC GCGCATGCACATCTGTCCGCGTGTGCCGCAGCGCTGGTATTTTTGTGA GGGCAGAGCCCTGCCTCCCCGCCTCTCTGCCGTTGGCAGGTGAAGCGA AAACGAAGCGAGAGGGCAGTCTGCATGTGTGTGCGAGGGCATGCGGAG CCCCCCTCCCCCCGCCCCCTGCCGTGCTGCACCGCTATTGTGGCGTCT TCTCTCGTTGTGCGCAAGTGTGGCTGCACCACGGCCGCCTCATGTGCG TGTGTGCGCATGTACACACACACACACACACACACACACACGGGCA GGCGCACGCTCCTCTCTCTTCAGGGAGCGCCGCCCCGCTGGTGTCATT GGACGAGCATCCGCCGCGCATCTCTTCACCCCTCACCCCTCATCCCTC TCCCCTCTCCCCGCACACACACGCAGTCCTTCGCTTTCACTCTTCGAA CAAACACCTCAACCATCTTATCACCTTTCTCTCTTCCTTGTCAACCAT GATCGCGAGCAGCGTGCGCCACGCGGTGATCCTGCTGCTGGTGGCGGT GGCGATGATGGTGAACAACGTGATCGCGGAGGTGCAGCTGGTGGAGAG CGGCGGCGGCCTGGTGCAGCCGGGCCGCAGCCTGCGCCTGAGCTGCGC GGCGAGCGGCTTCACGTTCGACGACTACGCGATGCACTGGGTGCGCCA GGCGCCGGGCAAGGGCCTGGAGTGGGTGAGCGCGATCACGTGGAACAG CGGCCACATCGACTACGCGGACAGCGTGGAGGGCCGCTTCACGATCAG CCGCGACAACGCGAACAACAGCCTGTACCTGCAGATGAACAGCCTGCG CGCGGAGGACACGGCGGTGTACTACTGCGCGAAGGTGAGCTACCTGAG CACGGCGAGCAGCCTGGACTACTGGGGCCAGGGCACGCTGGTGACGGT GAGCAGCGCGAGCACGAAGGGCCCGAGCGTGTTCCCGCTGGCGCCGAG CAGCAAGAGCACGAGCGGCGGCACGGCGGCGCTGGGCTGCCTGGTGAA GGACTACTTCCCGGAGCCGGTGACGGTGAGCTGGAACAGCGGCGCGCT GACGAGCGGCGTGCACACGTTCCCGGCGGTGCTGCAGAGCAGCGGCCT GTACAGCCTGAGCAGCGTGGTGACGGTGCCGAGCAGCAGCCTGGGCAC GCAGACGTACATCTGCAACGTGAACCACAAGCCGAGCAACACGAAGGT

SEQ ID NO.	Description	Sequence
		GGACAAGAAGGTGGAGCCGAAGAGCTGCGACAAGACGCACGGTACCAT TTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGC TGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATAC GAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCT AACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAA ACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAG GCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGC TGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGG CGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACA TGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGT TGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAA ATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGAT ACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGA CCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCG TGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGG TCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCG ACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAA GACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCA GAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA ACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGA AGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAC AAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTA CGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGG GGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCA TGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAAT GAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACA GTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATAT CAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAG GAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATC GGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCC CCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGA CTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTT GTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAA CCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGC GATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGC GCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGAT ATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGA GTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAA GAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAA CATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCG CATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGA CATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGG AATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCA TACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTC TCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAG GGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAA CCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGC CCTTTCGTC

SEQ ID NO.	Description	Sequence
190	pLMTB 8803	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAATGGTACCAAA TTGGATAACTTGGCGAAACGCCAAGCTAATACATGAACCAACCGGGTG TTCTCCACTTCAGACGGTGGGCGACCATCGTCGTGAGACGCCCAGCGA ATGAATGACAGTAAAACCAATGCCTTCACTGGCAGTAACACCCAGCAG TGTTGACTCAATTCATTCCGTGCGAAAGCCGGCTTGTTCCGGCGTCTT TTGACGAACAACTGCCCTATCAGCTTGTGATGGCCGTGTAGTGGACTG CCATGGCGTTGACGGGAGCGGGGGATTAGGGTTCGATTCCGGAGAGGG AGCCTGAGAAATAGCTACCACTTCTACGGAGGGCAGCAGGCGCGCAAA TTGCCCAATGTCAAAACAAAACGATGAGGCAGCGAAAAGAAATAGAGT TGTCAGTCCATTTGGATTGTCATTTCAATGGGGGATATTTAAACCCAT CCAATATCGAGTAACAATTGGAGGACAAGTCTGGTGCCAGCACCCGCG GTAATTCCAGCTCCAAAAGCGTATATTAATGCTGTTGCTGTTAAAGGG TTCGTAGTTGAACTGTGGGCTGTGCAGGTTTGTCCCTGGTCGTCCCGT CCATGTCGGATTTGGTGACCCAGGCCCTTGCAGCCCGTGAACATTCAA AGAAACAAGAAACACGGGAGTGGTTCCTTTCCTGATTTACGCATGTCA TGCATGCGTCGAAGATCCAGTCGCAGCCTGACCGCATCACACATCAAG GCGTTACAGCCTCTCCGTCTTTGCTGCACCCAAGTGTATTCGTGTGAC CGCGTTGAGGGATCTAATGGATTCGGAACTTTGGTCGTTTGGTCTCTC ATGCTGCCCAATCCCATGCGCTTTTCTCCGTGCCTCTCTGTCTCCCCT TCCGTTCTATTTGGACAACGATGTGTACTGTAATGCGTGCGCCATCTG ACAACGAATAGATCAGCAGCATTCGCACACTTGCACATACCCAGTGAA GCTTTTGTGTCTGTCGTATTGACAACACCGACTGCAACAAGGTGTAGA TAGAAGTTGGCCTTCTCGCTCGCTCGCACGCTCTTCACGCTCCTGCTT TCCTTGCTGTGCCTTGCCACCATGATCGCGAGCAGCGTGCGCCACGCG GTGATCCTGCTGCTGGTGGCGGTGGCGATGATGGTGAACAACGTGATC GCGGACATCCAGATGACGCAGAGCCCGAGCAGCCTGAGCGCGAGCGTG GGCGACCGCGTGACGATCACGTGCCGCGCGAGCCAGGGCATCCGCAAC TACCTGGCGTGGTATCAGCAGAAGCCGGGCAAGGCGCCGAAGCTGCTG ATCTACGCGGCGAGCACGCTGCAGAGCGGCGTGCCGAGCCGCTTCAGC GGCAGCGGCAGCGGCACGAACTTCACGCTGACGATCAGCAGCCTGCAG CCGGAGGACGTGGCGACGTACTACTGCCAGCGCTACAACCGCGCGCCG TACACGTTCGGCCAGGGCACGAAGGTGGAGATCAAGCGCACGGTGGCG GCGCCGAGCGTGTTCATCTTCCCGCCGAGCGACGAGCAGCTGAAGAGC GGCACGGCGAGCGTGGTGTGCCTGCTGAACAACTTCTACCCGCGCGAG GCGAAGGTGCAGTGGAAGGTGGACAACGCGCTGCAGAGCGGCAACAGC CAGGAGAGCGTGACGGAGCAGGACAGCAAGGACAGCACGTACAGCCTG AGCAGCACGCTGACGCTGAGCAAGGCGGACTACGAGAAGCACAAGGTG TACGCGTGCGAGGTGACGCACCAGGGCCTGAGCAGCCCGGTGACGAAG AGCTTCAACCGCGGCGAGTGCTAACTCGAGGGAGGAGGAGGAGGCGCG TAGCATTGCGTGCGGGTTATGTGTGCGTGCGTGTGTGTGTGCGGTGCG

SEQ ID NO.	Description	Sequence
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		GACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTAT TGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAA TGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGA AAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACC TATAAAAATAGGCGTATCACGAGGCCCTTTCGTC
191	pLMTB 8821	GCAGCTCTCTCTAGCGACGGCCGCATCTTCACTGGTGTCAATGTATAT CATTTTACTGGGGGACCTTGTGCAGAACTCGTGGTGCTGGGCACTGCT GCTGCTGCGGCAGCTGGCAACCTGACTTGTATCGTCGCGATCGGAAAT GAGAACAGGGGCATCTTGAGCCCCTGCGGACGGTGCCGACAGGTGCTT CTCGATCTGCATCCTGGGATCAAAGCCATAGTGAAGGACAGTGATGGA CAGCCGACGGCAGTTGGGATTCGTGAATTGCTGCCCTCTGGTTATGTG TGGGAGGGCTAACTAGCCTCGGAGATCCACTAGTTCTAGTTCTAGGGG CCGAATTCAGATCCTCGTGTGAGCGTTCGCGGAATCGGTCGCTCGTGT TTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAGCAGGATACC GTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAATTCGCGATCTCA CAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTTTTCCCACCTCT CGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAGAAGGGACGGGCA TGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCTTCTCTTGCTTGTG GCACTCACGCTCATGCGTCAAGGCGGCCCCACGCCGAGCCCCTGCGCT CCCTTCCCTCTTGCGCATCCGTAGCGCGGATGCCGTCGATGCGCAAGG CCGGCATGAAGGAGCGCGTGCCCTCAAGAGGGCACACTATCATGCCCT ACGTGGGCCACGCAGCGATGAGGCCGGCTTCGGCGGAGATGCGTCACG CACGTGCCAGATGATGCGCTACGCCTTCCTTGACTTGCGCCCCCCTCT CTTCCTCCGTCTCTCACTCTCTCTCTCTCACACACACACACACACACA CACACACACAAATGATGTCCCCTGAAGATGCGACCGGGCTGGAGGCTG CACGCAAGCAGAAGATCCATAACCTGAAGCTGAAGACGGCGTGCCTAG AGAATGAGGAGCTTGTGCAGGAGCTGCACATCTCTGACTGGTCAGAGA CGCAGCGACAGAAGCTGCGCGGCGCCCATGAGAAGGGCGAGGAGCTGC TTGCGTCCGTGGAGGTTGGGACGAAGTGGAACCTGATGGAGGCGTACG ACCTGGCGAAGCTGATGCGCGTGTGCGGGCTGGAGATGAGTCAGCGCG AGCTGTACCGCCCGGAGGACAAGCCGCAGTTCATGGACATCATTGGCG TGAAGAAGGTGCTACAGGACCTTCGACAGAACCGGAACAAGACGCGCG TTGTGAGCTTCACGCAGCTGATCGACAACAGCATCGCGAAGATGGAGA AGGTGGAGGAGGAGCTGCGGCGGTCGCAGCTGGACGCGACGCAGCTCG CGCAGGTGCCGTCTCGGACGGTGAAGATGATATTTAAATATCCCAATG GCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAA ATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG CGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGC TGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTG GGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTC GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTAT CCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCC AGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC ATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTC AGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCC CTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCG GATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATA

SEQ ID NO.	Description	Sequence
		GCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGC TGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTAT CCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGC CACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG GCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTA GAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCG GAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTA GCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAG GATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGT GGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAA GGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAA TCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCAT CGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATAC CATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGA GGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGA CTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAA GGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGA ATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGC CATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCA TTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAG GACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCA GCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCT GGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCAT CAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCG TCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGC TACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCAT ACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCC ATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCC TAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTC AATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACA TATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACAT TTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGA CATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGC GTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGA CGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTC AGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATG CGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAA TACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGC CATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTT CGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAA GTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGG CCAGTGAATTGACGCGTATTGGGATATTTAAAT
192	pLMTB 8831	CAGTCGTCGGTCGCTGCCGTATGATCCGACATTCTCGTGATAAGAAGA ACGAGCCTAACCCACAGCGCTTCGACCGAATCGCTCATACTAAGGAAA CGATGCTCTCCGACGGGCTCAACTCTCTCACATACCAGGTCCTCGACG TGCAGCGCTATCCACTTTACACGCAGATTACGGTCGACATCGGCACCC CGTCGTGAGTCCTCCGGCTTGACAGCGCACACGCGCCGCTGTATGTGC GCGTGCGCGCGGGTCCCGACTGGGGCCGGCGATGAGGCGCATCATACC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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193	pLMTB 8832	ATGCGGCTCCGCGAGCCACTGCTGAGCGGCTCGGCAGCTATGCCGGGC GCGTCCCTGCAGCGTGCGTGCCGCCTCCTTGTTGCAGTATGCGCCTTG CACTTGGGCGTGACCCTCGTGTACTATCTGGCGGGCCGAGATCTGAGT CGTCTGCCGCAACTGGTCGGAGTGAGCACTCCGCTTCAAGGCGGATCA AACAGCGCCGCGGCCATCGGGCAGTCTTCTGGTGAGCTTCGCACCGGC GGAGCCCGCCCTCCACCTCCCTTGGGCGCCTCCAGCCAACCCCGGCCA GGCGGGGACTCCAGTCCCGTGGTAGATTCGGGCCCCGGCCCTGCTTCC AACCTCACATCGGTGCCTGTACCCCATACGACTGCCCTCTCATTGCCA GCCTGTCCAGAGGAGAGCCCGCTTCTGGTAGGCCCAATGCTGATAGAG TTCAACATGCCGGTCGACTTGGAACTGGTGGCTAAACAAAACCCGAAT GTGAAGATGGGGGGCCGCTATGCGCCGCGGGACTGCGTGAGCCCGCAT AAGGTGGCGATTATCATCCCGTTCCGTAACCGCCAGGAGCACCTCAAA TACTGGCTCTACTACCTTCATCCGGTACTGCAGCGGCAACAGCTGGAC TACGGGATCTACGTTATCAACCAGGCAGGGGACACAATATTCAATCGC GCTAAGTTGCTGAACGTCGGATTTCAGGAGGCGTTGAAGGACTATGAT TATACCTGCTTCGTATTCTCCGATGTCGACTTGATCCCGATGAACGAT CATAACGCCTATCGATGCTTCTCCCAGCCTCGGCACATCAGTGTGGCG ATGGACAAGTTCGGCTTTTCCCTCCCATACGTCCAGTATTTCGGTGGG GTGAGCGCGCTGTCGAAGCAGCAGTTCCTGACAATCAACGGCTTCCCG AATAATTATTGGGGTTGGGGGGGGGAGGATGACGACATTTTTAATCGC CTCGTCTTTCGGGGGATGTCGATTAGCCGACCGAATGCCGTGGTCGGT CGATGCCGTATGATTCGGCATTCGCGTGACAAGAAGAATGAACCAAAT CCCCAACGCTTCGACCGAATTGCGCATACCAAGGAGACAATGCTGTCG GACGGCCTTAACAGTTTGACATACCAGGTCCTGGACGTCCAGCGATAC CCACTCTATACTCAGATTACAGTCGACATCGGCACGCCTTCGTGAATT

SEQ ID NO.	Description	Sequence
		TAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCT GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACG AGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAA CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGG CGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGC GGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTT GCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAA TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGAC CCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT CGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGA CCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACA AACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTAC GCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG GTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT GAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATG AAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAG TTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATC AGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGG AGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCG GTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCC CTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC TGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTG TTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAAC CAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCG ATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCG CAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATA TTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAG TAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAG AGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAAC ATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGC ATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGA ATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCAT ACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGG GGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAAC CATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCC CTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACAT GCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAG

SEQ ID NO.	Description	Sequence
		CAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGG CTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCA TATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCAT CAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATC GGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGC TGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACG TTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT
194	pLMTB 8834	CCGTGGTCGGTCGATGCCGTATGATTCGGCATTCGCGTGACAAGAAGA ATGAACCAAATCCCCAACGCTTCGACCGAATTGCGCATACCAAGGAGA CAATGCTGTCGGACGGCCTTAACAGTTTGACATACCAGGTCCTGGACG TCCAGCGATACCCACTCTATACTCAGATTACAGTCGACATCGGCACGC CTTCGTGAGCCTGTGTGCTGCCTCCTCATTTCCGGCGGCTCGCACGCG CTCGCATGCTTCGCCACACAGACGTCCTCGTGTCTACTGAACAGCTAA CGGATTTCCATGTCATTTCTCGTTTCCCATCTTCAAACACAAGAGCAC CACTGCAACGTCAGCAGTGAACGCCCAACACTGCGGAGAGCGTGGTCA CGCCCCTTCTGACTTGCACCATGAAAAACGATGTGAGGCAGCGGCGCG TCCTCTCTCCCGTTCGCTGACTTGCCCCACGCGAGTATCTGCGCGCCG GCACCCCTCTCCGCAGCTCGGTTTGCCTGCAGGTGTGCGCTCTCGATA CCTCCCGCCTCTGTCATTCTGTTTGTCTCTTCCTCCCAGCTCCACTCT TCTTCTTTTCCTGCTTCTCCGTTTGTTTGTGCGGCGCAGTGCCGCGAC CAGCACATTTTGGCTCTCTCTCCGTTGCTAGCACCAGGGGTCGGGATC GACGTGCGCGTTGCTCCTCCGCTCTCCCCATTTTCATCTCCTTATTCT GCTTTGTTTTGCAAACTCGCCGGCGAACGCTGTCAAATCTTCACGGGT TGTTTTTCTCTCTTCCTCTCTCGTGGAACGCCGGCGTGCCAAGACGAG GCCATGCGGCTGCGCGAACCACTCCTGTCGGGAAGCGCCGCCATGCCT GGCGCCAGCCTGCAGCGCGCCTGTCGTCTCTTGGTTGCGGTGTGCGCC TTGCATCTTGGGGTGACGTTGGTCTATTACTTGGCCGGGCGCGACCTC TCCCGTCTCCCTCAACTTGTGGGCGTCTCTACCCCTCTGCAAGGCGGG AGCAATAGCGCATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGA GCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCC TAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCT TTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCG CTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAAC GCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGT AAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACA GGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTC CCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTC AGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAG TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATC TGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT

SEQ ID NO.	Description	Sequence
		TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGC AAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG ATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAA GGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTT TTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAA ACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGC AATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGT TTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCA AGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAA CCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCA CCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATT TCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAA TCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCG AGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATC GAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCA CCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGG ATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGC TTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACC ATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGA AACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCA CCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCA GCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGT TGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTAT CAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAA AATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT GACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGG CGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAA AACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAA GCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTT GGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTA CTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGG AGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGT TGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTT TCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGACGCGTATT GGGATATTTAAAT
195	pLMTB 8836	ATGCGGCTGCGCGAACCACTCCTGTCGGGAAGCGCCGCCATGCCTGGC GCCAGCCTGCAGCGCGCCTGTCGTCTCTTGGTTGCGGTGTGCGCCTTG CATCTTGGGGTGACGTTGGTCTATTACTTGGCCGGGCGCGACCTCTCC CGTCTCCCTCAACTTGTGGGCGTCTCTACCCCTCTGCAAGGCGGGAGC AATAGCGCGGCTGCGATTGGGCAGTCTTCCGGGGAGCTGCGCACGGGC GGGGCTCGCCCGCCGCCACCGCTTGGCGCATCCAGCCAACCACGGCCT GGGGGCGACTCAAGCCCAGTCGTTGACTCGGGCCCTGGTCCGGCCTCC AACCTTACGTCAGTTCCTGTCCCGCACACAACTGCGCTCTCCCTGCCA GCCTGCCCAGAAGAGTCGCCGCTCCTTGTCGGGCCAATGCTTATCGAG TTCAACATGCCAGTCGACCTCGAACTGGTAGCGAAGCAGAACCCTAAT GTGAAAATGGGTGGACGGTACGCACCTCGAGACTGCGTATCCCCGCAC AAGGTAGCTATCATCATCCCCTTCCGAAATCGGCAGGAACATCTTAAA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
		CAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTC GCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGA AATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGC AACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAA TCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCA GTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATG GTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCA TCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAAC TCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGAT TGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCC ATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATA TGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGT TATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAA CAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTC TAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATC ACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTC TGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGAT GCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGG TGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGA GTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAA TACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAA GGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGG GGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAG TCACGACGTTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATA TTTAAAT
196	pLMTB 9070	GCGCAGACCCGGTGCGTGTTATGTACTCCAATGCCAAGACATATCAGC GCGCCGCGAAAAAGCTCGGCCTGATGGACGACTTCCGCTCCGGGGTAC CGCGCACGGCCTACCGCGGCATCGTGACGTGTTTCATTCGGGGCCGAC GAGTATACCTTGCCCCGTCGTTTGAGTGGAACAAGTACGACCCGACCT GGGGATAGACTTTTGATGGCACTGTTTTTCTTTACTTTTATTTCTCTC AAAACATCAGAAGCAGTAATGTAAATATTCATTTTGTTTCAGCGCTCG TGCCAAACATCACGCGCTTGTTCAAGAGGCTATGCGAAGTGATCATTG CCGTTTTTTTTTTCCTCAGCGTAAGCGGTGCATATGCTCAAAATGCAT GTGCTTGTGGAAAATCAAGGCAACTTTGCATCTCCTGTTGAGAGTTCT AGTCCAGCAATCTATCCATGGCCTTTTCTTCTTTGGGATACTTTTATC GCGATGCTTTGCGCTTCGTCTCTACCCCTTCTGTATCCTACAAAAATA TCATAACGCCGATTATGTGCTCGATGCGCTGCTTCGAATAGCTCTGTT TTCTTCATTTAACACGATGGTGCGGAAGAAAGGGAGCCTGATCCTTTG CGGCGCGTTCCTCTTTGTGGCATGGAATGCCTTGCTGCTGTTGTTCCT TTGGGGCCGCCCCCCGATCGGGCGCCTCGGTGAGGGCGGGGGCGCCGA ACCGGGCGCCGGAGAAGAGTGGGGCGCTGGAAAATCAAAGGTGGGCGG CGCCAATGGTCTGGCAGGGGAAGTATTTAAATATCCCAATGGCGCGCC GAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAA AGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCG CTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTA ATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTC TTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG

SEQ ID NO.	Description	Sequence
		GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGA ATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAA GGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT CCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTG GCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAG CTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCT GTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACG CTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTG TGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAA CTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGC TACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAAC AGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAG AGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGG TTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCA AGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGA AAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTT CACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAG TATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCAT CAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTT TTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTT CCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCC AACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATC AAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAA AAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACG CTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGA TTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATT ACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATC AACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGC TGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGT ACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCA GTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTT GCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCG ATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATA CCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCA AGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTA TTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGA ATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCG AAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAAC CTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGG TGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCAC AGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGC GTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATC AGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCA CAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAG GCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATT ACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGT

SEQ ID NO.	Description	Sequence
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197	pLMTB9072	GTAGCGGGCCTTTCCGCGTCCAGTACTCCTCTCGTGATTCGTTCAAGG TGCTTGCACGGAACCTGGGGGTCATGGACGACCTGAAATCAGGCGTTC CACGCGCCGGATACCGCGGGGTCGTGAGTTTTATCTCGCGAGGCCGGC GCATTTACCTGGCACCCCCGGAGGGCTGGACGAAGTACGACGTTAGCT GGTCTTGAAGAGGGCGTGCCTGGGGAGAGGGAGACATTGGCGGCCCAG GTGGTGCGTGTGCGCGGATCTGCGTGCAGAGGTGCGCAGGGCGCGCGC TCTCGTCTTTTGGTCTCTTTCTGTTTTCGCTTTATTTCTGTTTTTTTC TCCTTTTCAACAGCAAGAACAGCCACCACGCGCACCAAGCGAAGGTAA CGTGAGACTCGGCTTGTGGGATTGCTTCGGTGCGCGGGGGGGGAACGG CGAGGAGGTGGGGTGGTGGGTGGGGACCTCCCCTCATCTGCCTCCTGC GCAGCACCCCATCACTCACGCGCACACAGATGAGCAAGTCCGCCGACG CACTGCAGGCCACCCAACTGTGCTTCGTGTTGCTCGTGCATCGATCTC CCTCTGTGCAAGCGAATAGGCTCTCCTCAGATCAGATGTGATTTTCGT TCCCCTCCACATCACTTCCTCGAGCAGCTGACCTTTACCATGTCTTCG CAGGCGATGACGGCGCCCACTAGGCCTCGCCCCCTCCACCGCTGTTGC CAACATTGCAACTGCTTCTCTGTACTTCTCTGTGTTTCTCGAACTCTC TTCCCCCTCCCCCACCGTTTCCATCTCCGCGCGTGTGCGCGTCGCTGT ACACTCTTCGCTGGATGCCGGATCCCACGCAAACACACACGCACACAC ACACACACACATCAGACGTGCCTCACAAACCCGTTCGTGCTCGAACAT CGACAGCGCACCCAGACGTGTGGTCTTGCTCTTCTTCCTTTCGCTCGT TCTCAGCTCTTCTTCCTCCTTACCCAGTACGACGAGCTCTGACCTCTT GTCGTGTGCCCGCCTGTGTGCCATACACCTGGCACCCACTCCTAAACA CGCACTTATCACACCTCCATCGCAACACCATGCGTTTCCGCATTTACA AGCGCAAGGTCCTCATTCTGACGCTCGTCGTGGCCGCCTGCGGCTTTG TGCTGTGGTCCAGCAACGGTCGCCAGCGTAAAAACGACGCCCTGGCAC CACCGCTGCTGGATTCGGAGCCCCTGCGAGGTGCTGGGCACTTTGCGG CGTCAGTGGGGATCCGCCGGGTGTCGAATGACTCGGCATTTAAATATC CCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTG TGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAA GCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACAT TAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGT GCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGC GTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGG TCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATAC GGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAA AAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGT TTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCT CAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGT TTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGC TTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTT CTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCT CCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCG CCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACT TATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGT ATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCT ACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTA

SEQ ID NO.	Description	Sequence
		CCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCG CTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAA AAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG CTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTAT CAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTA AATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAA ACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTAT CAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACT CACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGA TTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAA AAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCG GTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAG GCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGT TATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGT TAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACA CTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATATTCTTCTA ATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATG CATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAA ATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGG CAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCT TCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGC GAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGAATTTAATC GCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCC TTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCG GATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGC GCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTA TCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTC TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAAT
198	pLMTB 9077	GACGTGCACGCAGTCCTGTCCCCACCCCCGACAGCAGGAGTGCGGGAC TGGGTGCTCTAACAAGCGCATGGTACGAGCTATGTGCTGGTGTGTAGC CAGCGGGGCTGTCATGCCATGTCGATCTCTCCCCGTGAGCAGCCCCCC AAAAAGACAACCTGATTTCTCCCTTTTTCCGATATTTCTCCCTTTGTG CTAAGGGGACCCTTCAGCAGCTCCCAGCGCCGCACATGCACACACTGG CGCGTGCTTCCGAGGTCCTCGGTGCACATATTTTCTATTATCTCACAC ACCCGGTTGCAGGGCGGCTCAATGTCACGGCGCGCGCACGCACTGCCT TGAGTACGGAACGGCGAGCGATACGACCGAGACGGCGCTGCCAGTAGG GTGTAGGACGCTGCGCATCTCATGAATGTATGAAGCATGCAGCCAACC ACACAAACATATGGGCGCACGAGTCTTCCCTCACAGACAGCGCGGCTG GTGAGGCGGCAGAAGGTCGGCCGCGGAAGGGCACACACTACGTTTCAC GCGTACATGACCCCGTCCGCTTTCCGCGCTATTTTAGGCGCACACCCG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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199	pLMTB 9080	ATGCGTTTCCGCATTTACAAGCGCAAGGTCCTCATTCTGACGCTCGTC GTGGCCGCCTGCGGCTTTGTGCTGTGGTCCAGCAACGGTCGCCAGCGT AAAAACGACGCCCTGGCACCACCGCTGCTGGATTCGGAGCCCCTGCGA GGTGCTGGGCACTTTGCGGCGTCAGTGGGGATCCGCCGGGTGTCGAAT GACTCGGCCGCTCCCCTCGTACCGGCTGTCCCCCGCCCCGAGGTGGAC AACCTCACCCTGCGGTATCGCTCGTTGGTTTACCAGCTGAATTTCGAC CAAATGCTGCGAAACGTGGACAAGGACGGAACATGGAGTCCGGGTGAA CTCGTGCTTGTGGTGCAGGTTCATAACCGGCCAGAGTACCTTCGCCTC TTGATCGACTCGCTCCGCAAGGCTCAAGGAATTCGGGAGGTGCTTGTG ATCTTTAGCCATGACTTCTGGTCTGCGGAAATCAACTCACTCATTTCC AGCGTTGATTTCTGCCCAGTTCTCCAGGTGTTCTTTCCGTTCAGCATC CAGCTCTACCCAAGCGAGTTTCCGGGCAGTGACCCACGTGACTGCCCT CGCGACCTTAAGAAGAACGCAGCCCTGAAGCTCGGGTGCATAAATGCA GAGTACCCTGATTCCTTCGGGCACTACCGGGAAGCTAAATTCAGCCAG ACGAAGCACCACTGGTGGTGGAAGCTTCACTTCGTGTGGGAGCGCGTG AAGGTACTCCAGGACTACACCGGCCTCATCCTGTTCCTCGAGGAGGAT CACTACCTGGCACCCGACTTTTACCACGTGTTTAAGAAAATGTGGAAA CTGAAACAGCAGGAGTGCCCAGGCTGTGACGTGCTGTCTCTTGGCACG TACACCACCATCCGTAGCTTCTACGGCATCGCCGATAAAGTAGACGTC AAGACTTGGAAAAGTACAGAGCACAACATGGGGTTGGCCCTGACACGC GACGCATACCAGAAGCTTATTGAGTGTACAGACACATTTTGCACGTAC GACGACTACAATTGGGACTGGACTCTGCAATACCTCACTCTGGCCTGC CTGCCGAAGGTCTGGAAGGTGCTGGTGCCACAGGCCCCCCGAATTTTT CATGCCGGTGACTGCGGAATGCATCATAAGAAGACGTGTCGACCCTCT ACCCAGAGCGCCCAGATTGAGAGCTTGTTGAATAACAACAAGCAGTAC CTGTTTCCGGAGACTCTGGTGATTGGCGAGAAGTTTCCTATGGCCGCT ATTTCCCCCCCGCGGAAGAACGGCGGGTGGGGGGACATCCGTGACCAT GAGCTTTGTAAGAGCTACCGCCGCCTTCAGTAGATTTAAATATCCCAA TGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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200	pLMTB 9082	ATAAGAAGACGTGTCGACCCTCTACCCAGAGCGCCCAGATTGAGAGCT TGTTGAATAACAACAAGCAGTACCTGTTTCCGGAGACTCTGGTGATTG GCGAGAAGTTTCCTATGGCCGCTATTTCCCCCCCGCGGAAGAACGGCG GGTGGGGGGACATCCGTGACCATGAGCTTTGTAAGAGCTACCGCCGCC TTCAGTAGGGCACGCAGTGTGTGTCTCGTTTGCTCCGAATTCTTTTTC CTTTTTCGTTTTTCGTGTTTCGCGTGCCTCTCTTTTCGGCGCATGCGA AAAACAGCACAGCAATCCAGCAAACGAACAAAGAAAATCATCGATGGC GCACGCTACGCCAAGGTTGGGGGTGGAGCGGGGGTGGCGGCAACGCCG TGTGCAGCAGAGCAGACACCCATCGCAGAAGCCCCCGGTATCTGCGTG CATGTGTGTTCGGTGCACGACCGGGTCGTGCTGCTTGTATGTTTGGGG AGGGAGGGGCTGCGTTGCCTTCCTCACGCCTCCCATCCCTCCATCCCT GTCGCCTTCTAGGGGTCGCCGAGGCGCGTGCAGAGACGGACTCTACAG GCCCAGGCGAGATGGCAACGGGCGCACGCACACACGCACGCGGAGGGA GGAATGTTTGGGATGAATCACACTGCACTGAAACCTCTCTTCTACCCT CATCAGCCTTCATCTTCACTCGACACACAGACGCGCCGCTGTCGCCAC CGCCTCAGAAAAGGCAGCAAGCACACGTGAAACCCTAAAATGCGGTTT CGTATTTACAAGCGGAAGGTGCTTATTCTGACACTGGTGGTGGCTGCC TGCGGGTTCGTTCTGTGGTCATCGAACGGCCGGCAGCGGAAGAACGAC GCGCTGGCTCCACCACTGCTGGACTCGGAGCCGCTCCGGGGTGCCGGC CACTTCGCAGCTAGCGTCGGAATCCGTCGCGTTAGCAACGACTCCGCA TTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAG CTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATA CGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGC TAACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGA AACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGA GGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCG CTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAG GCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAAC ATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCG TTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAA AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGA TACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCG ACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGC GTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAG GTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCC GACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTA AGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGC AGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT AACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTG AAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA CAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATT ACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACG

SEQ ID NO.	Description	Sequence
		GGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTC ATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAA TGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGAC AGTTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATA TCAGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAA GGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTAT CGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTC CCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACG ACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACT TGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCA ACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACG CGATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGG CGCAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGA TATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTG AGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGA AGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTA ACATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGC GCATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCG ACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTG GAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTC ATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGT CTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATA GGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAA ACCATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGG CCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACAC ATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGG AGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGG GGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCAC CATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGC ATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGA TCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGT GCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGA CGTTGTAAAACGACGGCCAGTGAATTGACGCGTATTGGGATATTTAAA T
201	pLMTB 9083	ATGCGGTTTCGTATTTACAAGCGGAAGGTGCTTATTCTGACACTGGTG GTGGCTGCCTGCGGGTTCGTTCTGTGGTCATCGAACGGCCGGCAGCGG AAGAACGACGCGCTGGCTCCACCACTGCTGGACTCGGAGCCGCTCCGG GGTGCCGGCCACTTCGCAGCTAGCGTCGGAATCCGTCGCGTTAGCAAC GACTCCGCTGCCCCGTTGGTACCTGCAGTCCCGCGCCCTGAGGTAGAC AACCTGACCCTGCGCTATCGCAGCCTTGTTTACCAGTTGAACTTCGAT CAGATGTTGCGCAACGTTGACAAGGACGGGACTTGGTCGCCCGGTGAG CTTGTGCTCGTGGTGCAAGTGCACAACCGCCCCGAGTACCTGCGCCTG CTGATCGACAGCCTCCGGAAGGCCCAGGGTATCCGCGAAGTTTTGGTC ATTTTCTCGCACGACTTCTGGTCGGCGGAGATTAACTCGCTGATAAGC AGTGTCGACTTTTGCCCGGTCTTGCAGGTATTCTTCCCTTTTAGCATC CAACTTTACCCATCCGAGTTCCCGGGAAGCGATCCTCGGGACTGCCCA CGCGACCTTAAGAAGAACGCCGCGCTCAAGCTGGGTTGCATCAATGCG GAGTACCCCGACTCGTTCGGTCACTACCGGGAAGCGAAGTTCAGTCAG

SEQ ID NO.	Description	Sequence
		ACTAAGCATCACTGGTGGTGGAAACTGCACTTCGTATGGGAGCGGGTA AAGGTGCTGCAAGACTACACCGGTCTGATCCTGTTTCTGGAGGAGGAC CACTACCTGGCCCCGGATTTCTACCACGTGTTCAAAAAGATGTGGAAG CTGAAACAGCAGGAGTGTCCCGGCTGCGACGTCCTGAGTCTGGGGACG TACACGACAATACGCTCTTTCTACGGTATCGCAGATAAAGTGGATGTT AAGACTTGGAAATCAACTGAGCACAATATGGGCCTGGCACTCACTCGG GATGCTTACCAAAAGCTCATCGAGTGCACAGATACTTTCTGTACCTAC GATGACTACAACTGGGACTGGACTCTTCAGTACCTGACTCTCGCATGC CTGCCTAAGGTCTGGAAAGTGCTCGTGCCGCAGGCACCGCGAATTTTT CACGCCGGTGATTGCGGCATGCACCACAAGAAGACTTGCCGCCCGAGT ACACAAAGCGCGCAGATAGAGTCCCTCCTGAACAACAACAAGCAGTAC CTGTTCCCCGAGACTCTGGTGATTGGGGAGAAGTTTCCTATGGCCGCC ATCTCTCCACCTCGCAAAAACGGTGGATGGGGCGACATCCGTGACCAT GAGCTCTGTAAGTCGTACCGGCGACTCCAGTGAGACGTGCACGCAGTC CTGTCCCCACCCCCGACAGCAGGAGTGCGGGACTGGGTGCTCTAACAA GCGCATGGTACGAGCTATGTGCTGGTGTGTAGCCAGCGGGGCTGTCAT GCCATGTCGATCTCTCCCCGTGAGCAGCCCCCCAAAAAGACAACCTGA TTTCTCCCTTTTTCCGATATTTCTCCCTTTGTGCTAAGGGGATTTAAA TATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTT CCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCC GGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTC ACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTG TCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGT TTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGC TCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTA ATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGA GCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTG GCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGA CGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAG GCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTG CCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCG CTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTT CGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGC TGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACAC GACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCG AGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTAC GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCA GTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACC ACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGC AGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCT GACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGA TTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATGAAGT TTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTAG AAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGA TTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAA AACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCGGTCT GCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCG TCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAA

SEQ ID NO.	Description	Sequence
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202	pLMTB 9303	CGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTAT CCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTA CCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTA CTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGC ATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGCGCA TGCCCGACGGCGAGGATCTCGTCGTGACGCATGGCGATGCCTGCTTGC CGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTG GCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCC GTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCG TGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATC GCCTTCTTGACGAGTTCTTCTGACTAGCCTCGGAGATCCACTAGTTCT AGTTCTAGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGCGGAATCG GTCGCTCGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGC AGCAGGATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAAT TCGCGATCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTT TTCCCACCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAGA AGGGACGGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCTTC TCTTGCTTGTGGCACTCACGCTCATGCGTCAAGGCGGCCCCACGCCGA GCCCCTGCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGATGCCGTC GATGCGCAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAGGGCACAC TATCATGCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTCGGCGGA GATGCGTCACGCACGTGCCAGATGATGCGCTACGCCTTCCTTGACTTG CGCCCCCCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCACACACAC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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203	pLMTB 9305	CAGACGACGGCGCAGCGGTGGCAGTGTGGACGACACCAGAGAGCGTCG AGGCAGGCGCGGTGTTCGCAGAGATTGGCCCACGCATGGCGGAGCTGA GCGGCAGCCGCCTGGCAGCACAGCAGCAGATGGAGGGCCTGCTGGCAC CGCACCGCCCAAAGGAGCCAGCCTGGTTTCTGGCGACAGTGGGCGTGT CCCCGGACCACCAGGGCAAGGGCCTGGGCAGCGCAGTGGTGCTCCCAG GCGTCGAGGCTGCAGAGCGCGCAGGCGTGCCGGCATTCCTGGAGACAA GCGCGCCACGCAACCTGCCGTTCTACGAGCGCCTGGGCTTCACCGTGA CGGCGGACGTCGAGGTGCCAGAGGGCCCACGCACATGGTGCATGACAC GCAAGCCAGGCGCGTAGCTAGCCTCGGAGATCCACTAGTTCTAGTTCT AGGGGCCGAATTCAGATCCTCGTGTGAGCGTTCGCGGAATCGGTCGCT CGTGTTTATGCCCGTCTTGGTGTTGTGCTCGCAAGGCGGTGCAGCAGG ATACCGTCGCCCTCCTCTCTCCTTGCTTCTCTGTTCTTCAATTCGCGA TCTCACAGAGGCCGGCTGTGCACGCCCTTCCTCACCCTCCTTTTCCCA CCTCTCGGCCACCGGTCGGCTCCGTTCCGTCTGCCGTCGAGAAGGGAC GGGCATGTGCAGCTCCTCCCTTTCTCTCGCGCGCGCATCTTCTCTTGC TTGTGGCACTCACGCTCATGCGTCAAGGCGGCCCCACGCCGAGCCCCT GCGCTCCCTTCCCTCTTGCGCATCCGTAGCGCGGATGCCGTCGATGCG CAAGGCCGGCATGAAGGAGCGCGTGCCCTCAAGAGGGCACACTATCAT GCCCTACGTGGGCCACGCAGCGATGAGGCCGGCTTCGGCGGAGATGCG TCACGCACGTGCCAGATGATGCGCTACGCCTTCCTTGACTTGCGCCCC CCTCTCTTCCTCCGTCTCTCACTCTCTCTCTCTCACACACACACACAC ACACACACACACACAAAGCTCCGGTTCGTCCGGCCGTAACGCCTTTTC AACTCACGGCCTCTAGGAATGAAGGAGGGTAGTTCGGGGGAGAACGTA CTGGGGCGTCAGAGGTGAAATTCTTAGACCGCACCAAGACGAACTACA GCGAAGGCATTCTTCAAGGATACCTTCCTCAATCAAGAACCAAAGTGT GGAGATCGAAGATGATTAGAGACCATTGTAGTCCACACTGCAAACGAT GACACCCATGAATTGGGGATCTTATGGGCCGGCCTGCGGCAGGGTTTA CCCTGTGTCAGCACCGCGCCCGCTTTTACCAACTTACGTATCTTTTCT ATTCGGCCTTTACCGGCCACCCACGGGAATATCCTCAGCACGTTTTCT GTTTTTTCACGCGAAAGCTCTGAGGTTACAGTCTCAGGGGGGAGTACG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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204	pLMTB 9832	GGGAAGGATAATGTGAACGGACAACTTCTCTGTCCTTTTTCGTTTTAA TTTGTGATTGTTTCCCGAAGAAGAAAAGCAACAAAACCGAAAGGGGAA GGAGCGATGTGCGCTCGGCAGAATAGCCTGTGCAAAGTTGGCGGCAGC GCACGTGCGCACCTGGAGATGGCAACAGCGGCGGCAGTATGCACGCAT GCACACACCTGGCAGCGCCAGAGATGGAAAGGGACGAGGATAGAGAGG GTAAAGTGTCGGAGGAGAACAAGCACATAAAGGGAGGGGCGAGGTCGT GACGGCGCGCGTGCTTGTTTTGCCCCCCCCCCTTTCCTGTGGTTTTGC TCCGACCTCTCTCTTCCTGTGTGTTCCCACCCTCTCTCTGGATGCATA TCTGCGCGTGTTTTGCATAGGCACACACGCGACCCGCGCTGTTGCTGT CCGCTGCCATCATGTCACCTCCCGCCTTTTCTCTCCTCTGCACCCGCT GTGCTCGACAATCGCAGTGGAAAAAAAGGCGTGTGCTCCTTTTACATG CTTCATGCCCGACCCCTCTCCGTGGCGTGTTTACACTTCAACGCTACC TCTTGCTCCTCCCCCACCCCCGCCTTTGCGTGATCTGCCAGAGTCGGC AGTACACCACCCTCTCGCTCTCGTCCTCCCTTGCTGCTCAACATCCGC GCGGAGACACGCACCCACACAGGCACACCAGACGCCAAGAAGGTGAGA GGGCGAGTGAGAATCAGCAGGGGAAACCTCTTGCCGCGGTGTGCGTCC GTCTGTCTGTCTGCTCCTTGCCTCTCTCGACGATTGGCGTTTGTTTGC TCTCTTAGTGCATATACGATGCTTTACAGGTTTTCCAAATGTTCGCCA ACCTCAAGTACGTGAGCCTTGGAATCCTTGTGTTTCAGACAACGAGTC TGGTGCTTACGATGCGGTACAGTCGCACATTGAAGGAAGAGGGCCCGC GGTACCTCTCCTCCACAGCGGTTGTCGTAGCGGAGCTCCTTAAGATCA TGGCCTGTATCTTGCTCGTTTACAAGGACTCCAAGTGCAGCCTTCGCG CTCTCAACCGCGTGCTGCATGATGAGATCCTTAATAAACCTATGGAGA CGCTTAAGTTGGCGATCCCATCAGGCATCTACACGCTGCAAAATAACC TGCTCTACGTGGCGCTTTCGAACTTGGACGCCGCTACCTACCAGGTCA CCTACCAGCTCAAGATCTTGACGACGGCCCTGTTTTCCGTGTCTATGC TCTCTAAAAAGCTCGGTGTGTACCAGTGGCTGTCTCTGGTTATTCTGA TGACGGGAGTGGCATTTGTACAGTGGCCTTCGGACTCACAGCTTGACA GCAAGGAGCTCTCCGCCGGAAGTCAGTTTGTGGGCTTGATGGCGGTGC TGACCGCGTGCTTTTCCTCTGGCTTTGCGGGTGTGTACTTTGAGAAAA TTCTCAAGGAAACGAAGCAGAGTGTTTGGATTCGCAACATTCAGCTCG GCTTCTTCGGTTCTATTTTTGGCCTCATGGGGGTCTACATCTACGACG GTGAGCTGGTGAGCAAGAATGGGTTCTTTCAGGGATACAACCGTTTGA CGTGGATCGTTGTCGTGCTGCAGGCTCTTGGTGGCCTTGTGATCGCTG CCGTGATTAAGTACGCGGACAACATCCTCAAGGGGTTCGCAACGTCAT TGTCCATAATCCTCTCTACACTGATCTCATACTTTTGGCTCCAAGACT TCGTGCCGACGTCAGTTTTCTTCCTCGGAGCAATTCTGGTGATCACAG CCACCTTTTTTGTATGGGTACGACCCTAAGCCCGCCGGTAACCCGACGA AGGCCTGAGCTTCATGTACAATCATCGCGCACCTTTCTTTTTCATTGA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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205	pLMTB9833	GCTCCGGCCCCTTCCGGGTCCAGTATTCCTCCCGGGACTCCTTCAAGG TCCTGGCCCGGAACCTGGGCGTCATGGACGACCTGAAGTCCGGCGTCC CCCGGGCCGGCTATCGGGGCGTCGTCTCCTTCATCTCCCGGGGCCGGC GGATCTATCTGGCCCCCCCCGAGGGCTGGACCAAGTATGACGTCTCCT GGTCCTAATGCCCCGCCGCCGTTGCCGCCACACCGCCGTGGCCAATAC CAAAGCGTGCATATTTCGGGCGCGTCTGCATTTTTAGTCCCCCTTCTT AGGCCTTGTATTGTTCACTTCATCTTCCCTTCTGTAGGACGTCTCTCT GTTCCATTTCTTTTCTTGTATGCGCCCCCTCACTACCGCCTCCCACGC TCTCTCTCTCTCGCTCTGTGTGTATGTGTGTGTGTGTGTGCACACT TTCGCGTCTTCGACTTGTCCCTTTGTTTTTCTCACTCTCTCTGCCCCC TCCCCACCTCACCGCCTGTCTATGCGCTTCCCTCCCTGTTGTTCTGTA TGCGTAGGTGTATACGTGGTACACCTCGAGTGCCACGGCGTGGCGCAC ATAGCAGCGTTTTCGTTTTTTCGCTTGGTAGAAGATGCGCAAACGGCG TTCACGACCACTGAAACAGCGCGACATCGGCGCGCACGCAGTCCCCTT TGCCAATAGCGAAATCCGGCACCCGCACGTCAGTTCTGGCTCTCTTTC CTCCTCTTCCCATGACCCGATGGTGGAGCTGCAACCAGCTTCTCTTTT CGCCTTCTGGGAGGCGGGGGTCATGCCTACTCCCTCAGTCTTCATGCT TTATCCTTCATTGCCTACCCCTTTGTTTGCTGCCGTCTACCTCACTTT CTTCCGACACACACACACACACACATACACACACACATACACACACAC ATACACACACACATACACGTGCCGTTCATCTCTTCTTGCACCTCACAA TCTGCGCCTTCTTCTTTCAGCTGTTCACTGAACTAGAAGCATCTGGCG AATACCCTCCCCCCTCAACATACACACCGTACCACCCCCTTCTCTCCC CCTCCACCTCCAAAAAAAAAATATATATTTCTCCTCTGTGCCTTCGCC CATCTCATCATTTATCATGCGCTTCCGCATCTACAAGCGAAAGGTGGT GATACTCACGCTCGTCGTGATAATTTGCGGCTTCGCCGTGTGGAACTC CGGCAAACCGAAGAAGGCTAGCACGGTGTTTCCAAAGGAAGTGGAAAC TGTGAAGCGCTCGAGCGTGGGGTCTCAAATCCAGGCCACAATCCCGGT GACACGCAAGCCGATCAATGAGTCATTTAAATATCCCAATGGCGCGCC GAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTA TCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAA AGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCG CTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTA ATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTC TTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCG GCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGA ATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAA GGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCT

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206	pLMTB9834	ATGCATGCCCAGCGGTCAAAAAACGAAAATCGAGAACGTACTTCAGAA CTCGGGCAACCAGCTGTTTCCAAAGCAACTTCTGATCACCAAGCGCTT

SEQ ID NO.	Description	Sequence
		GCCAGCGTCCGGGGCGAAGGGCGTCGCTCCTCATGTTAAAAACGGTGG TTGGGGCGACATCCGGGACCACGAACTGTGTAAGTCGTACCTCCGGCT CCAGTGACTGCGTTACGCGCACACTCGCATGGGATAGAGGAGAGGAGT GTTTCGAATGTAAATAGTTTCTCCCCAGGAATGTGTCTAAGCGCGAAC AAATAATACGAACAGTGAACACGCCGCAGCCTTGCTGTGCATTCAGAC TGCCTTTGACAAAGAGACATACGCATAGCCACGCAAAGATGCCGTTGA CCCACCGTCTTGCTCTCGTGTTGCGCAACATGTCCTTCCGTCATTTTT TCACCTGTGTCCATGTCAACTTCCCTTCCTACCATTGATGCCGAGTCA TCATCTCCGCGGCTTTGGTTATGCGCACTTTTCCGAAACGCCGGCTAC TCTCAGCTTTTCCCTCCGCTTTTCACCTCTATTGACTTACATACCCTA AGCTGCAGGTGCTGAAGCTTCCCAGCTTGTGGTTGCAAAAGTAGCAGC TGCTGGTTCAAACACGCATCTACGAAAGCAAATAGAAAAAAACGCCGG AAACTCCGTGCACACGCAAACACGCGTACGGGCACAGCGCAGACAAGG AACACGGAACAACATCACAATGCTCAAGAAGAGCAGCCTCGTTCTTTG GGGAGTTGTATTGTTTGTGGCATGGAATGCTCTGATACTGTTTTTCCT GTGGACGCGTCCTCAGAGCCTGTCCGACCACTCGCACCTGACCGAGGA GGTGATCCGCTTGGCCCAGGATGCGGAATCGGAGCTGGAGCGTCAGAA GGATCTGCTTCAGCAGATCTACCGATAATTTAAATATCCCAATGGCGC GCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTG TTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTG TAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTT GCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCA TTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCG CTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCT GCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCAC AGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCA AAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAG GCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAG GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGG AAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATA CCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTC ACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGG CTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGG TAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACT GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGG TGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAG AACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAA AAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGG TGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATC TCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAA CGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGAT CTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTA AAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAG CATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATA TTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCA GTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCG TCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTT ATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGG

SEQ ID NO.	Description	Sequence
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207	pLMTB 9835	GCTCGGAACGGTGCGAGTGCAATACACGACTCGAGACTCCTTCAAGGC ATTCGCGAAGGCTCTGGGCGTAATGGATGACTTGAAGTCCGGCGTCCC ACGTGCCGGTTATCGCGGCATCGTCAGTTTTCTTTACCAGAGCCGACG TGTGTACCTGGCACCCCCGAGCGACTGGACTGGCTACGACCCGTCCTG GAGTTGATGGCCACTGCCTGGAAGTAGGCCACACAAATGCACAGGCAT TCATTAGTGAGCGTGCAAGAGCAGACGACCGCCTTCAACAGCGCTTCG CCCTCACGCATGCAGAAGCGTTGCTTTTTTTGTCTACTCAGCTTCCTT CTTCCCAGCTCACTCGGTCGCGTTGGCTGGGGTCTTCAAAGAAGAGGG CCAAACACCAAACAAGAACGAGCCAGCGCCACTCAGCTACGGGCTAAA GCACATGCGGACACGCTCACAGGCGCGTTCGCTGCGCAGAAGCACAGC TGAGCTGCAAAGATATAGATGCGCCCCCGCGAGGCGGCAGTGAGAGCG GTTCTCCTTCATTGACTGACACGTGAAGCTGGCCCCATCCACCCCTGC CCACGCAGCCCGTCGAAAGGGGGACACCGGCGCATGATAGGGTAAGGC GAGCGTGCGTGTGTATGTGCGTCTGATCGCTCCCTCACGGGCTCATGC TGCATCTTCCTCGGCGTCCTCTGCACGCCCGCTCTCTGCGTCTCACTC TCTTCCACCTGATGTATTTACCTCTCCGTATCTCTCCGTGTTCATTTC TACGTTCTCGCCTTCGCGCCCAACGTCACACCTGCTGTCTTTTGTTTC TTGCACACACGCGGCGTCCCTTCCGCACTACCCACAGTCCCAGCGCTT TCCACTCACCCCACCACCTCACCTCTACAATGCGCCCACGGAAAACAA TACTGCTTGTGGGAGTGCTGGTAATCTGGGTGCTTATGACCTACCTTG CCTTCATGCGCAGTGTGCGCGGTACAGACGGCTCTCGACCTCGGCCAG CATTCGCTTCAAACAAGCTCATGTTGGAGAAAGTCCAGGACTTTGAGC AGAACCTTAAGTCATTTGCGGACAGCCGCCAAAACCTATTTAAATATC

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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208	pLMTB 9836	ATGCGCCCACGGAAAACAATACTGCTTGTGGGAGTGCTGGTAATCTGG GTGCTTATGACCTACCTTGCCTTCATGCGCAGTGTGCGCGGTACAGAC GGCTCTCGACCTCGGCCAGCATTCGCTTCAAACAAGCTCATGTTGGAG AAAGTCCAGGACTTTGAGCAGAACCTTAAGTCATTTGCGGACAGCCGC CAAAACCTTTACCGGGACATTATCAACATCCTGCGCCGGACCGACAAG GTGTCAAGCGTGCCAGCACAGCCAATTCCGGCGGTGCCATCCCAGGAA AGCCCAGGGGCTGCGGTGCAGGAGTCTGAGGTGCCGAAGGAGCGTCAG GCGCCCCCGCAGCGCTACCTTAACAACGACCCGGCGTTTCCTGTCATC CCAGTGGTGGTCTTTGCATGCAACCGGATCAGCGTCAACAAGTGCCTC GATGATCTGATCCGGTACCGCCCGAGTGCAGAGCAGTTTCCAATCATC GTCTCCCAGGATTGTGACGACGAGGCCACCCGGAACACCATCCTCAGC TATCGTGACGAGGTCACACTGATCCAGCAACCCGATCAGTCCGACATC CCGGTTCCTCCCAAGGAGAAGAAGTACAAGGGTTACTACAAAATAAGC CGCCATTACGGGTGGGCTCTTCGCGCTGTGTTCGGACAGGGCTTTGAC TCTGTTATCCTGGTTGAGGACGACCTGAGCGTCGCACCCGACTTCTAC GAGTACTTTCTGGGGACCTACCCCATATTGAAACGCGATAAGTCCCTT TGGTGCGTAAGTGCCTGGAATGATAACGGTAAAGAGGGACTCATCGAC ACAACCGCGCACGATTTGTTGTATCGCAGCGACTTCTTTCCGGGCCTT GGGTGGATGATGACGAAGGACCTGTGGGACGAGTTGGAGCCTAAGTGG CCCAAGGCCTTTTGGGATGACTGGATTCGCCAGCCGGAGCAACGTAAG GAACGGGCGTGTATCCGTCCTGAGCTGCCCCGTACGCGTACATTTGGT AAGATCGGGGTGTCTAACGGACTTTTTTTTGATAAGCACCTGAAGTTC ATTAAGCTTAGCGAAGAGTTCGTGTCCTTTACGAAGACGAACCTCAGC TACCTGGTCAAAAGCGCGTACGACGACGCATTCCTGAAAACCGTCTAC CAGTCGCCAGTCGTGACGCTGGACGAACTGAAGCGCGGCATGGTTATG ACACGTGAACCCATCCGCATCGCGTACCATACGAAGGAGCAGTACAAA CGCGCGACAAAGAACCTTGGTCTGATGGACGATTTCAAGTCTGGTGTC CCTCGTACAGCCTATCGCGGGGTTGTGTCCTTCTTCTACAACGGCCAG CGCGTGTATCTCGCGCCTTCTGCTAACTGGAAGGGCTACGATCTGACA TGGTCCTAGGGGAAGGATAATGTGAACGGACAACTTCTCTGTCCTTTT TCGTTTTAATTTGTGATTGTTTCCCGAAGAAGAAAAGCAACAAAACCG AAAGGGGAAGGAGCGATGTGCGCTCGGCAGAATAGCCTGTGCAAAGTT GGCGGCAGCGCACGTGCGCACCTGGAGATGGCAACAGCGGCGGCAGTA TGCACGCATGCACACACATTTAAATATCCCAATGGCGCGCCGAGCTTG GCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTC ACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGG GGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTG CCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATC GGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCT TCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCG GTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGG

SEQ ID NO.	Description	Sequence
		GATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGG AACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCC CCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAC CCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTC GTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCC TTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGG TATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCAC GAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGT CTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTT GGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGT AGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTT GTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGAT CCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCA CGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAG ATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATAT GAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGA AACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAA AGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGG ATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCA ATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAG AAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTA TGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCA TCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCC TGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACA GGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATA TTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTC CCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATA AAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGT CTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGT TTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATT GTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATAT AAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTT TCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGC ATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATT TAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTG CCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAA AATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGAC GGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGT CTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCG GGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAG ATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGC GTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGC AACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAG CTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCA GGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGACG CGTATTGGGATATTTAAAT

SEQ ID NO.	Description	Sequence
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210	pLMTB 9839	GCTCCGGCCCCTTCCGGGTCCAGTATTCCTCCCGGGACTCCTTCAAGG TCCTGGCCCGGAACCTGGGCGTCATGGACGACCTGAAGTCCGGCGTCC CCCGGGCCGGCTATCGGGGCGTCGTCTCCTTCATCTCCCGGGGCCGGC GGATCTATCTGGCCCCCCCCGAGGGCTGGACCAAGTATGACGTCTCCT GGTCCTAAGCCCACACCCTCCCTCCTCTCTGTCTCTCTTAGATCTCTT TCAAAGGTCGTGGTGGAGATGAACATCTCGGCTCATCTCCTCCCGGAG AGGGAGAAGCACTGGGCCTCTGCACGCGGCAGCGGCACGCACACGCGC ACATGTCTGCGTGTGTAAGGGGCGTGGCAGGCAGCGTGTGTGCCTCCA CGCTGCCGCGCACGCCGTATCATAGATGCACTTCTGTTTTTTATTATT TTAAATGCGCCATGCAAAGGGGGGAGGGGAATATGTTCTGCGTAATGT GCGCGCACTCGATCTCTGTGACCCGGCGATGGCGTGCGTGAGAGAGGG CCGTGCGTGGGTGCGATGGACGGCGTCGTCCTCGCACTCCGTGCTGGC CGGCAGCTGAGGAGAGAGCGCAGAGGACGCAAAGGTAGCGAGCAAGGA GCGGCACGCCCACGCAGTGCGCGCGCGTATAGGTGGATGCCTCTCTGC GCGATGCGTGCGTGTGCCTGTGCCGCGCAAGTAACGAATGACGCGCCA GCGGTGCTGCTGCCGCTGCTTTTCCGCCCACCTCATCGAAGCGGCCCCG TCGTCGGCACACAGGGACGTCTGCGCTGCCGGCCCTGCGCTGATCCGC TTGTACGTGCGGCGCTTCAGCCCTCTACGCAGCAGCGGGGTGGGAGGG

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SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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213	pLMTB 9852	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGTGAAATGGTGTATCCCATGACACGTCTTACGTCATGTTCCTCC CTCCTTCGTATGCGTACGACTCTCCTCCGCCTCCGCCTCCGCCTCCGC CTCCGCCTCCGCCTCCGCCTTCTCTGCGCCGGTTTCCTGGAGGATGGA GAGCTCTTGCTCATAGATTGAAGAAAGACCAGGCAAGCCACGGAAAAC TCCGAACAAAAGCGGACTCACGCGGCCGTCTGCATTTGACGTGCTTGC ATACATATACGCACCAACCTTGTGCACGTCTTGTTGACATCCGTAACA CTTGCCTCATTTTTTCCGTGCTGCTCGGATGCACACTCCTGGTGTGGG GCGTAGTCACTATTCGTCTCTCACCAACACACACACACACACACACAC ACACCTGTACATCTCTCTCTCTCTCCTTTTCTGTGTGCCCCGGCGGAC GTGCGTGCGTGTCTAATCACTGAAATTCTTCACATTGCATAGAACGTA

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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214	pLMTB 9853	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAAGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCGAGATCGAG GGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCAAGCTG AAGGTGACCAAGGGTGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCC CCTCAGTTCATGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGAC ATCCCCGACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAG CGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGGAC TCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGC ACCAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACTATGGGC TGGGAGGCCTCCTCCGAGCGGATGTACCCCGAGGACGGCGCCCTGAAG GGCGAGATCAAGCAGAGGCTGAAGCTGAAGGACGGCGGCCACTACGAC GCTGAGGTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGCTGCCC GGCGCCTACAACGTCAACATCAAGTTGGACATCACCTCCCACAACGAG GACTACACCATCGTGGAACAGTACGAACGCGCCGAGGGCCGCCACTCC ACCGGCGGCATGGACGAGCTGTACAAGTAGCCTCGGAGATCCATGGGG TGTGCTTTCCAGGCCGCTGAGCGGAGAGGTGCGGAGGGCAGTCCAGGA AGGTGGGGAGGGAGGAGGGATGGTACCCAAGCGAGAAGGGGACGGACG AGCTCAAGGCTGAAAGTTTCAGCCAACGGTTTCCGGCGCTGCATCCGT TCTCATGTTTTGGCACTCGTCATATGCTTTTATTTCTGTAATCGTTTT TGGAGGAGGGAGGAGGGGAGGAGATGTGGGCGAGCAGAGACGGCGGCA GCAGCAAAAAAAAGGGGGGGCGCCCACCGGCGCTGGTGAGGCGTGCAG GGGGAAGAGGGTGGCATGCGACATGCACAACCAAACGTGCGCGTGTGC AGATGTGCTGGCGTGCGTCGTGAGTGTGTGATTTATTTTTGAATGACA CCTTATCATTGCTCTCTCTGCCTCACACTCTCTCGCTTCCACCGCTTT ACCTTGCTACGAGTGTCGCTTCGGTATACCGTCACTGACGTTGCCTCT CCCCTCTCCATACTTTCGCCTGCAGGATTTAAATGGTACCATCCCAAT GGCGCGCCGAGCTTGGTCGAGCATGGTCATAGCTGTTTCCTGTGTGAA

SEQ ID NO.	Description	Sequence
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215	pLMTB 9854	ATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGAGCATGGTCATA GCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACAT ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAG

SEQ ID NO.	Description	Sequence
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SEQ ID NO.	Description	Sequence
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216	pLMTB 9855	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAAGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCGAGATCGAG GGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCAAGCTG AAGGTGACCAAGGGTGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCC CCTCAGTTCATGTACGGCTCCAAGGCCTACGTGAAGCACCCCGCCGAC ATCCCCGACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAG CGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGGAC TCCTCCCTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGC ACCAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACTATGGGC TGGGAGGCCTCCTCCGAGCGGATGTACCCCGAGGACGGCGCCCTGAAG GGCGAGATCAAGCAGAGGCTGAAGCTGAAGGACGGCGGCCACTACGAC GCTGAGGTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGCTGCCC GGCGCCTACAACGTCAACATCAAGTTGGACATCACCTCCCACAACGAG GACTACACCATCGTGGAACAGTACGAACGCGCCGAGGGCCGCCACTCC ACCGGCGGCATGGACGAGCTGTACAAGTAGCCTCGGAGATCCATGGAG GGAGAATGATGATGTGACCGAGGTGGCGCGCTCGCACGTGTCCTCCTC CTCCCCCTCCTCCTCCTCTTCTTCTTCCTCCTCATGGCCGCCCTCTGC GGTGGTCCTCTCTCACCTTTTCATGTGTTCCTGTGTGGCGTGCGTGTC GCTCAGGGGATTCCCGTGTGTGTGTGGGGGGGGGGGATGCCGGCCACT GGGGCGTGGGGCGTGCGGGCGCGGCAGCAGGCTCTCGAGGTGATGGCT GGTTGGACTCTTGGCGTGGGGGGCGGTGCGGGTGTCCGTTGGTTGACC GGCCCGTAGTGGAGCACGGGCACAAGTGGACACCGGCAGGAACGTTCC TGCTGGTCACTGTTTCGATACTGCTTTCCTCGTCACCCTGTGCGTCGC TCTCTGTGCCCCTCTCCTCCCCTCTCTGTCTCTGTCTCTCTCTCTGTG TGAGTATGTGTGTATAGGTGGGGGGGGGAGAGAGAAGCTGTGCGTGTG CACGGTGGTATTGTGTGGCCTGCAGGATTTAAATGGTACCATCCCAAT GGCGCGCCGAGCTTGGTCGAGCATGGTCATAGCTGTTTCCTGTGTGAA ATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAA AGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTG CGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGC TGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTG GGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTC GGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTAT CCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCC AGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCC

SEQ ID NO.	Description	Sequence
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217	pLMTB 9856	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATCCT GCAGGTGAAATGGTGTATCCCATGACACGTCTTACGTCATGTTCCTCC CTCCTTCGTATGCGTACGACTCTCCTCCGCCTCCGCCTCCGCCTCCGC

SEQ ID NO.	Description	Sequence
		CTCCGCCTCCGCCTCCGCCTTCTCTGCGCCGGTTTCCTGGAGGATGGA GAGCTCTTGCTCATAGATTGAAGAAAGACCAGGCAAGCCACGGAAAAC TCCGAACAAAAGCGGACTCACGCGGCCGTCTGCATTTGACGTGCTTGC ATACATATACGCACCAACCTTGTGCACGTCTTGTTGACATCCGTAACA CTTGCCTCATTTTTTCCGTGCTGCTCGGATGCACACTCCTGGTGTGGG GCGTAGTCACTATTCGTCTCTCACCAACACACACACACACACACACAC ACACCTGTACATCTCTCTCTCTCTCCTTTTCTGTGTGCCCCGGCGGAC GTGCGTGCGTGTCTAATCACTGAAATTCTTCACATTGCATAGAACGTA GCGTCAGGACGCAGCCTCGAACGGCGATGAAGCCAGAACTCGAGAGTA TGAAAAAGCCTGAACTCACCGCGACGTCTGTCGAGAAGTTTCTGATCG AAAAGTTCGACAGCGTCTCCGACCTGATGCAGCTCTCGGAGGGCGAAG AATCTCGTGCTTTCAGCTTCGATGTAGGAGGGCGTGGATATGTCCTGC GGGTAAATAGCTGCGCCGATGGTTTCTACAAAGATCGTTATGTTTATC GGCACTTTGCATCGGCCGCGCTCCCGATTCCGGAAGTGCTTGACATTG GGGAATTCAGCGAGAGCCTGACCTATTGCATCTCCCGCCGTGCACAGG GTGTCACGTTGCAAGACCTGCCTGAAACCGAACTGCCCGCTGTTCTGC AGCCGGTCGCGGAGGCGATGGATGCGATCGCTGCGGCCGATCTTAGCC AGACGAGCGGGTTCGGCCCATTCGGACCGCAAGGAATCGGTCAATACA CTACATGGCGTGATTTCATATGCGCGATTGCTGATCCCCATGTGTATC ACTGGCAAACTGTGATGGACGACACCGTCAGTGCGTCCGTCGCGCAGG CTCTCGATGAGCTGATGCTTTGGGCCGAGGACTGCCCCGAAGTCCGGC ACCTCGTGTTCGAAATTTAAATGGTACCATCCCAATGGCGCGCCGAGC TTGGTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGC TCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCT GGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCAC TGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAA TCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCG CTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAG CGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAG GGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCA GGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCC CCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAA ACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCC TCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCG CCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTA GGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGC ACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATC GTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAG CCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAG AGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTG GTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTT TTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAG ATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACT CACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCT AGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATAT ATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAAT GAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTTGAA

SEQ ID NO.	Description	Sequence
		AAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATA GGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACAT CAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTG AGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTT TATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGT CATCAAAATCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCG CCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAA CAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAA TATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTT TCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGA TAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTA GTCTGACCATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCAT GTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGA TTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCAT ATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACG TTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAA GCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTA TTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAG TGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATA AAAATAGGCGTATCACGAGGCCCTTTCGTC
218	pLMTB 9857	TCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCC CGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAG CCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTA ACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGT GTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCC ATTCGCCATTCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGG CCTCTTCGCTATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGC GATTAAGTTGGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAA CGACGGCCAGTGAATTGACGCGTATTGGGATGGTACCATTTAAATTTA ATTAAACCGAACTGCCCGCTGTTCTGCAGCCGGTCGCGGAGGCGATGG ATGCGATCGCTGCGGCCGATCTTAGCCAGACGAGCGGGTTCGGCCCAT TCGGACCGCAAGGAATCGGTCAATACACTACATGGCGTGATTTCATAT GCGCGATTGCTGATCCCCATGTGTATCACTGGCAAACTGTGATGGACG ACACCGTCAGTGCGTCCGTCGCGCAGGCTCTCGATGAGCTGATGCTTT GGGCCGAGGACTGCCCCGAAGTCCGGCACCTCGTGCACGCGGATTTCG GCTCCAACAATGTCCTGACGGACAATGGCCGCATAACAGCGGTCATTG ACTGGAGCGAGGCGATGTTCGGGGATTCCCAATACGAGGTCGCCAACA TCTTCTTCTGGAGGCCGTGGTTGGCTTGTATGGAGCAGCAGACGCGCT ACTTCGAGCGGAGGCATCCGGAGCTTGCAGGATCGCCGCGGCTCCGGG CGTATATGCTCCGCATTGGTCTTGACCAACTCTATCAGAGCTTGGTTG ACGGCAATTTCGATGATGCAGCTTGGGCGCAGGGTCGATGCGACGCAA TCGTCCGATCCGGAGCCGGGACTGTCGGGCGTACACAAATCGCCCGCA GAAGCGCGGCCGTCTGGACCGATGGCTGTGTAGAAGTACTCGCCGATA GTGGAAACCGACGCCCCAGCACTCGTCCGAGGGCAAAGGAATAGCCTC GGAGATCCATGGGGTGTGCTTTCCAGGCCGCTGAGCGGAGAGGTGCGG AGGGCAGTCCAGGAAGGTGGGGAGGGAGGAGGGATGGTACCCAAGCGA GAAGGGGACGGACGAGCTCAAGGCTGAAAGTTTCAGCCAACGGTTTCC GGCGCTGCATCCGTTCTCATGTTTTGGCACTCGTCATATGCTTTTATT

SEQ ID NO.	Description	Sequence
		TCTGTAATCGTTTTTGGAGGAGGGAGGAGGGGAGGAGATGTGGGCGAG CAGAGACGGCGGCAGCAGCAAAAAAAAGGGGGGGCGCCCACCGGCGCT GGTGAGGCGTGCAGGGGGAAGAGGGTGGCATGCGACATGCACAACCAA ACGTGCGCGTGTGCAGATGTGCTGGCGTGCGTCGTGAGTGTGTGATTT ATTTTTGAATGACACCTTATCATTGCTCTCTCTGCCTCACACTCTCTC GCTTCCACCGCTTTACCTTGCTACGAGTGTCGCTTCGGTATACCGTCA CTGACGTTGCCTCTCCCCTCTCCATACTTTCGCCTGCAGGATTTAAAT GGTACCATCCCAATGGCGCGCCGAGCTTGGTCGAGCATGGTCATAGCT GTTTCCTGTGTGAAATTGTTATCCGCTCACAATTCCACACAACATACG AGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA ACTCACATTAATTGCGTTGCGCTCACTGCCCGCTTTCCAGTCGGGAAA CCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGG CGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCT GCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCAGCTCACTCAAAGGC GGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACAT GTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTT GCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAA TCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGAC CCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGT GGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGT CGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGA CCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAG AGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA CTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAA GCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACA AACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTAC GCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGG GTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCAT GAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAAAAATG AAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAG TTAGAAAAACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATC AGGATTATCAATACCATATTTTTGAAAAAGCCGTTTCTGTAATGAAGG AGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGATCCTGGTATCG GTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCC CTCGTCAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGAC TGAATCCGGTGAGAATGGCAAAAGTTTATGCATTTCTTTCCAGACTTG TTCAACAGGCCAGCCATTACGCTCGTCATCAAAATCACTCGCATCAAC CAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCG ATCGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCG CAGGAACACTGCCAGCGCATCAACAATATTTTCACCTGAATCAGGATA TTCTTCTAATACCTGGAATGCTGTTTTCCCAGGGATCGCAGTGGTGAG TAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAAG AGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAAC ATCATTGGCAACGCTACCTTTGCCATGTTTCAGAAACAACTCTGGCGC ATCGGGCTTCCCATACAATCGATAGATTGTCGCACCTGATTGCCCGAC ATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGTTGGA

SEQ ID NO.	Description	Sequence
		ATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCAT ACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCT CATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGG GGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAAC CATTATTATCATGACATTAACCTATAAAAATAGGCGTATCACGAGGCC CTTTCGTC
219	pLMTB 10054	GGCGTGTGCGCACCGGCGTGTGCCAACGCCCAGGTACTGTGCGCACGT TCGTATCTCCATACGCTAGCTGACCGAGACGCATGCCCTCCGCCACCC TCAGTGGCGCGCACCTTCTCTCGTTTGAGCTCTTTATGCTCTCGTGAA TGGCACACAACATCCCGTGACTATCACGATGATCCTTCTCAAGCCACA CCGCTTGCCTTTTCTACAGCTCTGCGTTCTCTGGCCCATCCTCCTCTT GTTTGCTTTCCCTCTTTGCACATCCGTGTGCGCGTCCTTGTTCTTCTC TTCTGCGCACACTATTCTGCGCCCGCGACCCGCGCTTCGACTGCTGTC GGGTCATGCCTTGTGCTGCGCGTTCAGCTCTTCATTGCCCCTCGGCCT TGTACATAGCGGCTCTCCGTCATCGACGTTTTCCTCTCTCTTCAGCTC TATACACTCCCTCCCTTGTCAACACACTACACTGTGTCTCCCCCTTTC ATCTCTCCTCCCCTGTCACAATGGTCCGGAAGAAGGGCTCCCTGATCC TGTGCGGCGCCTTCCTGTTCGTCGCCTGGAACGCCCTGCTGCTGCTGT TCCTGTGGGGCCGGCCCCCCATCGGCCGGCTGGGCGAGGGCGGCGGCG CCGAGCCCGGCGCCGGCGAGGAGTGGGGCGCCGGCAAGTCCAAGGTCG GCGGCGCCAACGGCCTGGCCGGCGAGGTCATCCGGCTGGCCGAGGAGG TCGAGTCCGAGCTGGAGACCCAGAAGAAGCTGCTGAAGCAGATCCAGT CCCACCGGGAGCTGTGGGAGCAGCGGAAGGAGCTGGAGAAGCGGGAGT CCGAGGACACCAAGGACGAGAAGATCGACGTCGAGCCCAAGAAGCCCC GGCAGATCCCCGCCGTCCACCTGTCCCACAAGGTCGTCGAGGACGCCC AGACCGTCACCAAGAAGATGCAGACCCTGATGGTCACCCCCCCCCAGC TGGTCATGAAGGAGCAGGAGACCGACCAGAAGAACAAGCAGATGATGG AGGACCAGCTGGGCCTGACCACCCCCTCCCCCCAGATCATCATCCCCA TCCTGGTCATCGCCTGCGACCGGGTCACCGTCAAGCGGTCCCTGGACC GGCTGATCCAGTATCGGCCCTCCGCCGAGCTGTATCCCATCATCGTCT CCCAGGACTGCGGCCACGCCGACACCGCCCGGGTCATCGGCTCCTATG GCTCCCAGATCACCCACATCTCCCAGCCCGACCTGGCCGACATCCCCG TCCGGCCCGACCACCGGAAGTTCCAGGGCTATTATAAGATCGCCCGGC ACTATCGGTGGGCCCTGAACCAGGTCTTCAACGTCTTCGCCTATTCCA CCGTCGTCATCGTCGAGGACGACCTGGAGGTCGCCCCCGACTTCTTCG AGTATTTCCGGGCCCTGTATCCCATCCTGCGGTCCGACCCCACCCTGT GGTGCATCTCCGCCTGGAACGACAACGGCCGGGACGGCCTGGTCGACC CCGGCAAGGCCGAGCTGCTGTATCGGACCGACTTCTTCCCCGGCCTGG GCTGGATGCTGCTGAAGGAGGTCTGGGCCGAGCTGGAGCCCAAGTGGC CCAAGGCCTTCTGGGACGACTGGATGCGGCACCCCGAGCAGCGGAAGA ACCGGTCCTGCATCCGGCCCGAAATTTCTCGGACCATCACCTTCGGCC GGAAGGGCGTCTCCCTGGGCCAGTTCTTCGACCAGTATCTGCGGTATA TCAAGCTGAACACCGAGTTCGTCCCCTTCACCAAGCACGACCTGTCCT ATCTGGTCCGGGAGAAGTATGACGTCTCCTTCGAGAAGGACGTCTATT CCGCCCCCCTGGTCAAGGTCGAGGAGCTGCAGCACGGCGGCTCCCTGA AGGGCTCCGGCCCCTTCCGGGTCCAGTATTCCTCCCGGGACTCCTTCA AGGTCCTGGCCCGGAACCTGGGCGTCATGGACGACCTGAAGTCCGGCG TCCCCCGGGCCGGCTATCGGGGCGTCGTCTCCTTCATCTCCCGGGGCC

SEQ ID NO.	Description	Sequence
		GGCGGATCTATCTGGCCCCCCCCGAGGGCTGGACCAAGTATGACGTCT CCTGGTCCTAAATTTAAATATCCCAATGGCGCGCCGAGCTTGGCTCGA GCATGGTCATAGCTGTTTCCTGTGTGAAATTGTTATCCGCTCACAATT CCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCC TAATGAGTGAGCTAACTCACATTAATTGCGTTGCGCTCACTGCCCGCT TTCCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA CGCGCGGGGAGAGGCGGTTTGCGTATTGGGCGCTCTTCCGCTTCCTCG CTCACTGACTCGCTGCGCTCGGTCGTTCGGCTGCGGCGAGCGGTATCA GCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAAC GCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGT AAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGAC GAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACA GGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGC TCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTC CCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTC AGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCC CCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAG TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGT AACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG AAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATC TGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCT TGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGC AAGCAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG ATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAA GGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTT TTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAA ACTTGGTCTGACAGTTAGAAAAACTCATCGAGCATCAAATGAAACTGC AATTTATTCATATCAGGATTATCAATACCATATTTTTGAAAAAGCCGT TTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCA AGATCCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAA CCTATTAATTTCCCCTCGTCAAAAATAAGGTTATCAAGTGAGAAATCA CCATGAGTGACGACTGAATCCGGTGAGAATGGCAAAAGTTTATGCATT TCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAA TCACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCG AGACGAAATACGCGATCGCTGTTAAAAGGACAATTACAAACAGGAATC GAATGCAACCGGCGCAGGAACACTGCCAGCGCATCAACAATATTTTCA CCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCAGGG ATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGC TTGATGGTCGGAAGAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACC ATCTCATCTGTAACATCATTGGCAACGCTACCTTTGCCATGTTTCAGA AACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTGTCGCA CCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCA GCATCCATGTTGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGT TGAATATGGCTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTAT CAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAA AATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCT GACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAATAGG CGTATCACGAGGCCCTTTCGTCTCGCGCGTTTCGGTGATGACGGTGAA

SEQ ID NO.	Description	Sequence
		AACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAA GCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTT GGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTA CTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGG AGAAAATACCGCATCAGGCGCCATTCGCCATTCAGGCTGCGCAACTGT TGGGAAGGGCGATCGGTGCGGGCCTCTTCGCTATTACGCCAGCTGGCG AAAGGGGGATGTGCTGCAAGGCGATTAAGTTGGGTAACGCCAGGGTTT TCCCAGTCACGACGTTGTAAAACGACGGCCAGTGAATTGACGCGTATT GGGATATTTAAAT
220	pLMTB 10055	GCTTCATGTACAATCATCGCGCACCTTTCTTTTTCATTGATTAGGGCC AACTCCCCACCGATGTAAAAAAAATCCTGAAAGTGGGATGACACAATT CAGTGACAATGGAAAAAAAAGAAGCGTGATTGGTATTCAAGCTTCACA CACGTATTTCCCCCCATACACAAGGATGTGTTATTGTTTTCTACTTGA TTCGGGTACGCTCACCACAGCGCACCTCGTCTGAAAAGCACTTGATAC TGTTCCTTCTTTCGCGTATGTTCATCTATGAAAGAGCAACATTATTCG GCCACCTGTTTCGCGTGGGCACACGCACACTAGGGCTATGATGTTTTG CTTCATCGGCAATCTGTGCTCTGCTGAGGCAGCCGCTGTTTTGCTTGG TGCTCTTTTTCCCTCTTCTTTGGTGCAATGCATTCCGCTTGTCGCAGC AACCATTCTCCCACTCTGTTTCTTTCAACTGTCGTCGCTTCTATTCCC TCGATCTTTTATCTGGATGCATGACAATATGCAGAACAAAAGCAAGAC CAGTGAGTTTGGTTTCGTTTCCACCTGAAAAATGCGCCTCCGCGAACC CCTCCTGAGCGGCTCCGCAGCGATGCCTGGGGCTTCGCTGCAGCGCGC CTGTCGGCTGCTCGTAGCGGTCTGCGCACTCCACCTTGGCGTGACTCT CGTCTACTATCTGGCGGGACGAGATCTGTCGCGCCTCCCACAGCTCGT GGGTGTGTCGACGCCGCTGCAAGGAGGCTCAAATTCGGCCGCGGCCAT CGGTCAGAGCTCCGGCGAGCTGCGCACGGGAGGAGCACGCCCGCCACC TCCGCTGGGTGCATCGTCTCAGCCCCGTCCGGGCGGCGACAGTTCACC GGTTGTGGACTCGGGTCCAGGACCTGCATCTAACCTTACGTCCGTGCC CGTACCACACACGACGGCTCTTTCGCTTCCAGCCTGTCCCGAAGAGTC CCCTCTGCTTGTTGGTCCGATGTTGATCGAGTTCAACATGCCTGTTGA TCTCGAATTGGTGGCAAAACAAAACCCAAACGTGAAAATGGGAGGCCG GTACGCCCCGCGAGATTGCGTGTCGCCTCACAAGGTTGCGATCATCAT CCCCTTTCGGAATCGCCAGGAACACCTTAAGTACTGGTTGTACTACCT CCACCCCGTTTTGCAGCGCCAGCAGTTGGATTATGGCATCTACGTCAT TAACCAGGCCGGTGATACGATTTTTAACCGCGCCAAGCTGCTCAACGT GGGTTTTCAGGAGGCGCTCAAGGACTACGATTACACGTGCTTCGTCTT TTCCGACGTTGATTTGATTCCTATGAACGACCACAATGCGTATCGGTG TTTCAGCCAGCCGCGCCACATTTCGGTAGCCATGGATAAGTTTGGATT CTCCCTGCCTTACGTACAATACTTCGGCGGCGTGAGCGCATTGTCGAA GCAACAGTTCCTGACGATCAACGGCTTTCCAAACAATTACTGGGGTTG GGGCGGGGAAGACGACGACATCTTCAATCGTCTGGTGTTTCGTGGGAT GTCTATTTCCCGCCCGAACGCAGTCGTCGGTCGCTGCCGTATGATCCG ACATTCTCGTGATAAGAAGAACGAGCCTAACCCACAGCGCTTCGACCG AATCGCTCATACTAAGGAAACGATGCTCTCCGACGGGCTCAACTCTCT CACATACCAGGTCCTCGACGTGCAGCGCTATCCACTTTACACGCAGAT TACGGTCGACATCGGCACCCCGTCGTGAATTTAAATATCCCAATGGCG CGCCGAGCTTGGCTCGAGCATGGTCATAGCTGTTTCCTGTGTGAAATT GTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGT

SEQ ID NO.	Description	Sequence
		GTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTGCGT TGCGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCGTGCCAGCTGC ATTAATGAATCGGCCAACGCGCGGGGAGAGGCGGTTTGCGTATTGGGC GCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCGTTCGGC TGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCA CAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGC AAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATA GGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGA GGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTG GAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGAT ACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCT CACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGG GCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCGCCTTATCCG GTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCAC TGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCG GTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAA GAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAA AAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCG GTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGAT CTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGA ACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGA TCTTCACCTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCT AAAGTATATATGAGTAAACTTGGTCTGACAGTTAGAAAAACTCATCGA GCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCAT ATTTTTGAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGC AGTTCCATAGGATGGCAAGATCCTGGTATCGGTCTGCGATTCCGACTC GTCCAACATCAATACAACCTATTAATTTCCCCTCGTCAAAAATAAGGT TATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATG GCAAAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCAT TACGCTCGTCATCAAAATCACTCGCATCAACCAAACCGTTATTCATTC GTGATTGCGCCTGAGCGAGACGAAATACGCGATCGCTGTTAAAAGGAC AATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCG CATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGA ATGCTGTTTTCCCAGGGATCGCAGTGGTGAGTAACCATGCATCATCAG GAGTACGGATAAAATGCTTGATGGTCGGAAGAGGCATAAATTCCGTCA GCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGCTAC CTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACA ATCGATAGATTGTCGCACCTGATTGCCCGACATTATCGCGAGCCCATT TATACCCATATAAATCAGCATCCATGTTGGAATTTAATCGCGGCCTAG AGCAAGACGTTTCCCGTTGAATATGGCTCATACTCTTCCTTTTTCAAT ATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATAT TTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTC CCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACAT TAACCTATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTCGCGCGTT TCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGG TCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGG GCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGG CATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATAC

SEQ ID NO.	Description	Sequence
		CGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCGCCATTCGCCAT TCAGGCTGCGCAACTGTTGGGAAGGGCGATCGGTGCGGGCCTCTTCGC TATTACGCCAGCTGGCGAAAGGGGGATGTGCTGCAAGGCGATTAAGTT GGGTAACGCCAGGGTTTTCCCAGTCACGACGTTGTAAAACGACGGCCA GTGAATTGACGCGTATTGGGATATTTAAAT
221	oLMTB 7173	CGCACCTCGGCTTCAACTGCCAATG
222	oLMTB 7174	AACGTGCCTGAAGCCCGTAGCTTTG
223	oLMTB 7175	GGCGACGGATGATGCCCACCATTTG
224	oLMTB 7176	GGAGGCAACCAAGAAGGCGTCAGAG
225	oLMTB 7492	CCATGGCCAGATGCCAAGCTTACTC
226	oLMTB 7495	CGGAACACAGACCTGCCATCTGTGG
227	tryptic peptide from Adalimumab carrying the O-HexNAc on Thr225	THTCPPCPAPELLGGPSVFLFPPKPK
228	tryptic peptide from Adalimumab carrying the N-glycan Man3	EEQYNSTYR
229	tryptic peptide from CD43 carrying three GalNAc	Mox-YTTSITSDPK
230	14 aa peptide produced by	THTCPPCPAPELLG

SEQ ID NO.	Description	Sequence
	double digestion of Adalimumab with FabRICATOR (IdeS) and GingisKHAN (Kgp)	
231	gRNA_OGNT-1_3	GTTCTTCGCGAAATCCGATGCGG
232	gRNA_OGNT-1_5	ACACGCATGCGGGTGAGGTGAGG
233	gRNA_OGNT-2_5	AGTGGTTCACAACCGAATCCCGG
234	gRNA_OGNT-2_3	GATGGGCACGGAACGGCCTGTGG
235	gRNA_OGNT-L_5	ACGGTGACGCGAACTCGCAGAGG
236	gRNA_OGNT-L_3	CTTGTCTCGGTGGCGCCAAGCGG
237	tryptic O-glycopeptide position [117-131] of LMSAP-rhEPO-Strep	EAISPPDAASAAPLR
238	Adalimumab peptide that likely has O-	LTVDKSRWQQGNVFSCSVMHEALHNHYTQK

SEQ ID NO.	Description	Sequence
	glycosylation	
239	tryptic peptide with one missed cleavage and the HexNAc	SCDKTHTCPPCPAPELLGGPSVFLFPPKPK

WHAT IS CLAIMED:

1. A *Leishmania* cell genetically engineered such that the formation of an O-linked GlcNAc on a polypeptide in the *Leishmania* cell is reduced or eliminated.

2. The *Leishmania* cell of claim 1, wherein the formation of O-linked GlcNAc in the *Leishmania* cell prior to genetic engineering is catalyzed by at least one N-acetylglucosamine (GlcNAc)-transferase.

3. The *Leishmania* cell of claim 2, wherein the gene encoding the at least one GlcNAc-transferase is functionally inactivated.

4. The *Leishmania* cell of any one of claims 2 to 3, wherein the gene encoding the at least one GlcNAc-transferase is downregulated.

5. The *Leishmania* cell of any one of claims 2 to 3, wherein the gene encoding the at least one GlcNAc-transferase is deleted or mutated.

6. The *Leishmania* cell of claim 2, wherein the gene encoding the at least one GlcNAc-transferase is overexpressed.

7. The *Leishmania* cell of any one of claims 1 to 6, wherein the formation of the O-linked GlcNAc is reduced by at least 5%, 7%, 10%, 12%, 15%, 18%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% from the formation of the O-linked GlcNAc in a reference *Leishmania* cell.

8. The *Leishmania* cell of any one of claims 2 to 7, wherein the at least one GlcNAc-transferase is selected from the group consisting of OGNT1, OGNT2 and OGNTL, and homologous GlcNAc-transferases thereof.

9. The *Leishmania* cell of claim 8, wherein the at least one GlcNAc-transferase is a GlcNAc-transferase that is homologous to OGNT1, OGNT2 and/or OGNTL.

10. The *Leishmania* cell of any one of claims 2 to 9, wherein the number of the at least one GlcNAc-transferase is one, two or three.

11. The *Leishmania* cell of any one of claims 1 to 10, wherein the growth rate of the *Leishmania* cell is at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, or 100% of the

growth rate of a reference *Leishmania* cell.

12. The *Leishmania* cell of any one of claims 1 to 11, wherein the *Leishmania* cell is *Leishmania tarentolae*.

13. The *Leishmania* cell of any one of claims 1 to 12, wherein the polypeptide is selected from the group consisting of adalimumab, rituximab and erythropoietin (EPO).

14. The *Leishmania* cell of any one of claims 1 to 13, wherein the *Leishmania* cell comprises a recombinant nucleic acid encoding a heterologous glycosyltransferase.

15. The *Leishmania* cell of claim 14, wherein the *Leishmania* cell comprises one or more heterologous glycosyltransferases.

16. The *Leishmania* cell of any one of claims 14 and 15, wherein the heterologous glycosyltranferase is an N-acetyl glucosamine transferase; and/or a heterologous galactosyltransferase; and/or a heterologous sialyltransferase.

17. A method of making a polypeptide comprising (a) culturing the *Leishmania* cell of any one of claims 1 to 16 under suitable conditions for polypeptide production; and (b) isolating the polypeptide.

18. A polypeptide produced by the method of claim 17.

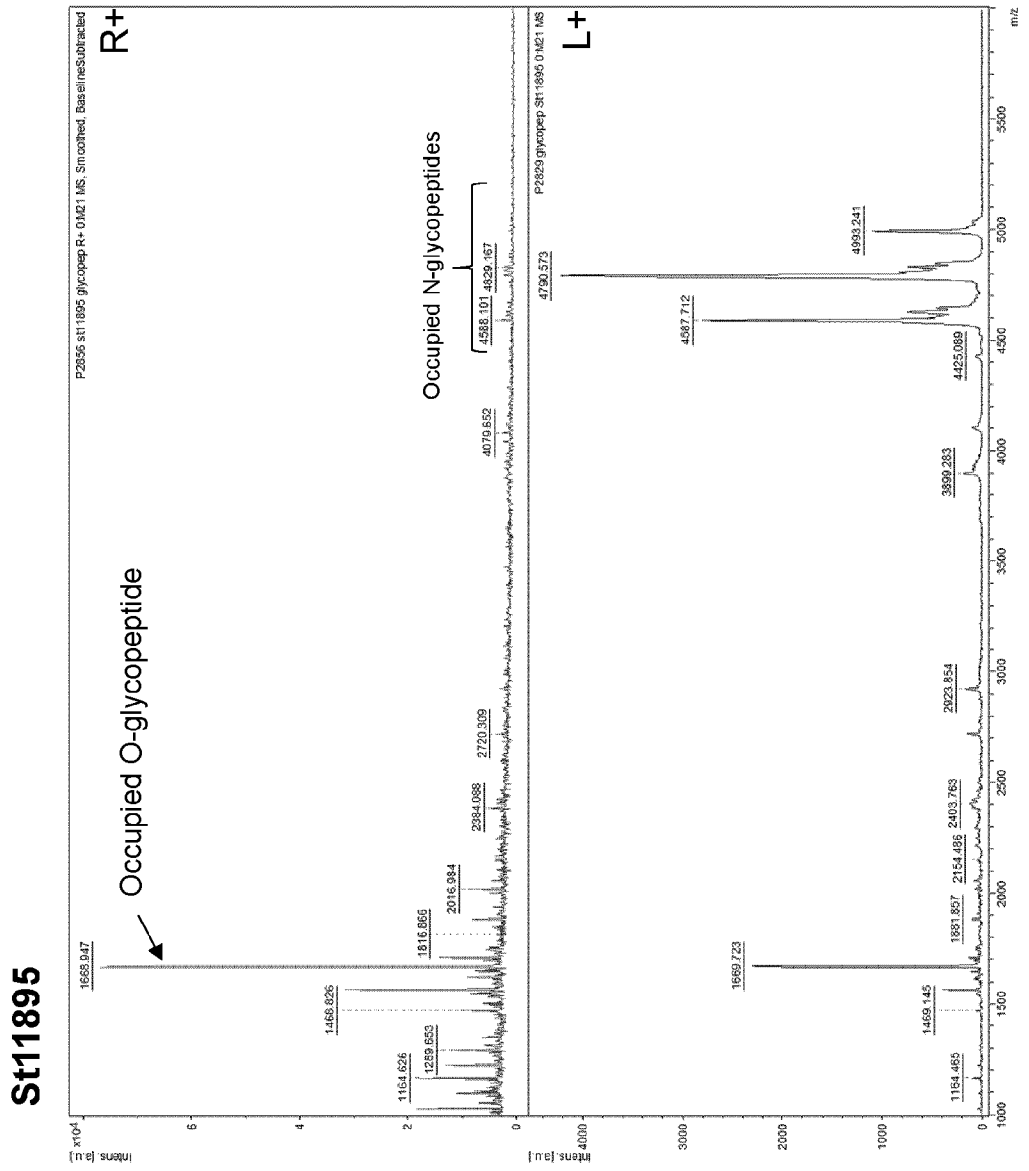

St11895
R+
L+
Occupied O-glycopeptide
Occupied N-glycopeptides
P2856 st11895 glycopep R+ 0M21 MS, Smoothed, BaselineSubtracted
P2829 glycopep St11895 0M21 MS
Intens. [a.u.]
m/z
1668.947
1468.826
1164.626
1289.653
1816.866
2016.984
2384.088
2720.309
4079.652
4588.101
4829.167
1669.723
1469.145
1164.465
1881.857
2154.486
2403.763
2923.854
3899.283
4425.089
4587.712
4790.573
4993.241

FIG. 1

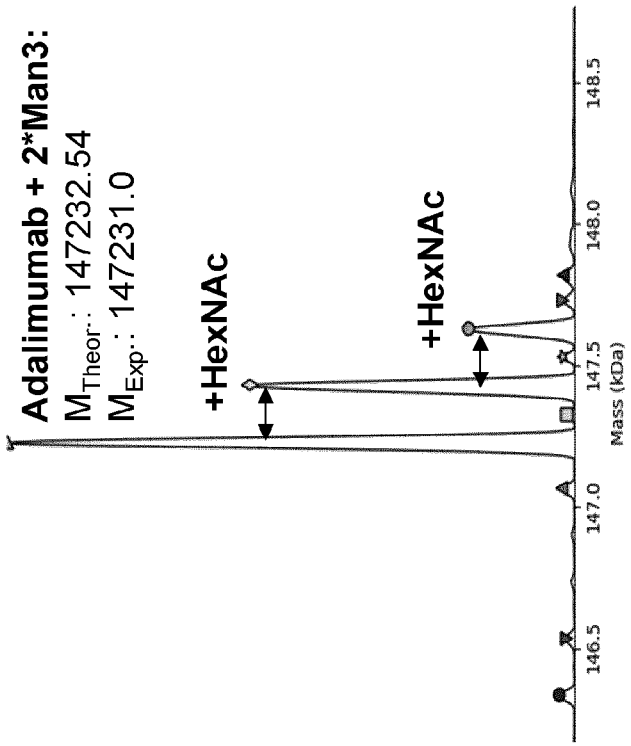

Adalimumab + 2*Man3:
$M_{Theor.}$: 147232.54
$M_{Exp.}$: 147231.0
+HexNAc
+HexNAc
146.5
147.0
147.5
148.0
148.5
Mass (kDa)

FIG. 2A

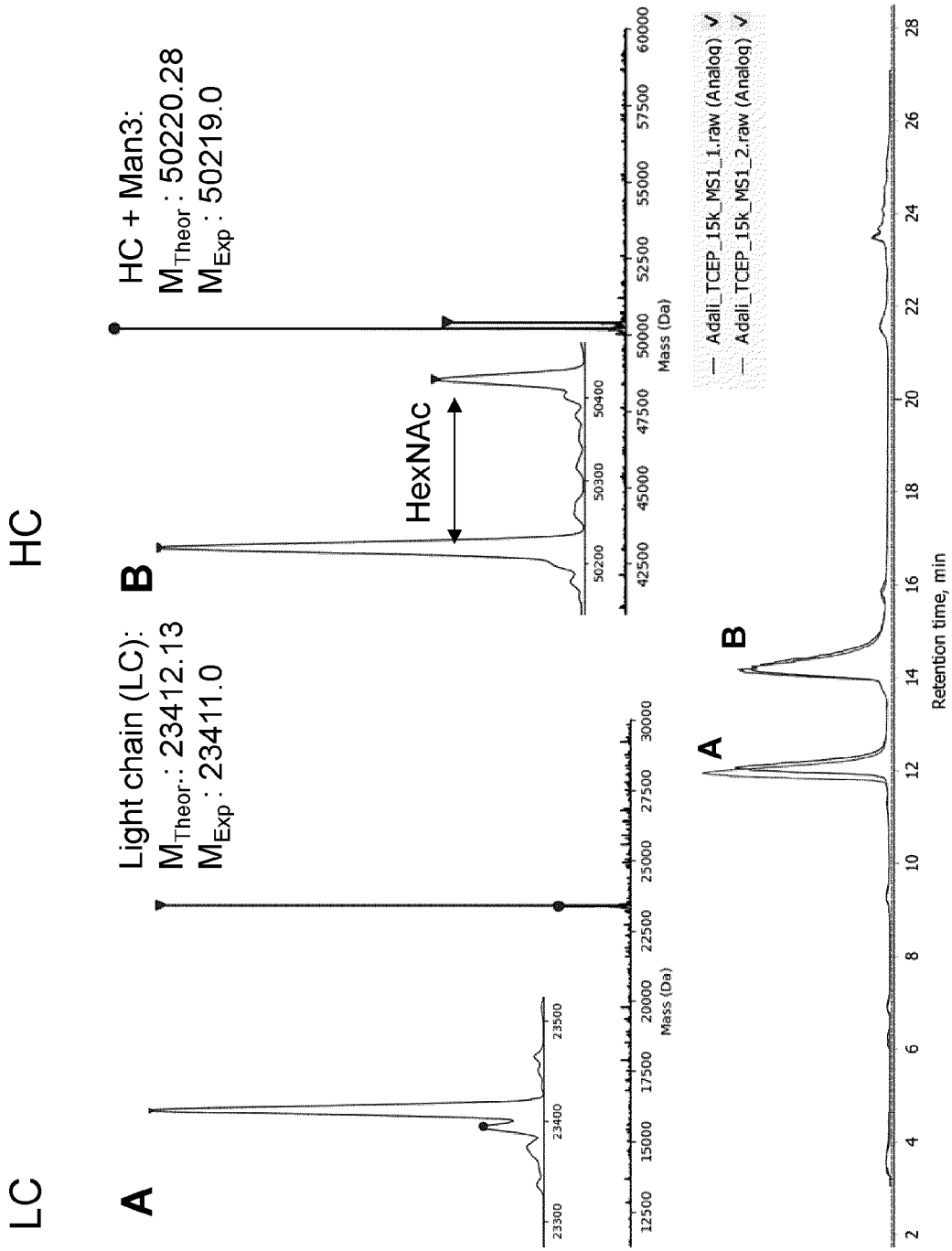

LC
HC
A
B
Light chain (LC):
$M_{Theor.}$: 23412.13
M_{Exp}: 23411.0
HC + Man3:
$M_{Theor.}$: 50220.28
M_{Exp}: 50219.0
HexNAc
Mass (Da)
Adali_TCEP_15k_MS1_1.raw (Analog)
Adali_TCEP_15k_MS1_2.raw (Analog)
Retention time, min

FIG. 2B

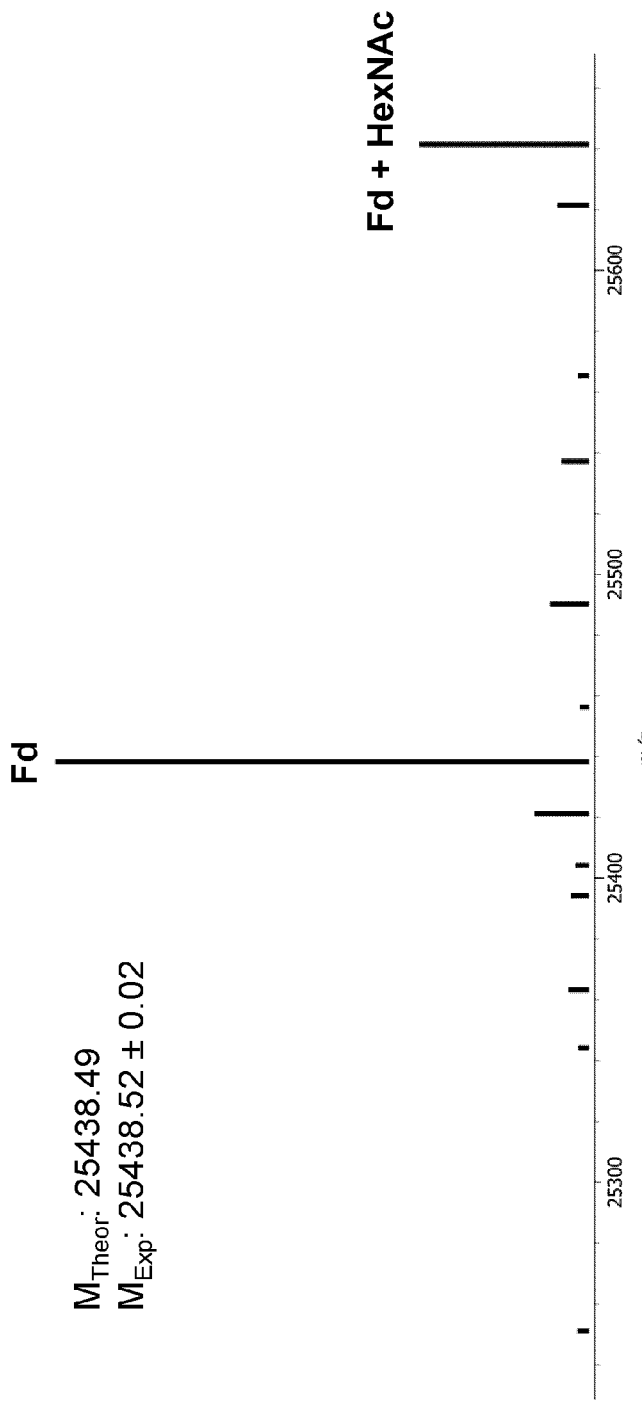


FIG. 2C (Subunit / IdeS)

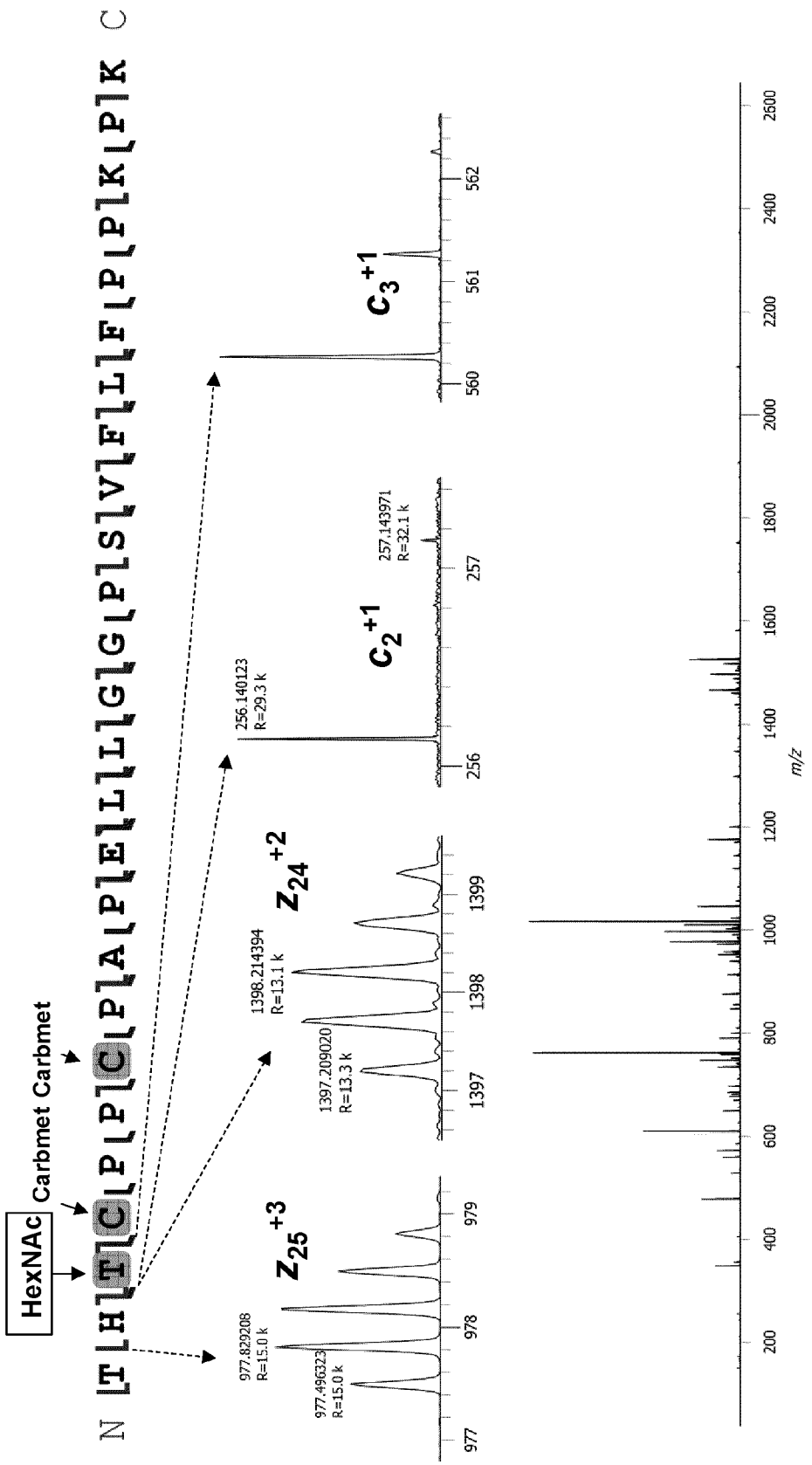

HexNAc
Carbmet Carbmet
N T H T C P C P A P E L L L G L G P S V L F L F P P K P K C
977.829208
R=15.0 k
977.496323
R=15.0 k
z_{25}^{+3}
1398.214394
R=13.1 k
1397.209020
R=13.3 k
z_{24}^{+2}
256.140123
R=29.3 k
257.143971
R=32.1 k
c_2^{+1}
c_3^{+1}
977
978
979
1397
1398
1399
256
257
560
561
562
200
400
600
800
1000
1200
1400
1600
1800
2000
2200
2400
2600
m/z

FIG. 2D

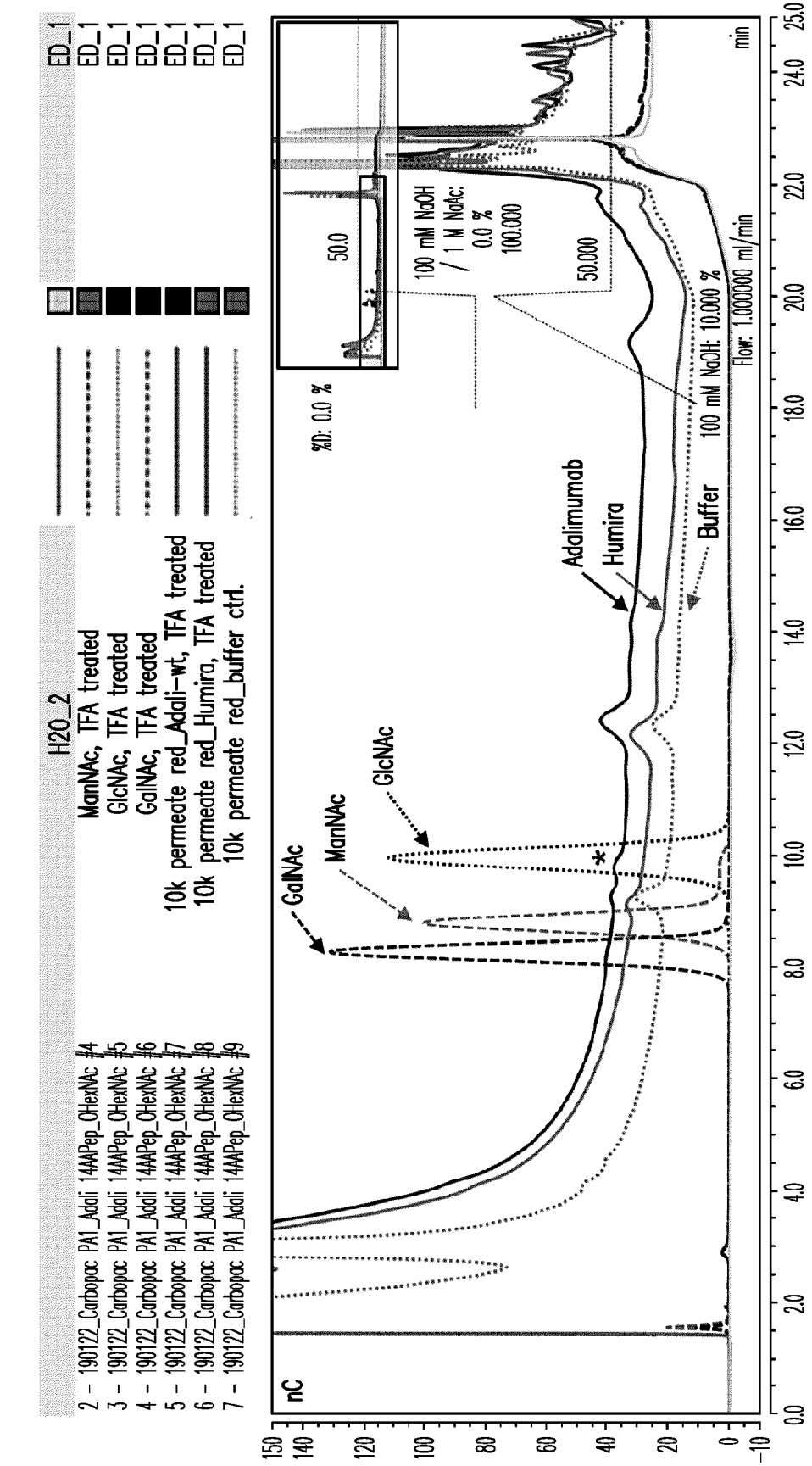

H2O_2
2 – 190122_Carbopac PA1_Adali 14AAPep_OHexNAc #4
3 – 190122_Carbopac PA1_Adali 14AAPep_OHexNAc #5
4 – 190122_Carbopac PA1_Adali 14AAPep_OHexNAc #6
5 – 190122_Carbopac PA1_Adali 14AAPep_OHexNAc #7
6 – 190122_Carbopac PA1_Adali 14AAPep_OHexNAc #8
7 – 190122_Carbopac PA1_Adali 14AAPep_OHexNAc #9
ManNAc, TFA treated
GlcNAc, TFA treated
GalNAc, TFA treated
10k permeate red_Adali-wt, TFA treated
10k permeate red_Humira, TFA treated
10k permeate red_buffer ctrl.
ED_1
nC
GalNAc
ManNAc
GlcNAc
Adalimumab
Humira
Buffer
%D: 0.0 %
50.0
100 mM NaOH
/ 1 M NaAc:
0.0 %
100.000
50.000
100 mM NaOH: 10.000 %
Flow: 1.000000 ml/min
min

FIG. 3A

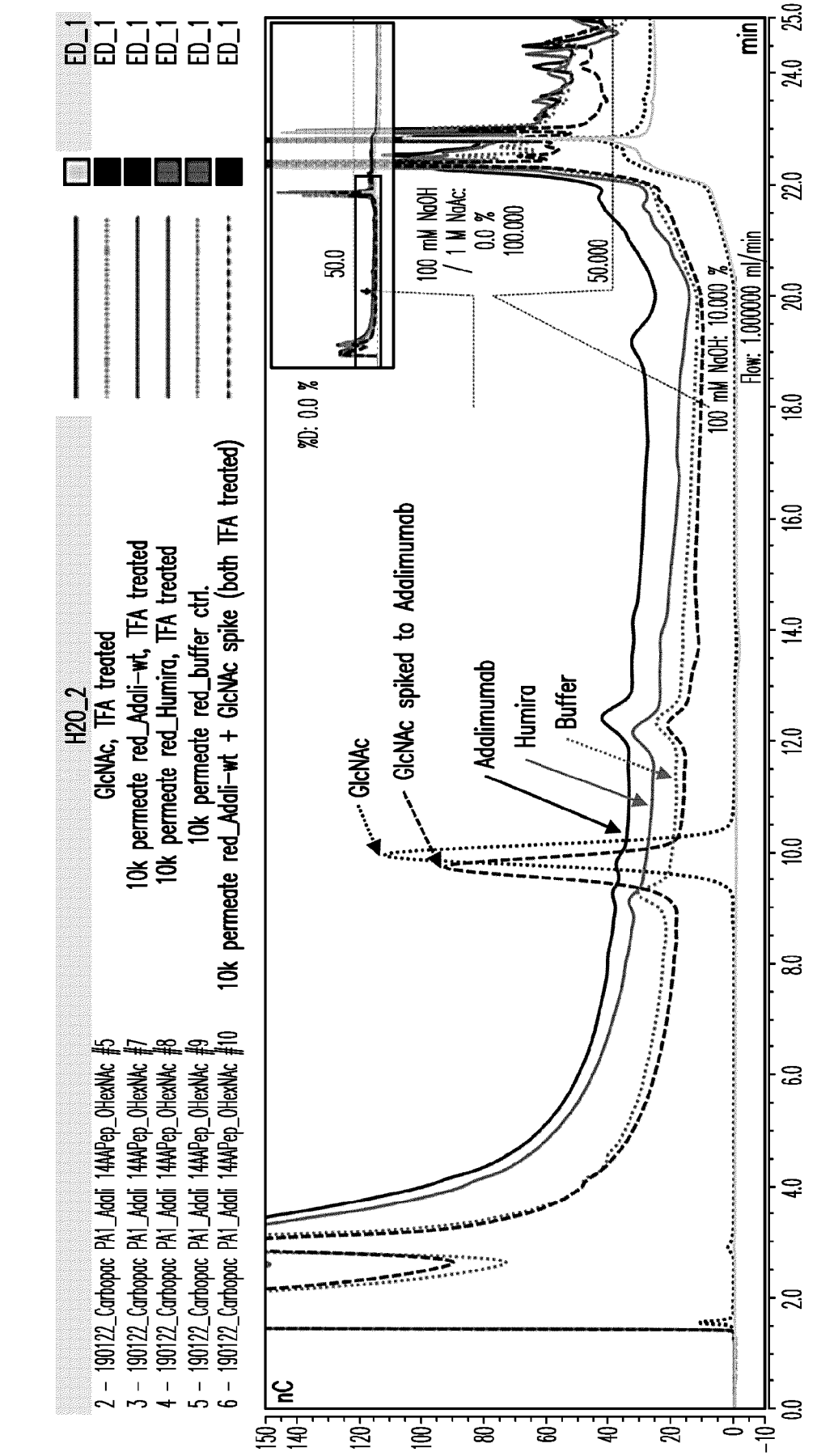

H2O_2
GlcNAc, TFA treated
10k permeate red_Adali-wt, TFA treated
10k permeate red_Humira, TFA treated
10k permeate red_buffer ctrl.
10k permeate red_Adali-wt + GlcNAc spike (both TFA treated)
2 - 190122_Carbopac PA1_Adali 14AAPep_0HexNAc #5
3 - 190122_Carbopac PA1_Adali 14AAPep_0HexNAc #7
4 - 190122_Carbopac PA1_Adali 14AAPep_0HexNAc #8
5 - 190122_Carbopac PA1_Adali 14AAPep_0HexNAc #9
6 - 190122_Carbopac PA1_Adali 14AAPep_0HexNAc #10
ED_1
nC
min
GlcNAc
GlcNAc spiked to Adalimumab
Adalimumab
Humira
Buffer
%D: 0.0 %
50.0
100 mM NaOH / 1 M NaAc: 0.0 % 100.000
50.000
100 mM NaOH: 10.000 %
Flow: 1.000000 ml/min

FIG. 3B

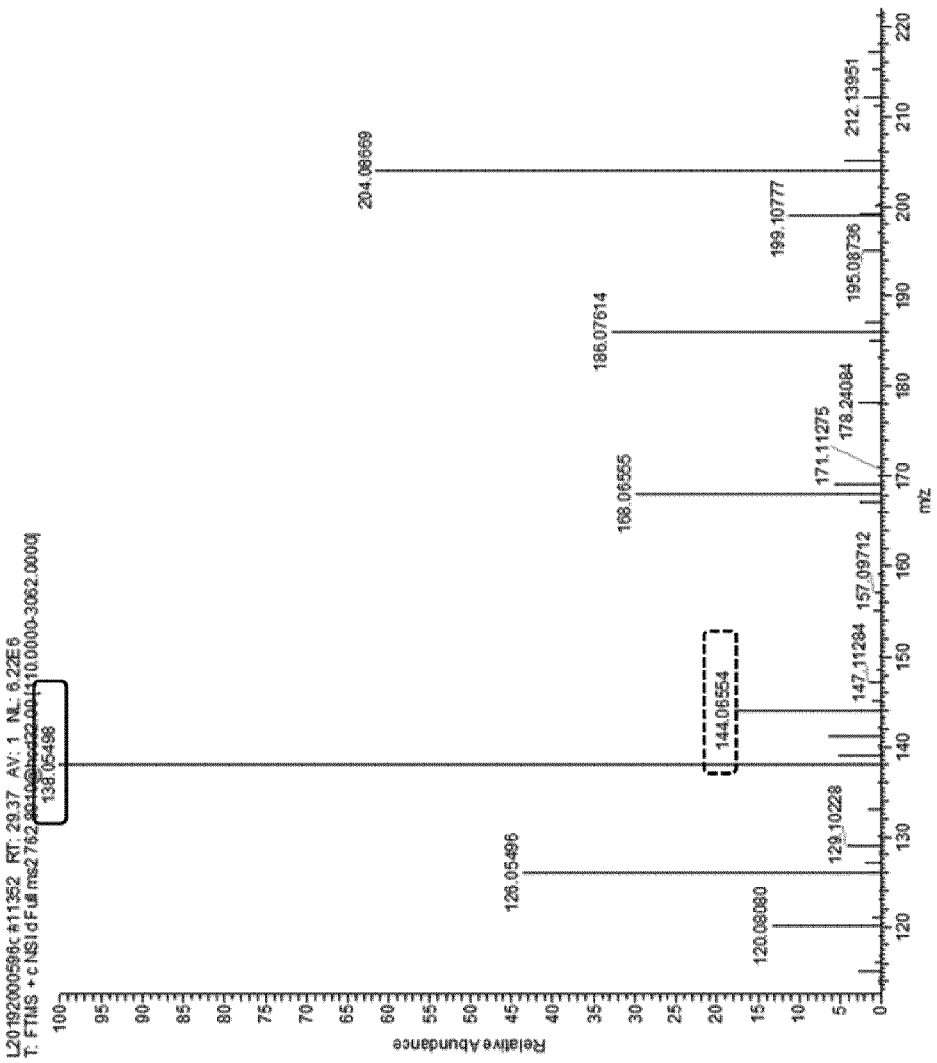

Relative Abundance
m/z
138.05498
144.06554
126.05496
120.08080
129.10228
147.11284
157.09712
168.06555
171.11275
178.24084
186.07614
195.08736
199.10777
204.08669
212.13951

FIG. 4A

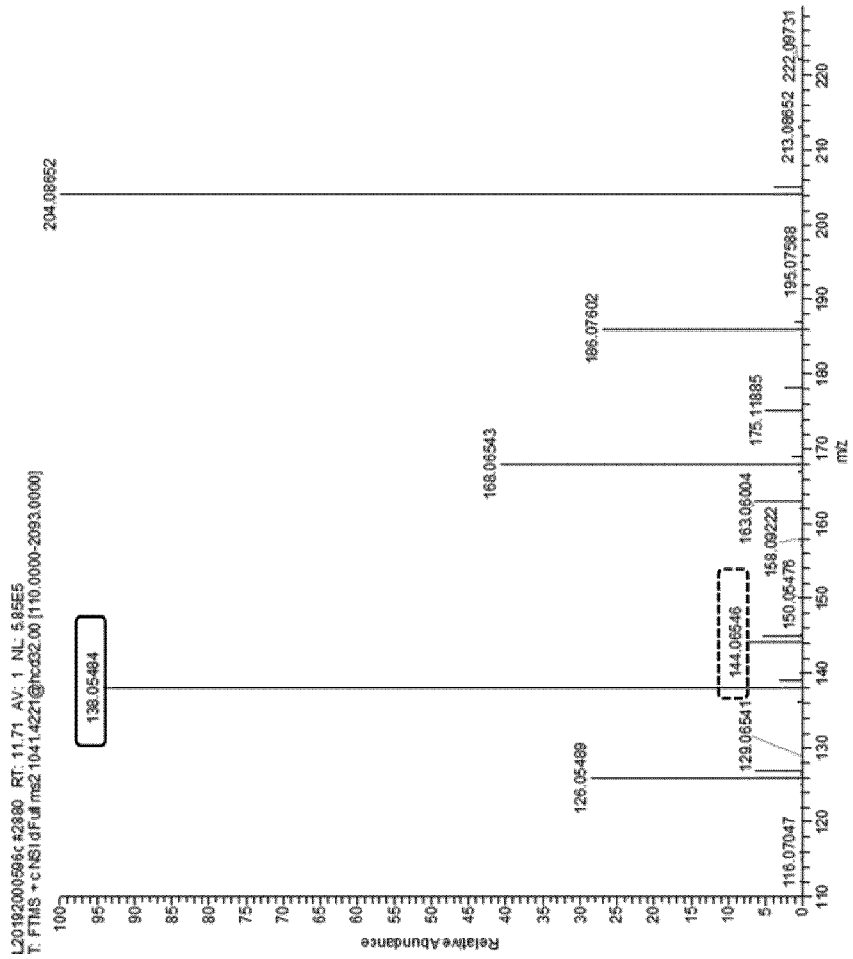

L20192008596c #2880 RT: 11.71 AV: 1 NL: 5.85E5
T: FTMS + c NSI dFull ms2 1041.4221@hcd32.00 [110.0000-2093.0000]
Relative Abundance
m/z
138.05484
204.08652
168.06543
186.07602
126.05489
129.06541
144.06546
150.05476
158.09222
163.06004
175.11885
195.07588
213.08852
222.09731
116.07047

FIG. 4B

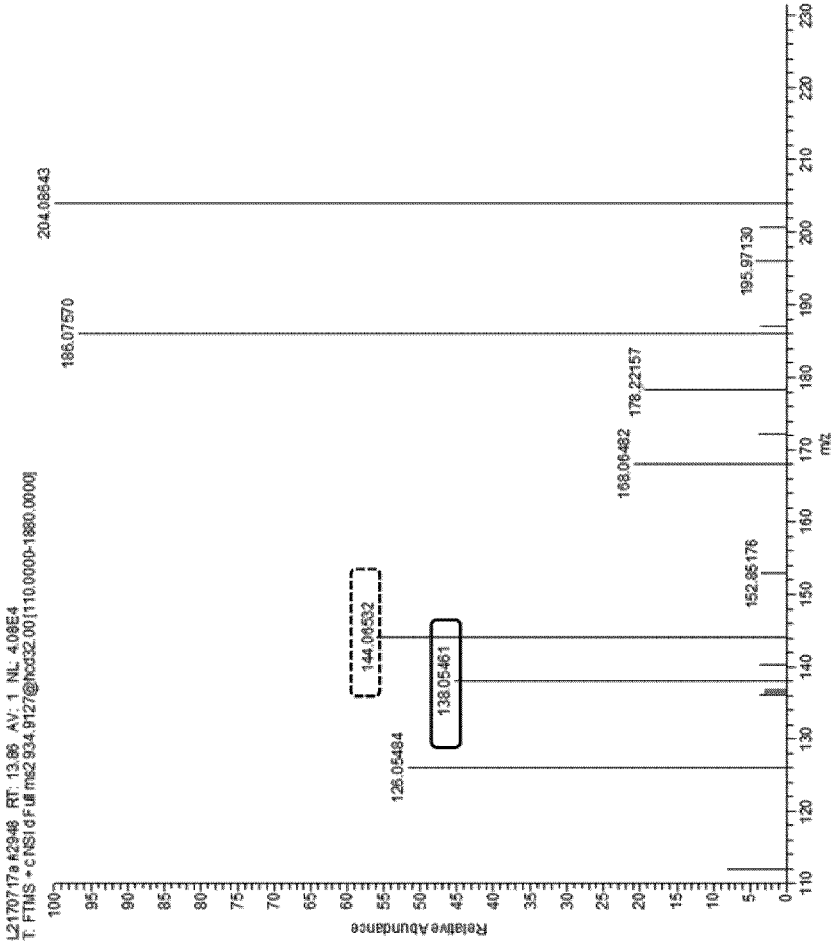

L2170717a #2948 RT: 13.86 AV: 1 NL: 4.08E4
T: FTMS + cNSI d Full ms2 934.9127@hcd32.00[110.0000-1880.0000]
Relative Abundance
m/z
204.08643
186.07570
195.97130
178.22157
168.06482
152.85176
144.09532
138.05461
126.05484

FIG. 4C

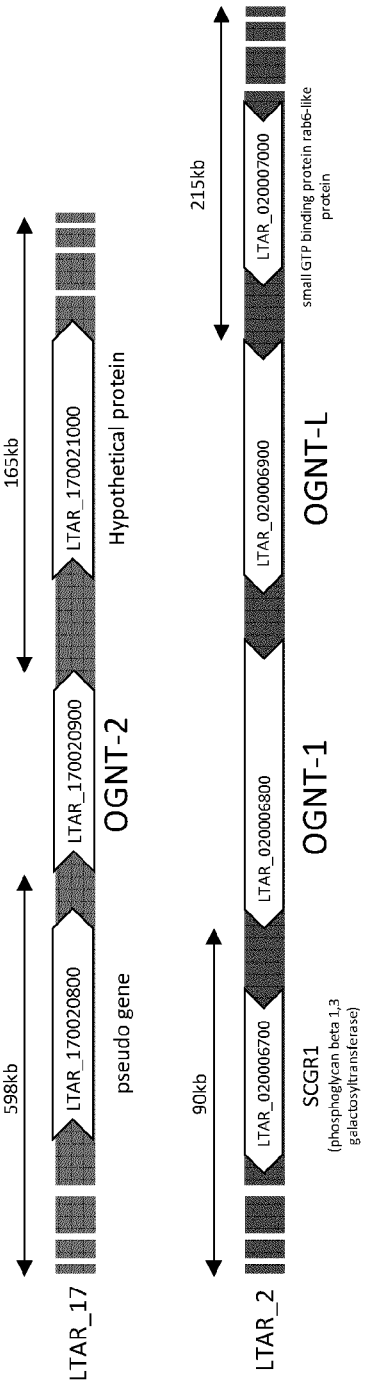

LTAR_17
LTAR_2
598kb
165kb
90kb
215kb
LTAR_170020800
LTAR_170020900
LTAR_170021000
LTAR_020006700
LTAR_020006800
LTAR_020006900
LTAR_020007000
pseudo gene
Hypothetical protein
SCGR1
(phosphoglycan beta 1,3 galactosyltransferase)
OGNT-2
OGNT-1
OGNT-L
small GTP binding protein rab6-like protein

FIG. 5A

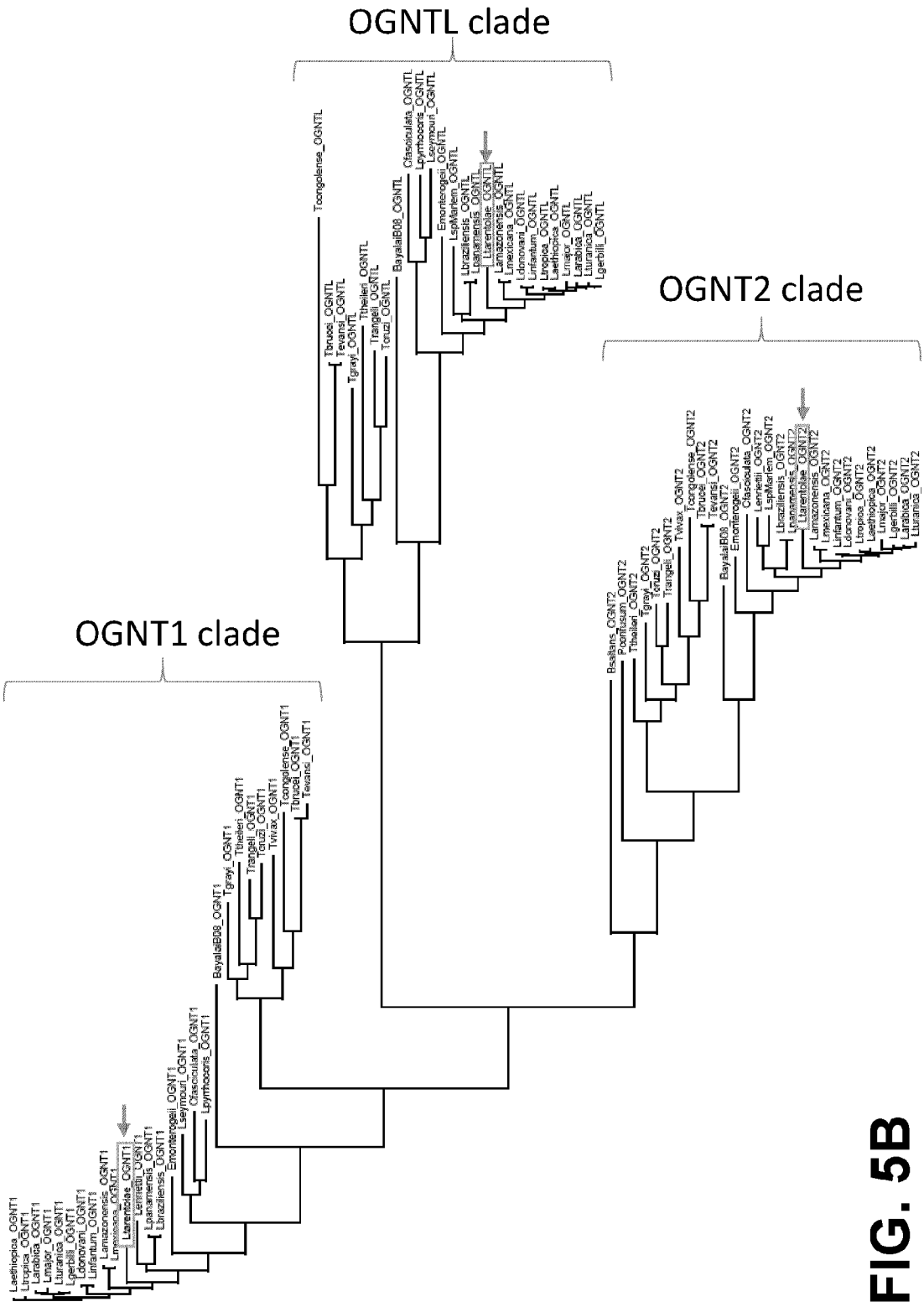

OGNTL clade
OGNT2 clade
OGNT1 clade
Tcongolense_OGNTL
Tbrucei_OGNTL
Tevansi_OGNTL
Tgrayi_OGNTL
Tbetleri_OGNTL
Trangeli_OGNTL
Tcruzi_OGNTL
BayalaIB08_OGNTL
Cfasciculata_OGNTL
Lpyrrhocoris_OGNTL
Lseymouri_OGNTL
Emonterogeii_OGNTL
LspMarlem_OGNTL
Lbraziliensis_OGNTL
Lpanamensis_OGNTL
Llaentoilae_OGNTL
Lamazonensis_OGNTL
Lmexicana_OGNTL
Ldonovani_OGNTL
Linfantum_OGNTL
Ltropica_OGNTL
Laethiopica_OGNTL
Lmajor_OGNTL
Larabica_OGNTL
Luranica_OGNTL
Lgerbili_OGNTL
Bsaltans_OGNT2
Pcontortus_OGNT2
Tbetleri_OGNT2
Tgrayi_OGNT2
Tcruzi_OGNT2
Trangeli_OGNT2
Tvivax_OGNT2
Tcongolense_OGNT2
Tbrucei_OGNT2
Tevansi_OGNT2
BayalaIB08_OGNT2
Emonterogeii_OGNT2
Cfasciculata_OGNT2
Lenriettii_OGNT2
LspMarlem_OGNT2
Lbraziliensis_OGNT2
Lpanamensis_OGNT2
Llaentoilae_OGNT2
Lamazonensis_OGNT2
Lmexicana_OGNT2
Linfantum_OGNT2
Ldonovani_OGNT2
Ltropica_OGNT2
Laethiopica_OGNT2
Lmajor_OGNT2
Lgerbili_OGNT2
Larabica_OGNT2
Luranica_OGNT2
Tcongolense_OGNT1
Tbrucei_OGNT1
Tevansi_OGNT1
BayalaIB08_OGNT1
Tgrayi_OGNT1
Tbetleri_OGNT1
Trangeli_OGNT1
Tcruzi_OGNT1
Tvivax_OGNT1
Emonterogeii_OGNT1
Lseymouri_OGNT1
Cfasciculata_OGNT1
Lpyrrhocoris_OGNT1
Lbraziliensis_OGNT1
Lpanamensis_OGNT1
Llaentoilae_OGNT1
Lamazonensis_OGNT1
Lmexicana_OGNT1
Linfantum_OGNT1
Ldonovani_OGNT1
Lgerbili_OGNT1
Luranica_OGNT1
Lmajor_OGNT1
Larabica_OGNT1
Ltropica_OGNT1
Laethiopica_OGNT1

FIG. 5B

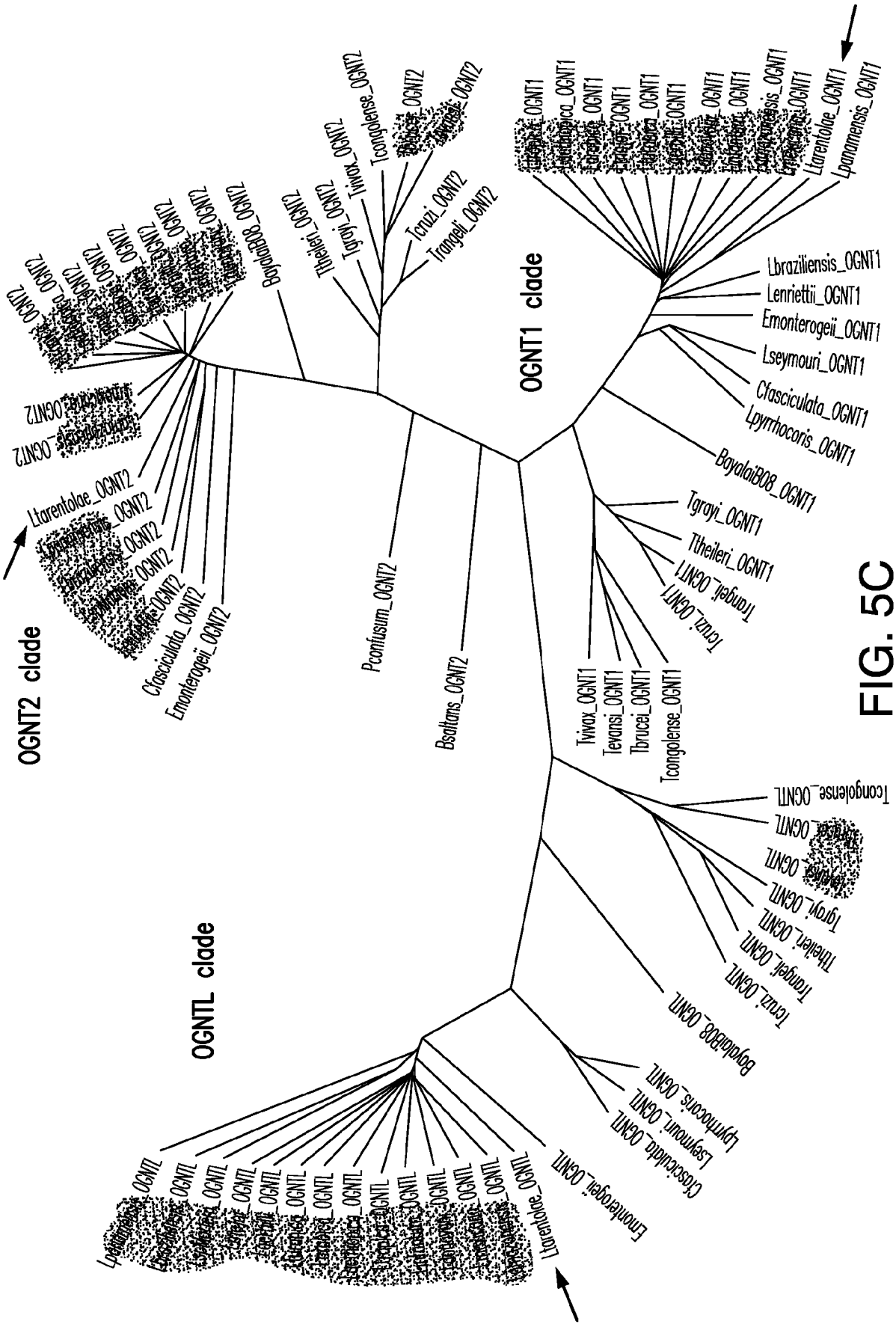

OGNT2 clade
OGNT1 clade
OGNTL clade
Ltarentolae_OGNT1
Lpanamensis_OGNT1
Lbraziliensis_OGNT1
Lenriettii_OGNT1
Emonterogeii_OGNT1
Lseymouri_OGNT1
Cfasciculata_OGNT1
Lpyrrhocoris_OGNT1
BayalaiB08_OGNT1
Tgrayi_OGNT1
Ttheileri_OGNT1
Trangeli_OGNT1
Tcruzi_OGNT1
Tvivax_OGNT1
Tevansi_OGNT1
Tbrucei_OGNT1
Tcongolense_OGNT1
Pconfusum_OGNT2
Bsaltans_OGNT2
Ltarentolae_OGNT2
Cfasciculata_OGNT2
Emonterogeii_OGNT2
Tcongolense_OGNTL
Tgrayi_OGNTL
Ttheileri_OGNTL
Trangeli_OGNTL
Tcruzi_OGNTL
BayalaiB08_OGNTL
Lpyrrhocoris_OGNTL
Lseymouri_OGNTL
Cfasciculata_OGNTL
Emonterogeii_OGNTL
Ltarentolae_OGNTL

FIG. 5C

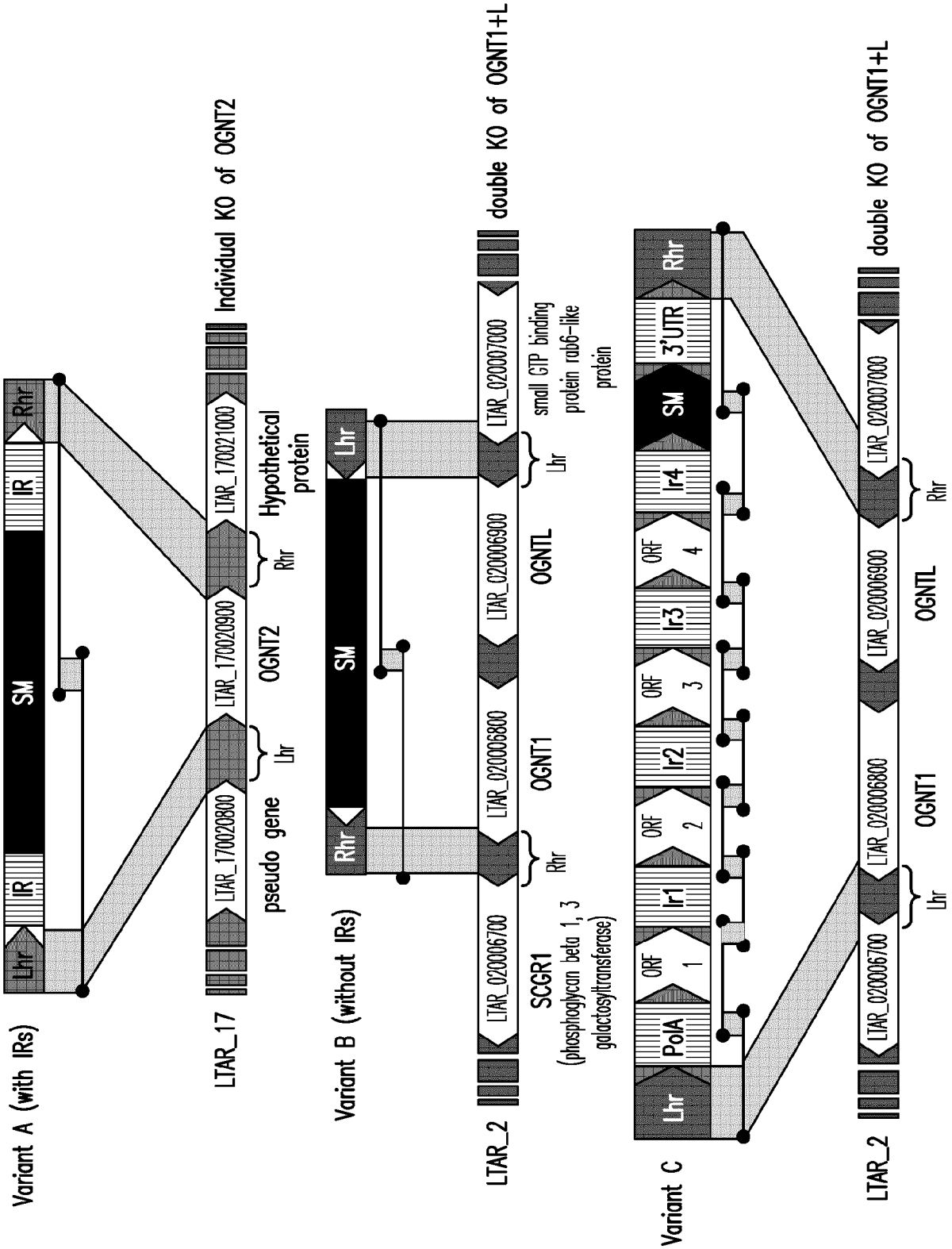

Variant A (with IRs)
LTAR_17
Individual KO of OGNT2
Lhr
IR
SM
IR
Rhr
LTAR_170020800
LTAR_170020900
LTAR_170021000
pseudo gene
OGNT2
Hypothetical protein
Lhr
Rhr
Variant B (without IRs)
LTAR_2
double KO of OGNT1+L
Lhr
SM
Rhr
LTAR_020006700
LTAR_020006800
LTAR_020006900
LTAR_020007000
SCGR1
(phosphoglycan beta 1, 3 galactosyltransferase)
OGNT1
OGNTL
small GTP binding protein rab6-like protein
Rhr
Lhr
Variant C
LTAR_2
double KO of OGNT1+L
Lhr
PolA
ORF 1
Ir1
ORF 2
Ir2
ORF 3
Ir3
ORF 4
Ir4
SM
3'UTR
Rhr
LTAR_020006700
LTAR_020006800
LTAR_020006900
LTAR_020007000
OGNT1
OGNTL
Lhr
Rhr

FIG. 6

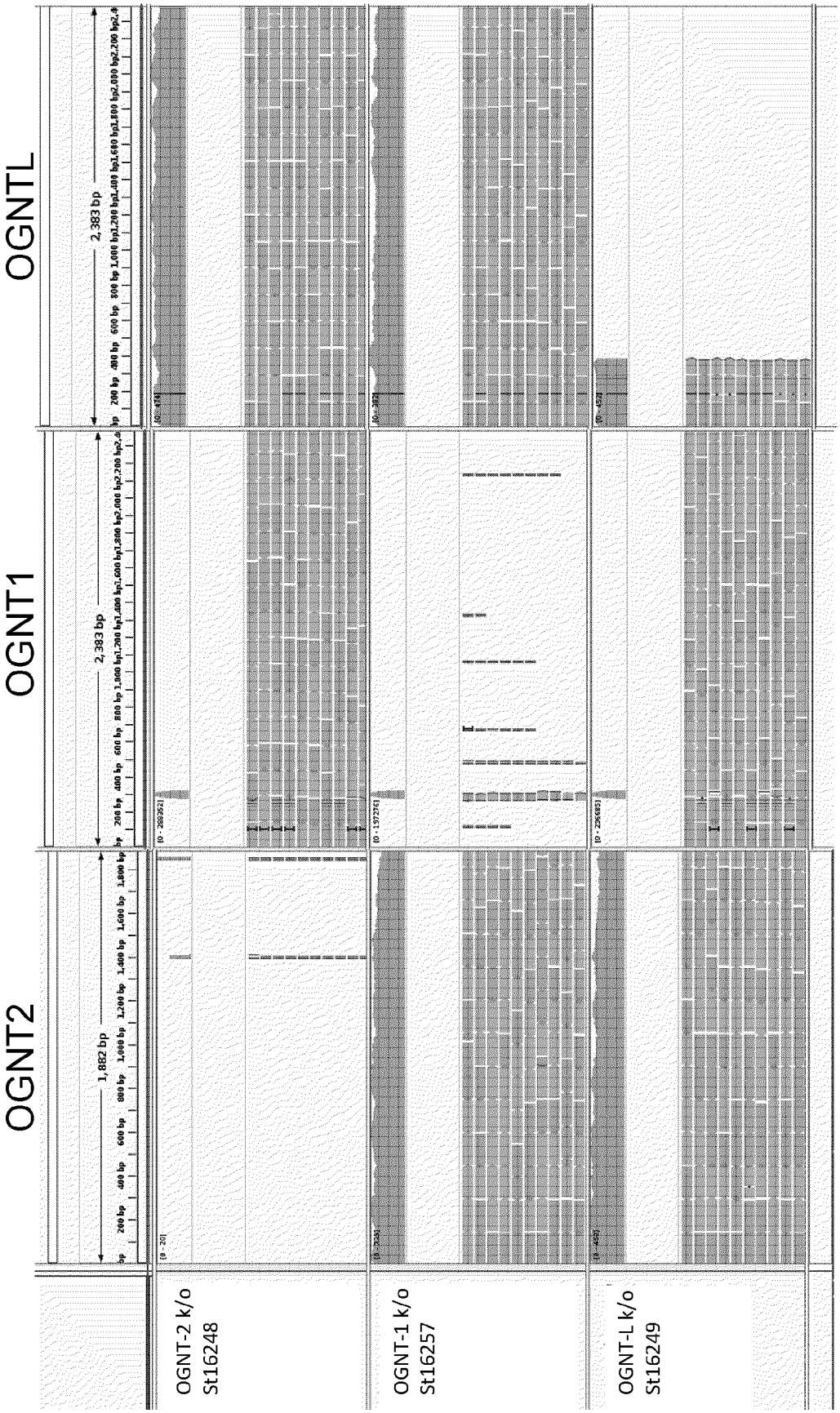
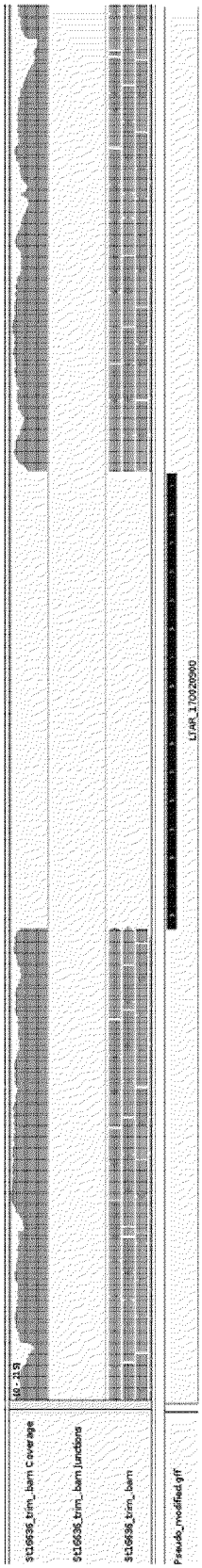

OGNT2
OGNT1
OGNTL
1,882 bp
2,383 bp
2,383 bp
OGNT-2 k/o
St16248
OGNT-1 k/o
St16257
OGNT-L k/o
St16249

FIG. 7A

OGNT2 (LTAR_170020900.1)



OGNT1 (LTAR_020006800.1), OGNTL (LTAR_020006900.1)

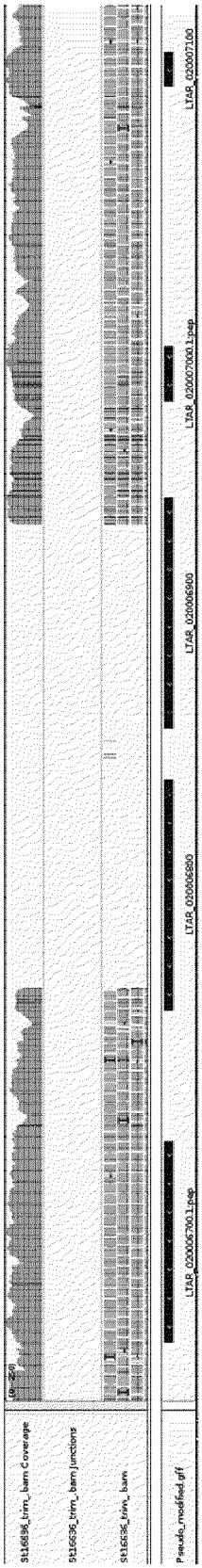


FIG. 7B

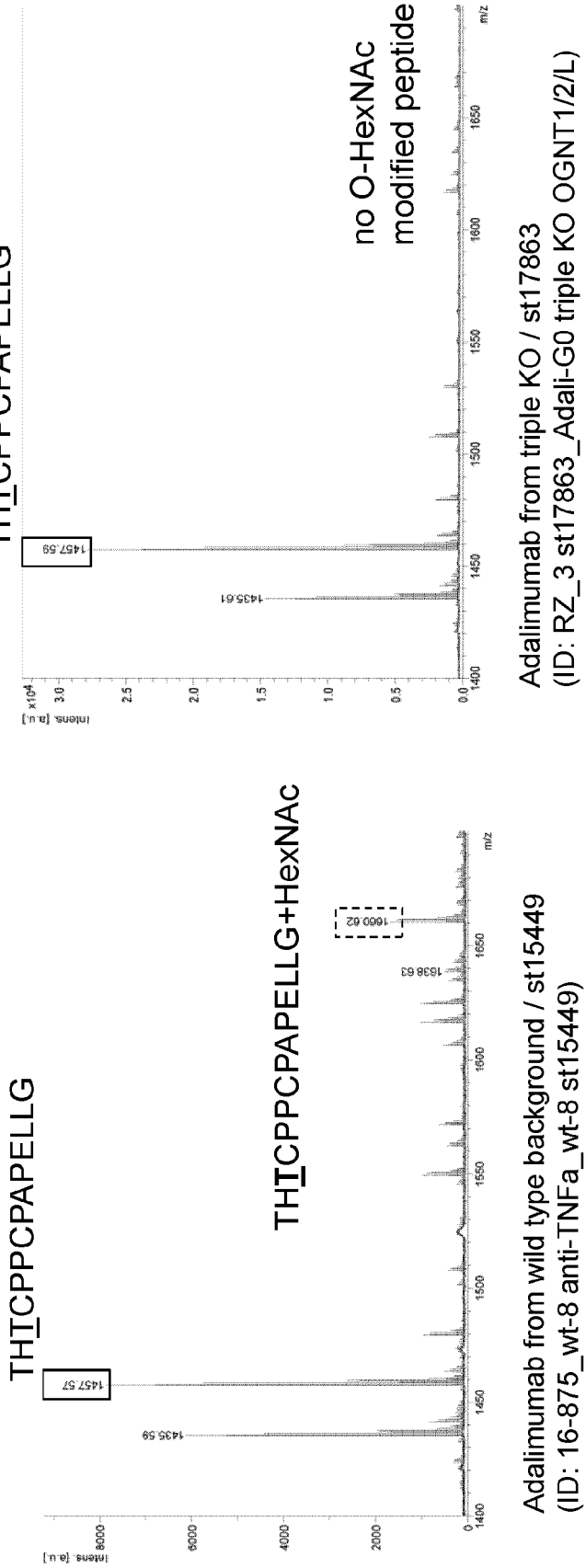

THTCPPCPAPELLG
1457.59
1435.61
no O-HexNAc
modified peptide
Intens. [a.u.]
m/z
Adalimumab from triple KO / st17863
(ID: RZ_3 st17863_Adali-G0 triple KO OGNT1/2/L)
THTCPPCPAPELLG
1457.57
1435.59
THTCPPCPAPELLG+HexNAc
1660.62
1638.63
Intens. [a.u.]
m/z
Adalimumab from wild type background / st15449
(ID: 16-875_wt-8 anti-TNFa_wt-8 st15449)

FIG. 8A

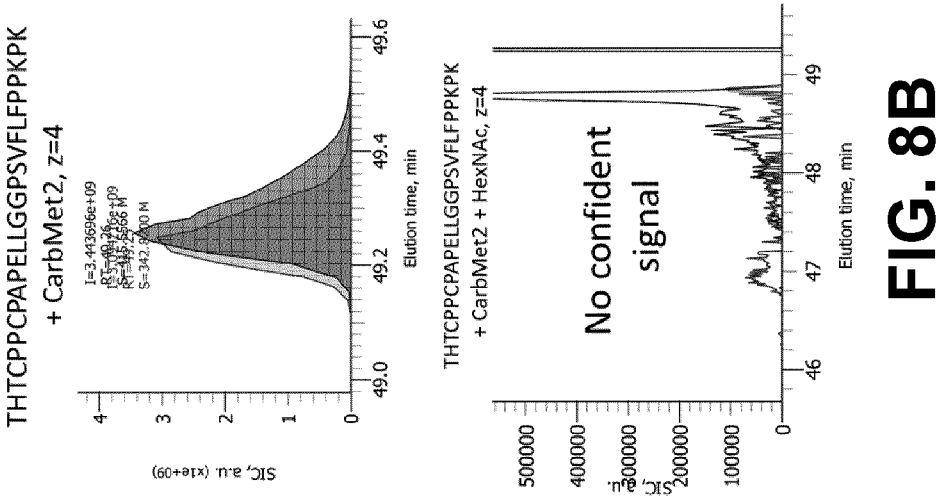

THTCPPCPAPELLGGPSVFLFPPKPK
+ CarbMet2, z=4
SIC, a.u. (x1e+09)
Elution time, min
THTCPPCPAPELLGGPSVFLFPPKPK
+ CarbMet2 + HexNAc, z=4
No confident signal
SIC, a.u.
Elution time, min

FIG. 8B

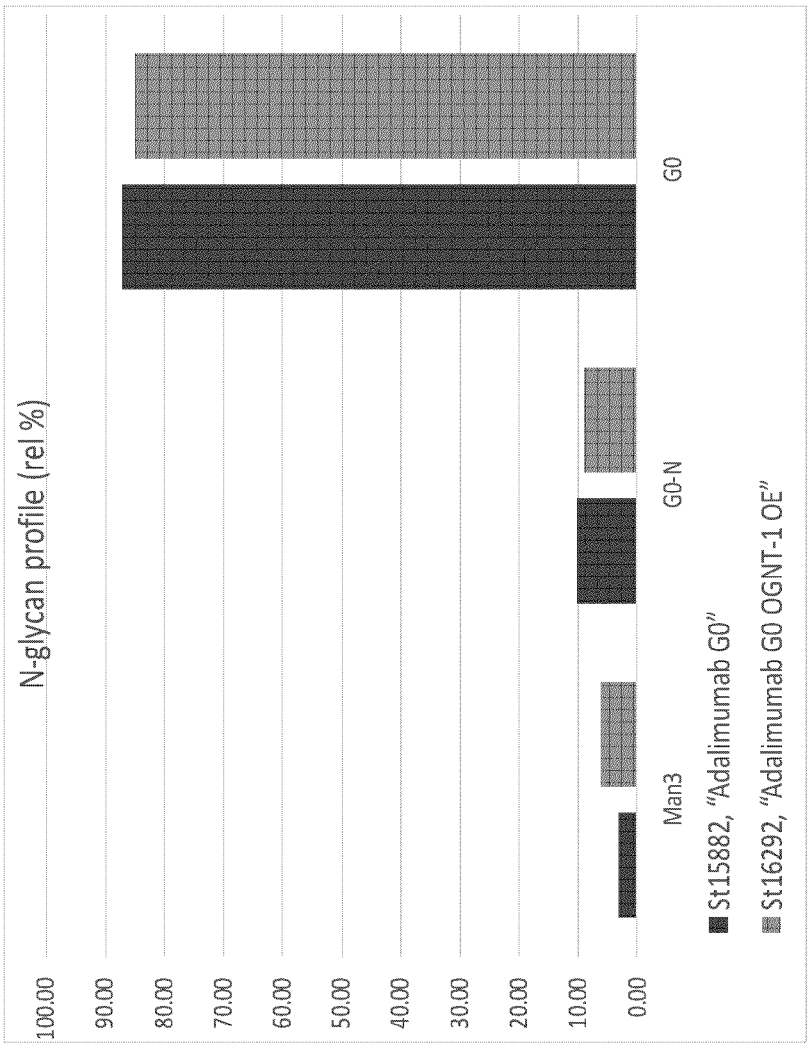

N-glycan profile (rel %)
100.00
90.00
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
Man3
G0-N
G0
St15882, "Adalimumab G0"
St16292, "Adalimumab G0 OGNT-1 OE"

FIG. 9A

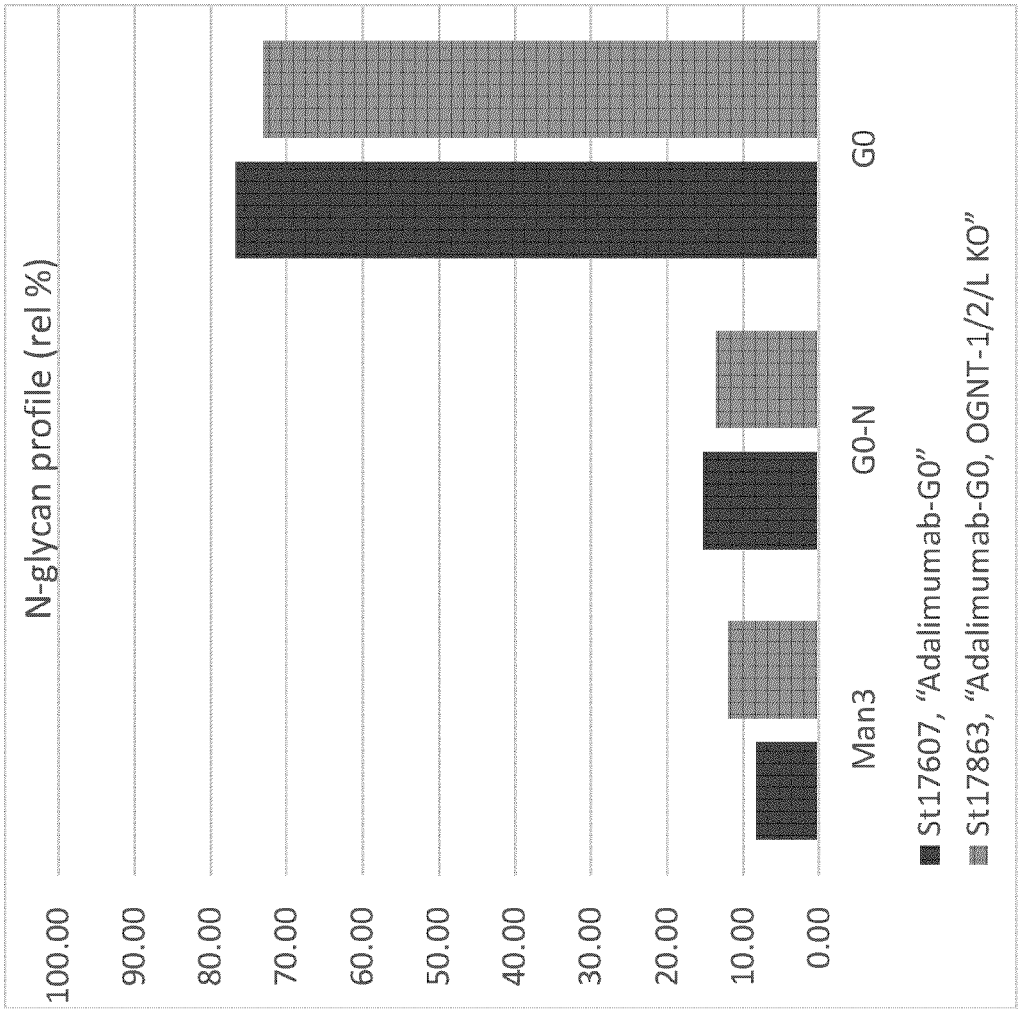

N-glycan profile (rel %)
100.00
90.00
80.00
70.00
60.00
50.00
40.00
30.00
20.00
10.00
0.00
Man3
G0-N
G0
St17607, "Adalimumab-G0"
St17863, "Adalimumab-G0, OGNT-1/2/L KO"

FIG. 9B

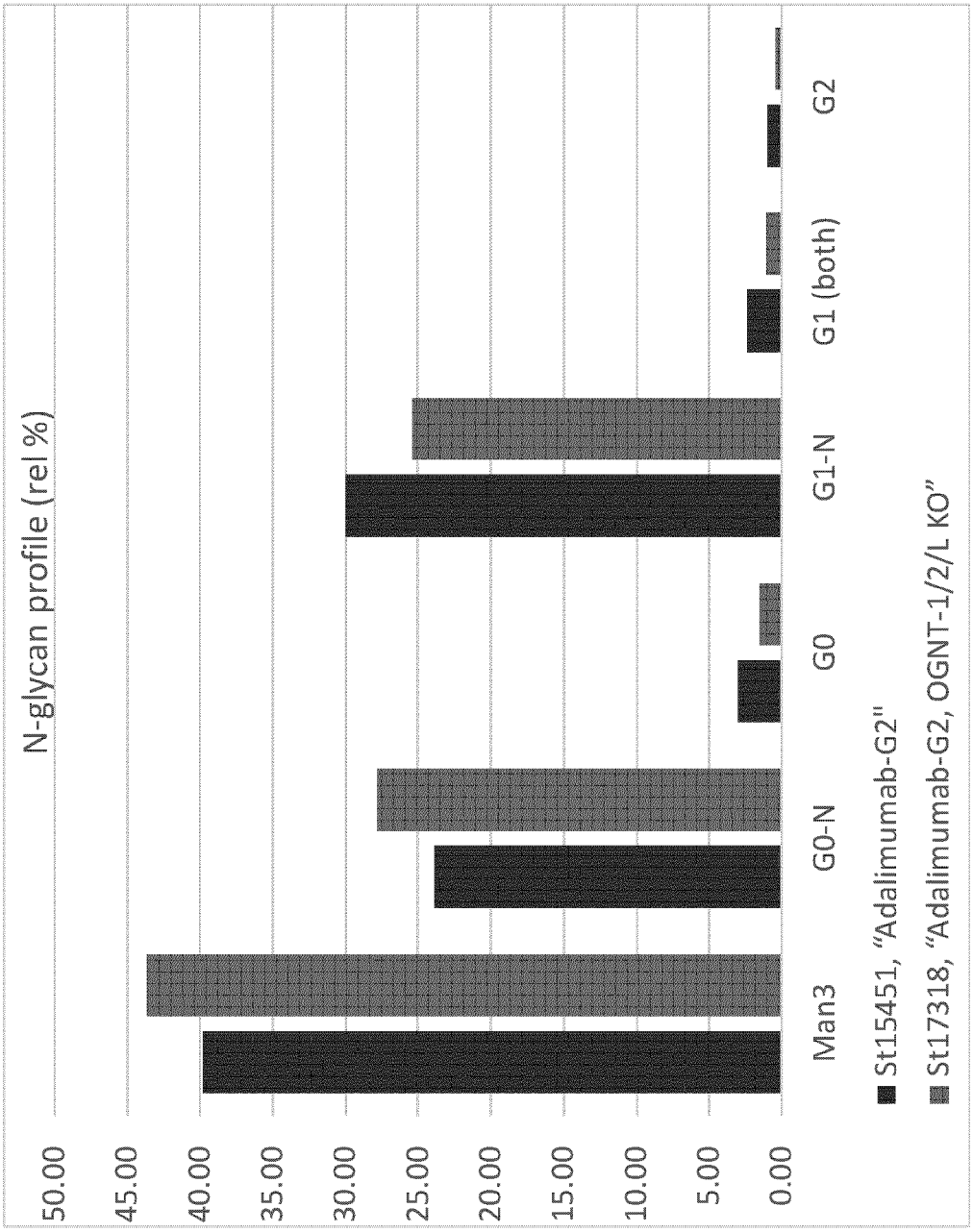

N-glycan profile (rel %)
50.00
45.00
40.00
35.00
30.00
25.00
20.00
15.00
10.00
5.00
0.00
Man3
G0-N
G0
G1-N
G1 (both)
G2
St15451, "Adalimumab-G2"
St17318, "Adalimumab-G2, OGNT-1/2/L KO"

FIG. 9C

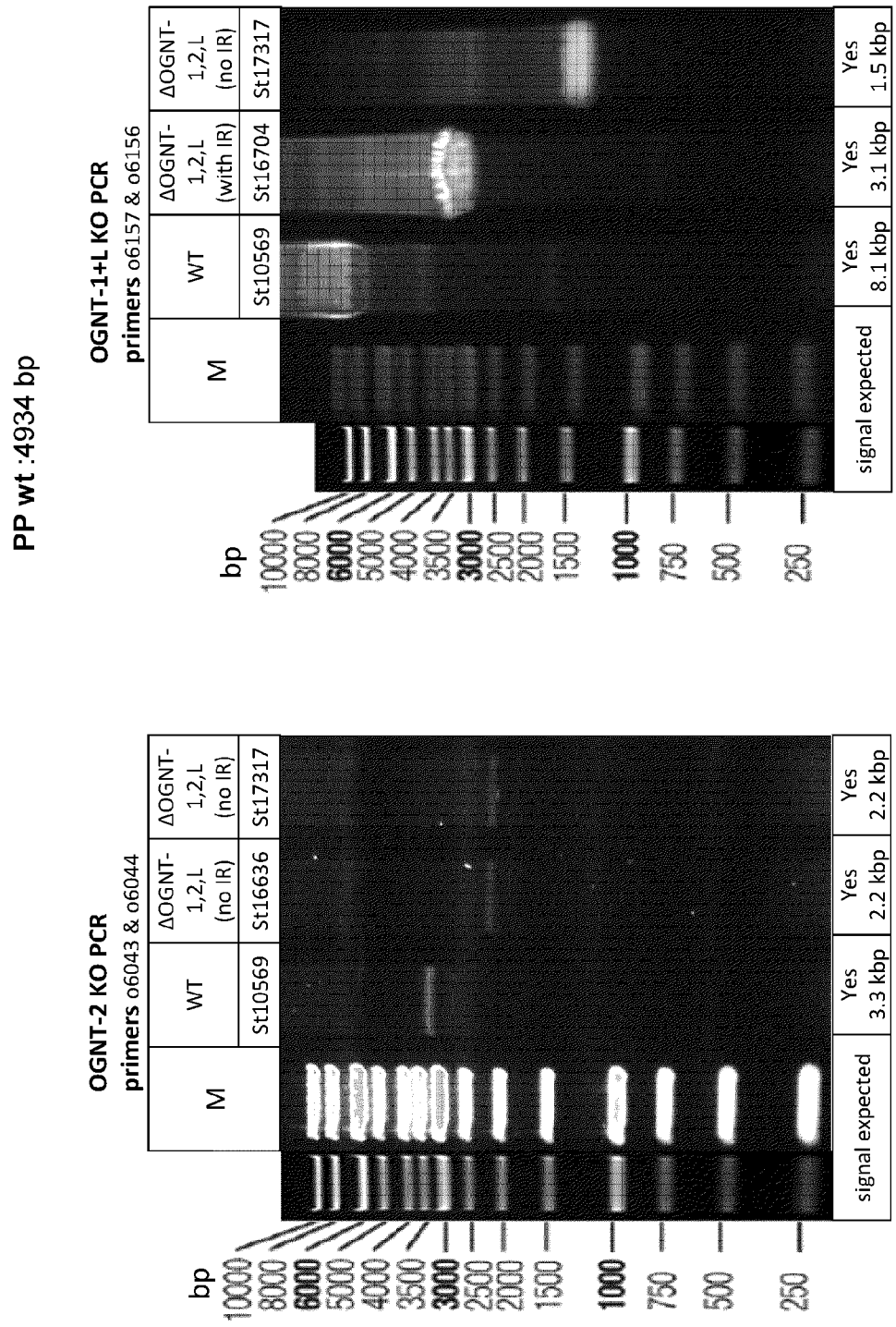

PP wt :4934 bp
OGNT-1+L KO PCR
primers o6157 & o6156
M
WT
ΔOGNT-1,2,L (with IR)
ΔOGNT-1,2,L (no IR)
St10569
St16704
St17317
signal expected
Yes 8.1 kbp
Yes 3.1 kbp
Yes 1.5 kbp
bp
10000
8000
6000
5000
4000
3500
3000
2500
2000
1500
1000
750
500
250
OGNT-2 KO PCR
primers o6043 & o6044
M
WT
ΔOGNT-1,2,L (no IR)
ΔOGNT-1,2,L (no IR)
St10569
St16636
St17317
signal expected
Yes 3.3 kbp
Yes 2.2 kbp
Yes 2.2 kbp
bp
10000
8000
6000
5000
4000
3500
3000
2500
2000
1500
1000
750
500
250

FIG. 9D

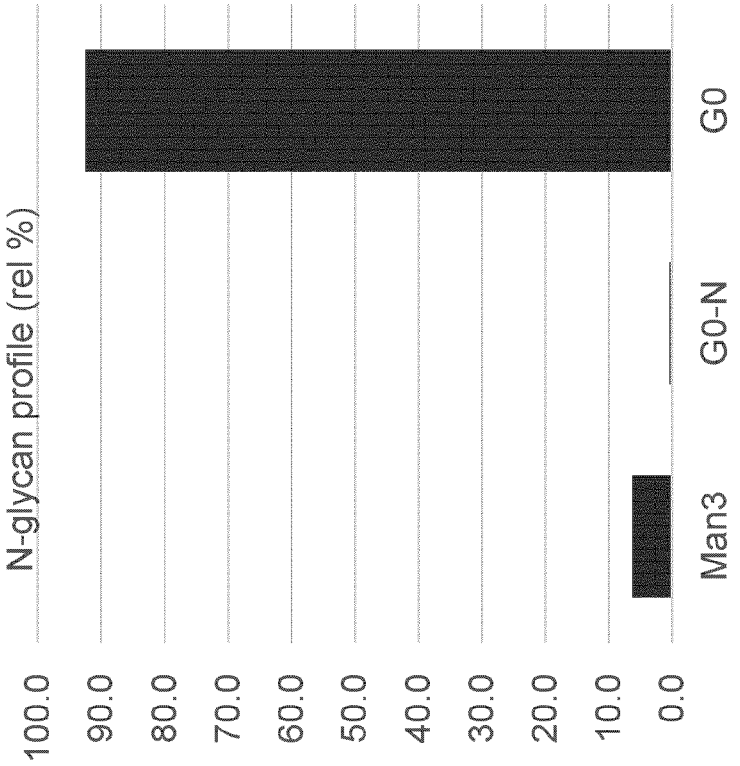

N-glycan profile (rel %)
100.0
90.0
80.0
70.0
60.0
50.0
40.0
30.0
20.0
10.0
0.0
Man3
G0-N
G0
St17846

FIG. 10A

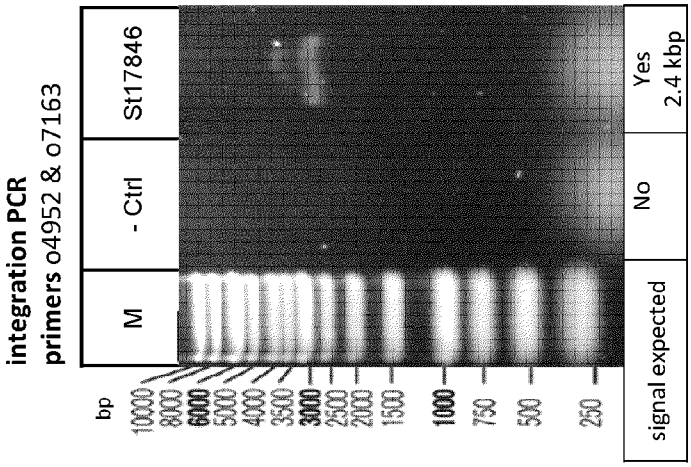

integration PCR
primers o4952 & o7163
M
- Ctrl
St17846
bp
10000
8000
6000
5000
4000
3500
3000
2500
2000
1500
1000
750
500
250
signal expected
No
Yes
2.4 kbp

FIG. 10B

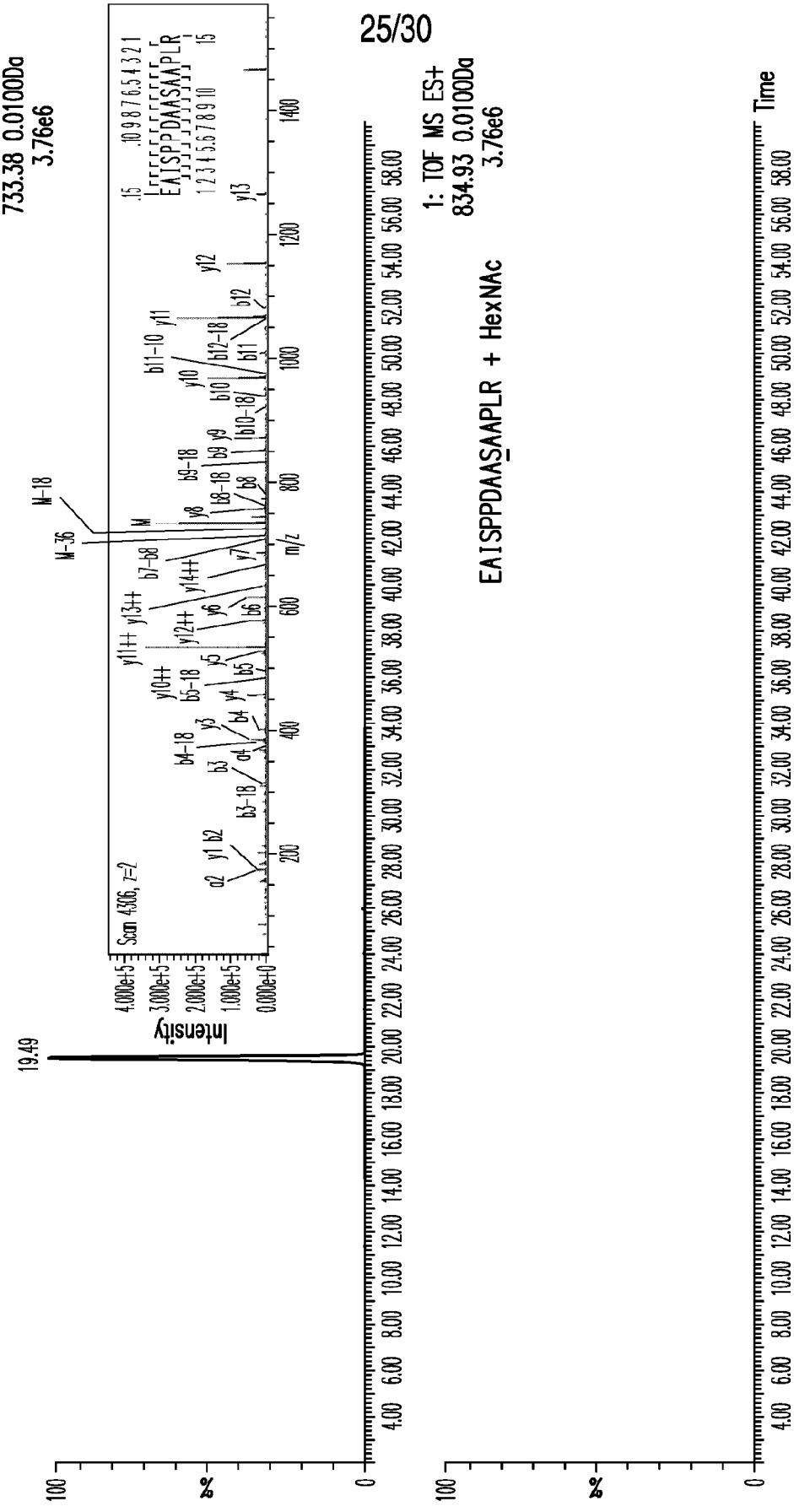

EAISPPDAASAAPLR
1: TOF MS ES+
733.38 0.0100Da
3.76e6
M-18
M-36
M
Scan 4306, z=2
Intensity
m/z
EAISPPDAASAAPLR + HexNAc
1: TOF MS ES+
834.93 0.0100Da
3.76e6
19.49
%
Time

FIG. 11

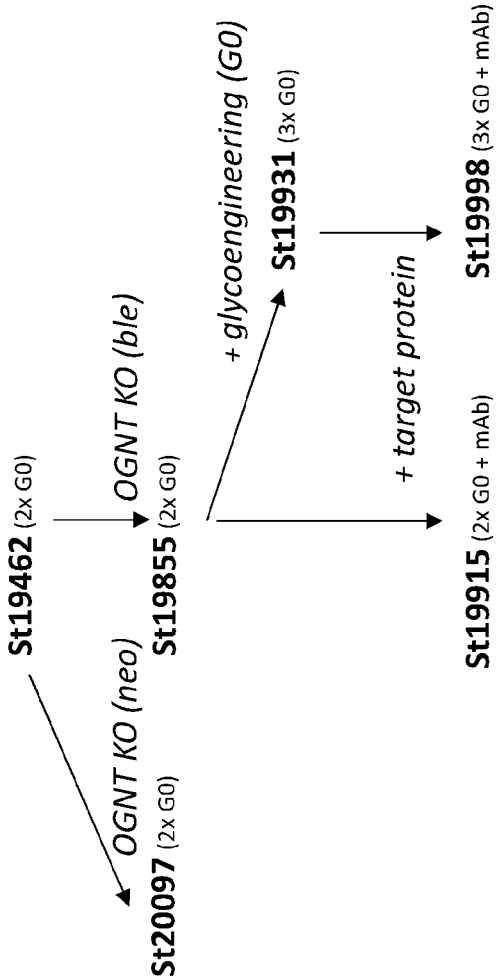

St19462 (2x G0)
OGNT KO (ble)
St19855 (2x G0)
OGNT KO (neo)
St20097 (2x G0)
+ glycoengineering (G0)
St19931 (3x G0)
+ target protein
St19915 (2x G0 + mAb)
St19998 (3x G0 + mAb)

FIG. 12A

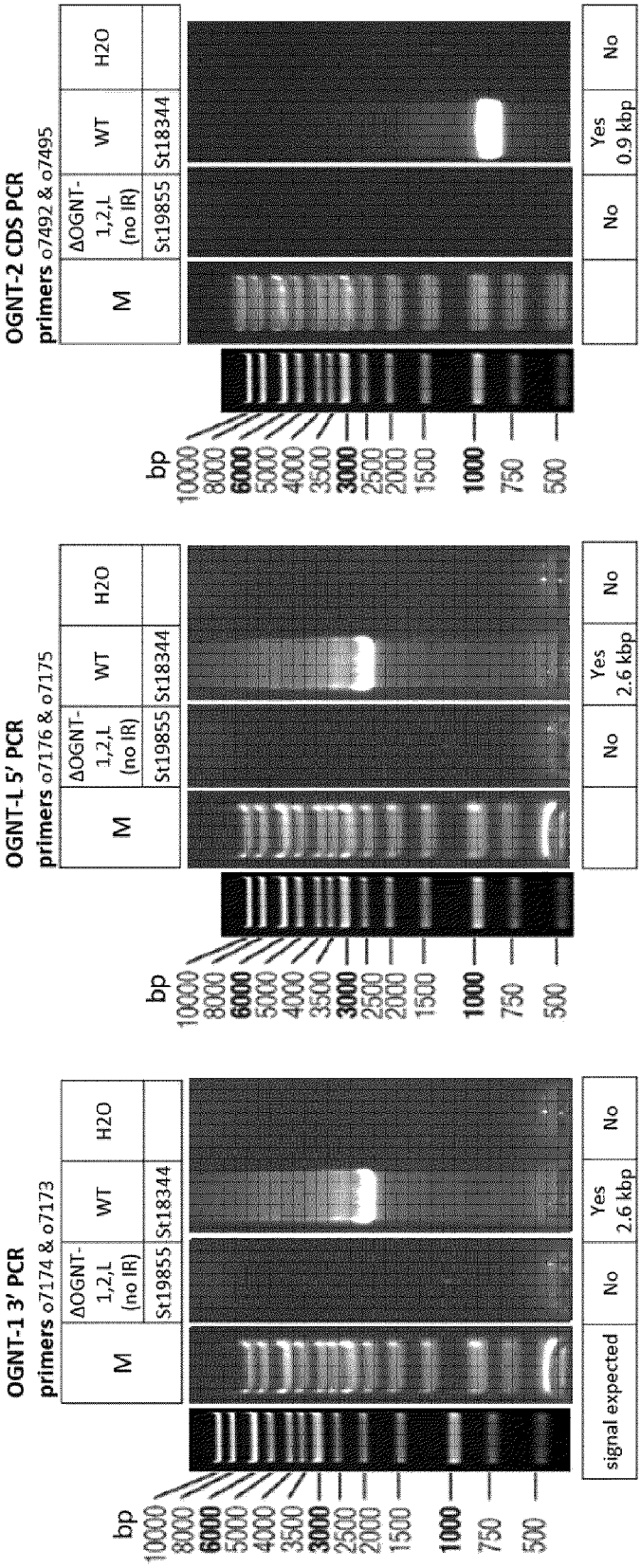

OGNT-1 3' PCR
primers o7174 & o7173
M
ΔOGNT-1,2,L (no IR)
St19855
WT
St18344
H2O
bp
10000
8000
6000
5000
4000
3500
3000
2500
2000
1500
1000
750
500
signal expected
No
Yes 2.6 kbp
No
OGNT-L 5' PCR
primers o7176 & o7175
M
ΔOGNT-1,2,L (no IR)
St19855
WT
St18344
H2O
bp
10000
8000
6000
5000
4000
3500
3000
2500
2000
1500
1000
750
500
No
Yes 2.6 kbp
No
OGNT-2 CDS PCR
primers o7492 & o7495
M
ΔOGNT-1,2,L (no IR)
St19855
WT
St18344
H2O
bp
10000
8000
6000
5000
4000
3500
3000
2500
2000
1500
1000
750
500
No
Yes 0.9 kbp
No

FIG. 12B

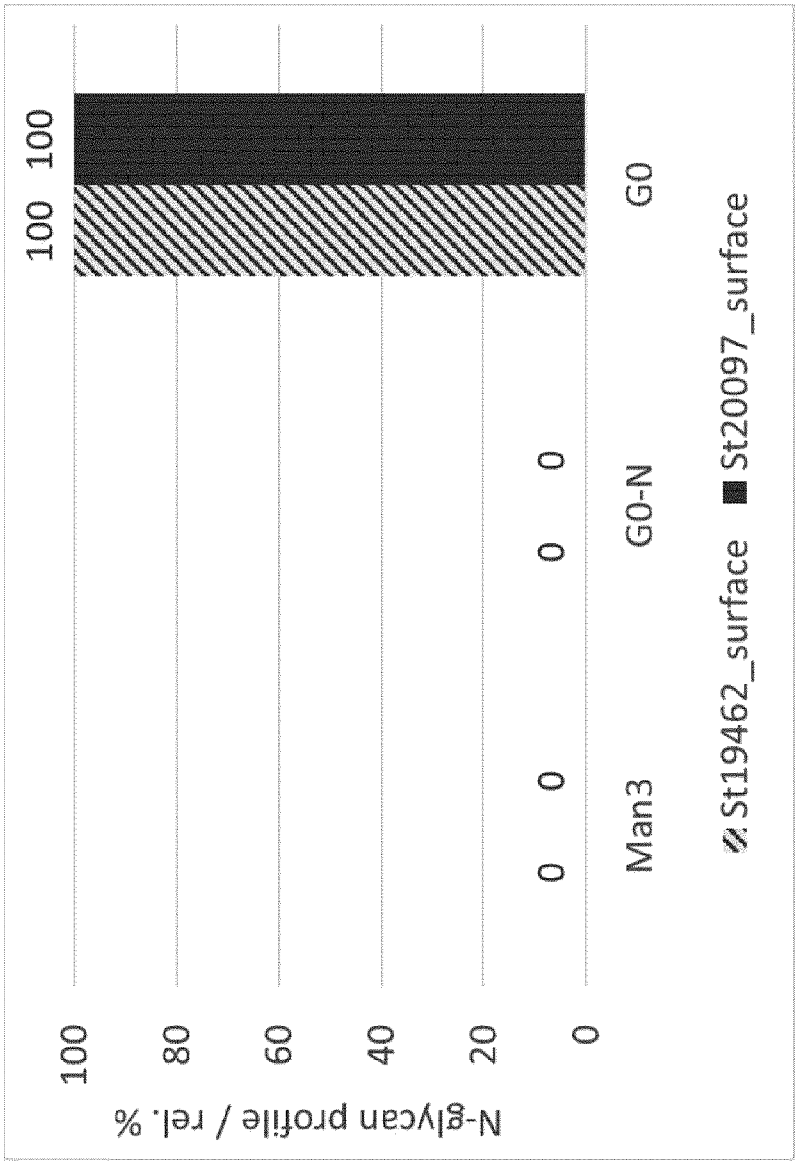
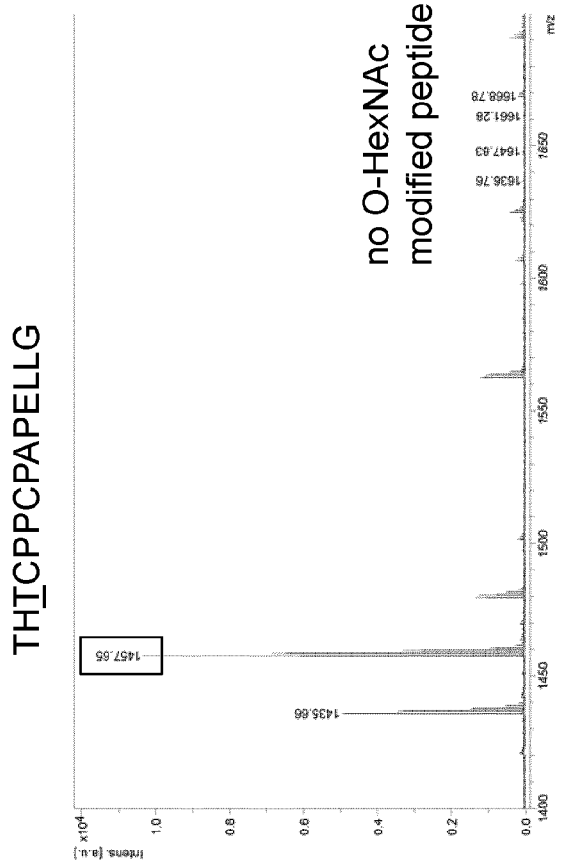

N-glycan profile / rel. %
100
80
60
40
20
0
0 0
Man3
0 0
G0-N
100 100
G0
St19462_surface
St20097_surface

FIG. 12C



Adalimumab from St19915
MSO_1201_15

FIG. 12D

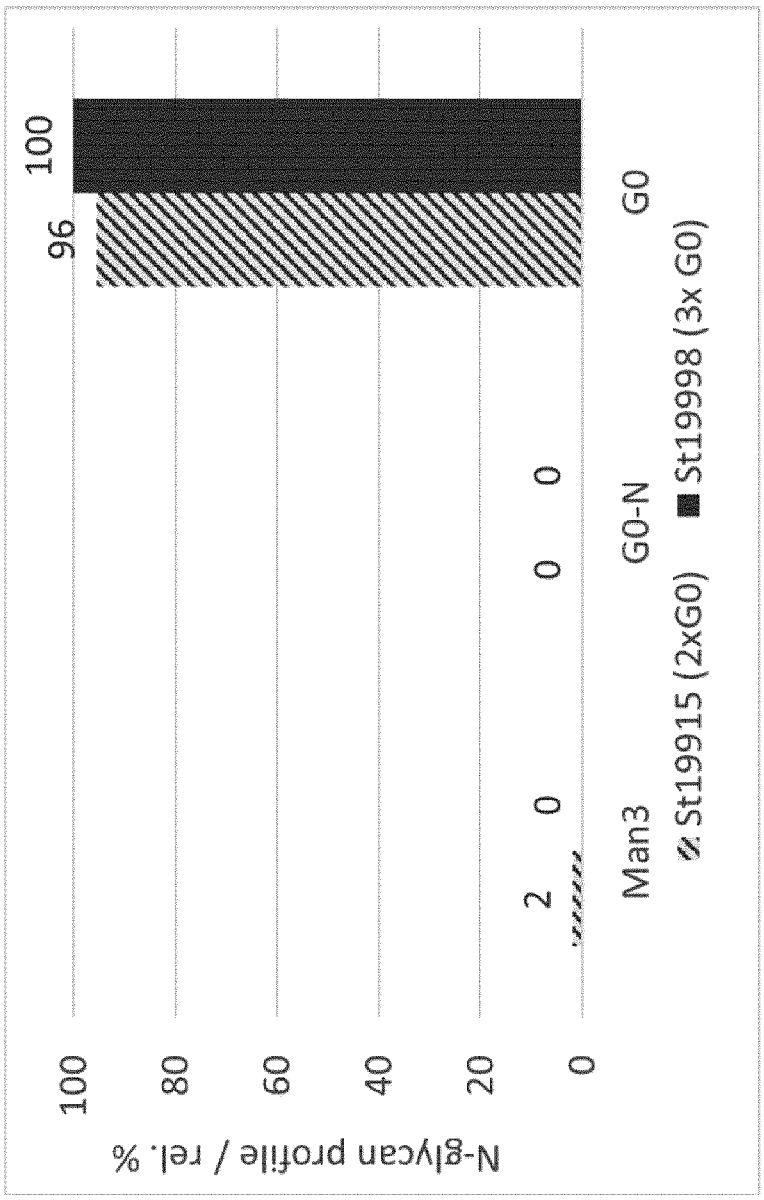

N-glycan profile / rel. %
100
80
60
40
20
0
2
0
0
0
96
100
Man3
G0-N
G0
St19915 (2xG0)
St19998 (3x G0)

FIG. 12E

INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2021/050172

A. CLASSIFICATION OF SUBJECT MATTER
INV. C12N9/10 C12N15/79 C12R1/90 C12P21/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
C12N C40B C12R C12P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
EPO-Internal, BIOSIS, Sequence Search, EMBASE, WPI Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 2019/234021 A1 (LIMMATECH BIOLOGICS AG [CH]) 12 December 2019 (2019-12-12)	18
A	the whole document	1-17

X	WO 2019/002512 A2 (LIMMATECH BIOLOGICS AG [CH]) 3 January 2019 (2019-01-03) cited in the application	18
A	the whole document	1-17

	-/--	

[X] Further documents are listed in the continuation of Box C.

[X] See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
8 April 2021	20/04/2021

Name and mailing address of the ISA/	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Kania, Thomas

2

Form PCT/ISA/210 (second sheet) (April 2005)

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KLATT STEPHAN ET AL: "Production of Glycosylated Soluble Amyloid Precursor Protein Alpha (sAPPalpha) in Leishmania tarentolae", JOURNAL OF PROTEOME RESEARCH, vol. 12, no. 1, 4 January 2013 (2013-01-04), pages 396-403, XP55793625, ISSN: 1535-3893, DOI: 10.1021/pr300693f	18
A	the whole document	1-17
A	WO 2016/091268 A2 (UNIV COPENHAGEN [DK]; NOVO NORDISK AS [DK]) 16 June 2016 (2016-06-16)	1-18
A	WO 2014/099632 A1 (MERCK SHARP & DOHME [US]; CHEN MING-TANG [US] ET AL.) 26 June 2014 (2014-06-26)	1-18
A	GIANCARLO BASILE ET AL: "Recombinant Protein Expression in Leishmania tarentolae", MOLECULAR BIOTECHNOLOGY, vol. 43, no. 3, 1 November 2009 (2009-11-01), pages 273-278, XP055059760, ISSN: 1073-6085, DOI: 10.1007/s12033-009-9213-5	1-18
A	KHAN AMJAD HAYAT ET AL: "Humanizing glycosylation pathways in eukaryotic expression systems", WORLD JOURNAL OF MICROBIOLOGY & BIOTECHNOLOGY, RAPID COMMUNICATIONS OF OXFORD, OXFORD, GB, vol. 33, no. 4, 1 January 2017 (2017-01-01), pages 1-12, XP036125448, ISSN: 0959-3993, DOI: 10.1007/S11274-016-2172-7 [retrieved on 2016-11-11]	1-18

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2021/050172

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2019234021 A1	12-12-2019	NONE	
WO 2019002512 A2	03-01-2019	AU 2018294504 A1	23-01-2020
		CN 111108211 A	05-05-2020
		EP 3645732 A2	06-05-2020
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		EP 2931895 A1	21-10-2015
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