

METHODS AND COMPOSITIONS FOR IMPROVING GUT MICROBIOTA POPULATION

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of the filing date of Chinese Patent Application No. 201210185004.2 filed June 6, 2012, the entire disclosure of which is incorporated by reference herein.

TECHNICAL FIELD

The present application relates to compositions and methods for improving gut microbiota populations and related application in drugs, nutritional supplements, health care products, food and beverage.

BACKGROUND

Unless otherwise indicated herein, the materials described in this section are not prior art to the claims in this application and are not admitted to be prior art by inclusion in this section.

Inside the human body lives a large number of symbiotic microbes, among which the gut microbiota acts as an important environmental factor to host health. There are more than 1000 species of bacteria, whose number exceeds 10 folds of the number of human cells, and whose gene number is about 150 folds of that in human cells. In this context, the human body as a "superorganism" made of host cells and symbiotic microbes including gut microbiota, and the genome encoding a consortium of gut microbes (microbiome) is considered as the second human genome, also known as "human metagenome". When human health status changes, the composition of symbiotic microbes changes accordingly. Conversely, changes in the composition of symbiotic microbes lead to the change in the human health status. Together, the diversity in human genome and the genome of gut microbiome affects immunity, nutrition, metabolism, and the health and disease status of the human host. However, up to now, it is not clear by what mechanisms the gut microbiota contribute to disease etiology and pathology, which type of bacteria is positively correlated with the health status of the host, and which type of bacteria is negatively correlated with the health status of the host.

SUMMARY

The following summary is illustrative only and is not intended to be in any way limiting. In addition to the illustrative aspects, embodiments, and features described above, further aspects, embodiments, and features will become apparent by reference to the drawings and the following detailed description.

In one aspect, the application provides methods for improving gut microbiota population. In one embodiment, the method includes administering to a subject a composition to increase a

first gut microbiota population while simultaneously decrease a second gut microbiota population in the subject. The first gut microbiota population may include a short-chain fatty acid (SCFA)-producing bacteria. The second gut microbiota population may include an endotoxin-producing bacterium.

In another aspect, the application provides methods for screening a test compound that may be active in improving gut microbiota population. In one embodiment, the method includes administering to a control subject an effective amount of a control composition to increase a first gut microbiota population while simultaneously decrease a second gut microbiota population in the control subject, administering to a test subject an amount of a test compound, and comparing the gut microbiota population of the controlled subject with the gut microbiota population of the test subject. A similarity of at least about 80% is indicative that the test compound is active in improving gut microbiota population. The first gut microbiota population may include a short-chain fatty acid (SCFA)-producing bacteria. The second gut microbiota population may include an endotoxin-producing bacterium.

In a further aspect, the application provides compositions for improving gut microbiota population. In one embodiment, the composition is capable of selectively increasing a first gut microbiota population while simultaneously decreasing a second gut microbiota population in a subject. The first gut microbiota population may include a short-chain fatty acid (SCFA)-producing bacteria. The second gut microbiota population may include an endotoxin-producing bacterium. In one embodiment, the composition is administered to the subject at a dosage of from about 50 mg/kg body weight to about 400 mg/body weight and with once a day administration for at least two weeks.

BRIEF DESCRIPTION OF THE DRAWINGS

The foregoing and other features of this disclosure will become more fully apparent from the following description and appended claims, taken in conjunction with the accompanying drawings. Understanding that these drawings depict only several embodiments arranged in accordance with the disclosure and are, therefore, not to be considered limiting of its scope, the disclosure will be described with additional specificity and detail through use of the accompanying drawings, in which:

FIGURE 1 illustrates the effect of berberine on the rat gut microbiota structure; FIGURE 1A is the PCoA score plot of changes in the rat gut microbiota structure in response to HFD feeding and berberine administration; FIGURE 1B shows the clustering of the gut microbiota based on mahalanobis distances calculated using MANOVA; and FIGURE 1C shows the Shannon-Wiener index, calculated after rarefying to an equal number of sequence reads for all samples;

FIGURE 2 illustrates some representative differences in the gut microbiota structure caused by berberine treatment using distance triplot of the RDA of gut microbiota;

FIGURE 3 illustrates the effect on the short-chain fatty acid contents in rat feces when the rats were fed with high fat diet or normal chow diet; FIGURE 3A shows the levels of total short-chain fatty acids (SCFAs); FIGURE 3B shows the level of acetic acid; FIGURE 3C shows the level of propionic acid; and FIGURE 3D shows the level of butyric acid (D);

FIGURE 4 illustrates the effect of berberine on obesity phenotypes and food intake in rats; FIGURE 4A shows the effect of berberine on the body weight gain; FIGURE 4B shows the effect of berberine on the adiposity index, calculated as the fat pad weight (sum of epididymal and perirenal fat pads) per 100 g of total body weight; and FIGURE 4C shows the food intake of rats during the entire trial;

FIGURE 5 illustrates the effect of berberine on the insulin sensitivity in rats; FIGURE 5A shows the effect of berberine on fasting blood glucose (FBG); FIGURE 5B shows the effect of berberine on fasting serum insulin (FINS); FIGURE 5C shows the effect of berberine on homeostasis assessment of insulin resistance (HOMA-IR) value, calculated according to the formula $\text{fasting insulin } (\mu\text{U/mL}) \times \text{fasting glucose (mmol/L)} / 22.5$; FIGURE 5D shows the effect of berberine on oral glucose tolerance test (OGTT); and FIGURE 5E shows the effect of berberine on intra-peritoneal insulin tolerance test (ITT); and

FIGURE 6 illustrates the effect of berberine on the level of inflammation factors in rats; FIGURE 6A shows the effect of berberine on serum lipopolysaccharide (LPS)-binding protein (LBP); FIGURE 6B shows the effect of berberine on serum leptin; FIGURE 6C shows the effect of berberine on serum MCP-1; and FIGURE 6D shows the effect of berberine on serum adiponectin corrected for body fat.

DETAILED DESCRIPTION

In the following detailed description, reference is made to the accompanying drawings, which form a part hereof. In the drawings, similar symbols typically identify similar components, unless context dictates otherwise. The illustrative embodiments described in the detailed description, drawings, and claims are not meant to be limiting. Other embodiments may be utilized, and other changes may be made, without departing from the spirit or scope of the subject matter presented herein. It will be readily understood that the aspects of the present disclosure, as generally described herein, and illustrated in the Figures, can be arranged, substituted, combined, separated, and designed in a wide variety of different configurations, all of which are explicitly contemplated herein.

This application is generally drawn, *inter alia*, to compositions, methods, processes, apparatus, systems, devices, and/or products related to improving gut microbiota population.

The application provides novel compositions and methods for improving gut microbiota population. The application identifies bacteria families that are closely related to host metabolism utilizing, for example, high throughput sequencing and multivariate statistical methods.

In one aspect, the application provides methods for improving gut microbiota population. In one embodiment, the method may include selectively enriching a first gut microbiota population. The first gut microbiota population may include, for example, an short-chain fatty acid (SCFA)-producing bacterium. In one embodiment, the method may include suppressing a second gut microbiota population. The second gut microbiota population may include, for example, an endotoxin-producing bacterium.

In one embodiment, the method may include the step of administering to a subject a composition. The composition may be an oral or parenteral formulation. The composition may

selectively increase the first gut microbiota population while simultaneously decrease the second gut microbiota population.

The enrichment of the first gut microbiota population and suppression of the second microbiota population may be carried out simultaneously. The method may result in the prevention or treatment of metabolic syndrome including, without limitation, obesity, diabetes mellitus, insulin resistance, hyperlipoproteinemia, hyperuricemia, hepatic steatosis, hypercholesterolemia, hypertriglyceridemia, inflammation, and other disorders.

The short-chain fatty acid (SCFA)-producing bacteria inside gut are mostly beneficial bacteria. These bacteria either directly or, by increasing short-chain fatty acid inside gut, thus indirectly, perform functions including without limitation anti-inflammation, protecting intestinal barrier function, and regulating metabolism and immune system. These functions lead to the prevention or treatment of obesity, insulin resistance, diabetes, and other metabolic diseases.

Using the disclosed methods for improving gut microbiota population, the increased gut microbiota population may include *Alistipes*, *Allobaculum*, *Bacteroides*, *Barnesiella*, *Blautia*, *Butyricoccus*, *Butyricimonas*, *Dorea*, *Helicobacter*, *Hespellia*, *Holdemania*, *Lawsonia*, *Oscillibacter*, *Parabacteroides*, *Phascolarctobacterium*, *Prevotella*, or *Sedimentibacter*. In one embodiment, the increased gut microbiota population may include *Bacteroidaceae*, *Coriobacteriaceae*, *Desulfovibrionaceae*, *Erysipelotrichaceae*, *Flavobacteriaceae*, *Helicobacteraceae*, *Incertae Sedis XI*, *Incertae Sedis XIV*, *Lachnospiraceae*, *Porphyromonadaceae*, *Prevotellaceae*, *Rikenellaceae*, *Ruminococcaceae*, or *Veillonellaceae*; alternatively, the increased gut bacteria may include *Campylobacteriales*, *Desulfovibrionales*, *Bacteroidales*, *Coriobacteriales*, *Flavobacteriales*, *Clostridiales*, or *Erysipelotrichales*; alternatively, the increased gut bacteria may include *Epsilonproteobacteria*, *Deltaproteobacteria*, *Bacteroidia*, *Coriobacteridae*, *Flavobacteria*, *Clostridia*, or *Erysipelotrichi*; alternatively, the increased gut bacteria may include *Proteobacteria*, *Bacteroidetes*, *Actinobacteria*, or *Firmicutes*.

For example, the increased gut microbiota population may include a bacterium whose V3 region of 16S rRNA gene sequence has at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-93.

The endotoxin-producing bacteria inside gut are mostly harmful bacteria, which, either directly or indirectly by increasing endotoxin, promote inflammation, damage intestinal barrier function, and increase disorder in metabolism and immune system, as a result inducing obesity, insulin resistance, diabetes and other metabolic diseases.

According to the methods for improving gut microbiota population disclosed herein, the decreased gut bacteria may include *Alistipes*, *Anaeroplasmataceae*, *Barnesiella*, *Bifidobacterium*, *Butyricimonas*, *Butyrivibrio*, *Coprococcus*, *Fastidiosipila*, *Helicobacter*, *Hespellia*, *Marvinbryantia*, *Oribacterium*, *Oscillibacter*, *Prevotella*, *Roseburia*, *Ruminococcus*, or *TM7_genera_incertae_sedis*; alternatively, the decreased gut bacteria may include *Helicobacteraceae*, *Lachnospiraceae*, *Porphyromonadaceae*, *Prevotellaceae*, *Rikenellaceae*, *Ruminococcaceae*, *Anaeroplasmataceae*, or *Bifidobacteriaceae*. In one embodiment, the decreased gut microbiota population may include *Campylobacteriales*,

Bacteroidales, *Clostridiales*, *Anaeroplasmatales*, or *Bifidobacteriales*; alternatively, the decreased gut bacteria may include *Epsilonproteobacteria*, *Alphaaproteobacteria*, *Bacteroidia*, *Clostridia*, *Actinobacteridae*, or *Mollicutes*. In one embodiment, the decreased gut microbiota population may include *Proteobacteria*, *Bacteroidetes*, *Actinobacteria*, *Firmicutes*, or *Tenericutes*.

For example, the decreased gut bacteria may include a bacteria whose V3 region of 16S rRNA gene sequence has at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 94-268.

The methods may cause decrease of the serum level of pro-inflammatory factors. Example pro-inflammatory factors include without limitation cytokines such as lipopolysaccharide-binding protein, monocyte chemoattractant protein-1, or leptin. Additionally and optionally, the methods may increase the serum level of cytokine such as adiponectin.

The level of gut short-chain fatty acids may be increased using the disclosed methods. The short-chain fatty acids may include without limitation acetic acid, propionic acid, butyric acid, valeric acid, isobutyric acid, and isovaleric acid.

To improve the gut microbiota population, the compositions may be administered orally or parentally. In one embodiment, the composition may be a food, a drink, a supplement, or a pharmaceutical formulation. In one embodiment, the composition may be in the form of suppository, tablet, pill, granule, powder, film, microcapsule, aerosol, spirit, tincture, tonic, liquid suspension, or syrup. The composition may be administered at a dosage of from about 50 mg/kg body weight to about 400 mg/body weight.

In one example, the composition including berberine was administered to a subject. The gut microbiota population of the subject was then analyzed using 454 pyrosequencing techniques and the level of short-chain fatty acid was assayed by gas chromatography. The results demonstrated that berberine is capable of altering gut microbiota population: enriching certain bacteria including those that produce short-chain fatty acid while simultaneously suppressing or eliminating certain bacteria including those that produce endotoxin. It is further demonstrated that berberine administered orally is capable of increasing the level of short-chain fatty acid inside the gut, and the increase is more pronounced in individuals who have metabolic syndrome. Additional experimentation and observation further demonstrated that above described effects by berberine on the gut microbiota population have beneficial results including without limitation improving insulin sensitivity, reducing inflammation, controlling weight gain, and preventing obesity induced by over-eating, chronic inflammation and insulin resistance.

In another aspect, the application provides methods for screening drugs, compounds, compositions, extracts, or formulations capable of improving gut microbiota population. The methods may be used in the development of drugs, nutritional supplements, health care products, food, and beverages that improve health and/or prevent obesity or other related metabolic syndromes by targeting gut microbiota population in a subject.

In one embodiment, the screening method may include administering to a control subject an effective amount of a control composition to increase the first gut microbiota population while

simultaneously decrease the second gut microbiota population in the control subject, administering to a test subject an amount of a test composition, and comparing the gut microbiota population of the controlled subject and the gut microbiota population of the test subject.

As used herein, the term "subject" refers to an animal, such as a mammal, for example a human. In some embodiments, the subject may be a rat. In some embodiments, the subject may be a mouse. In some embodiments, the subject may be a human.

If the test compound demonstrates similar effect on gut microbiota as the control, the test compound is active in improving gut microbiota population. As used therein, "similar" refers to a similarity of at least about 75%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99%.

The test composition may be a single compound, a mixture, a food, a food additive, a nutritional supplement, health care product, a pharmaceutical formulation, or a beverage.

In a further aspect, the application provides compositions for improving gut microbiota population. In one embodiment, the composition may be capable of selectively increasing the first gut microbiota population while simultaneously decreasing the second gut microbiota population in a subject.

The composition may include a chemical compound, a natural medicine, a natural product, or an herbal extract. In one embodiment, the chemical compound may include, without limitation, berberine, berberine derivatives, isoquinoline alkaloids, or any combinations thereof.

In one embodiment, the composition may include natural medicine, whole, fragmented or powdered herb, or herbal extract derived from plants of *Berberis*, *Coptis*, *Scutellaria*, *Phellodendron*, *Momordica*, *Ilex*, *Sophora*, *Gentiana*, *Anemarrhena*, *Gardenia*, *Rheum*, or *Taraxacum*. In one embodiment, the composition may include natural medicine, whole, fragmented or powdered herb, or herbal extract derived from plants of *Berberidaceae*, *Ranunculaceae*, *Lamiaceae*, *Rutaceae*, *Cucurbitaceae*, *Aquifoliaceae*, *Leguminosae*, *Gentianaceae*, *Agavaceae*, *Rubiaceae*, *Polygonaceae*, *Asteraceae*, *Menispermaceae*, or *Cucurbitaceae*. In one embodiment, the composition may include natural medicine, whole, fragmented or powdered herb, or herbal extract derived from *Berberis vulgaris*, *Coptis chinensis*, *Scutellaria baicalensis*, *Phellodendron chinensis*, *Momordica charantia*, *Ilex kudingcha*, *Sophora flavescens*, *Gentiana scabra*, *Anemarrhena asphodeloides*, *Gardenia jasminoides*, *Rheum palmatum*, or *Herba Taraxaci*.

The following examples are for illustration of the execution and property of representative method of the application. These examples are not intended to limit the scope of the application.

EXAMPLES

These examples use Wistar rats (8 weeks old, male) as testing subjects and berberine as a representative compound. 40 Wistar rats were acclimatized for two weeks and were subsequently randomly divided into four groups: normal diet group (NCD), normal diet plus berberine

treatment (NCD+BBR), high fat diet (HFD), and high fat diet plus berberine treatment (HFD+BBR). Each group continued for another 18 weeks. During these 18 weeks, the NCD+BBR group received intragastric administration of berberine at stated levels. Feces samples from each animal were collected at various time points. 454 pyrosequencing was performed to analyze gut microbiota structure. Gas chromatography was used to assay the short-chain fatty acid level of the feces. In addition, weight, food intake, insulin sensitivity, systemic inflammation levels were monitored and measured during the 18-week period.

Berberine Altered the Gut Microbiota Population Under Both Normal Diet and High Fat Diet Conditions

The gut microbiota populations in rats from all four experimental groups were analyzed by 454 pyrosequencing and multivariate statistical analyses. PCoA analysis based on unweightedUnifrac distance demonstrated that berberine altered gut microbiota structure in both the normal diet group and high fat diet group at a statistically significant level; and berberine accounts for 12.6% of overall changes in the gut microbiota population (FIGURE 1A). Diet also exerted statistically significant influence on gut microbiota population. FIGURE 1A reveals a statistically significant difference (3.7%) in gut microbiota population between two different diets (NCD versus HFD) along the vertical axis. The multivariate variance analysis (MANOVA) on the four groups demonstrated that berberine or diet has a statistically significant influence on the gut microbiota ($P < 0.01$), but the most pronounced difference derives from the presence of berberine (FIGURE 1B). Shannon-Wiener parameter indicates that berberine reduces diversity of gut microbiota population at a statistically significant level ($P < 0.05$).

Berberine Enriches the Short-Chain Fatty Acid-Producing Bacteria and Reduces Endotoxin-Producing Bacteria in Gut Microbiota Population

268 berberine-related OTU were identified by redundancy analysis (RDA) and the detailed results are shown in FIGURE 2, TABLE 1, and TABLE 2. 93 OTU (SEQ_ID_NO 1-93) (TABLE 1) are enriched by berberine, while 175 OTU (SEQ_ID_NO 94-268) (TABLE 2) were suppressed or eliminated.

The taxonomy of these 268 OTU was analyzed using RDP classifier with representative sequence of the OTU. It was revealed that the berberine-suppressed bacteria included those of *Alistipes*, *Anaeroplasma*, *Barnesiella*, *Bifidobacterium*, *Butyricimonas*, *Butyrivibrio*, *Coprococcus*, *Fastidiosipila*, *Helicobacter*, *Hespellia*, *Marvinbryantia*, *Oribacterium*, *Oscillibacter*, *Prevotella*, *Roseburia*, *Ruminococcus*, *TM7_genera_incertae_sedis*, and others. Among them, the *Helicobacter*, belonging to Proteobacteria phylum, is capable of producing highly active endotoxin. In addition, it was revealed that the berberine-increased bacteria included those of *Alistipes*, *Allobaculum*, *Bacteroides*, *Barnesiella*, *Blautia*, *Butyricococcus*, *Butyricimonas*, *Dorea*, *Helicobacter*, *Hespellia*, *Holdemania*, *Lawsonia*, *Oscillibacter*, *Parabacteroides*, *Phascolarctobacterium*, *Prevotella*, and *Sedimentibacter*. Among them, *Blautia*, *Allobaculum*, *Prevotella*, *Bacteroides*, and *Butyricimonas* are relatively abundant and are capable of producing short-chain fatty acid.

Therefore, when administered to a subject, berberine is capable of enriching the short-chain fatty acid-producing bacteria and reducing endotoxin-producing bacteria in gut microbiota population.

Berberine Increases Gut Short-Chain Fatty Acid Level in Rats

Fed Normal Diet or High Fat Diet

The levels of short-chain fatty acid (including acetic acid, propionic acid, butyric acid, valeric acid, isobutyric acid, isovaleric acid, etc.) in rat feces were assayed by gas chromatography. The result demonstrated that oral administration of 100mg/kg body weight may increase the level of gut short-chain fatty acid in rats fed with normal diet or high fat diet. The effect on the levels of acetic acid and propionic acid are especially pronounced (FIGURE 3). Therefore, berberine is capable of increasing gut short-chain fatty acid level in rats fed normal diet or high fat diet.

Berberine Reduces Obesity Phenotype of Rats

The body weight of all four groups of rats were monitored during the duration of the experiments and analyzed. The results demonstrated that, after 18 weeks of high fat diet, the HFD group has significantly higher body weight than the normal diet group ($P < 0.01$); intragastric administration of berberine at the dosage of 100mg/kg effectively limits rat body weight growth, especially for rats fed high fat diet. The result is especially surprising that during the entire experimental process, the body weight of the HFD+BBR group is limited to a level similar to that of normal diet group, displaying no statistically significant difference ($P > 0.05$). Berberine also influences, to a certain degree, the body weight of rats fed a normal diet (FIGURE 4).

At the end of experiment, animals were euthanized. Fasting body weight, epididymal fat weight, and perirenal fat weight were measured. Adiposity index ([epididymal fat weight + perirenal fat] / fasting weight $\times 100$) is shown in FIGURE 4B. After 18 weeks of high fat diet, the adiposity index of the HFD group is significantly higher than that of NCD, and berberine treatment significantly reduces adiposity index. Moreover, neither high fat diet nor berberine had significant effect on liver and pancreas, indicating surprisingly that long term use of berberine has no obvious side effect to rat's normal physiological function. Results of the calorie intake of these rats demonstrated that oral administration of berberine at 100mg/kg body weight has a significant inhibitory effect on rat food intake, especially on rats fed a high fat diet (Figure 4C).

Berberine Reduces Insulin sensitivity in Rats Fed a Normal Diet or High Fat Diet

The fasting blood glucose (FBG) and fasting insulin in serum (FINS) were measured for all four experimental groups of rats. Rats fed a HFD for 18 months had a significant higher level of FBG than that of NCD. Surprisingly, berberine effectively reduced FBG in NCD and HFD rats, especially in HFD rats where the FBG reduction was significant ($P < 0.05$) (FIGURE 5A). The result of berberine effect on insulin level is shown in FIGURE 5B. The FINS of rat fed a HFD was significantly higher than that of NCD group; however, after 18 month of berberine intervention at the level of 100mg/kg body weight, FINS level was significantly reduced even in rats fed a HFD (HFD+BBR), to reach a level comparable to that of normal diet. FIGURE 5C shows the result of HOMA insulin resistance index to evaluate the insulin resistance status in rats, which demonstrates that after 18 weeks of HFD induction, rats formed apparent insulin

resistance; yet berberine intervention at 100mg/kg body weight prevented the formation of insulin resistance ($P<0.05$).

In order to further examine insulin sensitivity, oral glucose tolerance test and intraperitoneal injection of insulin tolerance test were conducted, and the results are shown in FIGURE 5D, and 5E, respectively. Consistent with the FBG and FINS result, after 18 weeks of high fat diet inducement, oral glucose tolerance and intraperitoneal injection of insulin tolerance were significantly damaged, meanwhile, berberine intervention at 100mg/kg body weight significantly prevented the loss of glucose tolerance and insulin tolerance, demonstrating the berberine may play an important role in improving glucose metabolism.

Berberine Reduces Systemic inflammation Level in Rats

Fed a High Fat Diet

In order to evaluate the systemic inflammation levels of all four experimental groups of rats, the serum levels of lipopolysaccharide (LPS)-binding protein (LBP), monocyte chemoattractant protein-1 (MCP-1), leptin, and adiponectin were measured, and results are shown in FIGURE 6. The experiments demonstrate that HFD significantly increased LBP level in serum; but administering berberine at 100mg/kg significantly abrogated the increase of serum LBP ($P<0.05$, FIGURE 6A).

MCP-1 is a pro-inflammatory cytokine that functions in chemotaxis and activation of monocytes/macrophages. Occurrence and development of many inflammation-related diseases are closely related to MCP-1, including atherosclerosis, obesity, type 2 diabetes, arthritis, sepsis, and chronic bacterial infection. The results from the experiment demonstrated that, in the process of the gradual onset of obesity and insulin resistance in rat induced by HFD, MCP-1 level is gradually elevated; however, after intervention with berberine administering, MCP-1 level was significantly reduced, and, surprisingly, was even lower than that of NCD group (FIGURE 6B).

Leptin is a hormone secreted by adipose tissue, and broadly participates in lipid, glucose, and energy metabolism. The results from the experiment demonstrated that serum leptin level in HFD group is significantly higher than that of NCD group ($P<0.01$); however, berberine significantly reduced the serum leptin level in rat, especially in rats fed a HFD ($P<0.05$, FIGURE 6C).

The adiponectin levels in all four groups were analyzed. The results show that the adiponectin level normalized against body fat weight, was significantly lower in HFD group when compared to that of NCD group ($P<0.001$); however, berberine administration significantly increased adiponectin level in rats fed a HFD ($P<0.01$, FIGURE 6D). Therefore, berberine improves gut microbiota population, reduces LBP, MCP-1, and leptin level, and increases adiponectin secretion. TABLE 1 16S rRNA gene V3 region sequence of those bacteria enriched by berberine.

List	OTUName	16S rRNA Gene V3 Region Sequence
SEQ_ID_NO_ 1	R_U00449939	TAGGGAATATTGCTCAATGGGGGAAACCCTGAAGCA GCAACGCCGCGTGAGGATGAAGGTTTTCGGATTGT AAACTCCTTTTCTAAGAGAAGATTATGACGGTATCTT AGGAATAAGCACCGGCTAACTCCGTGCC
SEQ_ID_NO_ 2	R_U01131573	GGGGAAACCCTGAAGCAGCAACGCCGCGTGAGGAT GAAGGTTTCGGATTGTAAACTCCTTTCTAAGAGAAGA TTATGACGGTATCTTAGGAATAAGCACCGGCTAACTC CGTGCC
SEQ_ID_NO_ 3	R_U00442991	TGGGGAATATTGCGCAATGGGCGAAAGCCTGACGCA GCGACGCCGCGTGAGGGATGAAGGTCCTCGGATCGT AAACCTCTGTCAGGGGGGAAGAAGCGCCTGTGAGCA AATAGTTCATGGGTTTGACGGTACCCCCAAAGGAAG CACCGGCTAACTCCGTGCC
SEQ_ID_NO_ 4	R_U01131468	TGAGGAATATTGGTCAATGGGCGCAGGCCTGAACCA GCCAAGTAGCGTGAAGGATGACTGCCCTATGGGTTGT AAACTTCTTTTATATGGGAATAAAGTTTTCCACGTGT GGAATTTTGTATGTGCCATATGAATAAGGATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 5	R_U00000076	TGAGGAATATTGGTCAATGGACGAGAGTCTGAACCA GCCAAGTAGCGTGAAGGATGACTGCCCTATGGGTTGT AAACTTCTTTTATATGGGAATAAAGTGAGCCACGTGT GGCTTTTTGTATGTACCATACGAATAAGGATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 6	R_U00000261	TGAGGAATATTGGTCAATGGGCGCAGGCCTGAACCA GCCAAGTAGCGTGAAGGATGACTGCCCTATGGGTTGT AAACTTCTTTTATATGGGAATAAAGTTTTCCACGTGT GGAATTTTGTATGTACCATATGAATAAGGATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 7	R_U00277049	TGAGGAATATTGGTCAATGGGCGCAGGCCTGAACCA GCCAAGTAGCGTGAAGGATGACTGCCCTATGGGTTGT AAACTTCTTTTATATGGGAATAAAGTTTTCTACGTG TGGAATTTTGTATGTACCATATGAATAAGGATCGGC TAACTCCGTGCC
SEQ_ID_NO_ 8	R_U01140154	TGAGGAATATTGGTCAATGGGCGCGAGCCTGAACCA GCCAAGTAGCGTGCAGGACGACGGCCCTATGGGTTG TAAACTGTCTTTTATACGGGGATAAAGTATGCCACGT GTGGTTTATTGCAGGTACCGTATGAATAAGGACCGGC TAATTCCGTGCC

SEQ_ID_NO_ 9	R_U00797917	TGAGGAATATTGGTCAATGGGCGCGAGCCTGAACCA GCCAAGTAGCGTGACAGGACGACGGCCCTATGGGTTG TAAACTGCTTTTATACGGGGATAAAGTATGCCACGTG TGGTTTATTGCAGGTACCGTATGAATAAGGACCGGCT AATTCCGTGCC
SEQ_ID_NO_ 10	R_U01135802	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTTGCCGGGGAGGCAATGCCCACGCTCG CGAGCTGGGAAGGAGAGTACCCGGAGAAAAAGACAT CGGCTAACTCCGTGCC
SEQ_ID_NO_ 11	R_U01199632	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTTGCCGGGGAGCAATGCCCACGCTCGC GAGCTGGGAAGGAGAGTACCCGGAGAAAAAGACATC GGCTAACTCCGTGCC
SEQ_ID_NO_ 12	R_U01136954	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTTGCCGGGGAGCAAATGCCCAGCTCGC GAGCTGGGAAGGAGAGTACCCGGAGAAAAAGCATCG GCTAACTCCGTGCC
SEQ_ID_NO_ 13	R_U01156163	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTTGTGAGGGAGCAAGAACAGGCACGT GTGCCTGACTGAGAGTACCTGAAGAAAAAGACATCG GCTAACTCCGTGCC
SEQ_ID_NO_ 14	R_U00436427	TGAGGAATATTGGTCAATGGCCGGAAGGCTGAACCA GCCAAGTCGCGTGAGGGACTAAGGCCCTACGGGTCG TAAACCTCTTTTGCCGGGGAGCAATGGGGCCCTTGCG AGGGCCCAGGGAGAGTACCCGGAGAAAAAGCATCGG CTAACTCCGTGCC
SEQ_ID_NO_ 15	R_U01161731	TGAGGAATATTGGTCAATGGCCGGGAGGCTGAACCA GCCAAGTCGCGTGAGGGATGACGGCCCTACGGGTTG TAAACCTCTTTTGTGCGGGGAGCAAAGGACTTCACGAG TGGAGTTTCGAGAGTACCCGAAGAAAAAGACATCGG CTAACTCCGTGCC
SEQ_ID_NO_ 16	R_U00804243	TGAGGAATATTGGTCAATGGCCGGGAGGCTGAACCA GCCAAGTCGCGTGAGGGATGACGGCCCTACGGGTTG TAAACCTCTTTTGTGCGGGGAGCAAAGGACTTCACGAG TGGAGTTTCGAGAGTACCCGAAGAAAAAGCATCGGC TAACTCCGTGCC

SEQ_ID_NO_ 17	R_U00832647	TGAGGAATATTGGTCAATGGCCGGGAGGCTGAACCA GCCAAGTCGCGTGAGGGATGACGGCCCTACGGGTTG TAAACCTCTTTGTCGGGGAGCAAAGGACTTCACGAGT GGAGTTTCGAGAGTACCCGAAGAAAGACATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 18	R_U00013412	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTTGTGTCAGGGAGCAAGAACAGGCACGT GTGCCTGACTGAGAGTACCTGAAGAAAAAGCATCGG CTAACTCCGTGCC
SEQ_ID_NO_ 19	R_U00807079	TGAGGAATATTGGTCAATGGCCGAGAGGCTGAACCA GCCAAGTCGCGTGAGGGATGACGGCCCTACGGGTTG TAAACCTCTTTTGTGTCGGGGAGCAAAGGACTTCACGTG TGAAGTTTCGAGAGTACCCGAAGAAAAAGCATCGGC TAACTCCGTGCC
SEQ_ID_NO_ 20	R_U00005346	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTG TAAACCTCTTTTGCCGGGGAGCAATGCCGCTCTTGCG AGAGCGGAGGGAGAGTACCCGGAGAAAAAGCATCG GCTAACTCCGTGCC
SEQ_ID_NO_ 21	R_U00004086	TGAGGAATATTGGTCAATGGCCGGAAGGCTGAACCA GCCAAGTCGCGTGAGGGAATAAGGCCCTACGGGTCG TAAACCTCTTTTGTGTCAGGGAGCAAAGCTGGCTACGCG TAGCCAGAAGGAGAGTACCTGAAGAAAAAGCATCGG CTAACTCCGTGCC
SEQ_ID_NO_ 22	R_U01130438	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTGCCGGGAGCAATGCCCAGCTCGCGAG CTGGGAAGGAGAGTACCCGGAGAAAAGACATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 23	R_U01131459	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTGCCGGGGAGCAATGCCCAGCTCGCGA GCTGGGAAGGAGAGTACCCGGAGAAAAGACATCGGC TAACTCCGTGCC
SEQ_ID_NO_ 24	R_U00436448	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGACTAAGGCCCTACGGGTCG TAAACCTCTTTTGCCGGGGAGCAAGCCGTCCCACGTG TGGGCCGGTGGAGAGTACCCGGAGAAAAAGCATCGG CTAACTCCGTGCC

SEQ_ID_NO_ 25	R_U00474862	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGGACTAAGGCCCTACGGGTCG TAAACCTCTTTTGCCGGGGAGCAAGCCGTCCCACGTG TGGGCCGGTGAGAGTACCCGGAGAAAAAGACATCG GCTAACTCCGTGCC
SEQ_ID_NO_ 26	R_U00001388	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTTGCCGGGGAGCAATGCCCAGCTCGCG AGCTGGGAAGGAGAGTACCCGGAGAAAAAGCATCGG CTAACTCCGTGCC
SEQ_ID_NO_ 27	R_U01185184	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCA GCCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTG TAAACCTCTTTTGCCGGGGAGCAATGCCCAGCTCG CGAGCTGGGAAGGAGAGTACCCGGAGAAAAAAGCAT CGGCTAACTCCGTGCC
SEQ_ID_NO_ 28	R_U00000528	TGAGGAATATTGGTCAATGGGCGGAGAGCCTGAACCA GCCAAGTCGCGTGAAGGATGAAGGATCTATGGTTTGT AAACTTCTTTTATATGGGAATAAAGTGAGGAACGTGT TCCTTTTTGTATGTACCATATGAATAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 29	R_U00000002	TGAGGAATATTGGTCAATGGACGAGAGTCTGAACCA GCCAAGTAGCGTGAAGGATGACTGCCCTATGGGTTGT AAACTTCTTTTATACGGGAATAAAGTGAGGCACGTGT GCCTTTTTGTATGTACCGTATGAATAAGGATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 30	R_U00147566	TGAGGAATATTGGTCAATGGACGCAAGTCTGAACCA GCCATGCCGCGTGCAGGAAGACGGCTCTATGAGTTGT AAACTGTCTTTTGTACTAGGGTAAACGCTCTTACGTG TAGGAGCCTGAAAGTATAGTACGAATAAGGATCGGC TAACTCCGTGCC
SEQ_ID_NO_ 31	R_U00000394	TGAGGAATATTGGTCAATGGACGCAAGTCTGAACCA GCCATGCCGCGTGCAGGAAGACGGCTCTATGAGTTGT AAACTGCTTTTGTACTAGGGTAAACGCTTCTACGTGT AGGAGCCTGAAAGTATAGTACGAATAAGGATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 32	R_U00047397	TGGGGAATTTTGC GCAATGGGGGGAACCCTGACGCA GCAACGCCGCGTGCGGGATGACGGCCCTCGGGTTGT AAACCGCTTTCAGCAGGGAAGACCACGACGGTACCT GCAGAAGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 33	R_U00000552	TGAGGAATATTGGGCAATGGGCGGAAGCCTGACCCA

33		GCCATGCCGCGTGCAGGAAGACAGCCCTATGGGTGCTAAACTGCTTTTTTAGAGGAAGAATAAAGTCTACGTGTAGACCGATGACGGTACTTTAAGAAAAAGCATCGGCTAACTCCGTGCC
SEQ_ID_NO_34	R_U00441706	GTAGGGAATATTGCACAATGGGGGAAACCCTGATGCAAGCAGCGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAACTTCTATCAGCAGGGAAGACAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_35	R_U00119974	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCAGCGCCGCGTGAAGGAAGAAGTATTTTCGGTATGTAAGTCTATCAGCAGGGAAGAAAGTGACAGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_36	R_U00104206	TGGGGAATATTGCACAATGGGGGAAACCCGTACGATGCAGCAGCGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAACTTCTATCAGCAGGGAAGATAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_37	R_U00580795	TGGGGAATATTGCACAATGGGGGAAACCCGTACGATGCAGCAGCGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAACTTACTATCAGCAGGGAAGATAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_38	R_U01129900	AAACCCTGATGCAGCAGCGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAACTTCTATCAGCAGGGAAGACAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_39	R_U00016467	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCAGCGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAGTCTATCAGCAGGGAAGATAATGACGGTACCTGACTAAGAAGCCCCGGCTAATTACGTGCC
SEQ_ID_NO_40	R_U00000367	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCAGCGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAGTCTATCAGCAGGGAAGATAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_41	R_U00459481	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCAACGCCGCGTGGGTGAAGGAGCGTTTCGGCGCGTAAAGCCCTGTCAGCGGGGAAGAAAAAGACGGTACCTGACCAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_42	R_U00000215	TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGCAGCGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCT

		GACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 43	R_U00071963	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCA GCGACGCCGCGTGAAAGATGAAGTATTTTCGGTATGT AAACTTCTATCAGCAGGGAAGAAAATGACGGTACCT GACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 44	R_U00000939	TGGGGAATATTGCACAATGGAGGAAACTCTGATGCA GCGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGT AAAGCTCTATCAGCAGGGAAGACAGTGACGGTACCT GACTAAGAAGCTCCGGCTAAATACGTGCC
SEQ_ID_NO_ 45	R_U00472681	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCA GCGACGCCGCGTGAGTGACGAAGTATCTCGGTATGT AAAGCTCTGTGACGAGGGAAGAAGAATGACGGTACC TGAAGAAGAAGCACCGGCTAAATACGTGCC
SEQ_ID_NO_ 46	R_U00000105	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCA GCGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGT AAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCT GACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 47	R_U00000279	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCA GCAACGCCGCGTGGAAGGAAGACGGTTTTTCGGATTGT AAACTTCTATCAATAGGGAAGAAAGAAATGACGGTA CCTAAATAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 48	R_U00022935	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCA GCAACGCCGCGTGGAAGGAAGACGGTTTTTCGGATTGT AAACTTCTATCAATAGGGAAGAAAGAAATGACGGTA CCTAAATAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 49	R_U00000550	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCA GCGACGCCGCGTGAGGAAGAAGGTCTTCGGATTGT AAACTCCTGTCCCAGGGGACGATAATGACGGTACCCT GGGAGGAAGCACCGGCTAACTACGTGCC
SEQ_ID_NO_ 50	R_U00009280	TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCA GCAACGCCGCGTGGAAGGAAGACGGTTTTTCGGATTGT AAACTTCTGTTCTTAGTGAAGAAGAATGACGGTAGCT AAGGAGCAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 51	R_U00164237	TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCA GCAACGCCGCGTGGAAGGAAGACGGTTTTTCGGATTGT AAACTTCTGTTCTTAGTGAAGAATAATGACGGTAACT AAGGAGCAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 52	R_U00032911	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCA GCGACGCCGAGTGAGGGAAGAAGGTTTTTTCGGATTGT

52		AAACCTCTGTCCTTGGTGAAGATAATGACGGTAGCCA AGGAGGAAGCTACGGCTAACTACGTGCC
SEQ_ID_NO_ 53	R_U00040533	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCA GCGACGCCGCGTGAGGGAAGACGGCCTTCGGGTTGT AAACCTCTGTCGCAGGGGACGAAGGAAGTGACGGTA CCCTGTGAGGAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 54	R_U01145869	GAATATTGCGCAATGGGGGCAACCCTGACGCAGCAA CGCCGCGTGAAGGATGAAGGTTTTTCGGATTGTAACT TCTTTTATCAAGGACGAAGGACGTGACGGTACTTGAT GAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 55	R_U00211687	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCA GCAACGCCGCGTGAAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTACCAGGGGACGAAGGACGTGACGGT ACCTGGAGAAAAAGCAACGGCTAACTACGTGCC
SEQ_ID_NO_ 56	R_U01206474	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCA GCAACGCCGCGTGAAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTACCTAGGGACGAAGGACGTGACGGTA CCTGGAGAAAAAGACAACGGCTAACTACGTGCC
SEQ_ID_NO_ 57	R_U01219720	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCA GCAACGCCGCGTGAAAGGAAGAAGGTTTTTCGGGTTGT AAACTTCTTTTACCAGGGACGAAGGACGTGACGGTA CCTGGAGAAAAAGCAACGGCTAACTACGTGCC
SEQ_ID_NO_ 58	R_U01210669	GACCCAGCAACGCCGCGTGAAAGGAAGAAGGTCGTTT CGGGTTAGTAACTTCTTTTACCGAGGGACGAAGGAC GTGACGGTACCTGGAGAAAAAGCAACGGCTAACTAC GTGCC
SEQ_ID_NO_ 59	R_U00001394	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCA GCAACGCCGCGTGAAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTACCAGGGACGAAGGACGTGACGGTA CCTGGAGAAAAAGCAACGGCTAACTACGTGCC
SEQ_ID_NO_ 60	R_U00460521	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCA GCAACGCCGCGTGAAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTACCTAGGGACGAAGGACGTGACGGTA CCTGGAGAAAAAGACAACGGCTAACTACGTGCC
SEQ_ID_NO_ 61	R_U00831992	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCA GCAACGCCGCGTGAAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTACCAGGGACGAAGGACGTGACGGTA CCTGGAGAAAAAGACAACGGCTAACTACGTGCC

SEQ_ID_NO_ 62	R_U01143501	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCA GCAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTCTGGGGGACGAAGAAAGTGACGGTA CCCCACGGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 63	R_U00815791	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCA GCAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTCTGGGGGGCGAAGAAAGTGACGGTA CCCCAGGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 64	R_U00043629	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCA GCAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTCTGGGGGACGAAGAAAGTGACGGTA CCCCAGGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 65	R_U00164098	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCA GCAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGT AAACTTCTTTTCTCGGGGACGAACAAATGACGGTACC CGAGGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 66	R_U00000374	TGGGGAATATTGCGCAATGGGGGCAACCCTGACGCA GCAACGCCGCGTGATTGAAGAAGGTCTTCGGATTGTA AAAATCTTTTATCAAGGACGAAGAAGTGACGGTACTT GATGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 67	R_U00003296	TGGGGAATATTGGGCAATGGGGGGAACCCTGACCCA GCAACGCCGCGTGAGGGAAGAAGGTTTTTCGGATCGT AAACCTCTGTCCTTGGTGAAGAGGAGAAGACGGTAG CCAAGGAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 68	R_U00027329	TGGGGAATATTGGGCAATGGGGGGAACCCTGACCCA GCAACGCCGCGTGAGGGAAGAAGGTTTTTCGGATCGT AAACCTCTGTCCTTGGTGAAGAGAAGAAGACGGTAG CCAAGGAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 69	R_U00003420	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCA GCAACGCCGCGTGAAGGATGAAGTATTTTCGGTATGT AAACTTCTATCAGCAGGGAAGATAACGACGGTACCT GACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 70	R_U00436238	TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCA GCAACGCCGCGTGAACGAAGAAGGTCTTCGGATTGT AAAGTTCTGTCCTTAGGGAAGAAGAAAGTGACGGTA CCTAAGGAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 71	R_U00439751	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCA GCGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGT AAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCT

		G
SEQ_ID_NO_ 72	R_U00004741	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCA GCGACGCCGCGTGAAGGAAGAAGTATTTTCGGTATGT AAACTTCTATCAGCAGGGAAGAAAATGACGGTACCT GACTAAGAAGCCCCGGCTAATTACGTGCC
SEQ_ID_NO_ 73	R_U01160251	TAGGGAATTTTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGGGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGAAAAAGGAAGGGAAGAG GAAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAGT CACGGCTAACTACGTGCC
SEQ_ID_NO_ 74	R_U01166410	TAGGGAATTTTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGAAAAAGGAAGGAAAGAG GAAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAGT CACGGCTAACTACGTGCC
SEQ_ID_NO_ 75	R_U01169117	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGGGCGAAGAAGGTCTTCGGATCGT AAAAACTCTGTTGCGGGGGAAAAAAGGAAGGGAAG AGGAAATGCTTTTCTTTTGATGGTACCCCGCCAGAAA GTCACGGCTAACTACGTGCC
SEQ_ID_NO_ 76	R_U01180557	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGGGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTTGCGGGGGGAAAAAGGAAGGGAAGA GGAAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAG TCACGGCTAACTACGTGCC
SEQ_ID_NO_ 77	R_U00804007	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGGGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGGAAAAAGGAAGGGAAGAG GAAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAGT CACGGCTAACTACGTGCC
SEQ_ID_NO_ 78	R_U01143008	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGAAAAGGAAGGGAAGAGGA AATGCTTTTCTTTTGATGGTACCCCGCCAGAAAGTC ACGGCTAACTACGTGCC
SEQ_ID_NO_ 79	R_U01145549	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGGGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGGAAAAGGAAGGGAAGAGG AAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAGT CACGGCTAACTACGTGCC

SEQ_ID_NO_ 80	R_U00808391	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGGGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGAAAAAGGAAGGGAAGAGG AAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAGTC ACGGCTAACTACGTGCC
SEQ_ID_NO_ 81	R_U01144224	GGTAATTTTTCGTCAATGGGCGCAAGCCTGAACGAGC AATGCCGCGTGGGCGAAGAAGGTCTTCGGATACGTA AACTCTGTTGCGGGGGAAAAAGGAAGGGAAGAGGA AATGCTTTCTTTTGATGGTACCCCGCCAGAAAGTCAC GGCTAACTACGTGCC
SEQ_ID_NO_ 82	R_U01214804	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGAAAAAGGAAGGGAAGAG GAAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAG TCACGGCTAACTACGTGCC
SEQ_ID_NO_ 83	R_U01173110	TAGGGAATTTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGAAAAAAGGAAGGGAAGA GGAAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAG TCACGGCTAACTACGTGCC
SEQ_ID_NO_ 84	R_U00305232	TAGGGAATTTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGAAAAAGGAAGGGAAGAG GAAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAGT CACGGCTAACTACGTGCC
SEQ_ID_NO_ 85	R_U00043735	TAGGGAATTTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAACGAGGAAGGTCTTCGGATCGT AAAGTTCTGTTGAGAGGGAAAAAGGGTCACCAGAGG AAATGCTGGTGAAGTGATATTACCTTTCGAGGAAGTC ACGGCTAACTACGTGCC
SEQ_ID_NO_ 86	R_U00000409	TAGGGAATTTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAACGAGGAAGGTCTTCGGATCGT AAAGTTCTGTTGAGAGGGAAAAAGGGTCACCAGAGG AAATGCTGGTGAAGTGATATTACCTTTCGAGGAAGTC ACGGCTAACTACGTGCC
SEQ_ID_NO_ 87	R_U00029718	GGTAATTTTTCGTCAATGGGCGCAAGCCTGAACGAGC AATGCCGCGTGAACGAGGAAGGTCTTCGGATCGTAA AGTTCTGTTGAGAGGGAAAAAGGGTCACCAGAGGAA ATGCTGGTGAAGTGATATTACCTTTCGAGGAAGTCAC GGCTAACTACGTGCC

SEQ_ID_NO_ 88	R_U00007185	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAACGAGGAAGGTCTTCGGATCGT AAAGTTCTGTTGAGAGGGAAAAAGGGTCACCAGAG GAAATGCTGGTGAAGTGATATTACCTTTCGAGGAAGT CACGGCTAACTACGTGCC
SEQ_ID_NO_ 89	R_U00011248	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAACGAGGAAGGTCTTCGGATCGT AAAGTTCTGTTGAGAGGGAAAAAGGGTCACCAGAGGA AATGCTGGTGAAGTGATATTACCTTTCGAGGAAGTCA CGGCTAACTACGTGCC
SEQ_ID_NO_ 90	R_U01156257	TAGGGAATTTTCGTCAAGTGGGCGCAAGCCTGAACG AGCAATGCCGCGTGAACGAGGAAGGTCTTCGGATAC GTAAAGTTCTGTTGAGAGGAAAAAGGGTCACCAGAG GAAATGCTGGTGAAGTGATATTACCTTTCGAGGAAGT CACGGCTAACTACGTGCC
SEQ_ID_NO_ 91	R_U00808203	TAGGGAATTTTCGTCAATGGGCGCAAGCCTGAACGA GCAATGCCGCGTGAGCGAAGAAGGTCTTCGGATCGT AAAACCTCTGTTGCGGGGGAAAAAGGAAGGGAAGAGG AAATGCTTTTCTTTTGATGGTACCCCGCCAGAAAGTC ACGGCTAACTACGTGCC
SEQ_ID_NO_ 92	R_U00003073	TAGGGAATTTTCGGCAATGGGCGAAAGCCTGACCGA GCAACGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGT AAAGCTCTGTTGTGAAGGAAGAACGGCTCATAGAGG GAATGCTATGGGAGTGACGGTACTTTACCAGAAAGC CACGGCTAACTACGTGCC
SEQ_ID_NO_ 93	R_U00000235	TGGGGAATCTTCCGCAATGGACGAAAGTCTGACGGA GCAACGCCGCGTGAGTGATGAAGGATTTTCGGTCTGTA AAGCTCTGTTGTTTATGACGAACGTGCAGTGTGTGAA CAATGCATTGCAATGACGGTAGTAAACGAGGAAGCC ACGGCTAACTACGTGCC

TABLE 2 16S rRNA gene V3 region sequence of those bacteria suppressed/eliminated by berberine.

List	OTUName	16S rRNA Gene V3 Region Sequence
SEQ_ID_NO_ 94	R_U0043619 5	TGAGGAATATTGGGCAATGGGGGCAACCCTGACCCAG CCATGCCGCGTGAGTGAAGAAGGTTTTCGGATTGTAA AGCTCTTTCGGATGTGACGATGATGACGGTAGCATCT AAAGAAGCCCCGGCAAACCTTCGTGCC
SEQ_ID_NO_ 95	R_U0010141 6	GNGGGAAACCCTGAAGCAGCAACGCCGCGTGAGGA TGAAGGTTTTCGGATTGTAACTCCTTTGTTAGAGAAG ATAATGACGGTATCTAACGAATAAGCACCGGCTAACT CCGTGCC
SEQ_ID_NO_ 96	R_U0000040 7	TAGGGAATATTGCTCAATGGGGGAAACCCTGAAGCAG CAACGCCGCGTGAGGATGAAGGTTTTCGGATTGTAA ACTCCTTTTGTAGAGAAGATAATGACGGTATCTAAC GAATAAGCACCGGCTAACTCCGTGCC
SEQ_ID_NO_ 97	R_U0080096 6	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTAGCGTGCAGGAAGACGGCCCTACGGGTGTGA AACTGCTTTTTATGCGGGGATAAAGTGCAATACGTGTA TTGCTTTGCAGGTACCGCATGAATAAGGACCGGCTAA TTCCGTGCC
SEQ_ID_NO_ 98	R_U0113198 2	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTAGCGTGCAGGATGACGGCCCTACGGGTGTGA AACTGCTTTTTTGCAGGAATAAAGCGGCTCACGTGTG AGCCTTTGCATGTACCGCACGAATAAGGACCGGCTAA TTCCGTGCC
SEQ_ID_NO_ 99	R_U0079783 9	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTAGCGTGCAGGATGACGGCCCTATGGGTGTGA AACTGCTTTTTATACGGGGATAAAGTTGGGGACGTGTC CCCATTTGTAGGTACCGTATGAATAAGGACCGGCTAA TTCCGTGCC
SEQ_ID_NO_ 100	R_U0000398 1	TGAGGAATATTGGTCAATGGTTCGTGAGACTGAACCAG CCAAGTAGCGTGCAGGATGAAGGCCCTCCGGGTGCGTA AACCGCTTTTAGACGGGGATAAAAGGGCATACTGTGA TGCCGTATTGCATGTACCGTCAGAAAAAGGACCGGCT AATTCGTGCC
SEQ_ID_NO_ 101	R_U0000140 4	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTAGCGTGAAGGAAGACTGCCCTATGGGTGTGA AACTTCTTTTATAAGGGAATAAAGAGCGCCACGTGTG GTGTGTTGTATGTACCTTATGAATAAGCATCGGCTAAT

		TCCGTGCC
SEQ_ID_NO_ 102	R_U0000005 2	TGAGGAATATTGGTCAATGGGCGTGAGCCTGAACCAG CCAAGCCGCGTGAGGGAAGAAGGCGCCAGGCGTCGT AAACCTCTTTTGCCGGGGAACAAAGGGCGCCACGTGT GGCGTTGTGAGTGTACCCGGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 103	R_U0000096 4	TGAGGAATATTGGTCAATGGGCGTGAGCCTGAACCAG CCAAGCCGCGTGAGGGAGGAAGGCGCCAGGCGTCGT AAACCTCTTTTGCCGGGGAACAAAGGGCGCCACGTGT GGCGTTGTGAGTGTACCCGGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 104	R_U0004069 0	TGAGGAATATTGGTCAATGGGCGTGAGCCTGAACCAG CCAAGCCGCGTGAGGGAGGAAGGCGCCAGGCGTCGT AAACCTCTTTTGCCGGGGAACAAAGGGCGCCACGTGT GGCGTTGTGAGTGTACCCGGAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 105	R_U0082399 1	TGAGGAATATTGGTCAATGGGCGTGAGCCTGAACCAG CCAAGCCGCGTGAGGGAGGAAGGCGCCAGGCGTCGT AAACCTCTTTTGCCGGGGAACAAAGGGCGCCACGTGT GGCGTTGTGAGTGTACCCGGAGAAAAAGCATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 106	R_U0000080 4	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGCCGCGTGAGGGAATAAGGCGCCAAGCGTCGTA AACCTCTTTTGTCAGGGAACAAAAGCGGGCACGCGTG CCCGTCCGAGTGTACCTGAAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 107	R_U0115591 5	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGCCGCGTGAAGGAAGAAGGTGCTAAGCATTGTA AACTTCTTTTGTCAGGGAACAAAGAGCGCGACGAGTC GCGCCGTGAGTGTACCTGAAGAAAAAGACATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 108	R_U0045985 0	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGCCGCGTGAAGGAAGAAGGTGCTAAGCATTGTA AACTTCTTTTGTCAGGGAACAAAGAGCGCGACGAGTC GCGCCGTGAGTGTACCTGAAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 109	R_U0079809 8	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGCCGCGTGAAGGAAGAAGGTGCTAAGCATTGTA AACTTCTTTTGTCAGGGAACAAAGAGCGCGACGAGTC GCGCCGTGAGTGTACCTGAAGAAAAAGCATCGGCTAAC

		TCCGTGCC
SEQ_ID_NO_ 110	R_U0000917 0	TGAGGAATATTGGTCAATGGTCGGAAGACTGAACCAG CCAAGCCGCGTGAAGGAAGAAGGTGCTCGGCATCGTA AACTTCTTTTGTGAGGGAACAAAGGGCGGTACGTGTA CCGCTGTGAGTGTACCTGAAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 111	R_U0110215 3	TGAGGAATATTGGTCAATGGTCGGAAGACTGAACCAG CCAAGCCGCGTGAAGGAAGAAGGTGCTCGGCATCGTA AACTTCTTTTGTGAGGGAACAAAGGGCGGTACGTGTA CCGCTGTGAGTGTACCTGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 112	R_U0000623 0	TGAGGAATATTGGTCAATGGGCGTGAGCCTGAACCAG CCAAGCCGCGTGAAGGAAGAAGGTGCAGGGCATCGT AACTTCTTTTGCCGGGGAACAATAAGCGGGACTAGT CCCGCGACGAGTGTACCCGGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 113	R_U0046534 4	TGAGGAATATTGGTCAATGGGCGTGAGCCTGAACCAG CCAAGCCGCGTGAAGGAAGAAGGTGCAGGGCATCGT AACTTCTTTTGCCGGGGAACAATAAGCGGGACTAGT CCCGCGACGAGTGTACCCGGAGAAAAAGACATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 114	R_U0000120 2	TGAGGAATATTGGTCAATGGTCGGGAGACTGAACCAG CCAAGCCGCGTGAGGGATGGAGGTACAGAGTATCGTA AACCTCTTTTGTGAGGGAACAAAGGGCGCCACGTGTG GCGCTATGAGGGTACCTGAAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 115	R_U0000138 4	TGAGGAATATTGGTCAATGGGAGAGATCCTGAACCAG CCAAGCCGCGTGAGGGAAGACGGCACTACGTGTTGTA AACCTCTTTTGCCGGGGAACAAAAGCGGGGACGCGTC CCCGTCCGCGTGTACCCGGAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 116	R_U0080279 9	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTGTA AACCTCTTTTGTGCGGGGAGCAAAGAGCGCCACGCGTG GCGAGATGAGAGTACCCGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 117	R_U0080845 3	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTGTA AACCTCTTTTGTGCGGGGAGCAAAGAGCGCCACGCGTG GCGAGATGAGAGTACCCGAAGAAAAAGACATCGGCT

		AACTCCGTGCC
SEQ_ID_NO_ 118	R_U0002671 1	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGCCGCGTGAGGGAAGACGGCCCTACGGGTGTA AACTTCTTTTGTTCAGGACAACACCCCGGACGCGTCC GGGCATGAGTGTATGCAAAGAAAAAGCATCGGCTAAC TCCGTGCC
SEQ_ID_NO_ 119	R_U0000065 0	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGCCGCGTGAGGGAATAAGGCCCTACGGGTCGTA AACCTCTTTTGTTCGGGAACAAAACCGGAGACGAGTC TCCGGCTGCGTGTACCCGAAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 120	R_U0000083 9	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGCCGCGTGAGGGAAGAAGGCGCTCAGCGTCGTA AACCTCTTTAGCCGGGGAACAAAGAGCTGCTCGGGAA GCAGCGTTGAGCGTACCCGGAGAATAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 121	R_U0115793 0	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTCGCGTGAGGGACGACGGTCCTACGGATTGTA AACCTCTTTTGCCGGGGAGCAATGCGCGGTACGCGTA CCGCGACGGAGAGTACCCGGAGAAAAAGCATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 122	R_U0079842 0	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTGTA AACCTCTTTTGTTCGGGGAGCAAAGAGCGCCACGCGTG GCGAGATGAGAGTACCCGAAGAAAAAGACATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 123	R_U0000193 3	TGAGGAATATTGGTCAATGGGCGCGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTGTA AACCTCTTTTGTTCGGGGAGCAAGGACTGCCACGAGTG GCAGGGCGAGAGTACCCGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 124	R_U0000149 1	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCTTACGGATTGTA AACCTCTTTTGCCGGGGAGCAAAGGGCGCCACGCGTG GCGTTTCGAGAGTACCCGGAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 125	R_U0000647 6	TGAGGAATATTGGTCAATGGCCGAGAGGCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCTTATGGATTGTA AACCTCTTTTGTTCGGGGAGCAAAGGCGTCACGTGTG ACGCTATGAGAGTACCCGAAGAAAAAGCATCGGCTAA

		CTCCGTGCC
SEQ_ID_NO_ 126	R_U0000150 2	TGAGGAATATTGGTCAATGGCCGGAAGGCTGAACCAG CCAAGCCGCGTGAGGGGAGGAAGGCGCAGAGCGTCGC AGACCTCTTTTGCCGGGGGACAAAAGGCCGGACTCGT CCGGTCCTGAGGGTACCCGGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 127	R_U0000150 4	TGAGGAATATTGGTCAATGGGCGCGAGCCTGAACCAG CCAAGTCGCGTGAGGGATGACGGCCCTACGGGTTGTA AACCTCTTTTGTCGGGGAGCAAATTCGTTACGTGTAA CGGAGTCGAGAGTACCCGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 128	R_U0000060 9	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGACAGGGGAGCAAGGCACGGTACGTGTA CCGTGAAGGAGAGTACCCTGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 129	R_U0000926 1	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCGGGGAGCAAAGCCGCTCACGTGTG AGCGGAAGGAGAGTACCCGAAGAAAAAGCATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 130	R_U0113699 2	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTCGCGTGAGGGGAGGACGGTCCTATGGATTGTA AACCTCTTTTGTCGGGGAGCAAAGCCGCTCACGTGTG AGCGGAAGGAGAGTACCCGAAGAAAAAGCATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 131	R_U0000049 7	TGAGGAATATTGGTCAATGGCCGAAGGGCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTGTA AACCTCTTTTGCCGGGGAGCAAAGGCGGTCACTGGTG ACCGGATGAGAGTACCCGGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 132	R_U0000088 6	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCAGGGAGCAAGGAGGGCCACGAGTG GCGCTTCGGAGAGTACCTGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 133	R_U0114329 2	TGAGGAATATTGGTCAATGGCCGAGAGGCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTGTA AACCTCTTTTGTCGGGGAGCAAACAGCGCAACGCGCT TGCGCATTGAGAGTACCCGAAGAAAAAGCATCGGCTA

		ACTCCGTGCC
SEQ_ID_NO_ 134	R_U0080318 8	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTGTA AACCTCTTTTGTCTGGGGAGCAAAGAGCGCCACGCGTG GCGAGATGAGAGTACCCGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 135	R_U0000878 2	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTATGGGTTGTA AACCTCTTTTGCCGGGGAGCAAAGAACCGCACGTGTG CGGTCTGGAGAGTACCCGGAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 136	R_U0000140 6	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTCGCGTGAGGGAATAAGGCCCTAAGGGTCGTA AACCTCTTTTGCCGGGGAGCAATGGTTCGCTTGCGAG CGGACAGGGAGAGTACCCGGAGAAAAAGCATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 137	R_U0003088 0	TGAGGAATATTGGTCAATGGCCGTAAGGCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTACGGGTTGTA AACCTCTTTTGCCGGGGAGCAAAGGCGCCACGCGTG GCGTTTCGAGAGTACCCGGAGAAAAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 138	R_U0045093 8	TGAGGAATATTGGTCAATGGGCGTAAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTATGGGTTGTA AACCTCTTTTGTCTGGGGAGCAAAGCCGCCACGTGTG GGCGGAAGGAGAGTACCCGAAGAAAAAGCATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 139	R_U0000976 3	TGAGGAATATTGGTCAATGGGCGTAAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTATGGGTTGTA AACCTCTTTTGTCTGGGGAGCAAAGCCGCCACGAGTG GGCGGAAGGAGAGTACCCGAAGAAAAAGCATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 140	R_U0115549 5	TGAGGAATATTGGTCAATGGGCGTAAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTATGGGTTGTA AACCTCTTTTGTCTGGGGAGCAAAGCCGCCACGAGTG GGCGGAAGGAGAGTACCCGAAGAAAAAGACATCGGC TAACTCCGTGCC
SEQ_ID_NO_ 141	R_U0079869 4	TGAGGAATATTGGTCAATGGGCGTAAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGCCCTATGGGTTGTA AACCTCTTTTGTCTGGGGAGCAAAGCCGCCACGAGTG GGCGGAAGGAGAGTACCCGAAGAAAAAGACATCGGCT

		AACTCCGTGCC
SEQ_ID_NO_ 142	R_U0080236 0	TGAGGAATATTGGTCAATGGGCGGTAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGCCGGGGAGCAAGGCCATGTACGTGTA CGTGGCCTGAGAGTACCCGGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 143	R_U0116278 2	TGAGGAATATTGGTCAATGGGCGCGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTAAGGATTGTA AACCTCTTTTGTCAGGGAGCAAGGAGCGCCACGTGTG GCGCGGCGAGAGTACCTGAAGAAAAAGACATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 144	R_U0000270 9	TGAGGAATATTGGTCAATGGGCGCGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTAAGGATTGTA AACCTCTTTTGTCAGGGAGCAAGGAGCGCCACGTGTG GCGCGGCGAGAGTACCTGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 145	R_U0000523 2	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACAGTCCTATGGATTGTA AACCTCTTTTGCCGGGGAGCAAAGAGCGGCACGTGTG CCGCGCCGAGAGTACCCGGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 146	R_U0000030 5	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGCCGGGGAGCAAAGAGCGGCACGTGTG CCGCGCCGAGAGTACCCGGAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 147	R_U0000682 1	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCGGGGAGCAACGAAGGCACGTGTGC CAGAAGCGAGATTACCCGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 148	R_U0119940 5	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCGGGGAGCAACGAAGGCACGTGTGC CAGAAGCGAGATTACCCGAAGAAAAAGACATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 149	R_U0000615 0	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCGGGGAGCAACGAAGGCACGTGTGC CTGAAGCGAGATTACCCGAAGAAAAAGCATCGGCTAA

		CTCCGTGCC
SEQ_ID_NO_ 150	R_U0000020 6	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCTGGGGAGCAAAGAGGCCACGTGTGG TCAAAAGCGAGAGTACCCGAAGAAAAAGCATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 151	R_U0115067 3	TGAGGAATATTGGTCAATGGGCGGGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCTGGGGAGCAAAGAGGCCACGTGTGG TCAAAAGCGAGAGTACCCGAAGAAAAAGACATCGGC TAACTCCGTGCC
SEQ_ID_NO_ 152	R_U0080581 1	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCTGGGGAGCAAGGATCCGCACGAGTG CGGAGGCGAGAGTACCCGAAGAAAAAGCATCGGCTA ACTCCGTGCC
SEQ_ID_NO_ 153	R_U0119947 1	TGAGGAATATTGGTCAATGGGCGGAAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGACGGTCCTATGGATTGTA AACCTCTTTTGTCTGGGGAGCAAGGATCCGCACGAGTG CGGAGGCGAGAGTACCCGAAGAAAAAGACATCGGCT AACTCCGTGCC
SEQ_ID_NO_ 154	R_U0000006 8	TGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAG CCAAGTCGCGTGAGGGAAGAATGGTCTATGGCCTGTA AACCTCTTTTGTCTAGGGAAGAATAAGGATGACGAGTC ATTCGATGCCAGTACTTGACGAATAAGCATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 155	R_U0000555 9	TGAGGAATATTGGTCAATGGACGCAAGTCTGAACCAG CCATGCCGCGTGCAGGAAGACGGTCTATGAGTTGTA AACTGCTTTTGTACGAGGGTAAACCCGGATACGTGTA TCCGGCTGAAAGTATCGTACGAATAAGGATCGGCTAA CTCCGTGCC
SEQ_ID_NO_ 156	R_U0080196 1	CTAAGGATATTCCGCAACGGGCGGAAGCCCGGCGGAG CGACGCCGCGTGACGAGGAAGGCCGGAAGGTTGCA GAGTCCTTTTGTCTGGGGGAAGAAGGAGCCGCGGAGGG AATGCCGCGGCGGCGACCGAACCCCGCAATAAGGG GCGGCTAATTACGTGCC
SEQ_ID_NO_ 157	R_U0000012 6	TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAG CGACGCCGCGTGCGGGATGGAGGCCTTCGGGTTGTAA ACCGCTTTTGTTCAGGGCAAGGCACGGCTTCGGGCC GTGTTGAGTGGATTGTTCAATAAGCACCGGCTAACT

		ACGTGCC
SEQ_ID_NO_ 158	R_U0016410 5	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGGGTGAAGAAGTATTTTCGGTATGTAA AGCCCTATCAGCAGGGAAGAAAAAGACGGTACCTGA CTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 159	R_U0011807 8	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAAGGAAGAAGTATTTTCGGTATGTAA ACTTCTATCAGCAGGGAAGAAAATGACGGTATCTGAC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 160	R_U0114837 6	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGGGTGAAGAAGTATTTTCGGTATGTAA AGCCCTATCAGCAGGGAAGAAAATGACAGTACCTGAA TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 161	R_U0044400 2	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGGGTGAAGAAGTATTTTCGGTATGTAA AGCCCTATCAGCAGGGAAGAAAGAAGACGGTACCTG AGTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 162	R_U0113039 6	TGGGGAGTATTGCACAATGGGGGGAACCCGTGATGCA GCGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTA AAGCTCTATCAGCAGGGAAGAAAATAGACGGTACCTG ACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 163	R_U0001158 2	TGGGGGATATTGGACAATGGGGGGAACCCTGATCCAG CGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAGAAATGACGGTACCT GACCAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 164	R_U0043988 8	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTAATTCGTTACGTAA AGCTCTATCAGCAGGGAAGAAAAAGAAATGACGGTA CCTGATTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 165	R_U0116361 7	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CAATGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAAAAGACGGTACCTG ACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 166	R_U0002930 6	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CAATGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAAAAGACGGTACCTG ACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 167	R_U0079798	TGGGGAATATTGCACAATGGAGGAACTCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTAATTCGTTACGTAA

167	5	AGCTCTATCAGCAGGGAAGAAAAAATGACGGTACCTG ACTAAGAAGCACCGGCTAAATACGTGCC
SEQ_ID_NO_ 168	R_U0117359 4	TGGGGAATATTGCACAATGGAGGAACTCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTAATTCGTTACGTAA AGCTCTATCAGCAGGGAGAAAAAATGACGGTACCTG ACTAAGAAGCACCGGCTAAATACGTGCC
SEQ_ID_NO_ 169	R_U0000928 2	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAGATGACAGTACCTGAC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 170	R_U0016528 8	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CAACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGAC TAAGAAGCTCCGGCTAAATACGTGCC
SEQ_ID_NO_ 171	R_U0000348 1	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGATGCCGCGTGAGGGAAGAAGGTTTTTCGGATTGTAA ACTCCTGTCTTAAAGGACGATAATGACGGTACTTTAG GAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 172	R_U0000354 8	TGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAG CGACGCCGCGTGAGTGAGGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAGAATGACGGTACCTGA CTAAGAAGCACCGGCTAAATACGTGCC
SEQ_ID_NO_ 173	R_U0079847 2	TGGGGAATATTGCACAATGGAGGGAACCTCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTAATTCGTTATGTAA AGCTCTGTCAGCAGGGAAGAAAGTGACGGTACCTGAA AAAGAAGCTCCGGCTAAATACGTGCC
SEQ_ID_NO_ 174	R_U0080400 5	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAATATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGAG TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 175	R_U0016481 4	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTAATTCGTTATGTAA AGCTCTATCAGCAAGGAAGAAAAAAGACGGTACTTGA CTAAGAAGCCCCGGCTAAATACGTGCC
SEQ_ID_NO_ 176	R_U0050740 9	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGGGTGAAGAAGTATTTTCGGTATGTAA AGCCCTATCAGCAGGGAAGAAGATGACAGTACCTGAC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 177	R_U0000995	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG

177	2	CGACGCCGCGTGGGTGAAGGAGTACTCCGGTATGTAA AGCCCTATCGGCAGGGAAGAAGATGACGGTACCTGAC TAAGAAGCTCCGGCTAAATACGTGCC
SEQ_ID_NO_ 178	R_U0083254 9	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAGTGACAGTACCTGAG TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 179	R_U0001347 6	TGGGGGATATTGGACAATGGGGGGAACCCTGATCCAG CGACGCCGCGTGAGTGAAGAAGTATCTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAGAAATGACGGTACCT GAGTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 180	R_U0000001 2	TGGGGGATATTGGACAATGGGGGGAACCCTGATCCAG CGACGCCGCGTGAGTGAAGAAGTATCTCGGTATGTAA AGCTCTGTCAGCAGGGAAGAAAGAAATGACGGTACCT GACCAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 181	R_U0080806 5	TGGGGGATATTGGACAATGGGGGGAACCCTGATCCAG CGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTGTCAGCAGGGAAGAAAGAAATGACGGTACCT GAAGAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 182	R_U0081662 5	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGGGTGAAGGAGTGCTTCGGCATGTAA AGCCCTATCGGCAGGGAAGAAGAAGGACGGTACCTG ACTAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 183	R_U0016460 5	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGGGTGAAGAAGCGCCCCGGCGCGTAA AGCCCTATCGGCAGGGAAGAAGATGACGGTACCTGGC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 184	R_U0023209 6	GGGGATATTGCACAATGGGGGAACCCGTGATGCAGCG ACGCCGCGTGGGTGAAGAAGCGCCCCGGCGCGTAA GCCCTATCGGCAGGGAAGAAGATGACGGTACCTGGCT AAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 185	R_U0003150 2	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGAACGAAGAAGACGGTACCTGAC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 186	R_U0113068 3	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTAATTCGTTACGTAA AGCTCTATCAGCAGGAAAGAAAGAAGACGGTACCTG ACTAAGAAGCCCCGGCTAACTACGTGCC

SEQ_ID_NO_ 187	R_U0113935 5	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGAGCGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCGGGGAAGAGAATGACGGTACCCGAC TAAGAAGCTCCGGCTAAATACGTGCC
SEQ_ID_NO_ 188	R_U0085159 9	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAGATGACAGTACCTGAA TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 189	R_U0001004 7	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGAGCGAGGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGAC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 190	R_U0016413 5	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAGCGATGAAGGTCTTCGGATTGTAA AGCTCTGTTCGAGGGGACGAAGTATGACGGTACCCTG TAAGAAAGCCCCGGCAAACACTACGTGCC
SEQ_ID_NO_ 191	R_U0003405 0	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGAGCGAAGAAGTATCTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAGAATGACGGTACCTGA GTAAGAAGCACCGGCTAAATACGTGCC
SEQ_ID_NO_ 192	R_U0113967 0	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGAGCGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGAA CAAGAAGCTCCGGCTAAATACGTGCC
SEQ_ID_NO_ 193	R_U0003367 0	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CAACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGAC TAAGAAGCACCGGCTAAATACGTGCC
SEQ_ID_NO_ 194	R_U0003369 3	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGTGAAGGAGTACTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAGCAAGACGGTACCTGA CCAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 195	R_U0000258 3	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGCGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGAC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 196	R_U0004412 9	TGGGGAATATTGGGCAATGGAGGCAACTCTGACCCAG CAACGCCGCGTGAGCGATGAAGGTCTTCGGATTGTAA AGCTCTTTAAGTGGGGACGAAGAAAGTGACTGTACCC

		ACAGAATAAGCCTCGGCTAACTACGTGCC
SEQ_ID_NO_ 197	R_U0004265 3	TGGGGAATATTGGGCAATGGAGGAACTCTGACCCAG CAACGCCGCGTGAATGATGAAGGTCTTCGGATTGTAA AGTTCTTTTCTAAGGGAAGAAGAAAGTGACGGTACCT TAGGAATAAGCCTCGGCTAACTACGTGCC
SEQ_ID_NO_ 198	R_U0085532 8	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CAATGCCGCGTGGGTGAAGAAGTACCCCGGTATGTAA AGCCCTATCAGCAGGGAAGAAAATGACGGTACCTGGC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 199	R_U0016419 6	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGCGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAAGGAAGATAATGACGGTACTTGAC TAAGAAGCTCCGGCTAAATACGTGCC
SEQ_ID_NO_ 200	R_U0016425 6	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAG CAACGCCGCGTGAAGGAAGAAGGGTTTCGGCTCGTAA ACTTCTATCAACAGGGACGAAGGAAGTGACGGTACCT GAATAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 201	R_U0000307 9	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CAACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGAC TAAGAAGCTCCGGCTAAATACGTGCC
SEQ_ID_NO_ 202	R_U0000240 4	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGGAAGAAGGCCCTCGGGTTGTAA ACTCCTGTCTTTGGGGACGATAATGACGGTACCCAAG GAGGAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 203	R_U0080437 5	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGGAAGAAGGCCCTCGGGTTGTAA ACTCCTGTCTTCGGGGACGATAATGACGGTACCCGAG GAGGAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 204	R_U0044387 2	TGGGGGATATTGCACAATGGGGGGAACCCTGATGCAG CGACGCCGCGTGAGCGAAGAAGATCTTCGGATTGTAA AGCTCTGTCTTAGGGGACGATGATGACGGTACCCTGA GAGGAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 205	R_U0000012 8	TGGGGGATATTGCGCAATGGGGGCAACCCTGACGCAG CAACGCCGCGTGAAGGATGAAGGTTTTTCGGATTGTAA ACTTCTTTTCTTAAGGACGAAATTTGACGGTACTTAAG GAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 206	R_U0000277	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTTCGGGTTGTAA

206	7	ACTTCTTTTAAGAGGGACGAAGGAAGTGACGGTACCT CTTGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 207	R_U0000116 6	TGAGGGATATTGGTCAATGGGGGAAACCCTGAACCAG CAACGCCGCGTGAGGGAAGACGGTCTTCGGATTGTAA ACCTTTGTCCTCTGTGAAGATAATGACGGTAGCAGAG GAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 208	R_U0000208 7	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCAG CAACGCCGCGTGGAAGGAAGAAGGTCTTCGGATTGTAA ACTTTTGTCTTGGTGAAGATAATGACGGTAGCCAAG GAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 209	R_U0000809 8	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTGTCTAGGGAAGAGCAGAAGACGGTACCTG ACGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 210	R_U0000098 1	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGTGGGAAGACGGTCTCTGGATTGTAA AACCCTGTCCCCAGGGACGAAGATGACGGTACCTGG GGAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 211	R_U0043629 2	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGATGCCGCGTGGAGGAAGAAGGTTTTTCGGATTGTAA ACTCCTGTCTGACAGGAAAGAAAAAGGACTGTACCTGT CAAGAAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 212	R_U0000255 1	TGGGGAATATTGCACAATGGGGGGAACCCTGATGCAG CGATGCCGCGTGGAGGAAGAAGGTTTTTCGGATTGTAA ACTCCTGTCTTAAAGGACGATAATGACGGTACTTTAG GAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 213	R_U0016429 7	TGGGGAATATTGCACAATGGAGGAAACTCTGATGCAG CGATGCCGCGTGAGGGAAGAAGGTTTTTCGGATTGTAA ACCTCTGTCTTAAAGGGACGATAATGACGGTACCTTAG GAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 214	R_U0080693 7	TGGGGGATATTGCACAATGGAGGGAACCTCTGATGCAG CGATGCCGCGTGAGGGAAGAAGGTTTTTCGGATTGTAA ACCTCTGTGGACAGAGACGATAATGACGGTATCTGTC AAGGAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 215	R_U0000272 3	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCAG CGATGCCGCGTGAGGGAAGAAGGTTTTTCGGATTGTAA ACCTCTGTGGAGGGGGACGATAATGACGGTACCCCTT AAGGAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 216	R_U0000487	TGGGGGATATTGGACAATGGGGGAAACCCTTATCCAG

216	8	CGACGCCGCGTGAGGGAAGAAGGTTTTCGGATTGTAA ACCTCTGTCAGCGGGGACGATAATGACGGTACCCGCG GAGGAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 217	R_U0114298 2	TGGGGAATATTGGGCAATGGGCGAAAGCCTGACCCAG CGACGCCGCGTGAAGGAAGACGGTCTTCGGATTGTAA ACTTTAGTACTCAGGGACGAAGAAATGACGGTACCTG AGGTTAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 218	R_U0080688 4	TGGGGGATATTGCGCAATGGGGGAAACCCTGACGCAG CAACGCCGCGTGAAGGAAGAAGGTTTTCGGATTGTAA ACTTCTTTTATTAAGGACGAAGATGACGGTACTTAAT GAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 219	R_U0081053 1	TGGGGAATATTGGGCAATGGACGCAAGTCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTGTGACGGGAAGAGAAGAAGACGGTACCTG ACGAACAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 220	R_U0000014 9	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTGACAGGGGAAGAGCAGAAGACGGTACCTG TCGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 221	R_U0000450 1	TGGGGGATATTGCGCAATGGGGGCAACCCTGACGCAG CAACGCCGCGTGAAGGATGAAGGTTTTCGGATTGTAA ACTTCTTTTATTAAGGACGAATTTTGACGGTACTTAAT GAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 222	R_U0013288 2	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTAAGAGGGGAAGAGCAGAAGACGGTACCTC TTGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 223	R_U0080038 7	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCAG CAACGCCGCGTGAGGGAAGAAGGCTTTCGGGTTGTAA ACCTCTTTTACCAGGGACGAAGGACGTGACGGTACCT GGAGAAAAAGCAACGGCTAACTACGTGCC
SEQ_ID_NO_ 224	R_U0000090 8	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCCTTCGGGTTGTAA ACTTCTTTTACCAGGGACGAAGGACGTGACGGTACCT GGAGAAAAAGCAACGGCTAACTACGTGCC
SEQ_ID_NO_ 225	R_U0020438 6	TGGGGAATATTGGGCAATGGGCGAAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCCTTCGGGTTGTAA ACTTCTTTTAAGAGGGACGAAGAAAGTGACGGTACCT CTTGAATAAGCCACGGCTAACTACGTGCC

SEQ_ID_NO_ 226	R_U0079945 3	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTGAGAGGGACGAAACAAATGACGGTACCT CTTGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 227	R_U0080607 1	TGGGGAATATTGGGCAATGGGCGGAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTCTTGGGGACGAAGAAAGTGACGGTACCC AAGGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 228	R_U0113290 7	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTGAGGGGGACGAAGGATGTGACGGTACCC CTTGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 229	R_U0046333 7	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTCTTGGGGACGAAGAAAGTGACGGTACCC GAGGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 230	R_U0081299 4	TGGGGAATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGGGTGAAGAAGTATTTTCGGTATGTAA AGCCCTATCAGCAGGGAAGATCATGACGGTACCTGAC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 231	R_U0001001 8	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTCTGAGGGACGAAGCAAGTGACGGTACCT TAGGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 232	R_U0016472 0	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCTTTCGGGTTGTAA ACTTCTTTTGACAGGGAAGAGGAGAAGACGGTACCTG TCGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 233	R_U0000441 8	TGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGCCCTCGGGTTGTAA ACTTCTTTTATCAGGGACGAAGAAGTGACGGTACCTG ATGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 234	R_U0020815 3	TGGGGAATATTGCGCAATGGGGGAAACCCTGACGCAG CAACGCCGCGTGATTGAAGAAGGCCTTCGGGTTGTAA AGATCTTTAATCGGGGACGAATTTTGACGGTACCCGA AGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 235	R_U0003087 0	TGGGGAATATTGCGCAATGGGGGAAACCCTGACGCAG CAACGCCGCGTGATTGAAGAAGGCCCTCGGGTTGTAA AGATCTTTAATCGGGGACGAAGAATGACGGTACCCGA

		AGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 236	R_U0083779 7	TGGGGAATATTGCGCAATGGGGGAAACCCTGACGCAG CAACGCCGCGTGAGTGAAGAAGGCCTTCGGGTTGTAA AGCTCTTTAATCAGGGACGAAGAACGACGGTACCTGA AGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 237	R_U0044980 4	TGGGGAATATTGGGCAATGGGCGAAAGCCTGACCCAG CAACGCCGCGTGGAAGGAAGAAGGTCTTCGGATTGTAA ACTTCTTTTATCAGGGACGAAGGAAGTGACGGTACCT GATGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 238	R_U0043633 2	TCGGGAATATTGCGCAATGGAGGCAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTGTCCACAGGGAAGAAAAGGACTGTACCTGTG AAGAAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 239	R_U0000343 5	TCGGGAATATTGCGCAATGGAGGAAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTGTCCACAGGGAAGATAAAAAGACTGTACCTGT GAAGAAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 240	R_U0019867 3	TCGGGAATATTGCGCAATGGAGGAAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTGTTCGATAGGGAAGAAAAAAGACTGTACCTAT CAAGAAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 241	R_U0000272 0	TCGGGAATATTGCGCAATGGAGGGAACCTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTTTAGTCAGGGAAGAAAGCAGACGGTACCTGA AGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 242	R_U0019570 7	TCGGGAATATTGCACAATGGAGGAAACTCTGATGCAG TGACGCCGCGTGCAGGAAGAAGGTTTTTCGGATTGTAA ACTGCTTTAGACAGGGAAGAAAAAAGACAGTACCTGT AGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 243	R_U0000268 6	TCGGGAATATTGCGCAATGGAGGAAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGTTTTTCGGAATGTAA ACTATTGTTCGTTAGGGAAGAGAAAGGACAGTACCTAA GGAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 244	R_U0000895 9	TCGGGAATATTGCGCAATGGAGGGAACCTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTGTTCGTTAGGGAAGAAAAAAGACAGTACCTAA GGAGGAAGCCCCGGCTAACTATGTGCC
SEQ_ID_NO_ 245	R_U0003435	TCGGGAATATTGCGCAATGGAGGAAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTCTTCGGATTGTAA

245	1	ACTATTGTCGTTAGGGAAGAGAAAGGACAGTACCTAA GGAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 246	R_U0043700 9	TCGGGAATATTGCGCAATGGAGGAACTCTGACGCAG TGACGCCGCGTGCAGGAAGAAGGTTTTTCGGATTGTAA ACTGCTTTAGACAGGGAAGAAACAAATGACAGTACCT GTAGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 247	R_U0003248 6	TCGGGAATATTGCGCAATGGAGGAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTGTCGTGAGGGAAGAAATTGACAGTACCTCAG GAGGAAGCTCCGGCTAACTATGTGCC
SEQ_ID_NO_ 248	R_U0000099 9	TCGGGAATATTGCGCAATGGAGGAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTGTCGTTAGGGAAGAGAAAGGACAGTACCTAA GGAGGAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 249	R_U0000220 1	TCGGGAATATTGCGCAATGGAGGAACTCTGACGCAG TGACGCCGCGTGCAGGAAGAAGGTTTTTCGGATTGTAA ACTGCTTTAGACAGGGAAGAAAGAAATGACGGTACCT GTAGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 250	R_U0000189 1	TCGGGAATATTGCGCAATGGAGGAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTGTCGTTAGGGAAGATAAAAGACTGTACCTAA GGAGGAAGCCCCGGCTAACTATGTGCC
SEQ_ID_NO_ 251	R_U0080366 5	TCGGGAATATTGCGCAATGGAGGAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGTTTTTCGGAATGTAA ACTATTGTCATTAGGGAAGAGAAAGGACGGTACCTAA GGAGGAAGCCCCGGCTAACTATGTGCC
SEQ_ID_NO_ 252	R_U0002711 1	TCGGGAATATTGCGCAATGGAGGAACTCTGACGCAG TGACGCCGCGTATAGGAAGAAGGTTTTTCGGATTGTAA ACTATTGTCGTTAGGGAAGAAAAAAGACAGTACCTAA GGAGGAAGCCCCGGCTAACTATGTGCC
SEQ_ID_NO_ 253	R_U0045415 7	TTGGGAATATTGGACAATGGAGGAACTCTGATCCAG TGACGCCGCGTGAAGGAAGAAGGTCTTCGGATTGTAA ACTTATTTTGTGACGGGAAGATAAATGACTGTACCTG AAGAAAAAGCACCGGCTAACTACGTGCC
SEQ_ID_NO_ 254	R_U0008017 4	TGGGGAATATTGCGCAATGGGGGAAACCCTGACGCAG CAACGCCGCGTGCAGGAAGAAGGTCTTCGGATTGTAA ACTGTTGTGTCAGGGGAAGAAGACAGTGACGGTACCC TGTGAGAAAGTCACGGCTAACTACGTGCC
SEQ_ID_NO_ 255	R_U0080330	TGGGGAATATTGGGCAATGGGCGAAAGCCTGACCCAG

255	2	CAACGCCGCGTGAGGAAGAAGGTTTTTCGGATCGTAA ACTCCTGTCCTAAGAGACGAGGAAGAGACGGTATCTT AGGAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 256	R_U0003220 8	TGGGGAATATTGGGCAATGGGCGAAAGCCTGACCCAG CAACGCCGCGTGAGGGAAGAAGGTTTTTCGGATTGTAA ACCTCTGTCCTAAGTGACGAAGGAAGTGACGGTAGCT TAGGAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 257	R_U0000111 6	TGGGGAATATTGGGCAATGGGCGAAAGCCTTACCCAG CAACGCCGCGTGAGGGAAGAAGGTTTTTCGGATTGTAA ACCTCTGTCCTGGGGGACGAAGGAAGTGACGGTACCC CGGGAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 258	R_U0080770 4	TGGGGAATATTGGGCAATGGGGGAAACCCTGACCCAG CAACGCCGCGTGAAGGAAGAAGGTTTTTCGGATCGTAA ACTTCTATCCTTGGTGAAAATGATGATGGTAGCCAAG AAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 259	R_U0000027 2	TGGGGAATATTGGGCAATGGGCGAAAGCCTGACCCAG CAACGCCGCGTGAGGGAAGAAGGGTTTTTCGGCTCGTAA ACCTCTGTCCTATGGGACGAAGGAAGTGACGGTACCA TAGGAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 260	R_U0080527 7	TGGGGAATATTGCACAATGGGCGAAAGCCTGATGCAG CAACGCCGCGTGAGCGAAGAAGGTCTTCGGATCGTAA AGCTCTGTCCTTGGGGAAGATAATGACGGTACCCAAG GAGGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 261	R_U0113623 8	TGGGGAATATTGGGCAATGGAGGCAACTCTGACCCAG CAACGCCGCGTGAATGAAGAAGGTCCTAGGATTGTAA AGTTCTTTTATGATAGACGAATAAAATGACGGTATAT CATGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 262	R_U0084863 9	TGGGGAATATTGGGCAATGGAGGCAACTCTGACCCAG CAACGCCGCGTGAATGAAGAAGGCCTTCGGGTTGTAA AGTTCTTTAATGGGGGACGAAGAAAGTGACGGTACCC CAAGAATAAGCCACGGCTAACTACGTGCC
SEQ_ID_NO_ 263	R_U0000424 9	TGGGGGATATTGCACAATGGGGGAAACCCTGATGCAG CGACGCCGCGTGAGTGAAGAAGTATTTTCGGTATGTAA AGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGAC TAAGAAGCCCCGGCTAACTACGTGCC
SEQ_ID_NO_ 264	R_U0001209 6	TTAGGAATATTCGTCAATGGGGGAAACCCTGAACGAG CAATGCCGCGTGAGTGATGACGGTCTTTATGATTGTA AAACTCTGTTGTAAGGAAAGAACCCTTATCATAGGAA ATGATGATAAGTTGACGGTACCTTACCAGAAAGCCCC

		GGCTAACTACGTGCC
SEQ_ID_NO_ 265	R_U0115212 2	TAGGGAATTTTCGGCAATGGGGGGAACCCTGACCGAG CAACGCCGCGTGAAACGAAGAAGTTATTCGTAATGTAA AGTTCTTTTATCAGGGAAGAAAAGAAGGGAATTGACG GTACCTGATGAATAAGCTCCGGCTAACTACGTGCC
SEQ_ID_NO_ 266	R_U0112319 9	TGGGGAATCTTCCGCAATGGGCGAAAGCCTGACGGAG CGACGCCGCGTGAGTGAAGAAGGTCTTCGGACCGTAA AGCTCTTTTGTTCAGGCGAAAGGACTTAAGAGGAAA TGCTTAAGTTAAGACGGTATGGAACGAATAAGCCACG GCTAACTACGTGCC
SEQ_ID_NO_ 267	R_U0000073 7	TAGGGAATCTTTCACAATGGGCGAAAGCCTGATGGAG CAACGCCGCGTGACAGGATGAAGGCCTTCGGGTTGTAA ACTGCTTTTATAAGCGAGAAATATGATGGTAACTTAT GAATAAGGATCGGCTAACTACGTGCC
SEQ_ID_NO_ 268	R_U0082204 0	TGGGGAATTTTGGACAATGGACGGAAGTCTGATCCAG CAACGCAGCGTGAAAGGACGAAGGTCTCGGATTGTAA ACTTCTTTTGCAGGGGAAGAAAAAATGACGGTACCC TGTGAATAAGCCACGGCTAACTACGTGCC

In the above detailed description, reference is made to the accompanying drawings, which form a part hereof. In the drawings, similar symbols typically identify similar components, unless context dictates otherwise. The illustrative embodiments described in the detailed description, drawings, and claims are not meant to be limiting. Other embodiments may be used, and other changes may be made, without departing from the spirit or scope of the subject matter presented herein. It will be readily understood that the aspects of the present disclosure, as generally described herein, and illustrated in the Figures, may be arranged, substituted, combined, separated, and designed in a wide variety of different configurations, all of which are explicitly contemplated herein.

The present disclosure is not to be limited in terms of the particular embodiments described in this application, which are intended as illustrations of various aspects. Many modifications and variations can be made without departing from its spirit and scope, as will be apparent to those skilled in the art. Functionally equivalent methods and apparatuses within the scope of the disclosure, in addition to those enumerated herein, will be apparent to those skilled in the art from the foregoing descriptions. Such modifications and variations are intended to fall within the scope of the appended claims. The present disclosure is to be limited only by the terms of the appended claims, along with the full scope of equivalents to which such claims are entitled. It is to be understood that this disclosure is not limited to particular methods, reagents, compounds, compositions or biological systems, which can, of course, vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting.

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

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

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

As will be understood by one skilled in the art, for any and all purposes, such as in terms of providing a written description, all ranges disclosed herein also encompass any and all possible subranges and combinations of subranges thereof. Any listed range can be easily recognized as sufficiently describing and enabling the same range being broken down into at

least equal halves, thirds, quarters, fifths, tenths, etc. As a non-limiting example, each range discussed herein can be readily broken down into a lower third, middle third and upper third, etc. As will also be understood by one skilled in the art all language such as “up to,” “at least,” and the like include the number recited and refer to ranges which can be subsequently broken down into subranges as discussed above. Finally, as will be understood by one skilled in the art, a range includes each individual member. Thus, for example, a group having 1-3 cells refers to groups having 1, 2, or 3 cells. Similarly, a group having 1-5 cells refers to groups having 1, 2, 3, 4, or 5 cells, and so forth.

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

CLAIMS

WHAT IS CLAIMED IS:

1. A method for improving gut microbiota population, comprising administering to a subject a composition to increase a first gut microbiota population while simultaneously decrease a second gut microbiota population in the subject, wherein the first gut microbiota population comprises a short-chain fatty acid (SCFA)-producing bacterium, and wherein the second gut microbiota population comprises an endotoxin-producing bacterium.
2. The method of Claim 1, wherein the composition comprises a natural medicine, a natural product, an herb, or an herbal extract.
3. The method of Claim 1, wherein the composition comprises berberine, a berberine derivative, or anisoquinoline alkaloid.
4. The method of Claim 1, wherein the composition comprises a plant or its extract thereof, wherein the plant comprises *Berberis vulgaris*, *Coptischinensis*, *Scutellariabaicalensis*, *PhellodendriChinensis*, *Momordicacharantia*, *Ilex kudingcha*, *Sophoraflavescens*, *Gentianascabra*, *Anemarrhenaasphodeloides*, *Gardenia jasminoides*, *Rheum palmatum*, *HerbaTaraxaci*, or combinations thereof.
5. The method of Claim 1, wherein the composition comprises a plant or its extract, wherein the plant is a *Berberis*, *Coptis*, *Scutellaria*, *Phellodendron*, *Momordica*, *Ilex*, *Sophora*, *Gentiana*, *Anemarrhena*, *Gardenia*, *Rheum*, or *Taraxacum*.
6. The method of Claim 1, wherein the composition comprises a plant or its extract, wherein the plant is a *Berberidaceae*, *Ranunculaceae*, *Lamiaceae*, *Rutaceae*, *Cucurbitacea*, *Aquifoliaceae*, *Leguminosae*, *Gentianaceae*, *Agavaceae*, *Rubiaceae*, *Polygonaceae*, *Asteraceae*, *Menispermaceae*, or *Cucurbitaceae*.
7. The method of Claim 1, wherein the first gut microbiota population comprises *Alistipes*, *Allobaculum*, *Bacteroides*, *Barnesiella*, *Blautia*, *Butyricicoccus*, *Butyricimonas*, *Dorea*, *Helicobacter*, *Hespellia*, *Holdemania*, *Lawsonia*, *Oscillibacter*, *Parabacteroides*, *Phascolarctobacterium*, *Prevotella*, *Sedimentibacter*, or a combination thereof.
8. The method of Claim 1, wherein the first gut microbiota population comprises *Bacteroidaceae*, *Coriobacteriaceae*, *Desulfovibrionaceae*, *Erysipelotrichaceae*, *Flavobacteriaceae*, *Helicobacteraceae*, *IncertaeSedis XI*, *IncertaeSedis XIV*, *Lachnospiraceae*, *Porphyromonadaceae*, *Prevotellaceae*, *Rikenellaceae*, *Ruminococcaceae*, *Veillonellaceae*, or a combination thereof.
9. The method of Claim 1, wherein the first gut microbiota population comprises *Campylobacterales*, *Desulfovibrionales*, *Bacteroidales*, *Coriobacteriales*, *Flavobacteriales*, *Clostridiales*, *Erysipelotrichales*, or a combination thereof.

10. The method of Claim 1, wherein the first gut microbiota population comprises *Epsilonproteobacteria*, *Deltaproteobacteria*, *Bacteroidia*, *Coriobacteridae*, *Flavobacteria*, *Clostridia*, *Erysipelotrichi*, or a combination thereof.
11. The method of Claim 1, wherein the first gut microbiota population comprises *Proteobacteria*, *Bacteroidetes*, *Actinobacteria*, *Firmicutes*, or a combination thereof.
12. The method of Claim 1, wherein the short-chain fatty acid (SCFA)-producing bacteria comprises *Blautia*, *Allobaculum*, *Prevotella*, *Bacterioides*, *Butyricimonas*, or a combination thereof.
13. The method of Claim 1, wherein the first gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 95% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-93.
14. The method of Claim 1, wherein the first gut microbiota population comprises a bacteria whose V3 region of 16S rRNA gene sequence has at least about 80% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-93.
15. The method of Claim 1, wherein the second gut microbiota population comprises *Alistipes*, *Anaeroplasma*, *Barnesiella*, *Bifidobacterium*, *Butyricimonas*, *Butyrivibrio*, *Coprococcus*, *Fastidiosipila*, *Helicobacter*, *Hespellia*, *Marvinbryantia*, *Oribacterium*, *Oscillibacter*, *Prevotella*, *Roseburia*, *Ruminococcus*, *TM7_genera_incertae_sedis*, or a combination thereof.
16. The method of Claim 1, wherein the second gut microbiota population comprises *Helicobacteraceae*, *Lachnospiraceae*, *Porphyromonadaceae*, *Prevotellaceae*, *Rikenellaceae*, *Ruminococcaceae*, *Anaeroplasmataceae*, *Bifidobacteriaceae*, or a combination thereof.
17. The method of Claim 1, wherein the second gut microbiota population comprises *Campylobacteriales*, *Bacteroidales*, *Clostridiales*, *Anaeroplasmatales*, *Bifidobacteriales*, or a combination thereof.
18. The method of Claim 1, wherein the second gut microbiota population comprises *Epsilonproteobacteria*, *Alphaaproteobacteria*, *Bacteroidia*, *Clostridia*, *Actinobacteridae*, *Mollicutes*, or a combination thereof.
19. The method of Claim 1, wherein the second gut microbiota population comprises *Proteobacteria*, *Bacteroidetes*, *Actinobacteria*, *Firmicutes*, *Tenericutes*, or a combination thereof.
20. The method of Claim 1, wherein the endotoxin-producing bacteria comprises *Proteobacteria*.
21. The method of Claim 1, wherein the second gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 95% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 94 -268.
22. The method of Claim 1, wherein the second gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 80% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 94-268.

23. The method of Claim 1, wherein the composition is an oral formulation or a parenteral formulation.
24. The method of Claim 1, wherein the composition is in a form of suppository, tablet, pill, granule, powder, film, microcapsule, aerosol, spirit, tincture, tonic, liquid suspension, or syrup.
25. The method of Claim 1, wherein the composition may decrease the serum level of a first cytokine and increase the serum level of a second cytokine, wherein the first cytokine comprises lipopolysaccharide-binding protein, monocyte chemoattractant protein-1, leptin, or a combination thereof, and wherein the second cytokine comprises adiponectin.
26. The method of Claim 1, wherein the composition may increase the level of fecal short-chain fatty acids.
27. A method for screening a test compound that is active in improving gut microbiota population, comprising:
- administering to a control subject an effective amount of a control composition to increase a first gut microbiota population while simultaneously decrease a second gut microbiota population in the control subject, wherein the first gut microbiota population comprises a short-chain fatty acid (SCFA)-producing bacteria, and wherein the second gut microbiota population comprises an endotoxin-producing bacteria;
 - administering to a test subject an amount of a test compound; and
 - comparing the gut microbiota population of the controlled subject and the gut microbiota population of the test subject, wherein a similarity of at least about 80% is indicative that the test compound is active in improving gut microbiota population.
28. The method of Claim 27, wherein a similarity of at least about 95% is indicative that the test compound is active in improving gut microbiota population.
29. The method of Claim 27, wherein a similarity of at least about 75% is indicative that the test compound is active in improving gut microbiota population.
30. The method of Claim 27, wherein the composition comprises a natural medicine, a natural product, an herb, or an herbal extract.
31. The method of Claim 27, wherein the composition comprises berberine, a berberine derivative, or an isoquinoline alkaloid.
32. The method of Claim 27, wherein the composition comprises a plant or its extract thereof, wherein the plant comprises *Berberis vulgaris*, *Coptischinensis*, *Scutellariabaicalensis*, *PhellodendriChinensis*, *Momordicacharantia*, *Ilex kudingcha*, *Sophoraflavescens*, *Gentianascabra*, *Anemarrhenaasphodeloides*, *Gardenia jasminoides*, *Rheum palmatum*, *HerbaTaraxaci*, or combinations thereof.
33. The method of Claim 27, wherein the composition comprises a plant or its extract thereof, wherein the plant is *Berberis*, *Coptis*, *Scutellaria*, *Phellodendron*, *Momordica*, *Ilex*, *Sophora*, *Gentiana*, *Anemarrhena*, *Gardenia*, *Rheum*, or *Taraxacum*.

34. The method of Claim 27, wherein the composition comprises a plant or its extract thereof, wherein the plant is *Berberidaceae*, *Ranunculaceae*, *Lamiaceae*, *Rutaceae*, *Cucurbitaceae*, *Aquifoliaceae*, *Leguminosae*, *Gentianaceae*, *Agavaceae*, *Rubiaceae*, *Polygonaceae*, *Asteraceae*, *Menispermaceae*, or *Cucurbitaceae*.
35. The method of Claim 27, wherein the first gut microbiota population comprises *Alistipes*, *Allobaculum*, *Bacteroides*, *Barnesiella*, *Blautia*, *Butyricicoccus*, *Butyricimonas*, *Dorea*, *Helicobacter*, *Hespellia*, *Holdemania*, *Lawsonia*, *Oscillibacter*, *Parabacteroides*, *Phascolarctobacterium*, *Prevotella*, *Sedimentibacter*, or a combination thereof.
36. The method of Claim 27, wherein the short-chain fatty acid (SCFA)-producing bacteria comprises *Blautia*, *Allobaculum*, *Prevotella*, *Bacterioides*, *Bacterioides*, *Butyricimonas*, or a combination thereof.
37. The method of Claim 27, wherein the first gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 95% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO:1-93.
38. The method of Claim 27, wherein the first gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 80% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO:1-93.
39. The method of Claim 27, wherein the second gut microbiota population comprises *Alistipes*, *Anaeroplasma*, *Barnesiella*, *Bifidobacterium*, *Butyricimonas*, *Butyrivibrio*, *Coprococcus*, *Fastidiosipila*, *Helicobacter*, *Hespellia*, *Marvinbryantia*, *Oribacterium*, *Oscillibacter*, *Prevotella*, *Roseburia*, *Ruminococcus*, *TM7_genera_incertae_sedis*, or a combination thereof.
40. The method of Claim 27, wherein the endotoxin-producing bacteria comprises *Proteobacteria*.
41. The method of Claim 27, wherein the second gut microbiota population comprises a bacteria whose V3 region of 16S rRNA gene sequence has at least about 95% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO. 94-268.
42. The method of Claim 27, wherein the second gut microbiota population comprises a bacteria whose V3 region of 16S rRNA gene sequence has at least about 80% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO. 94-268.
43. The method of Claim 27, wherein the composition may decrease the serum level of a first cytokine and increase the serum level of a second cytokine, wherein the first cytokine comprises lipopolysaccharide-binding protein, monocyte chemoattractant protein-1, leptin, or a combination thereof, and wherein the second cytokine comprises adiponectin.
44. The method of Claim 27, wherein the composition may increase the level of gut short-chain fatty acids.
45. A composition for improving gut microbiota population, wherein the composition is capable of selectively increasing a first gut microbiota population while simultaneously decreasing a second gut microbiota population in a subject, wherein the first gut microbiota population

comprises a short-chain fatty acid (SCFA)-producing bacterium, and wherein the second gut microbiota population comprises an endotoxin-producing bacterium.

46. The composition of Claim 45, wherein the composition comprises natural medicine, natural product, an herb, or an herbal extract.

47. The composition of Claim 45, wherein the composition comprises berberine, berberine derivative, or other isoquinoline alkaloid thereof.

48. The composition of Claim 45, wherein the composition comprises a plant or its extract thereof, wherein the plant comprises *Berberis vulgaris*, *Coptischinensis*, *Scutellariabaicalensis*, *PhellodendriChinensis*, *Momordicacharantia*, *Ilex kudingcha*, *Sophoraflavescens*, *Gentianascabra*, *Anemarrhenaasphodeloides*, *Gardenia jasminoides*, *Rheum palmatum*, *HerbaTaraxaci*, or any combinations thereof.

49. The composition of Claim 45, wherein the composition comprises a plant or its extract thereof, wherein the plant is *Berberis*, *Coptis*, *Scutellaria*, *Phellodendron*, *Momordica*, *Ilex*, *Sophora*, *Gentiana*, *Anemarrhena*, *Gardenia*, *Rheum*, or *Taraxacum*.

50. The composition of Claim 45, wherein the composition comprises a plant or its extract thereof, wherein the plant is *Berberidaceae*, *Ranunculaceae*, *Lamiaceae*, *Rutaceae*, *Cucurbitaceae*, *Aquifoliaceae*, *Leguminosae*, *Gentianaceae*, *Agavaceae*, *Rubiaceae*, *Polygonaceae*, *Asteraceae*, *Menispermaceae*, or *Cucurbitaceae*.

51. The composition of Claim 45, wherein the composition is a food, a drink, a supplement, or a pharmaceutical formulation.

52. The composition of Claim 45, wherein the composition is capable of selectively increasing a first gut microbiota population while simultaneously decreasing a second gut microbiota population in a subject at a dosage of from about 50 mg/kg body weight to about 400 mg/body weight and with once a day administration for at least two weeks, wherein the first gut microbiota population comprises a short-chain fatty acid (SCFA)-producing bacterium, wherein the second gut microbiota population comprises an endotoxin producing bacterium.

53. The composition of Claim 45, wherein the first gut microbiota population comprises *Alistipes*, *Allobaculum*, *Bacteroides*, *Barnesiella*, *Blautia*, *Butyricicoccus*, *Butyricimonas*, *Dorea*, *Helicobacter*, *Hespellia*, *Holdemania*, *Lawsonia*, *Oscillibacter*, *Parabacteroides*, *Phascolarctobacterium*, *Prevotella*, *Sedimentibacter*, or a combination thereof.

54. The composition of Claim 45, wherein the short-chain fatty acid (SCFA)-producing bacteria comprises *Blautia*, *Allobaculum*, *Prevotella*, *Bacterioides*, *Butyricimonas*, or a combination thereof.

55. The composition of Claim 45, wherein the first gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 95% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-93.

56. The composition of Claim 45, wherein the first gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least about 80% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 1-93.

57. The composition of Claim 45, wherein the second gut microbiota population comprises *Alistipes*, *Anaeroplasma*, *Barnesiella*, *Bifidobacterium*, *Butyricimonas*, *Butyrivibrio*, *Coprococcus*, *Fastidiosipila*, *Helicobacter*, *Hespellia*, *Marvinbryantia*, *Oribacterium*, *Oscillibacter*, *Prevotella*, *Roseburia*, *Ruminococcus*, *TM7_genera_incertae_sedis*, or a combination thereof.

58. The composition of Claim 45, wherein the endotoxin-producing bacterium comprises *Proteobacteria*.

59. The composition of Claim 45, wherein the second gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least 95% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 94-268.

60. The composition of Claim 45, wherein the second gut microbiota population comprises a bacterium whose V3 region of 16S rRNA gene sequence has at least 80% similarity with a nucleic acid sequence selected from a group consisting of SEQ ID NO: 94-268.