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(54) ANTIBACTERIAL COMPOSITION AGAINST DRUG-RESISTANT BACTERIA OR PRO-INFLAMMATORY BACTERIA

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**Related U.S. Application Data**

(62) Division of application No. 17/436,148, filed on Sep. 3, 2021, now abandoned, filed as application No. PCT/JP2020/009423 on Mar. 5, 2020.

(60) Provisional application No. 62/815,101, filed on Mar. 7, 2019.

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A61P 31/04 (2006.01)

(52) U.S. Cl.

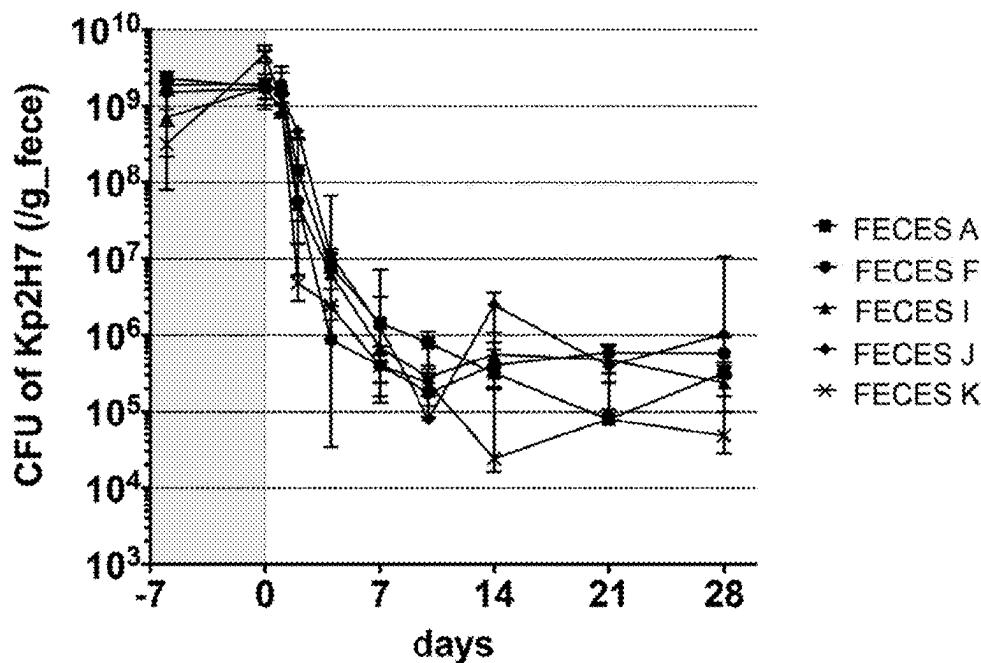
CPC ..... A61K 35/741 (2013.01); A61P 31/04 (2018.01); A61K 2035/115 (2013.01)

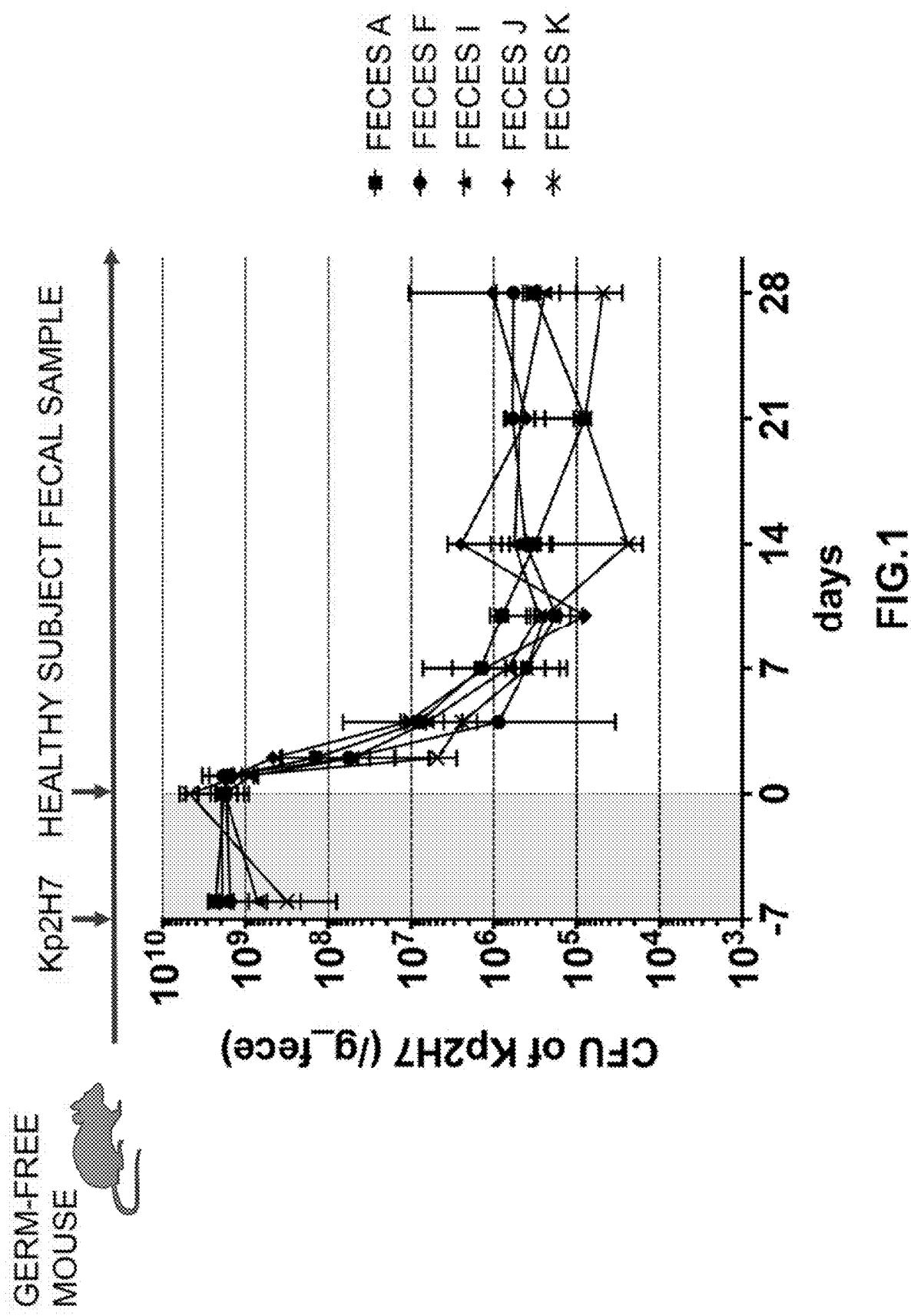
**ABSTRACT**

An antibacterial composition against drug-resistant bacteria or pro-inflammatory bacteria is disclosed. The antibacterial composition contains an intestinal bacterium as an active ingredient. Also uses of such composition useful for treating, ameliorating, or preventing an infectious disease or an inflammatory disease, and a pharmaceutical composition containing an intestinal bacterium as an active ingredient are disclosed.

**Specification includes a Sequence Listing.**GERM-FREE  
MOUSE

Kp2H7    HEALTHY SUBJECT FECAL SAMPLE





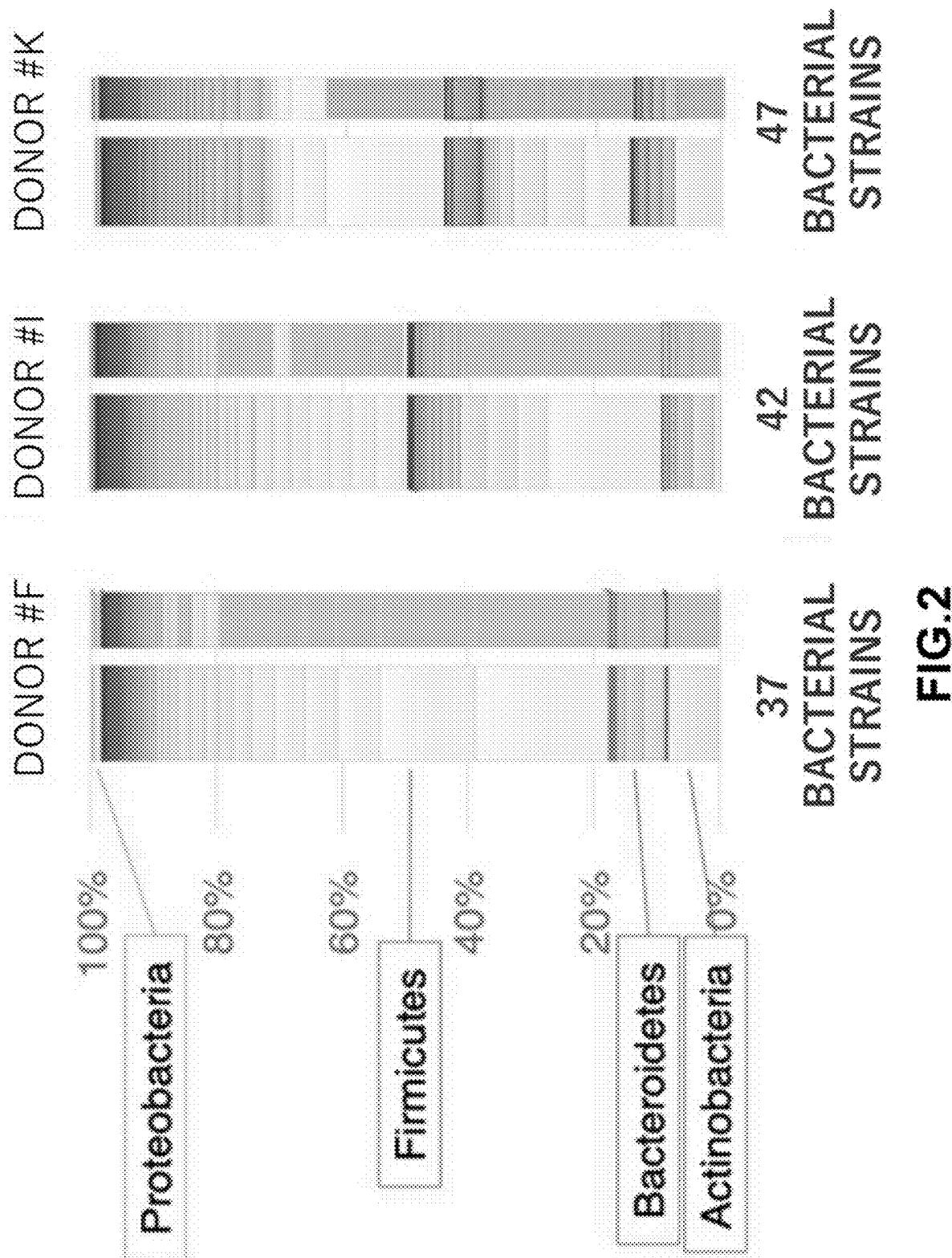
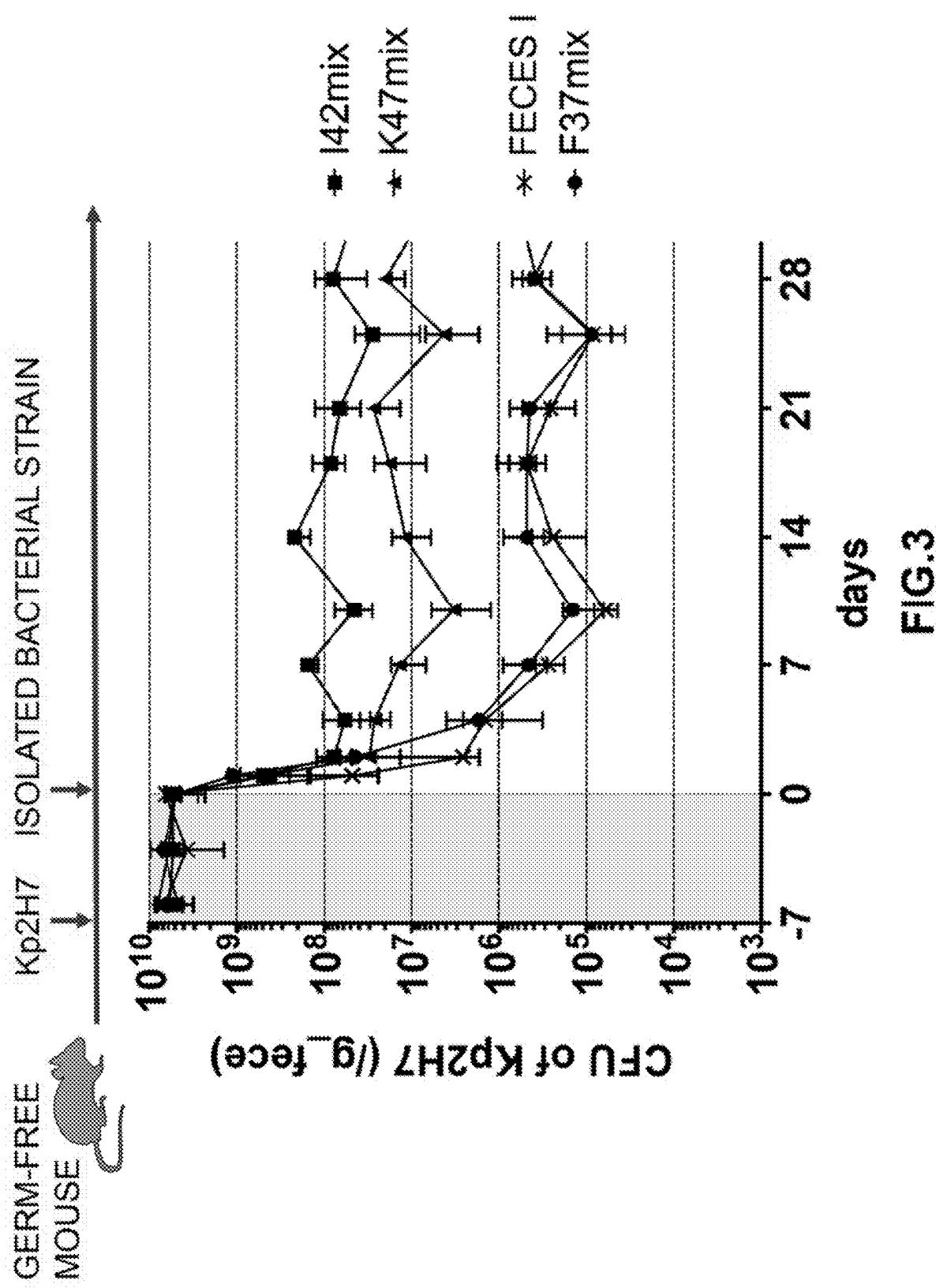
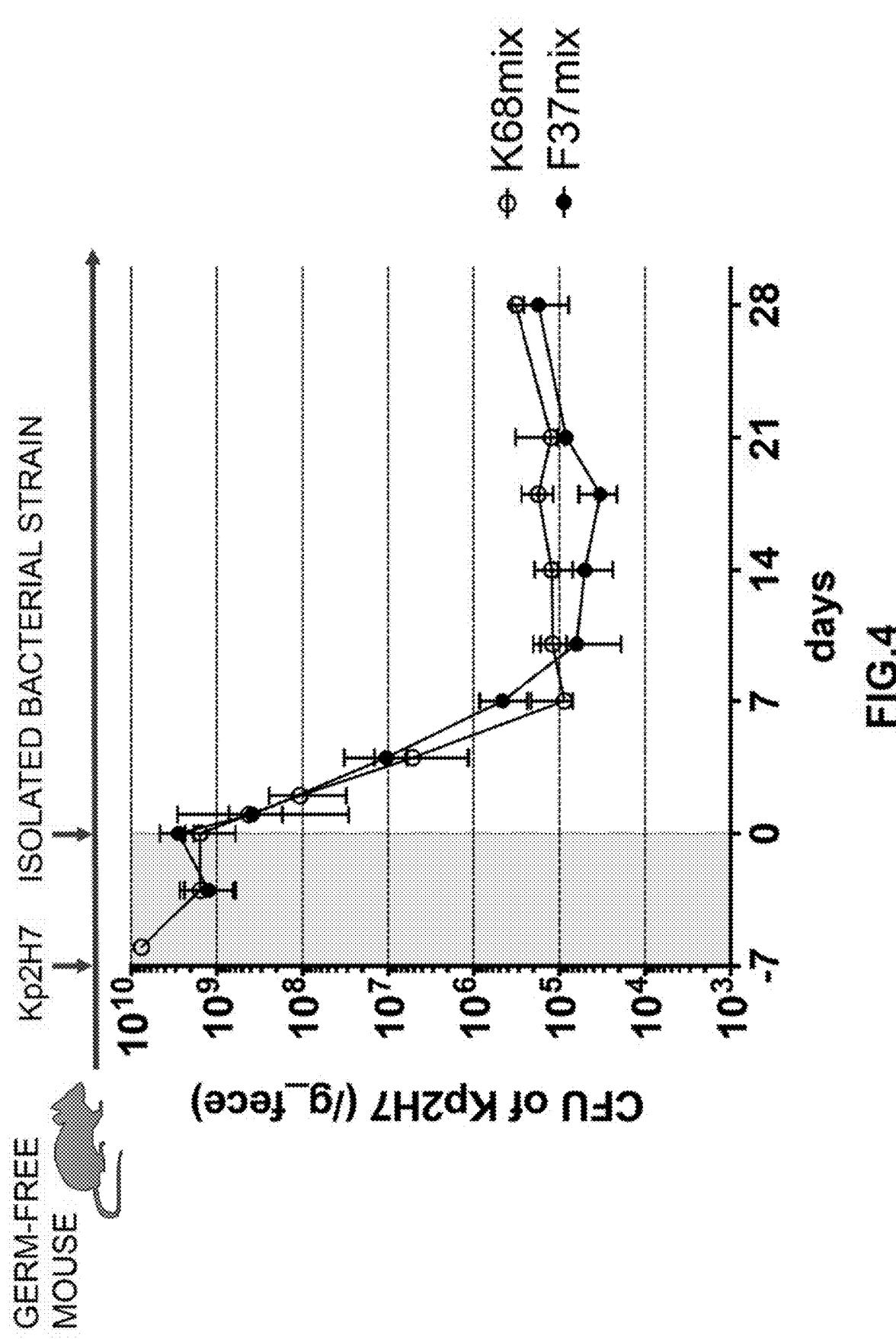


FIG.2





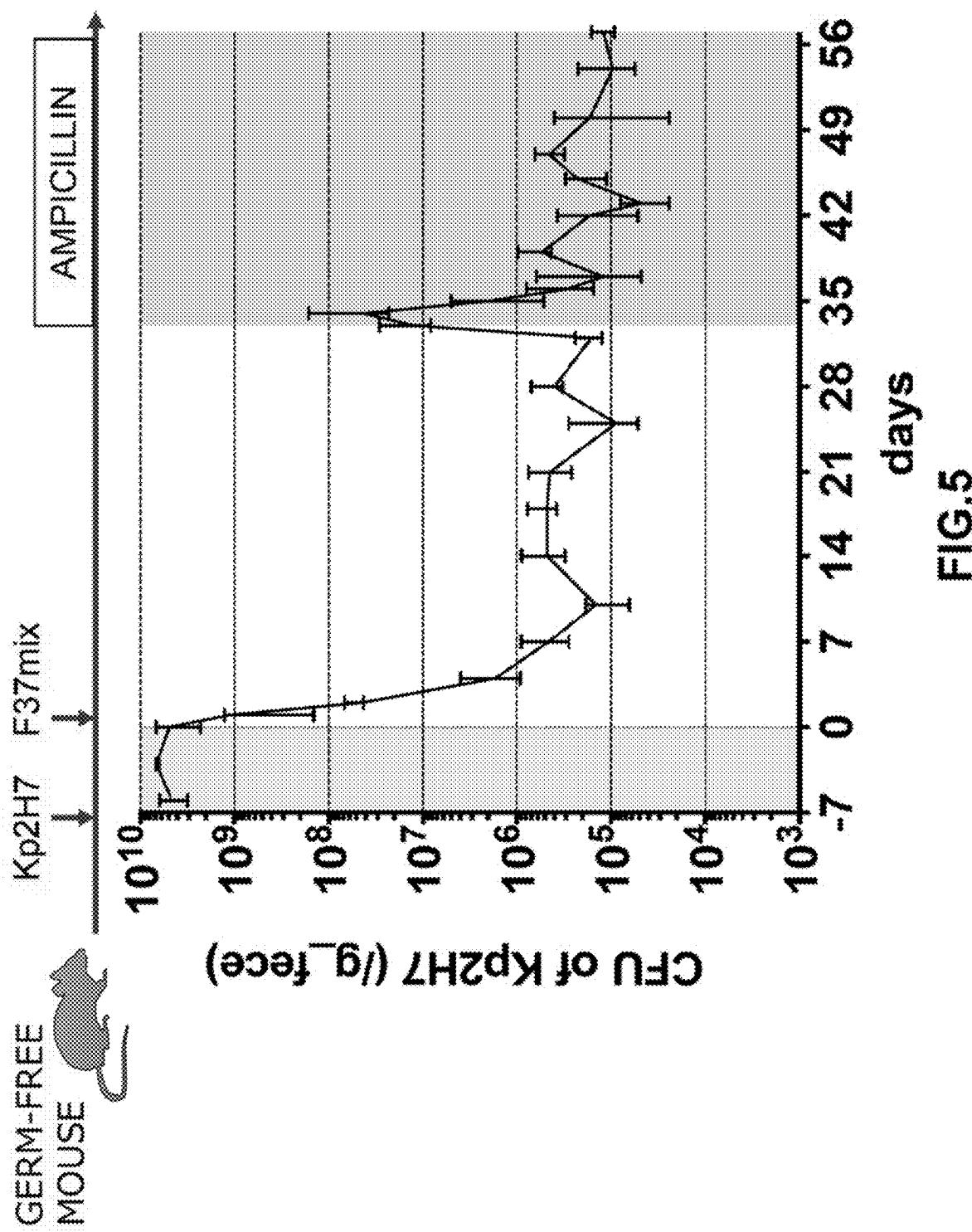


FIG.5

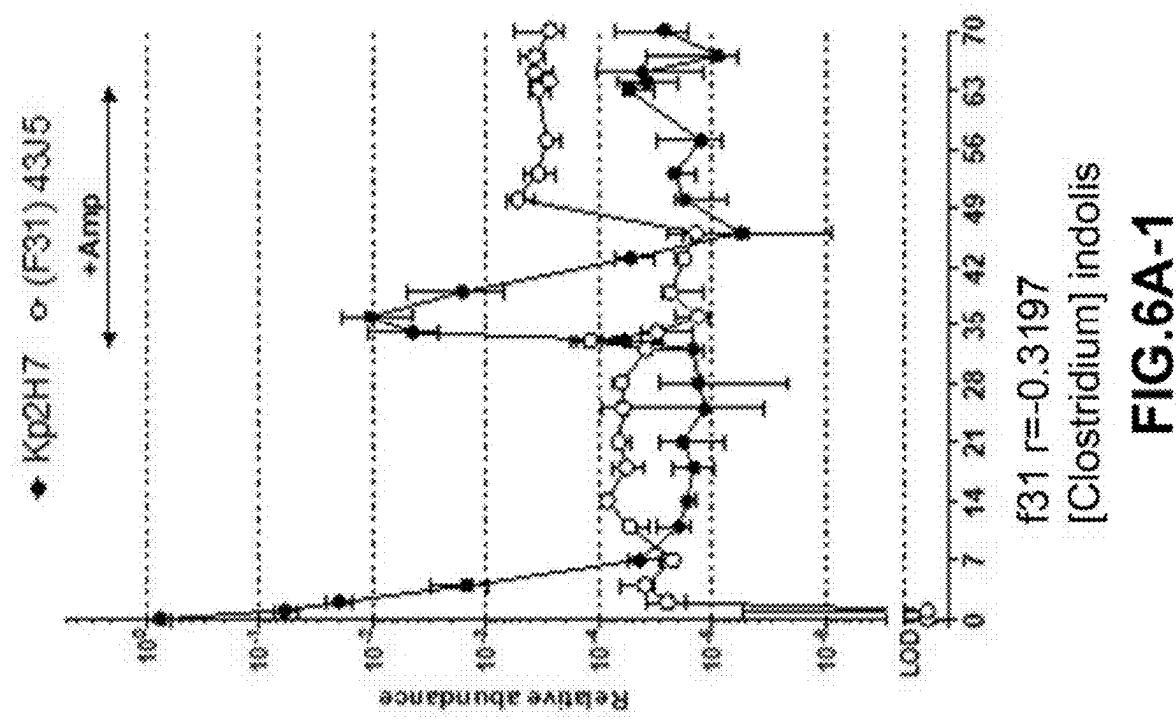
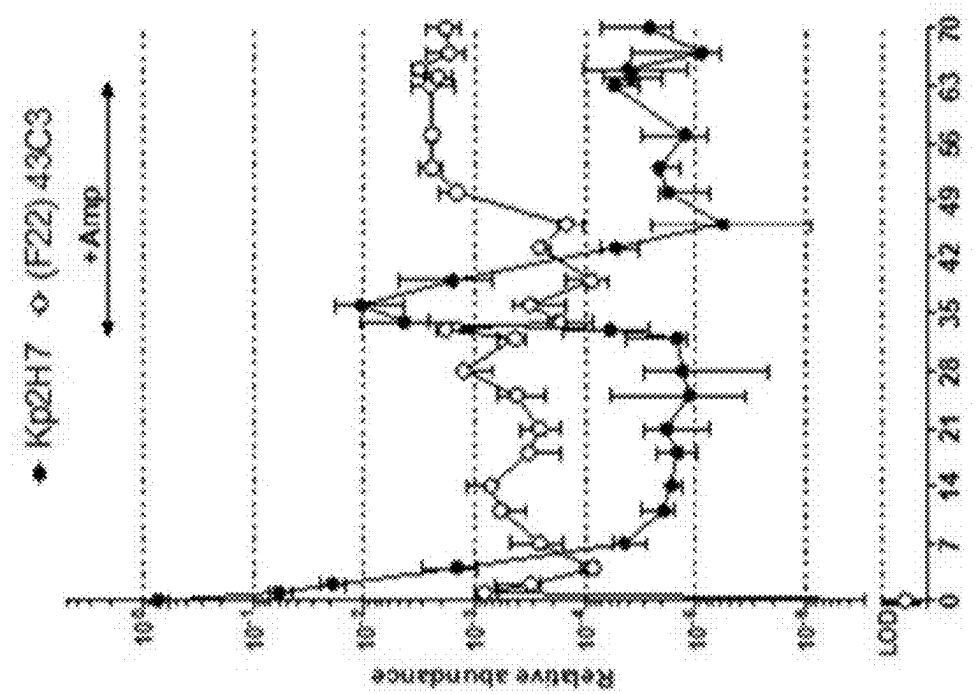
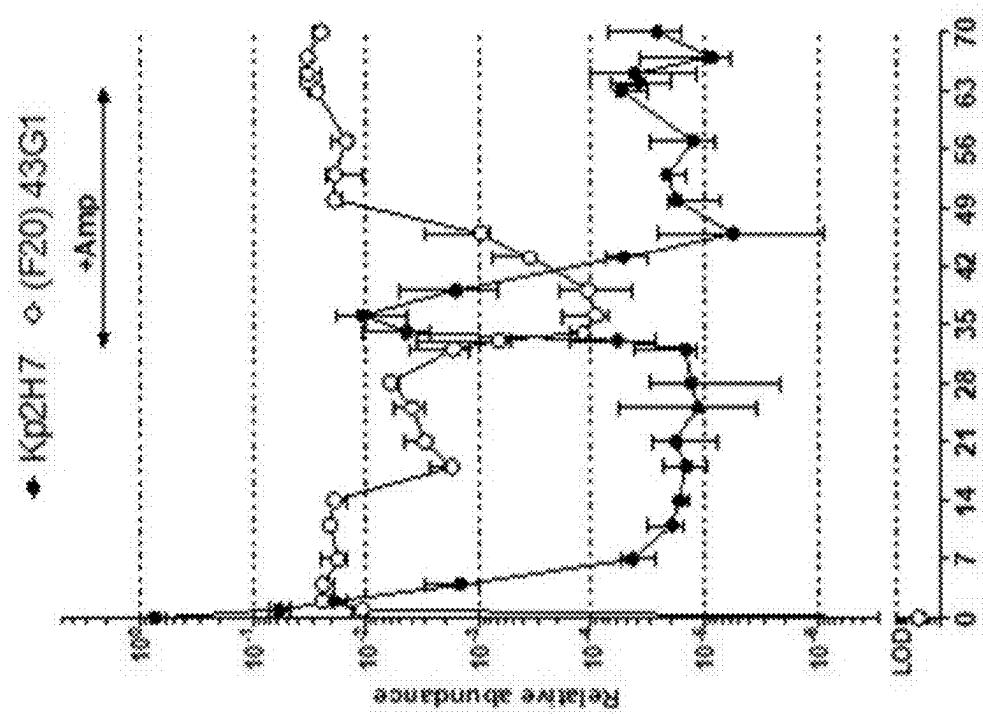


FIG.6A-1



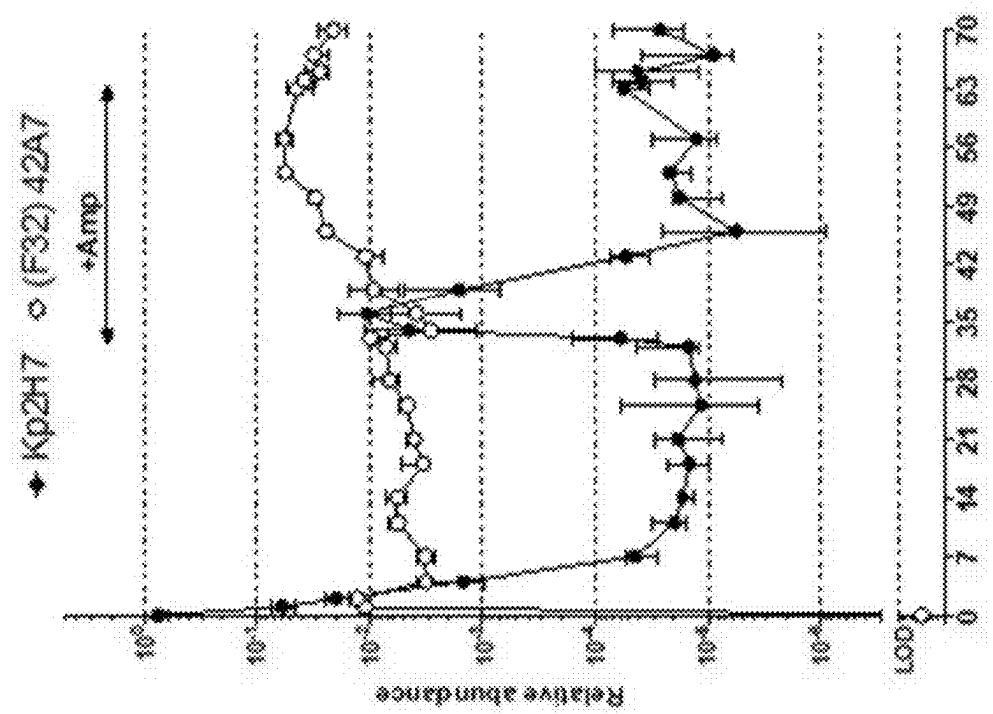
[Clostridium] asparagiforme

**FIG. 6A-2**



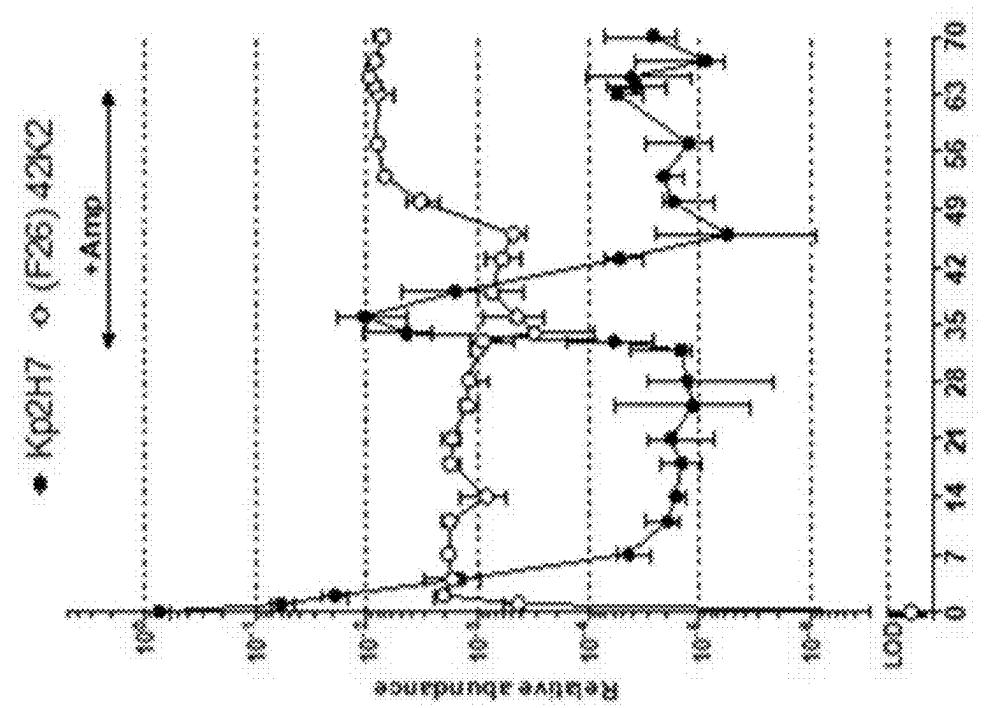
f20  $r=0.281$   
[Clostridium] innocuum

**FIG.6A-3**

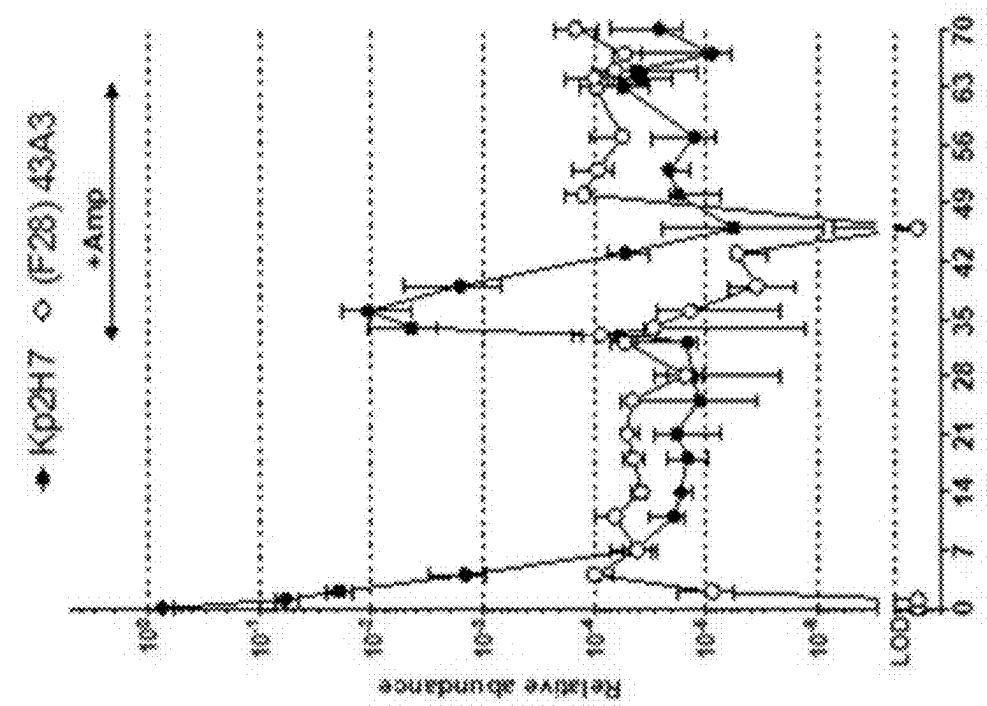


f32 r=-0.2529  
*Blautia producta*

**FIG.6A-4**

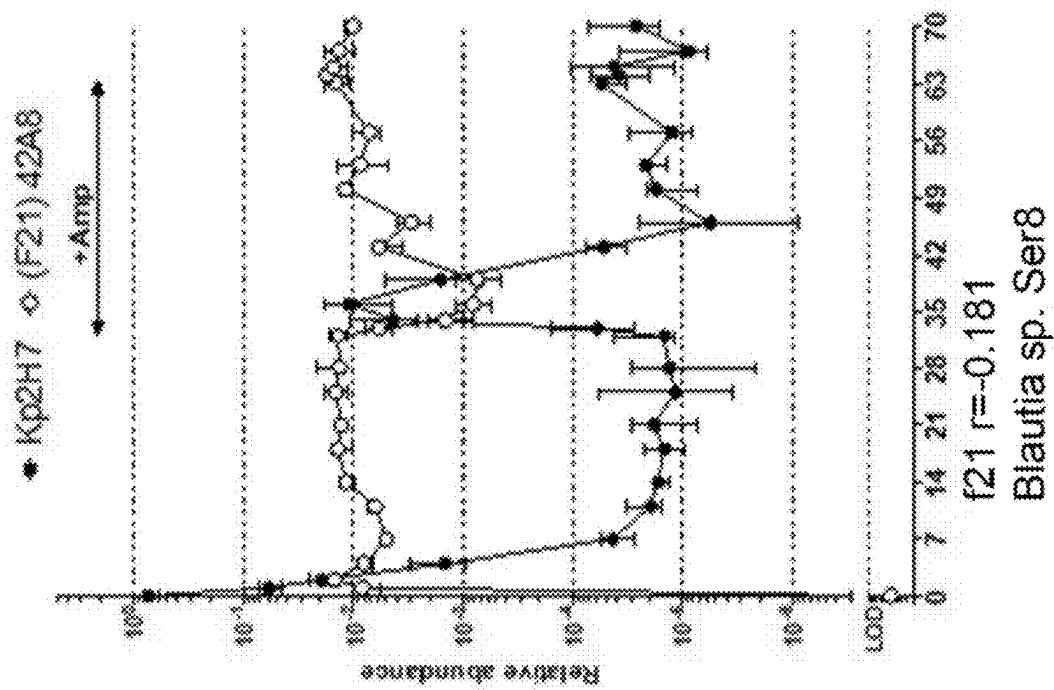


**FIG. 6B-1**  
f26 r=-0.2024  
*Flavonifractor plautii*

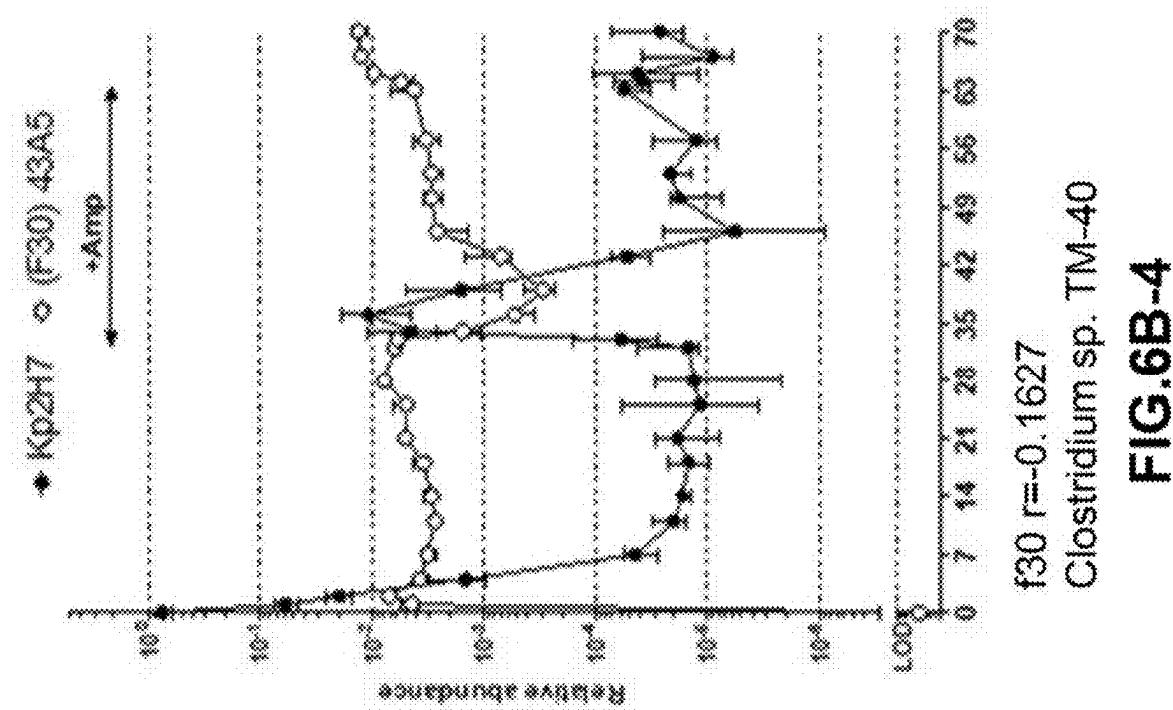


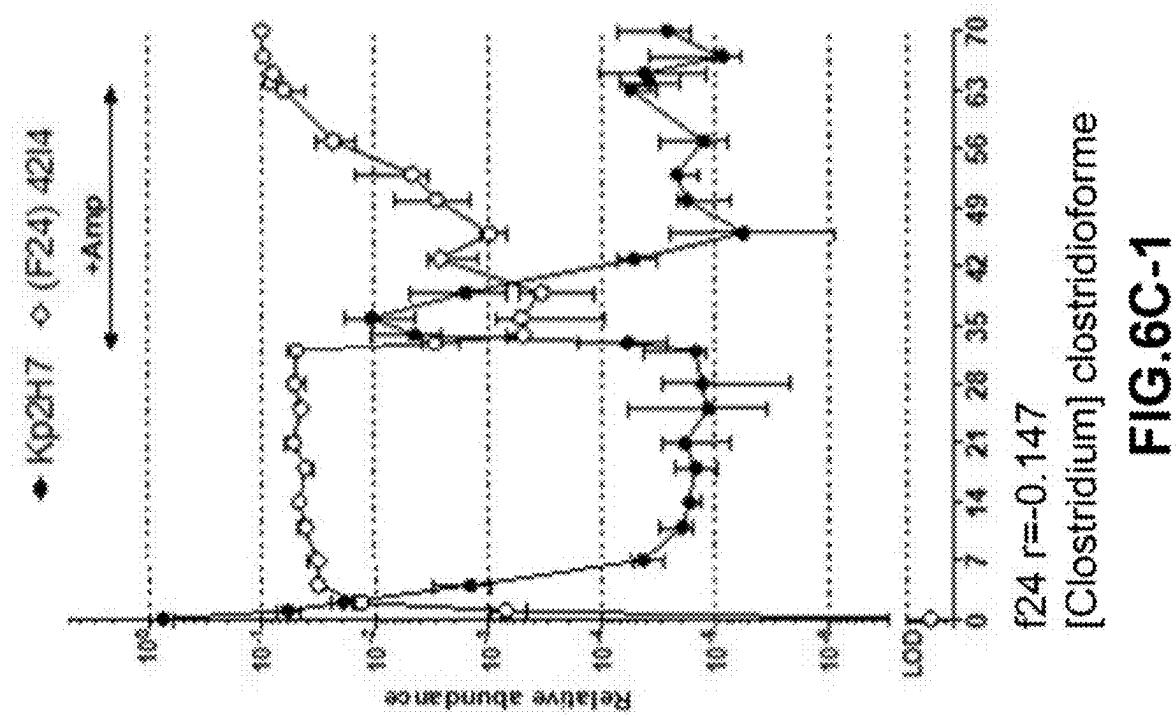
f28 r=0.1812  
Intestinibacter bartletti

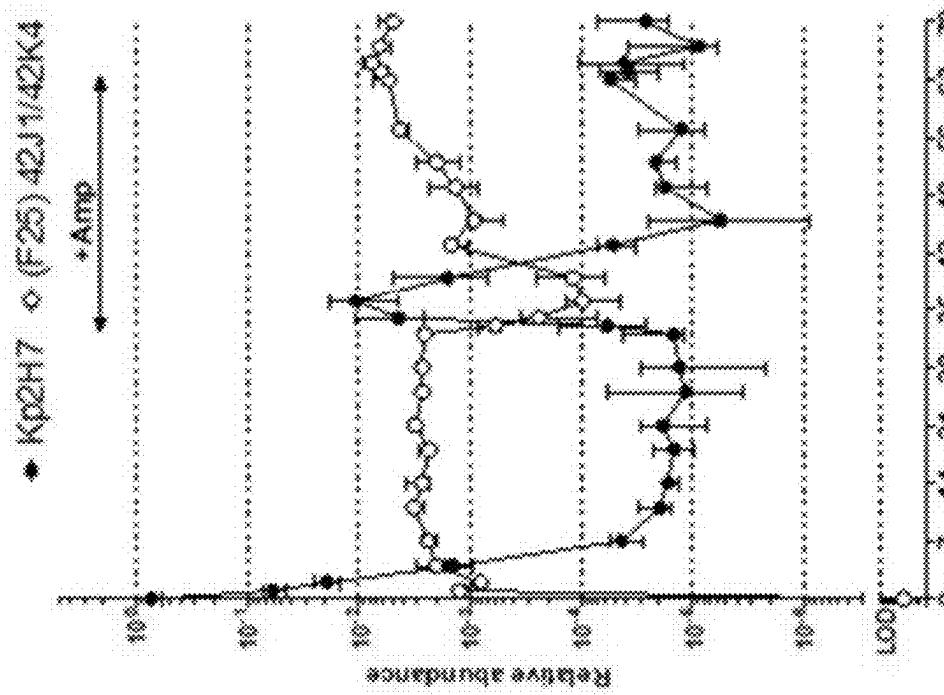
**FIG. 6B-2**



**FIG.6B-3**

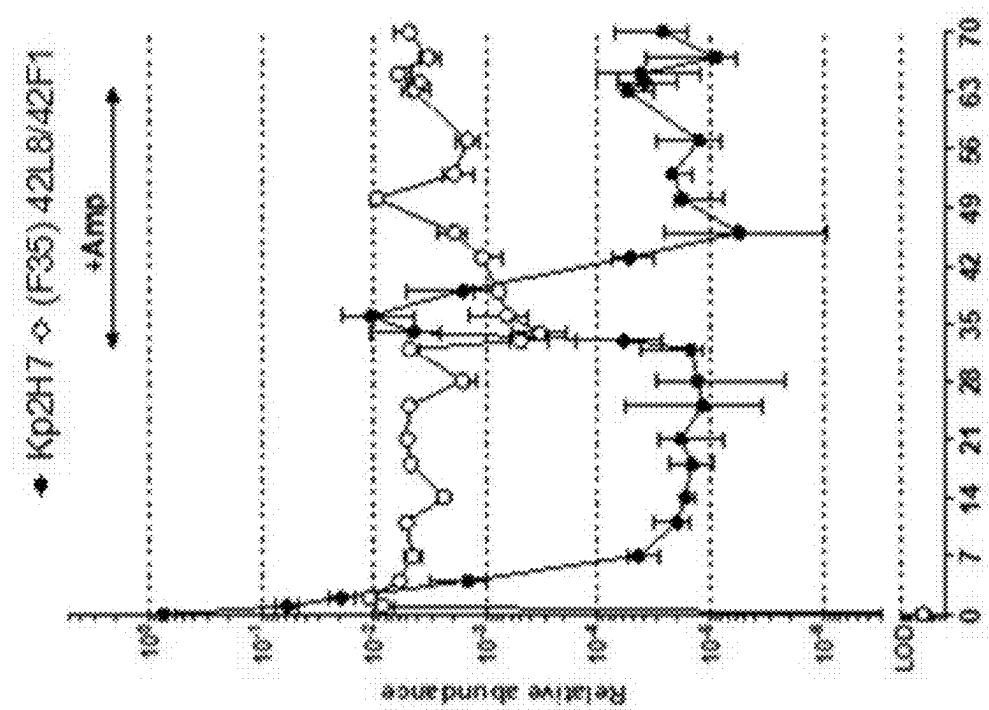




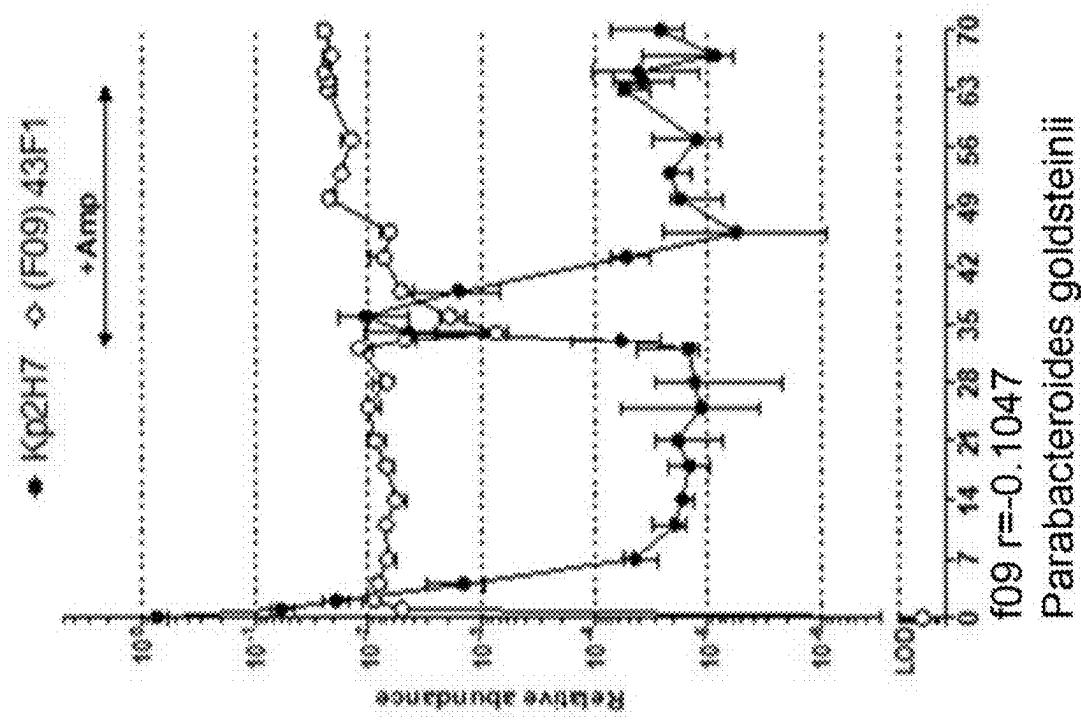


f23/f25  $r=0.1295$   
[Clostridium] glycyrhizinilyticum

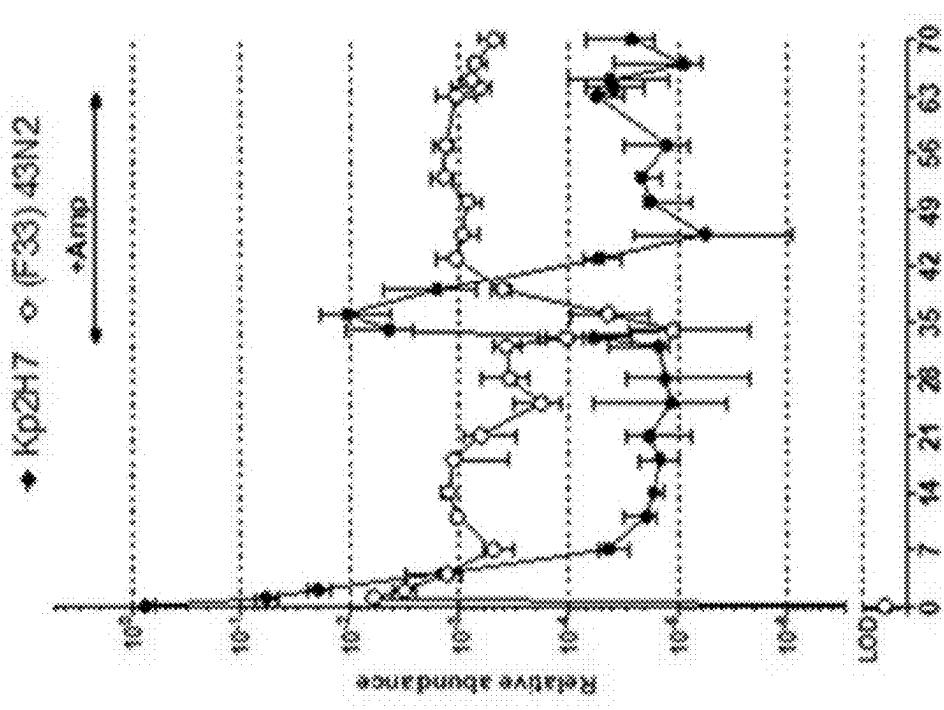
**FIG. 6C-2**



**FIG.6C-3**  
f35/f36 r=-0.1108  
*Fusobacterium ulcerans*

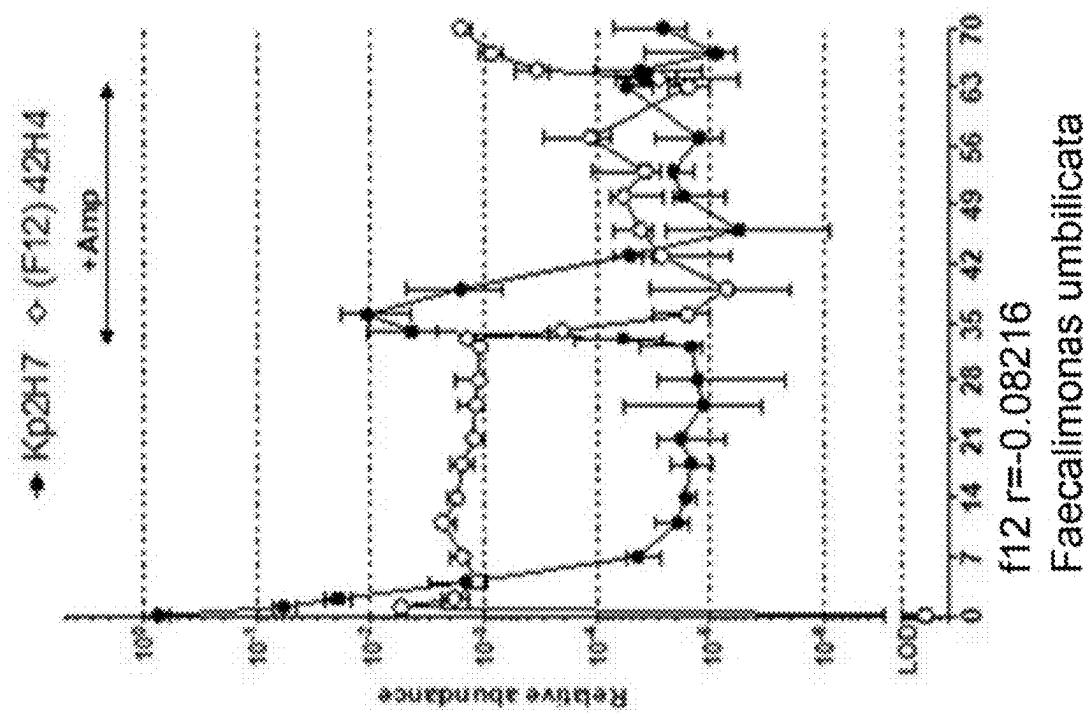


**FIG. 6C-4**

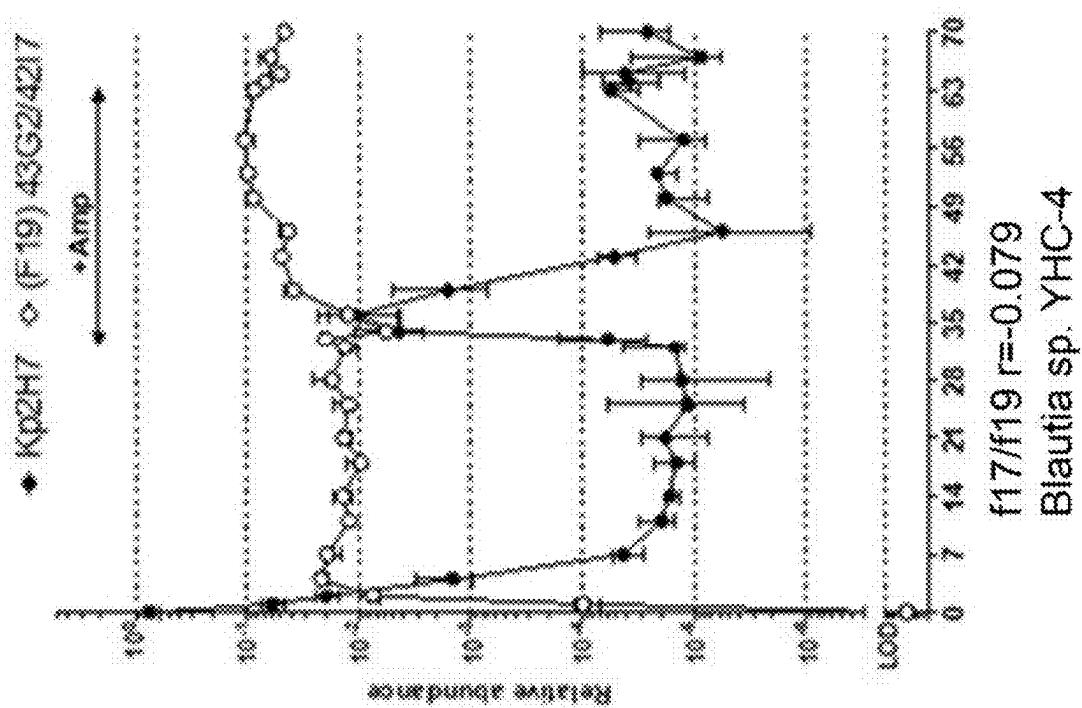


Erysipelotocidium ramosum  
f33  $r=0.08432$

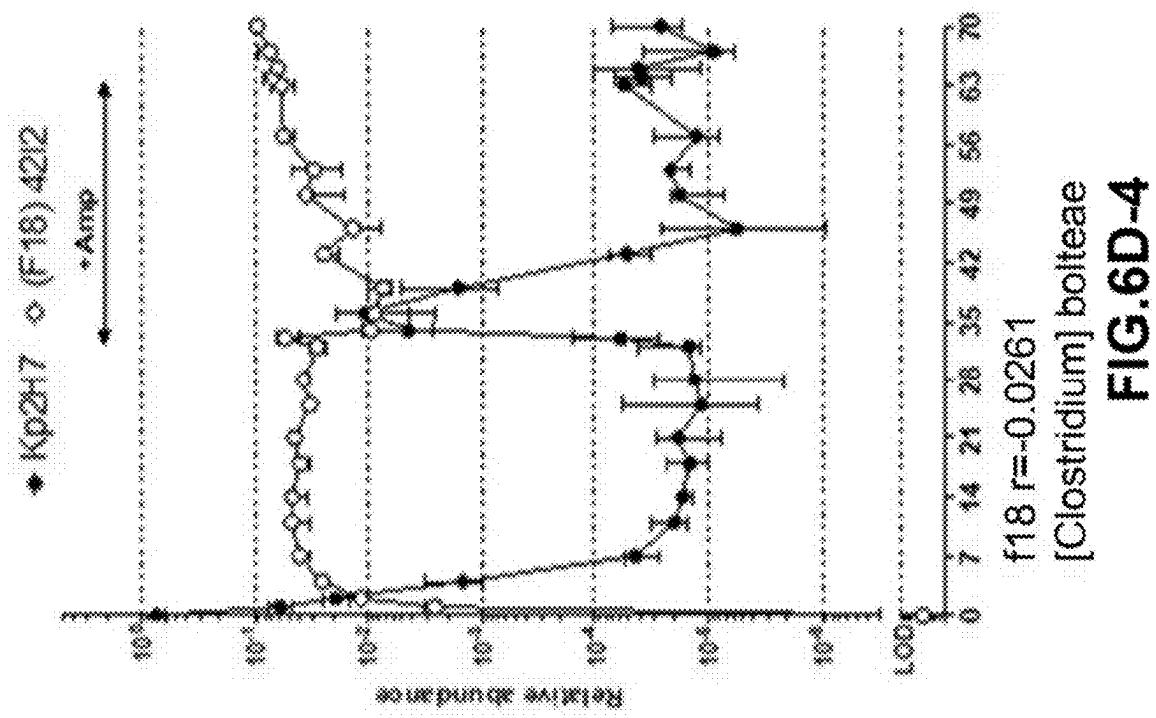
**FIG. 6D-1**

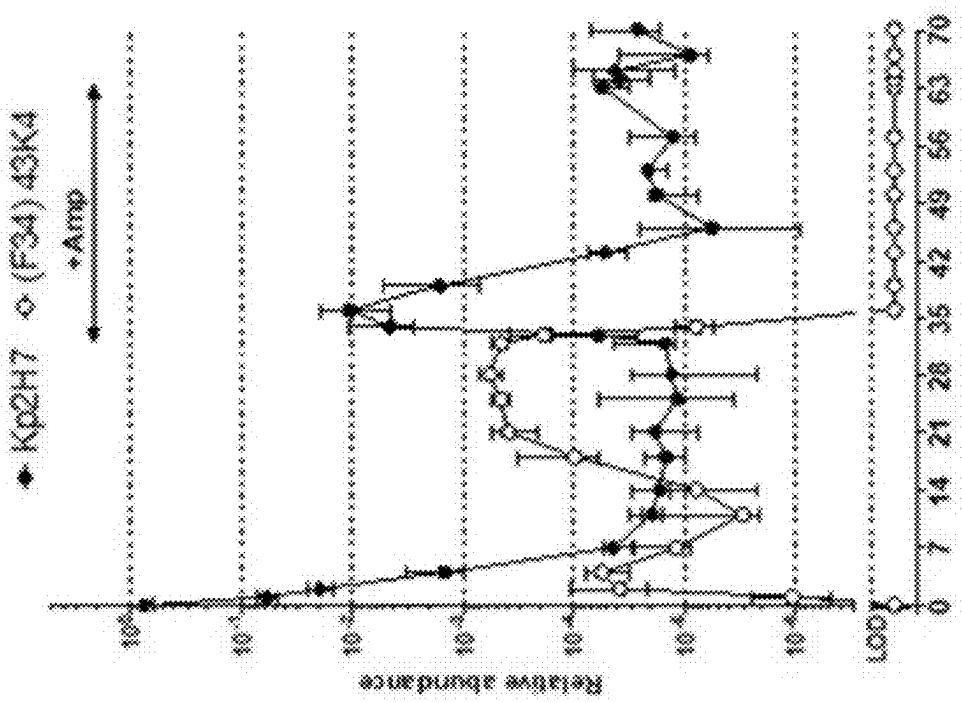


**FIG.6D-2**

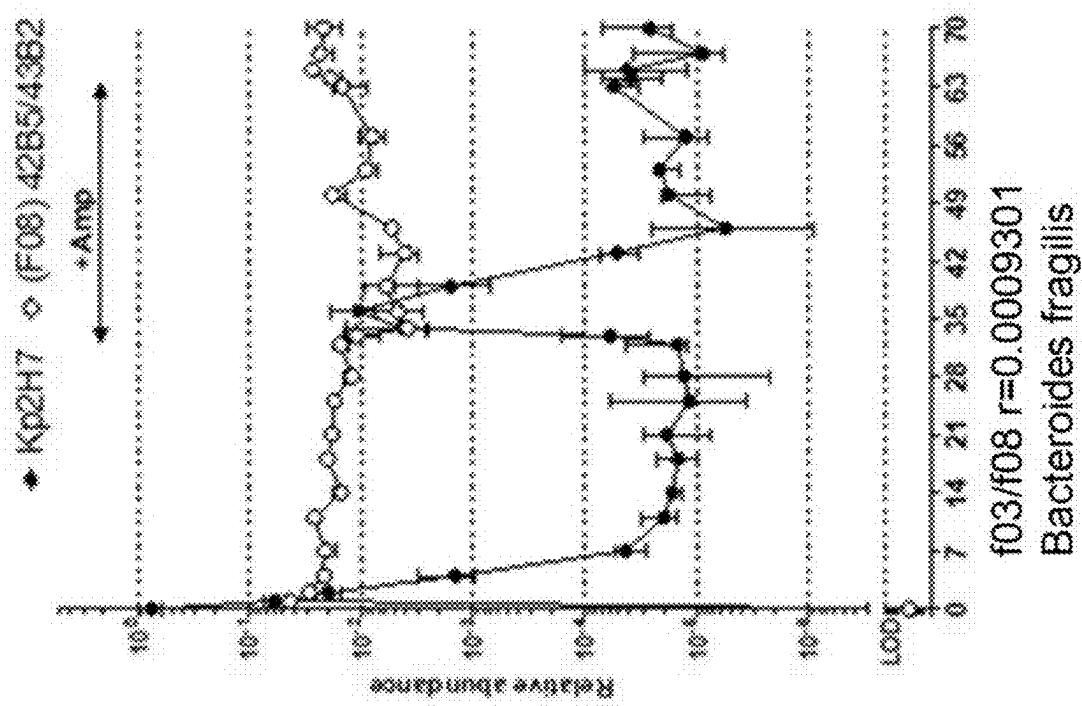


**FIG.6D-3**

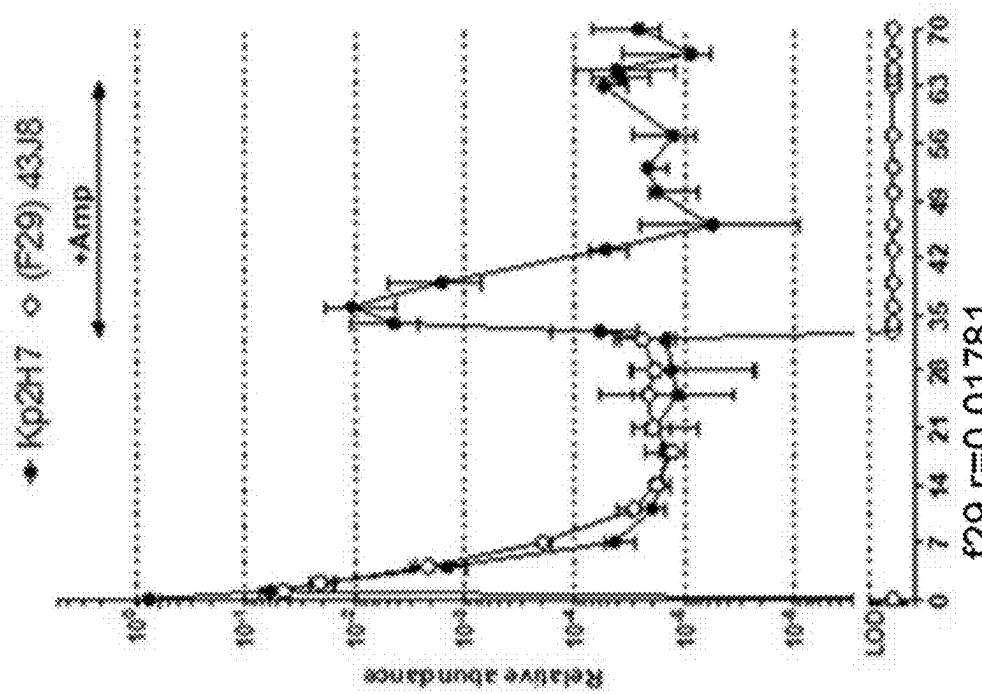




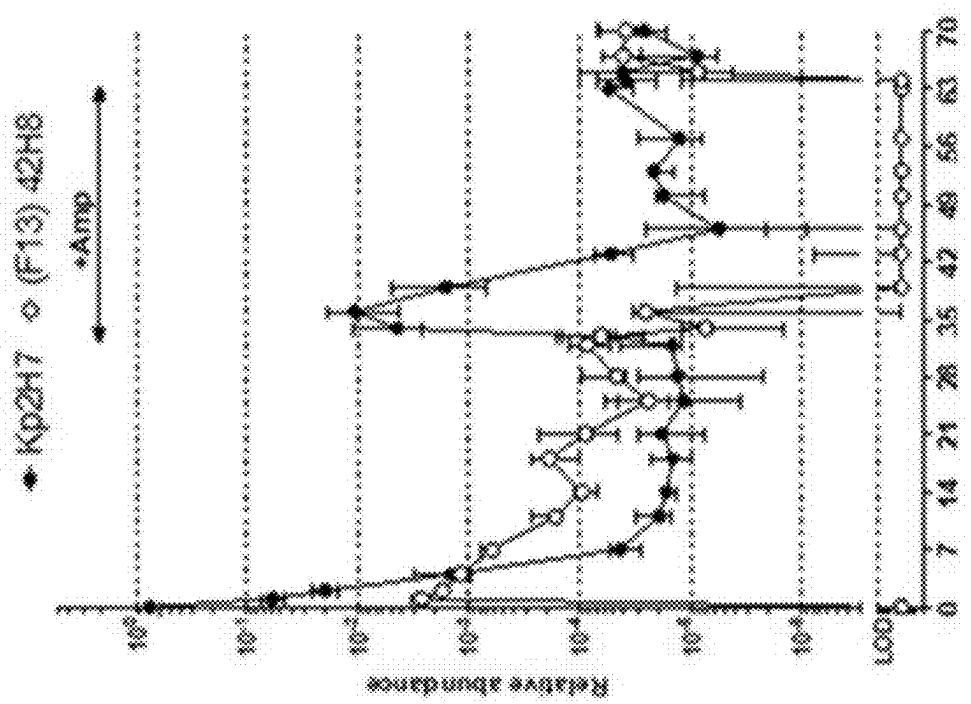
**FIG.6E-1**  
f34 r=-0.02255  
*Veillonella* sp. 6\_1\_27



**FIG. 6E-2**

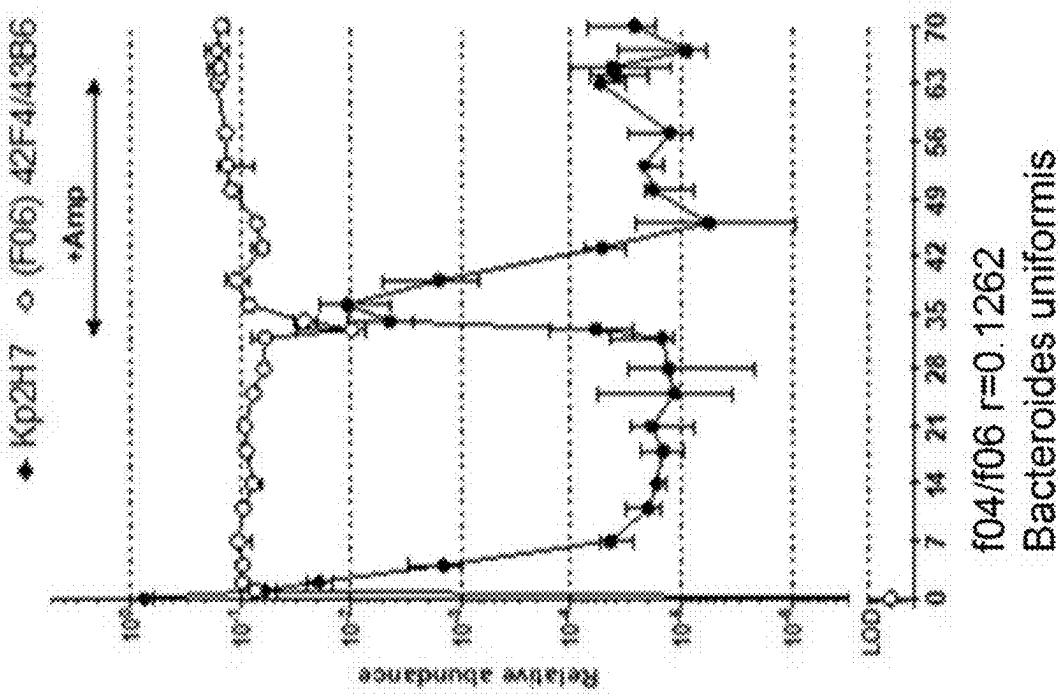


**FIG. 6E-3**



f13 r=0.1134  
Clostridium sp. M62/1

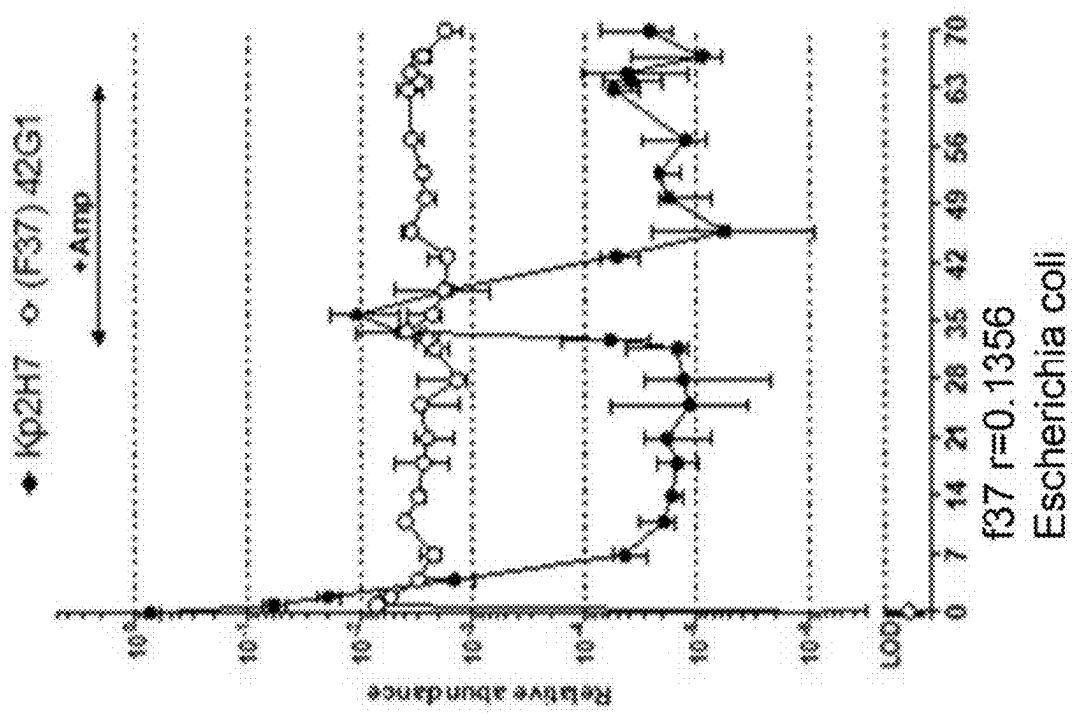
**FIG. 6E-4**



**FIG. 6F-1**

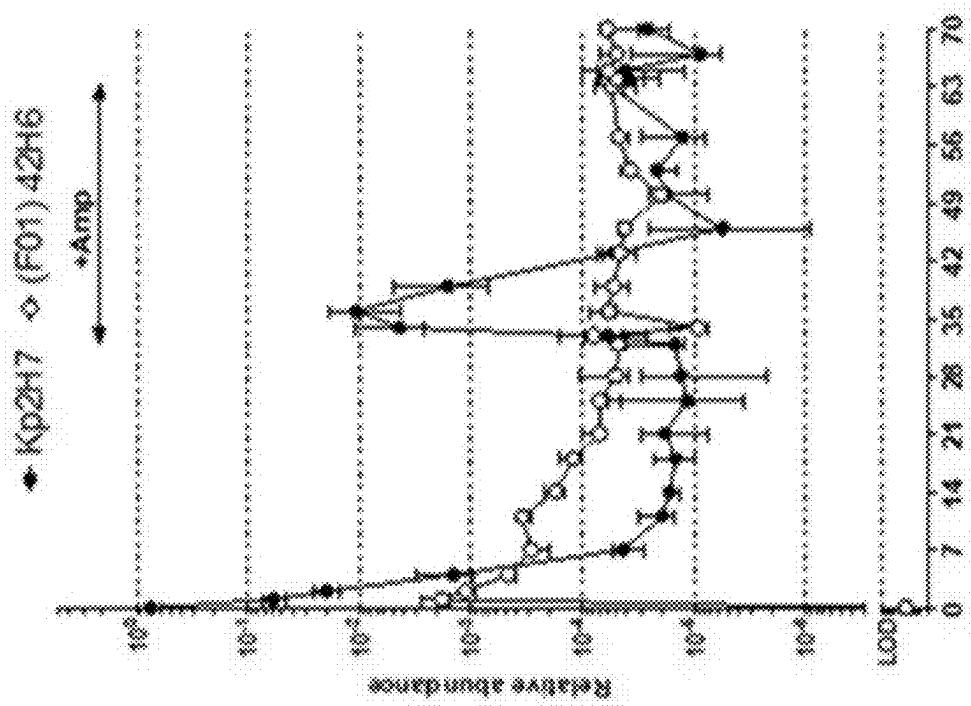
$f_04/f_06 = 0.1262$

*Bacteroides uniformis*



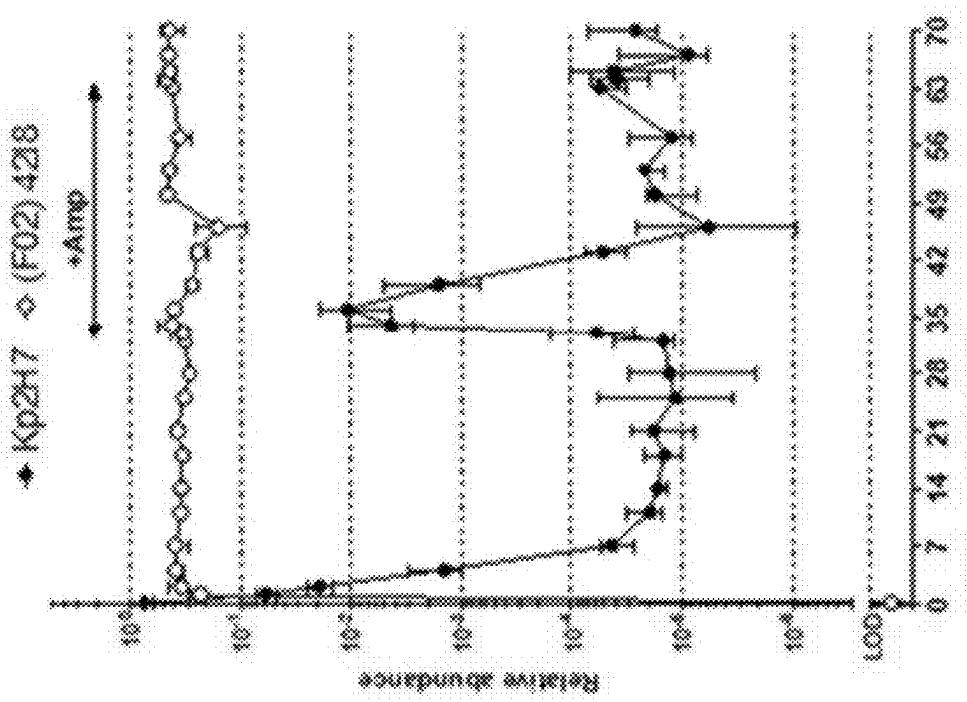
**FIG.6F-2**

f37 r=0.1356  
Escherichia coli



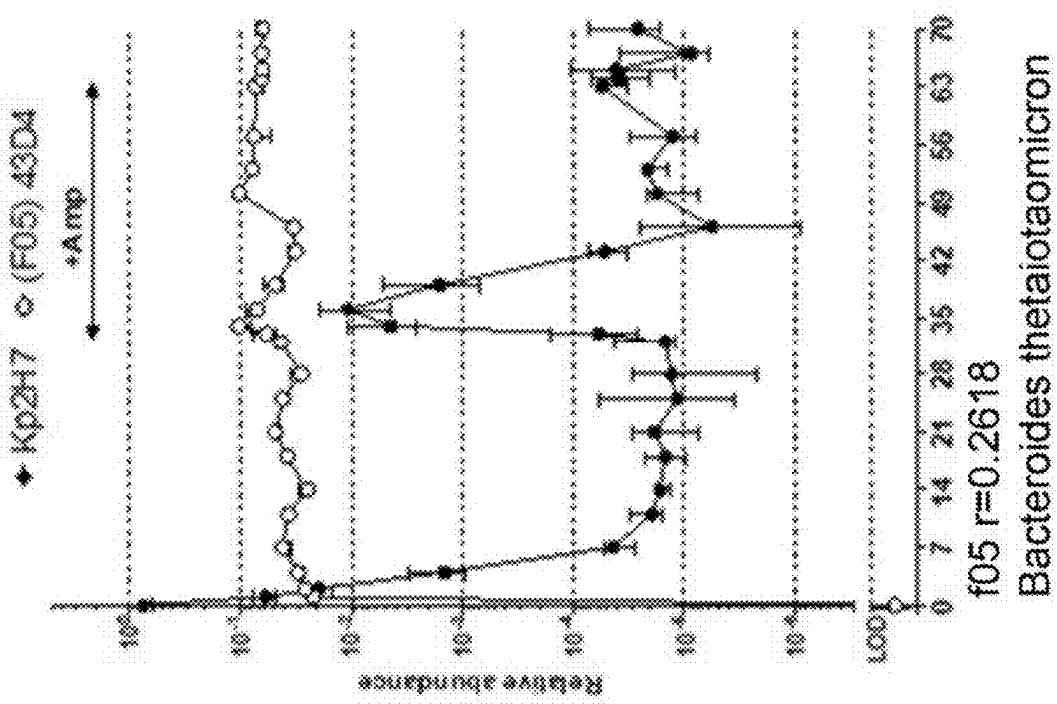
f01  $r=0.1671$   
*Bifidobacterium longum*

**FIG. 6F-3**



f02 r=0.2418  
Bacteroides xyloisolvans

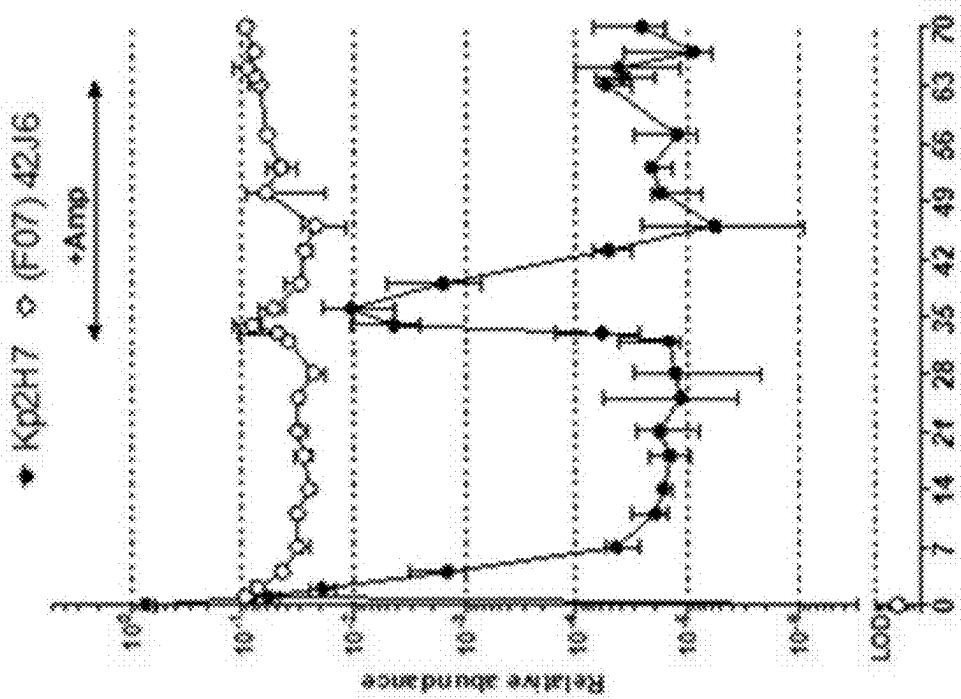
FIG. 6F-4



**FIG.6G-1**

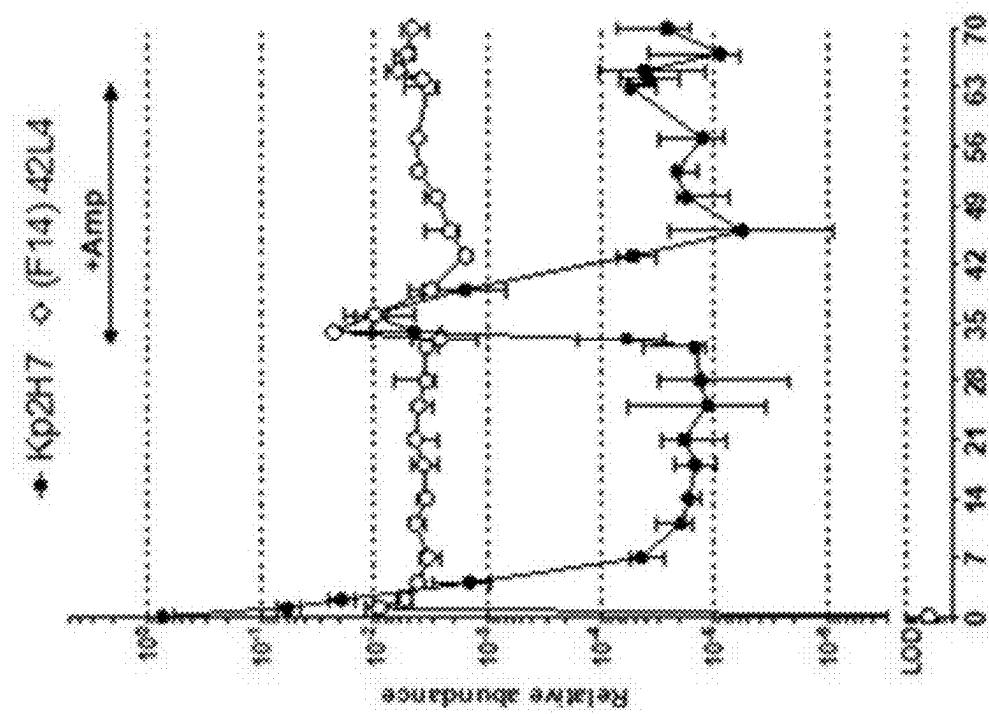
Bacteroides thetaiotaomicron

f05 r=0.2618



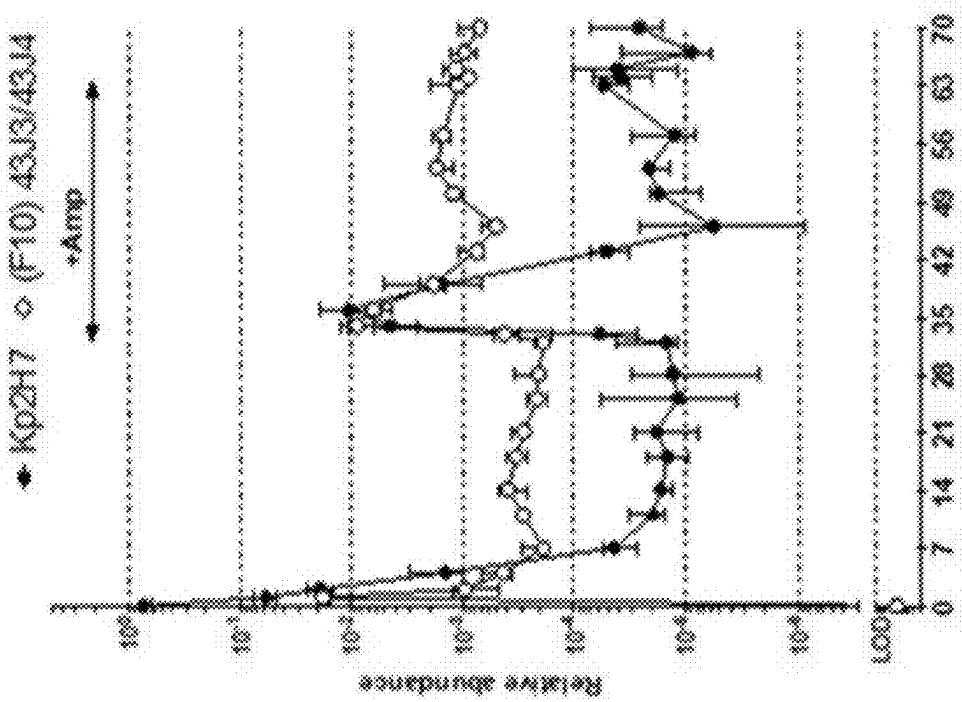
f07 r=0.3179  
Bacteroides sp. Smartlab 3302996

**FIG.6G-2**



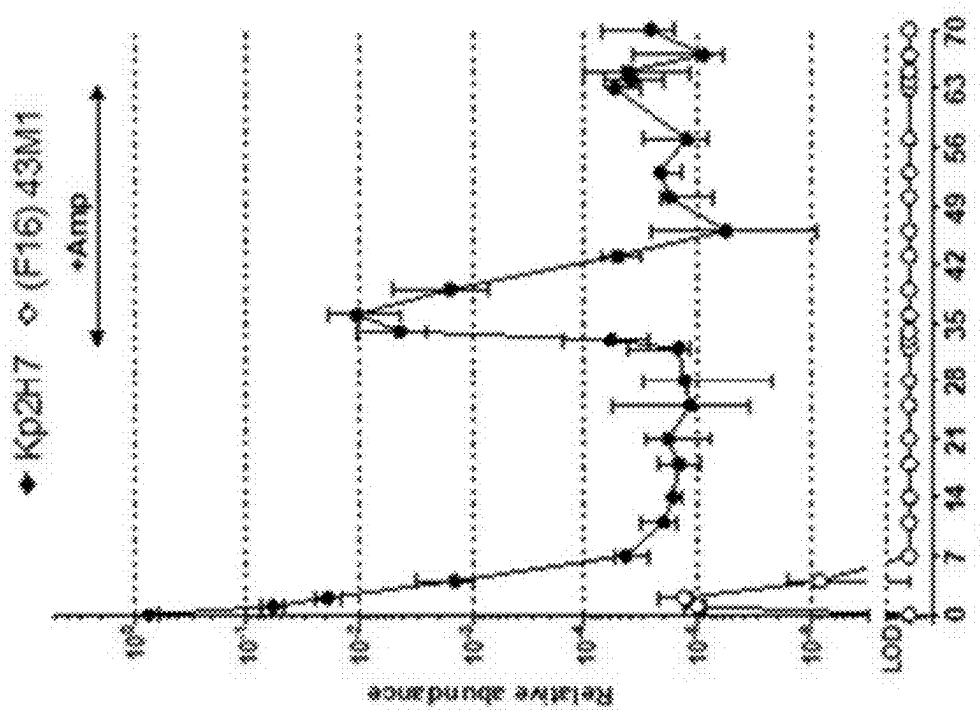
f14 r=0.451  
*Tyzzerella nexilis*

**FIG.6G-3**

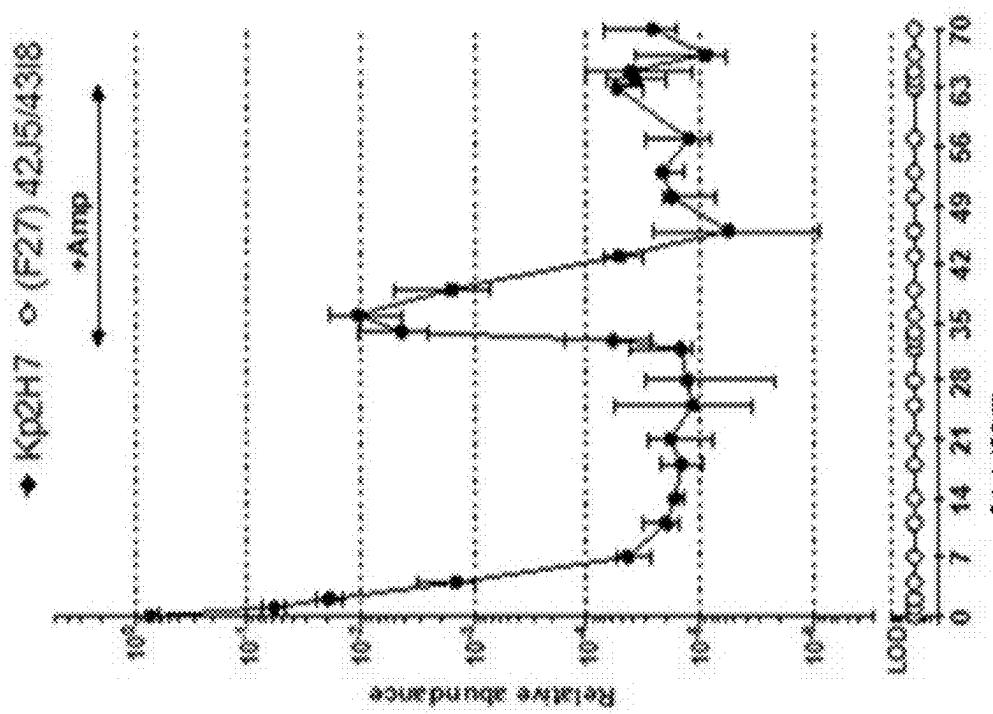


f10ff15 r=0.4664  
[Ruminococcus] gnavus

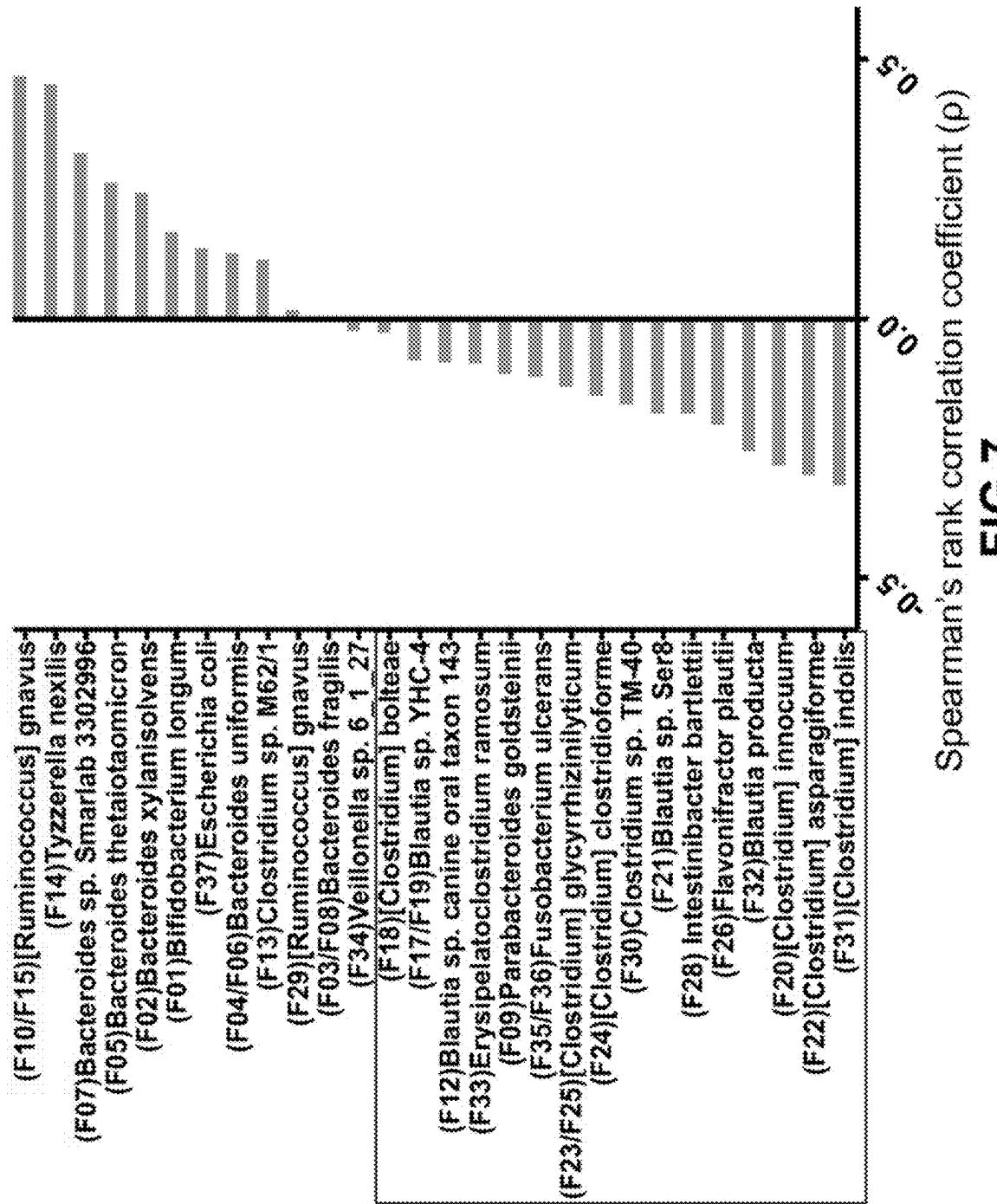
**FIG.6H-1**



**FIG.6H-2**  
Anaerostipes hadrus



Blautia wexlerae  
**FIG. 6H-3**



**FIG.7**

Spearman's rank correlation coefficient ( $\rho$ )

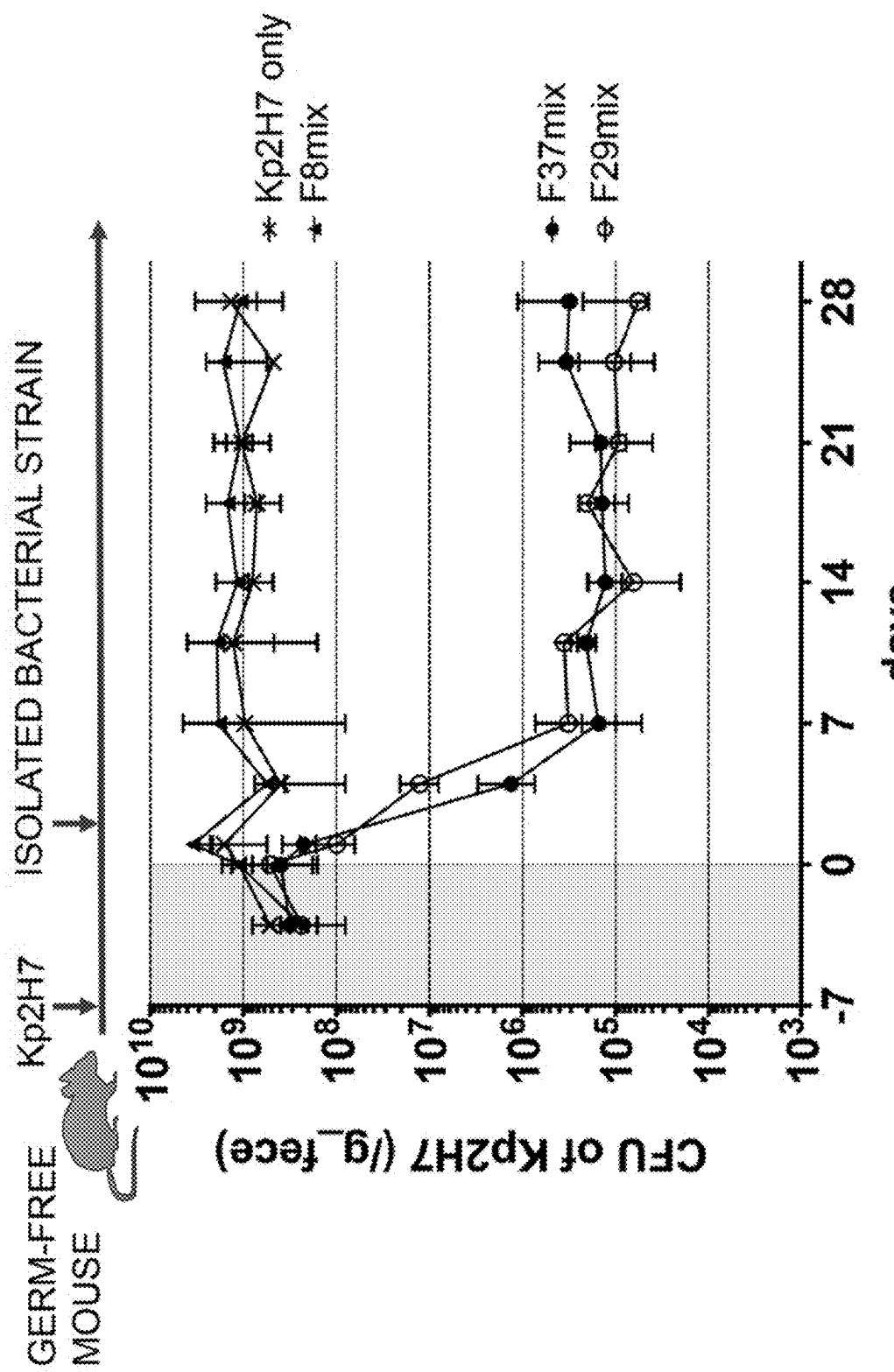
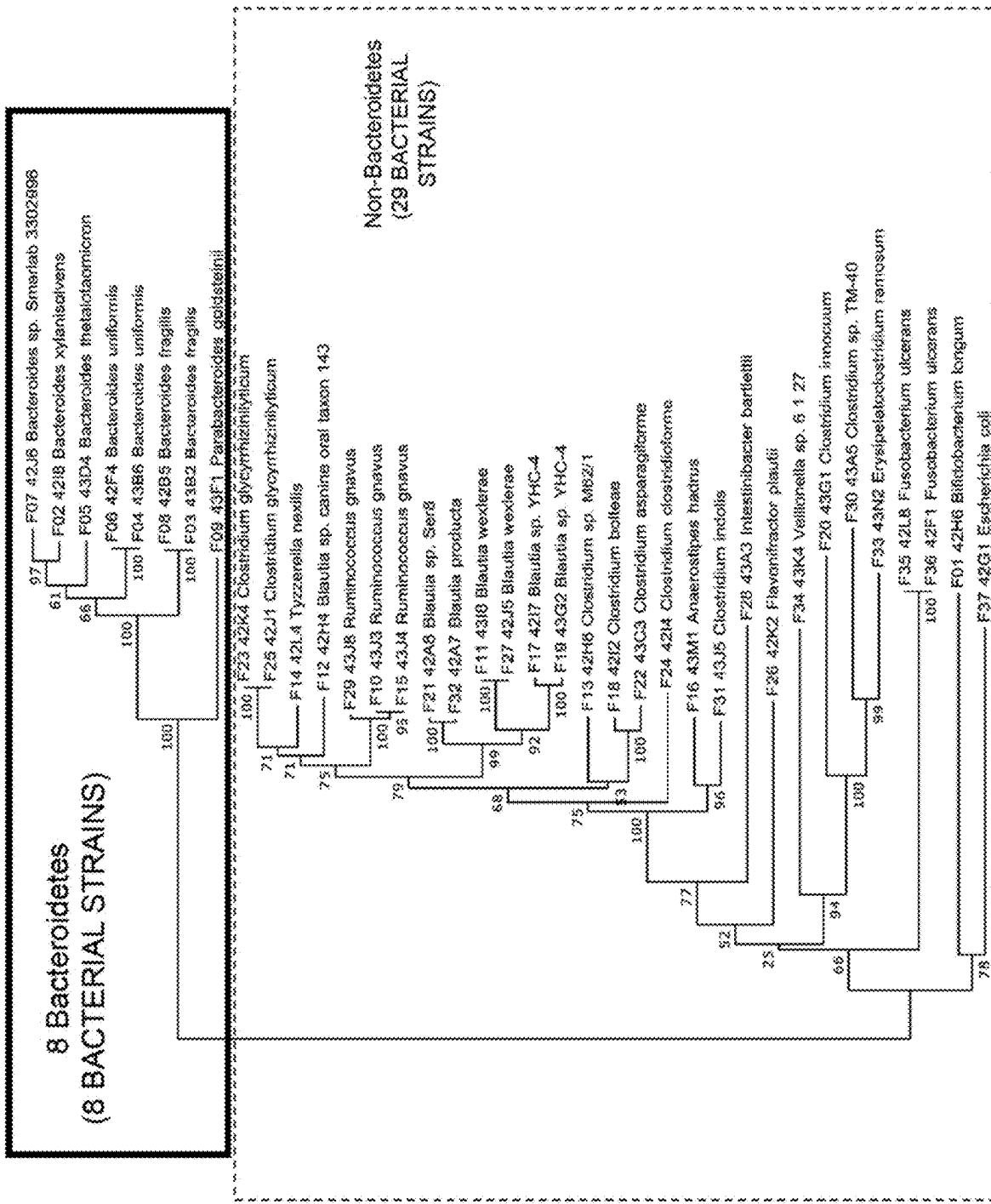


FIG. 8



**FIG.9**

F18 mix

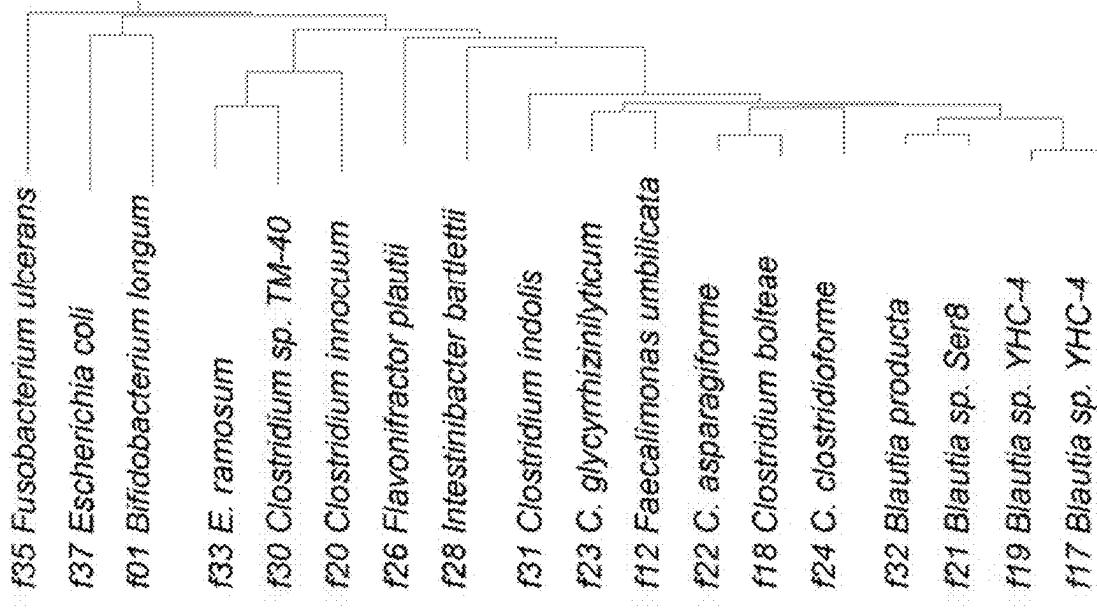
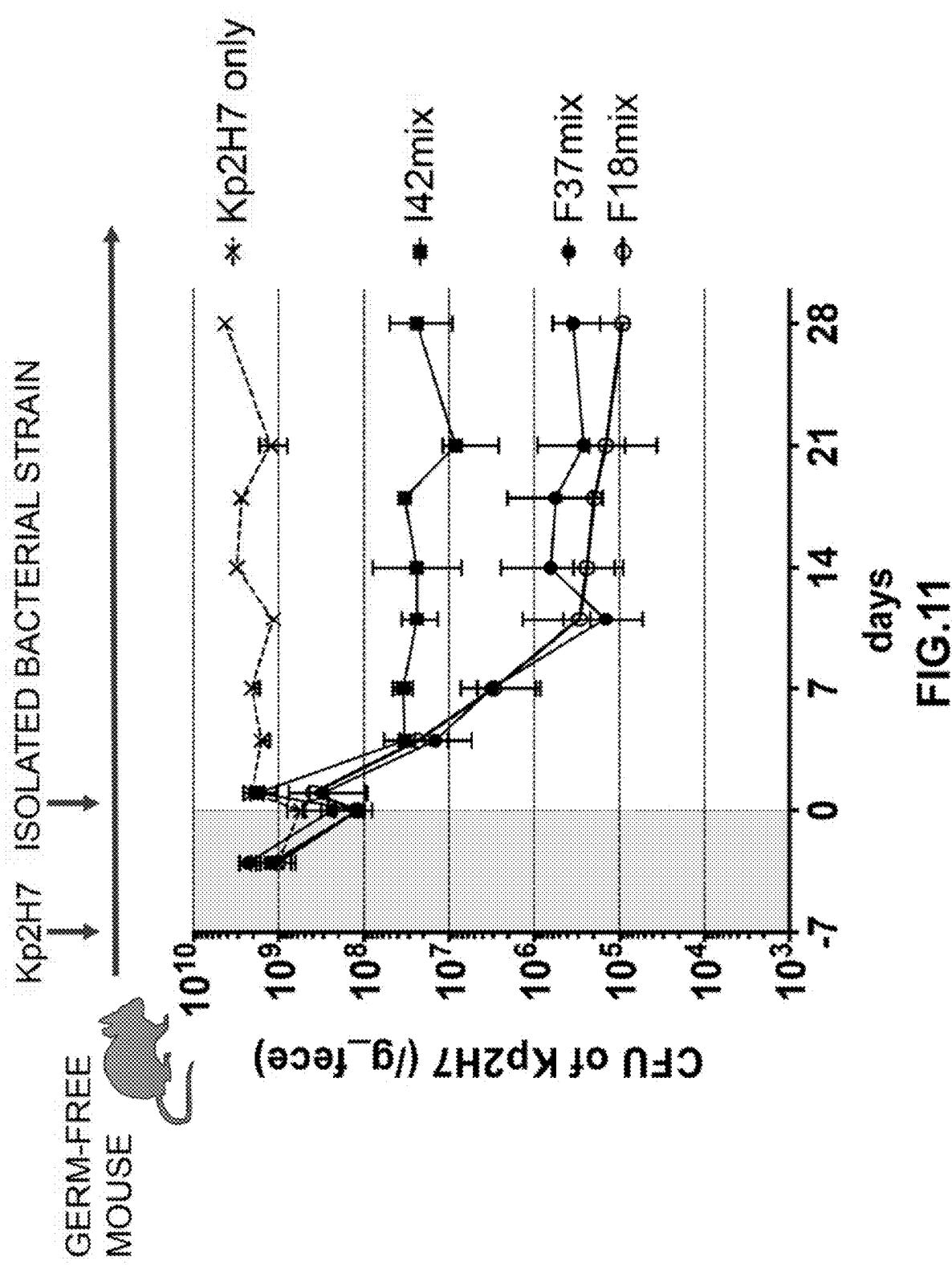


FIG.10



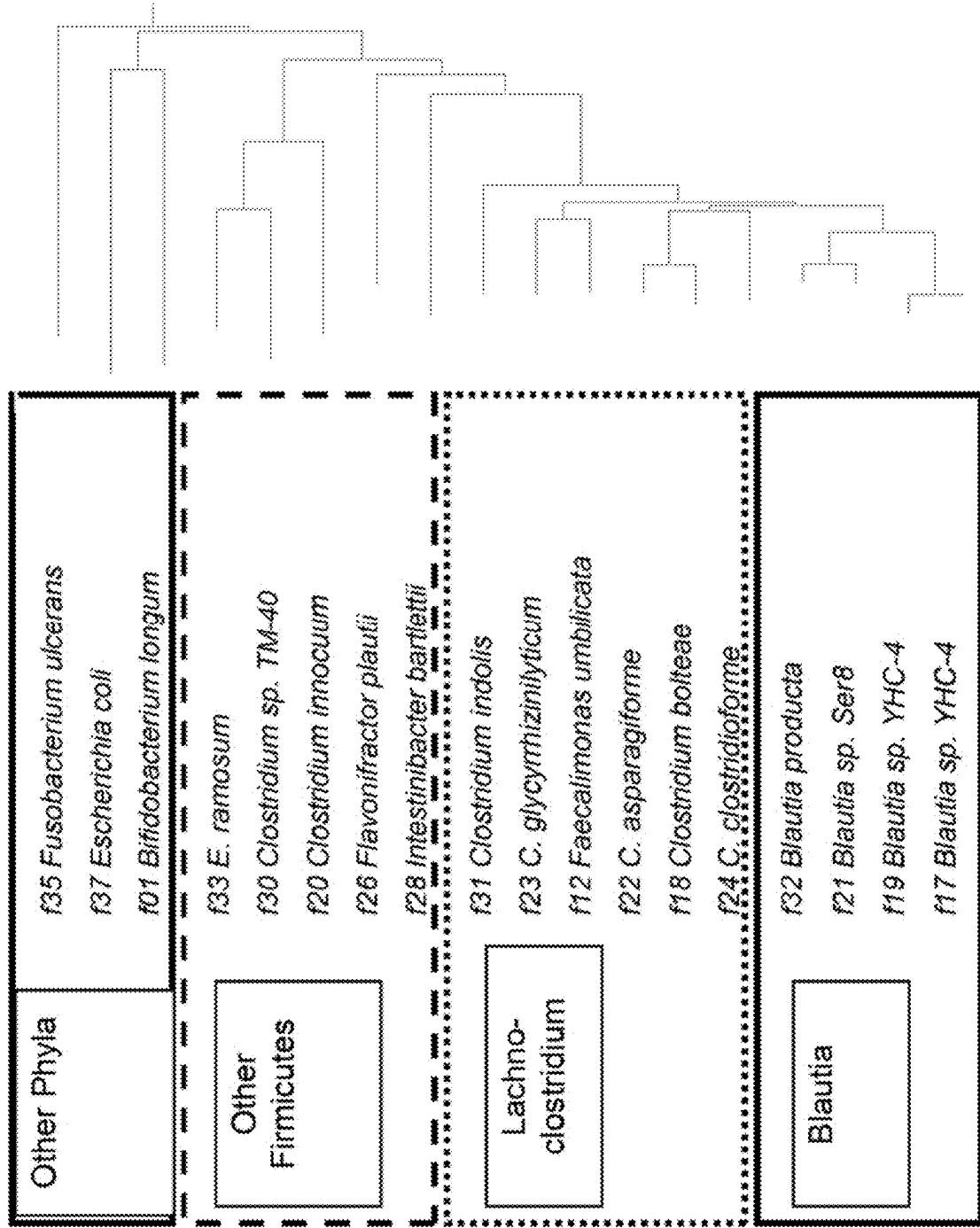


FIG.12

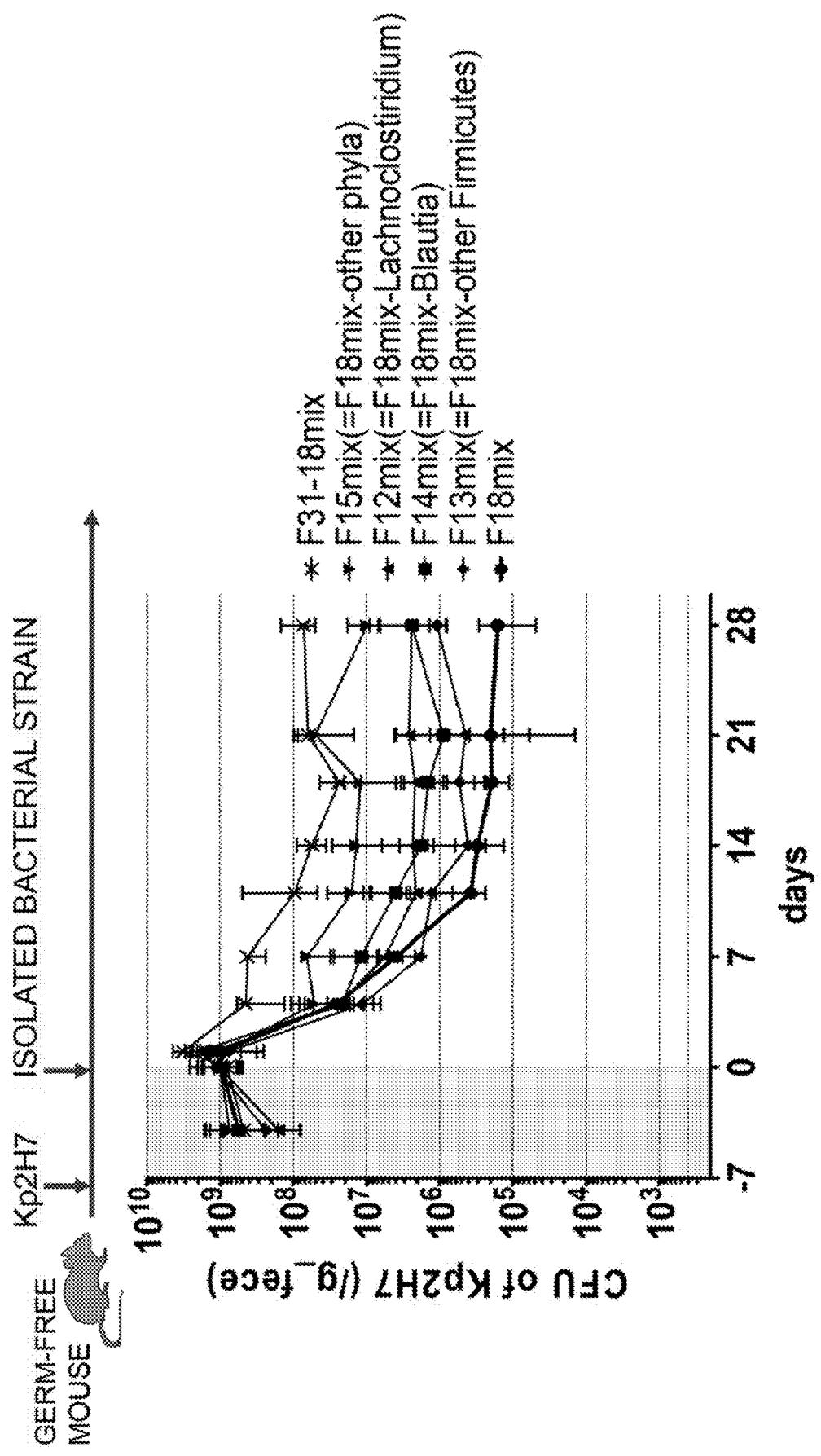
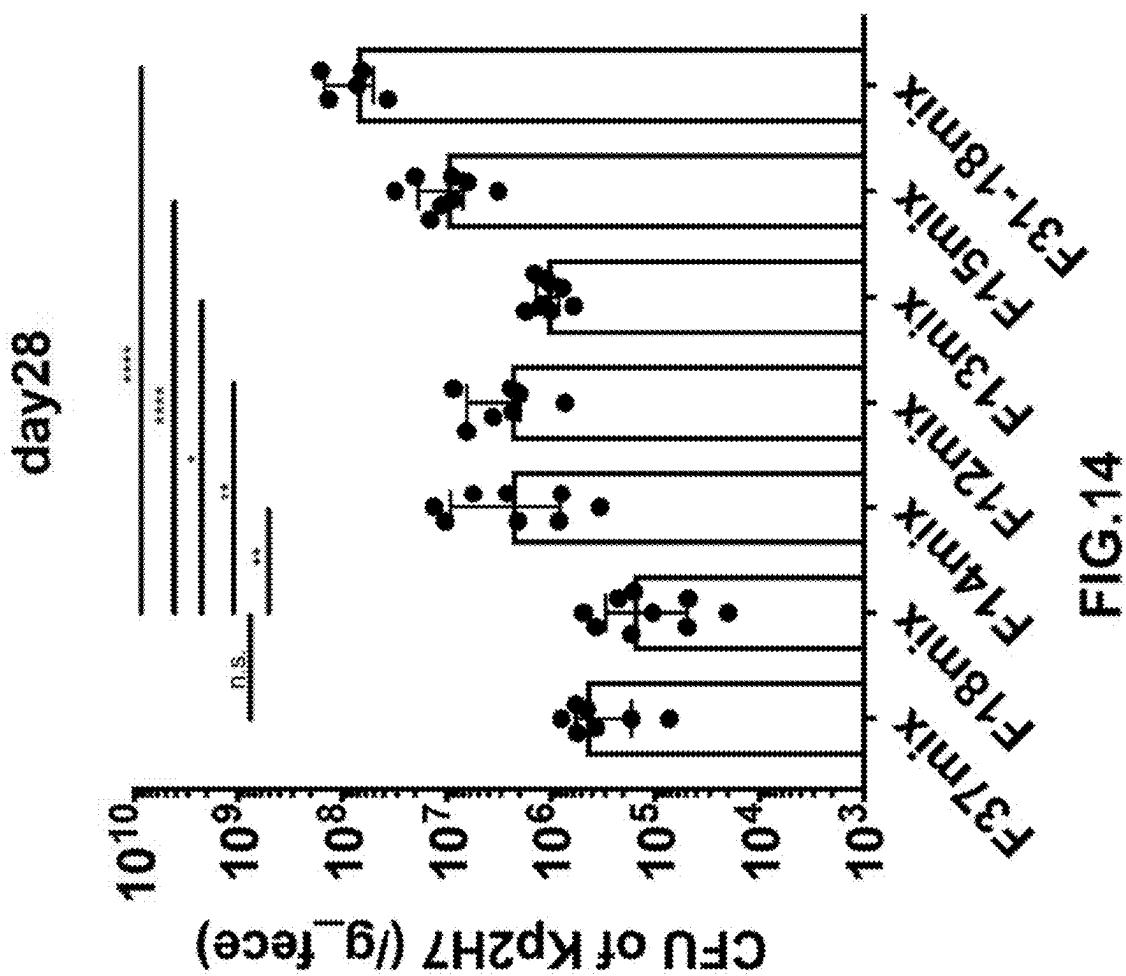
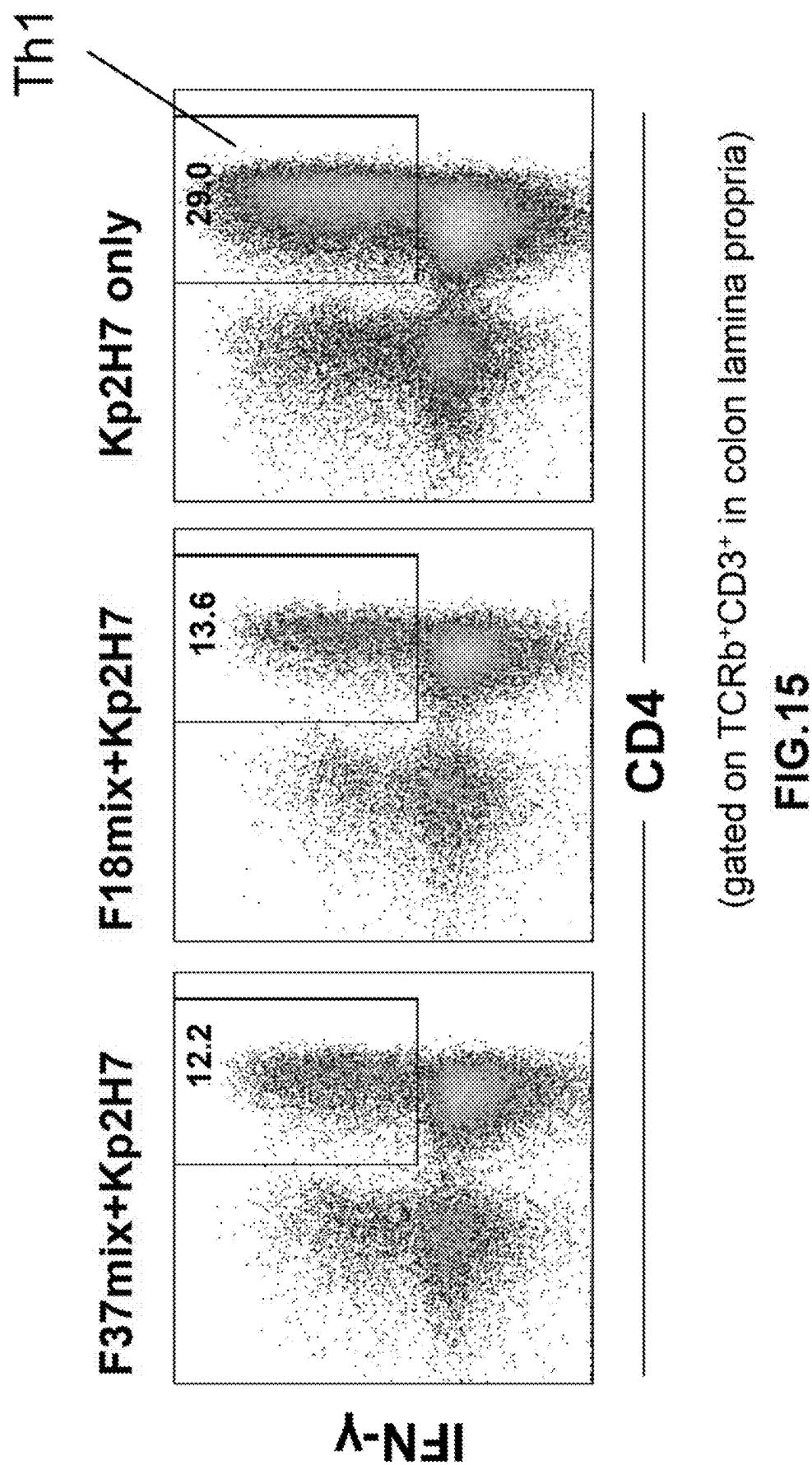


FIG.13





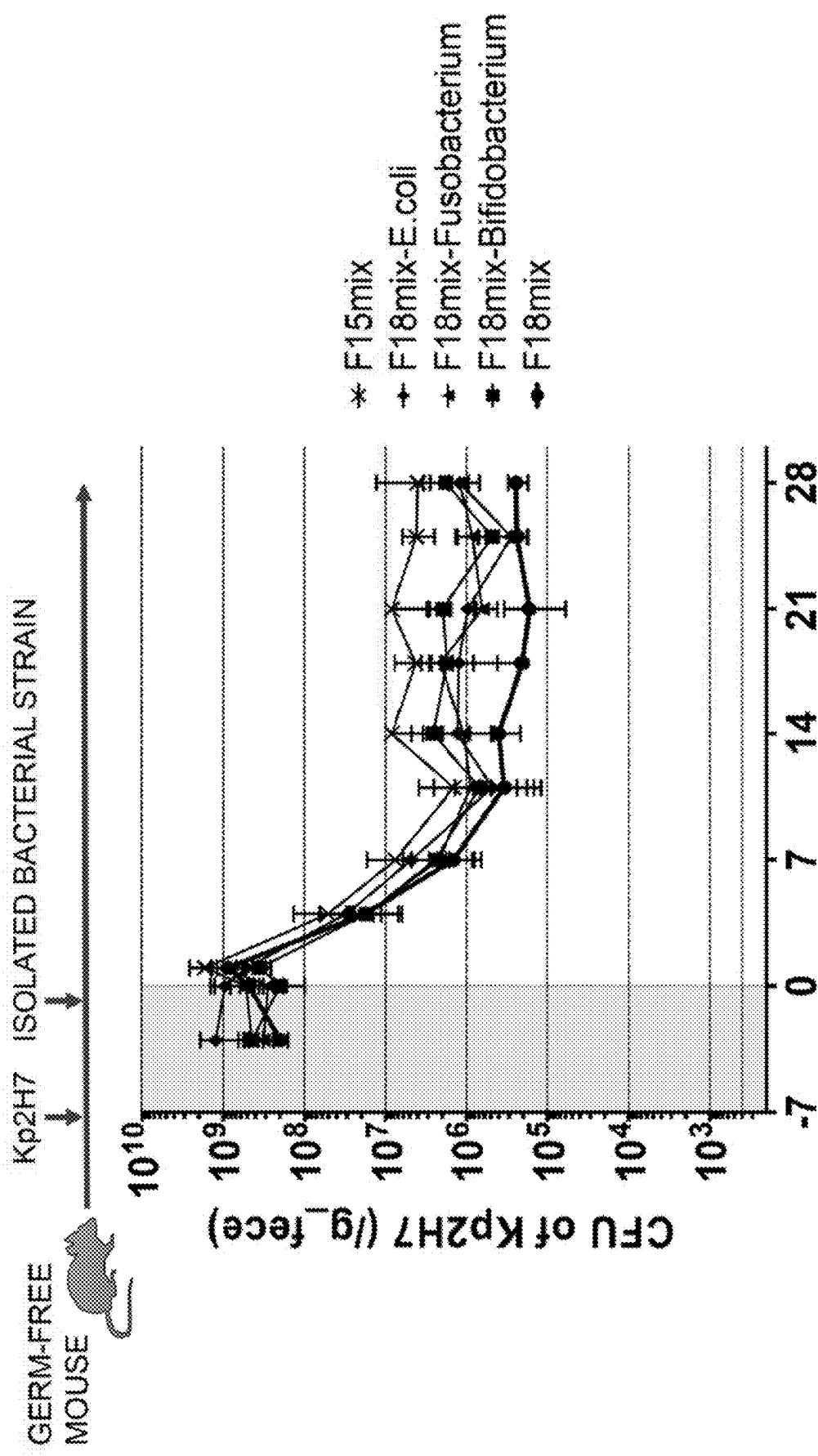


FIG. 16  
days

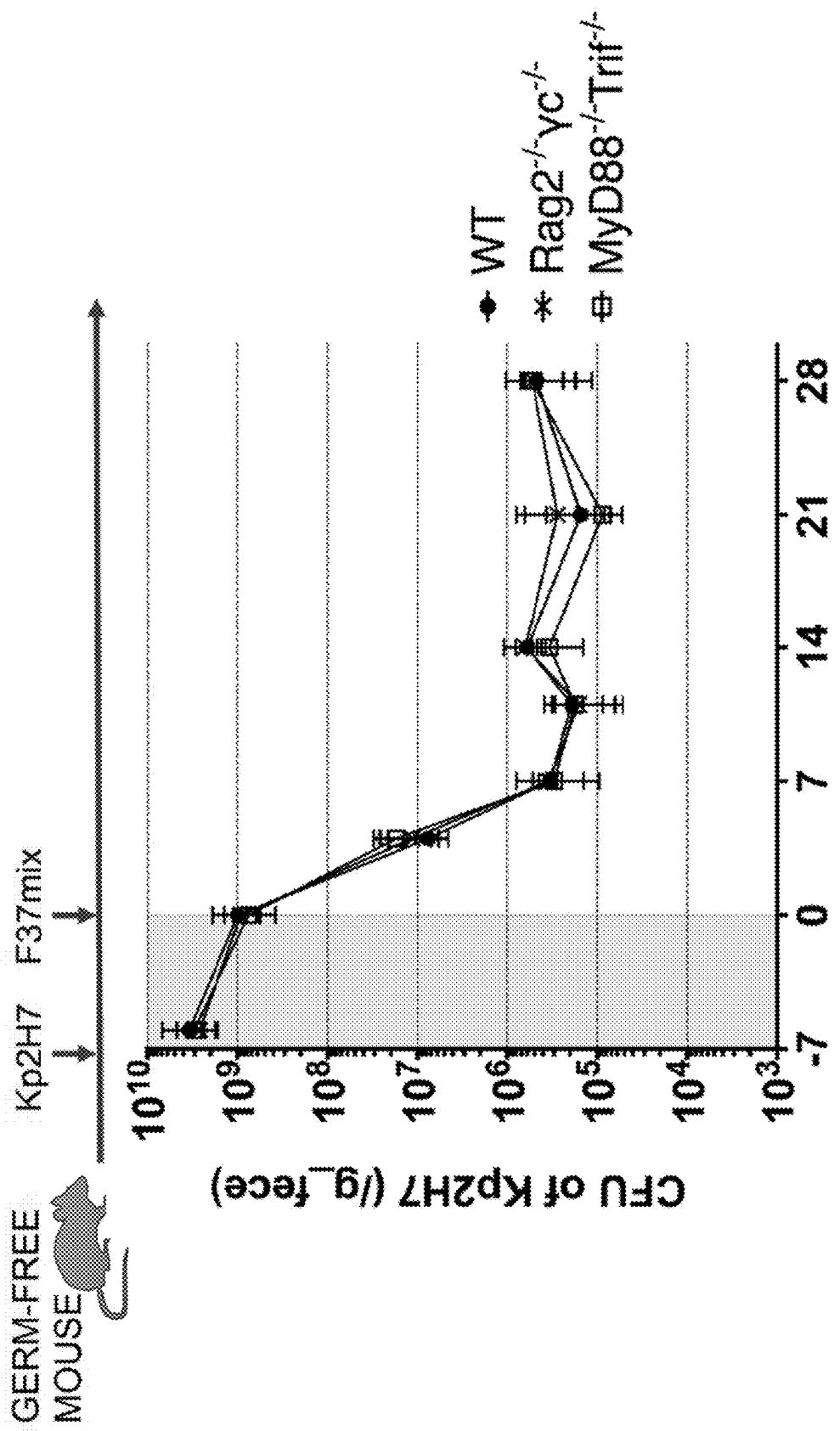


FIG. 17

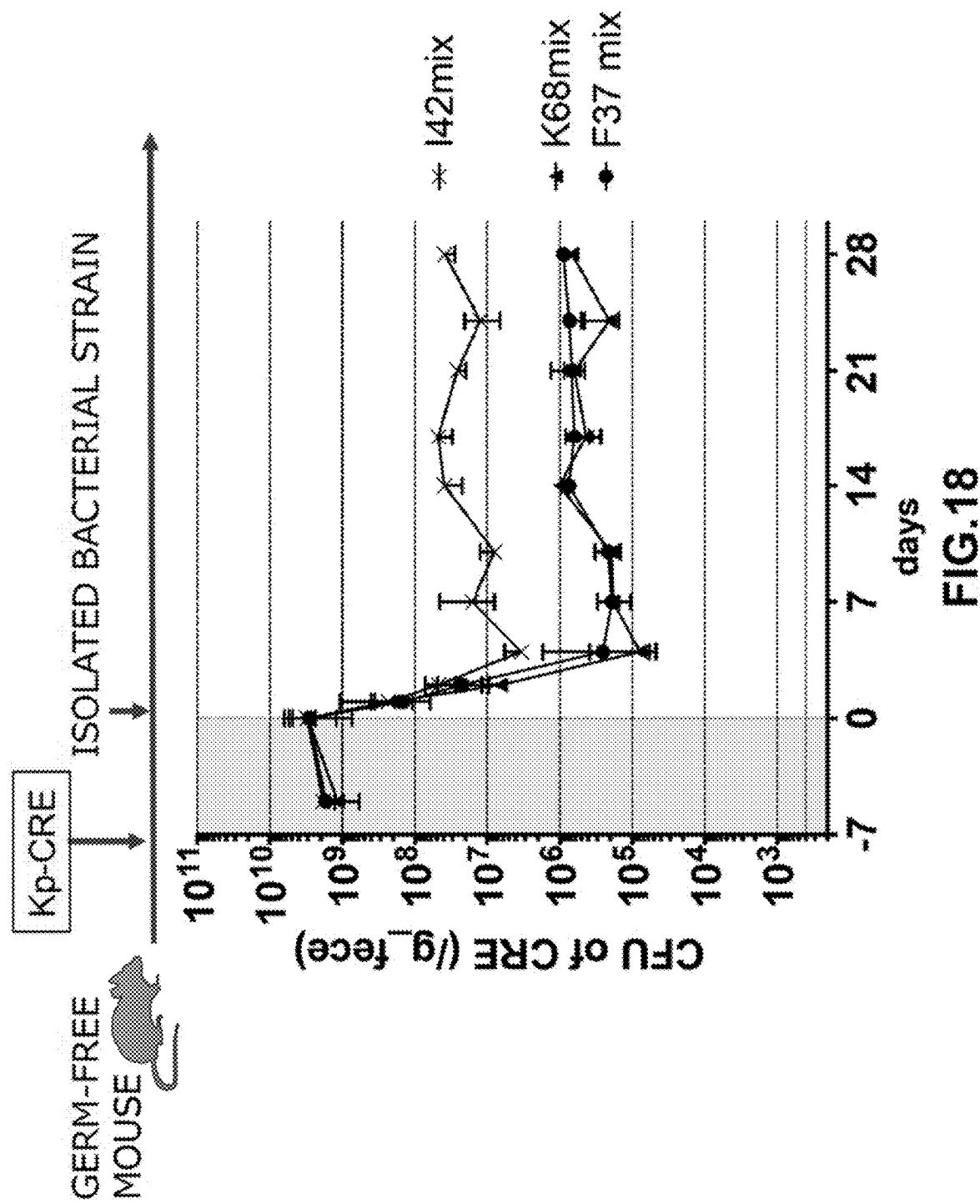
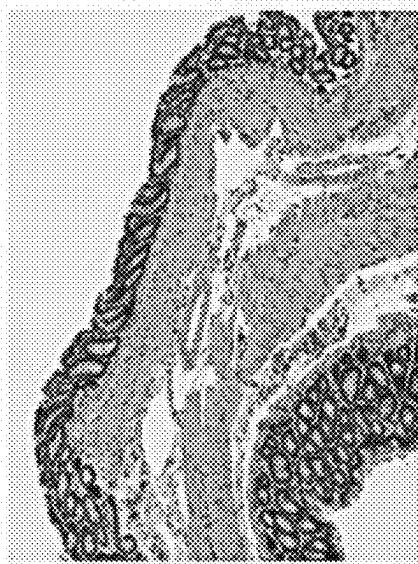


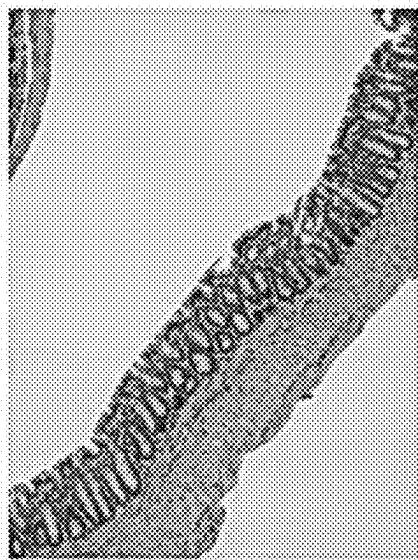
FIG. 18

Histology\_CRE

#2\_F37



#7\_K68



#10\_43

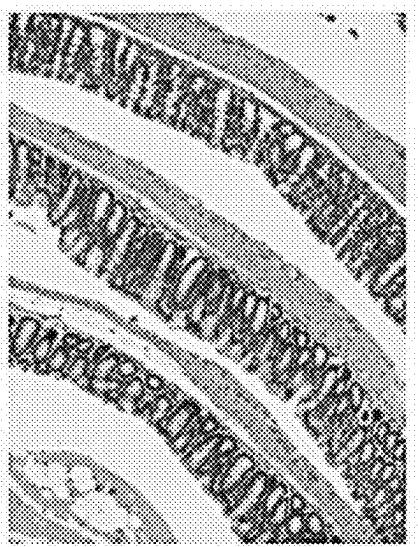
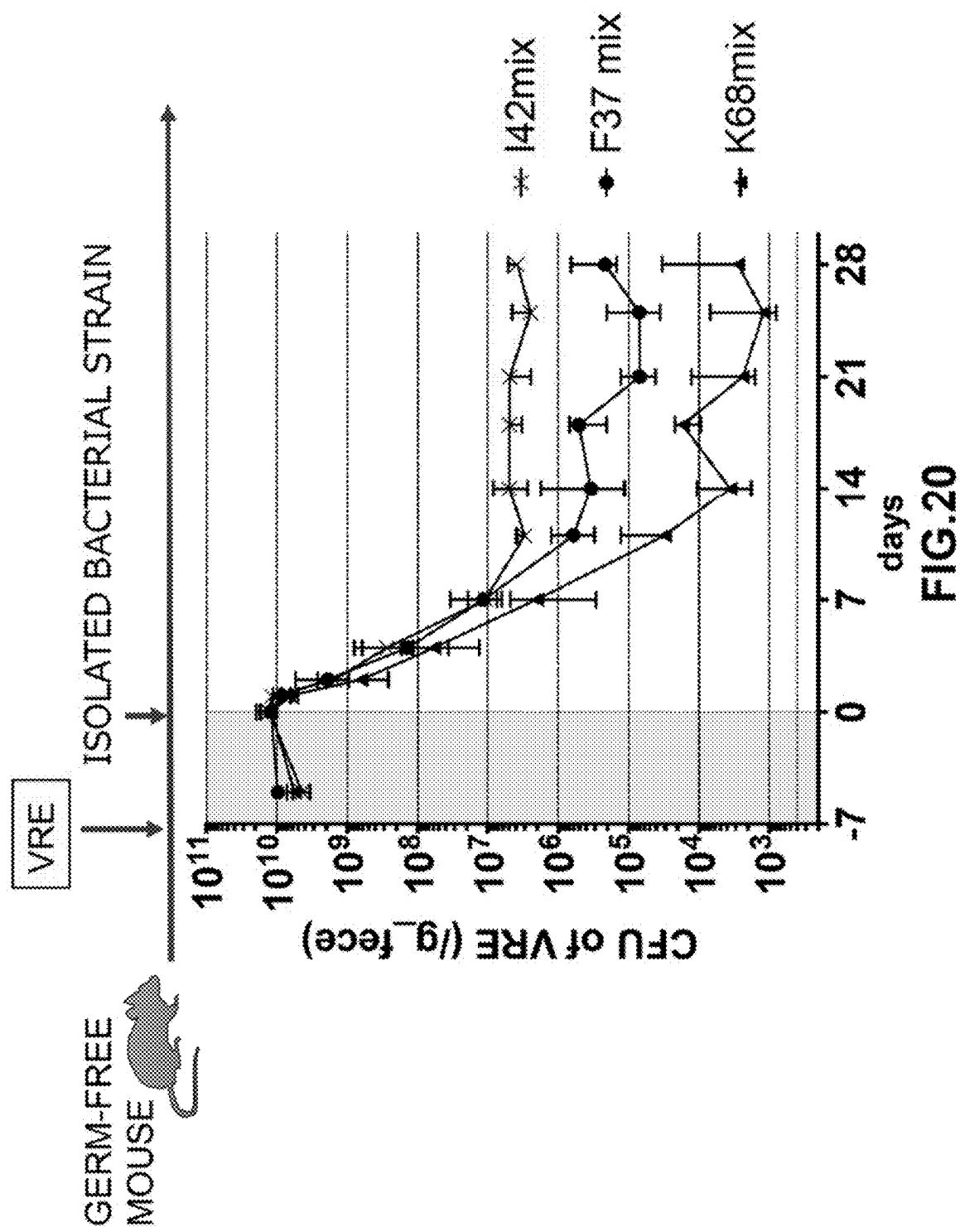


FIG.19



Histology\_VRE

#01\_F37

#19\_K68

#23\_I43

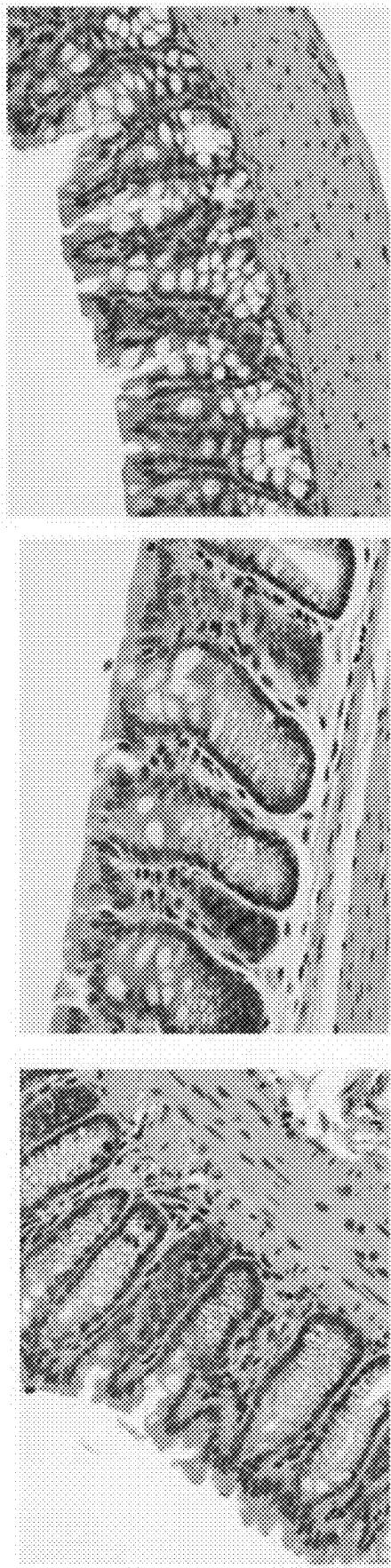
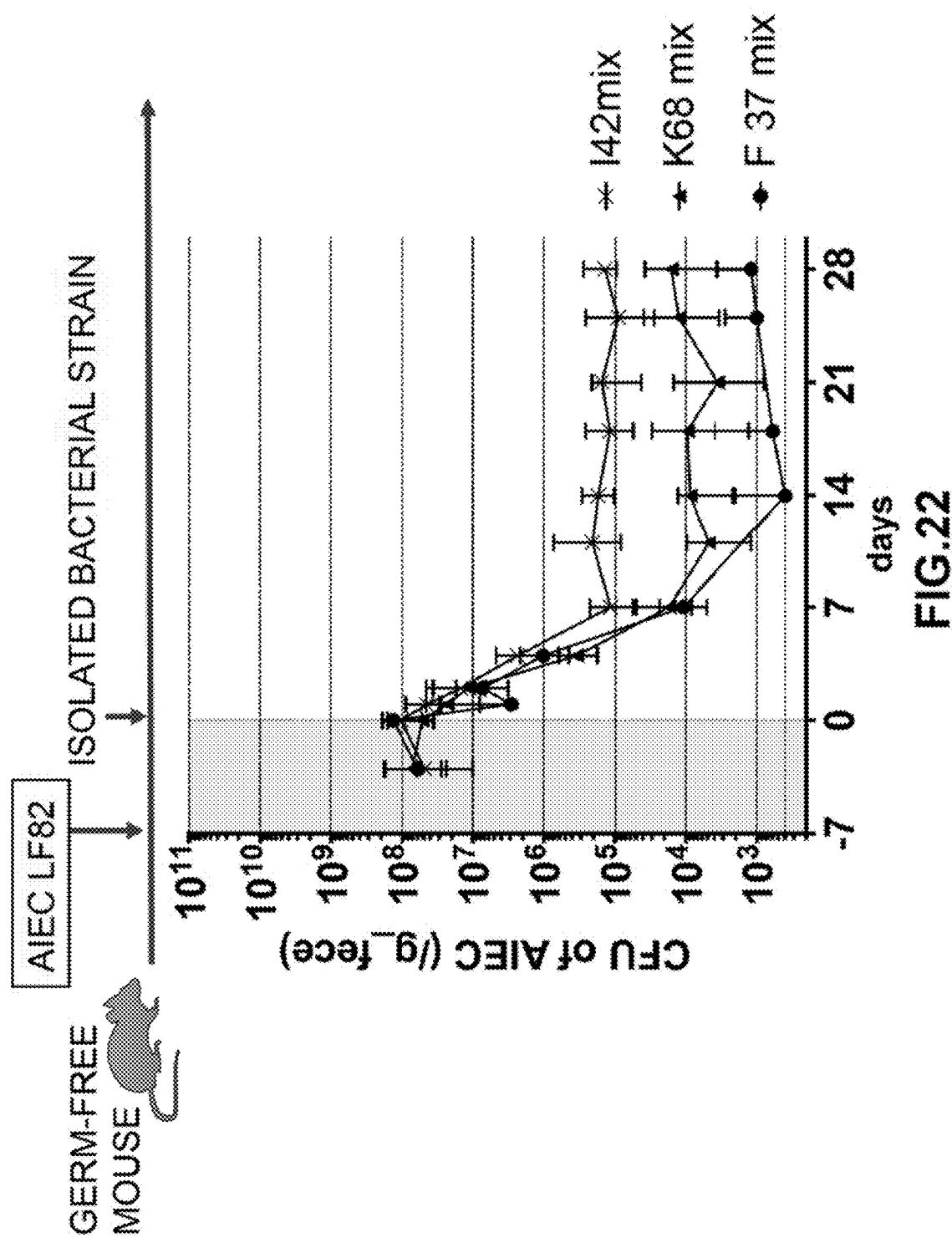


FIG.21



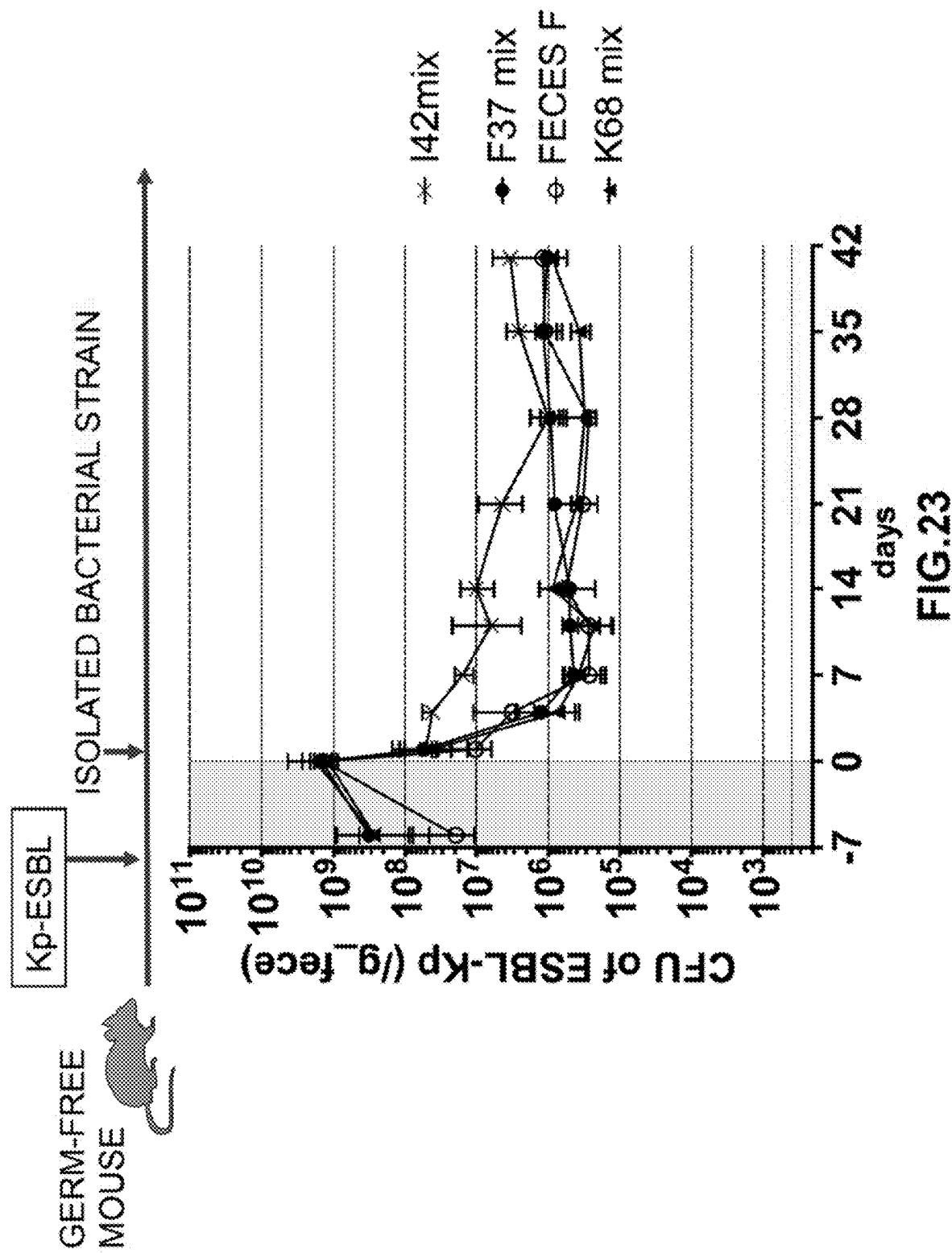


FIG.23

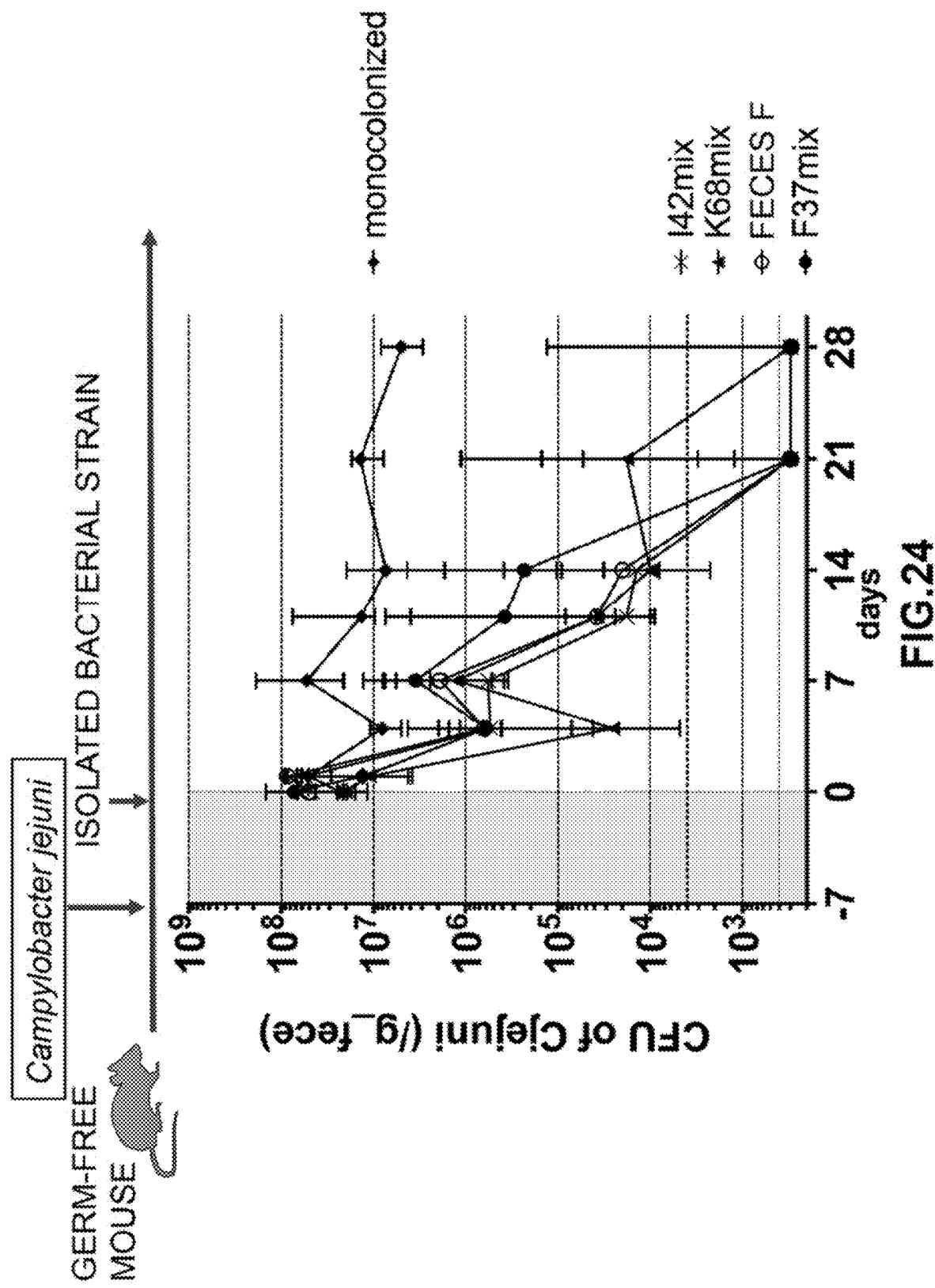


FIG.24

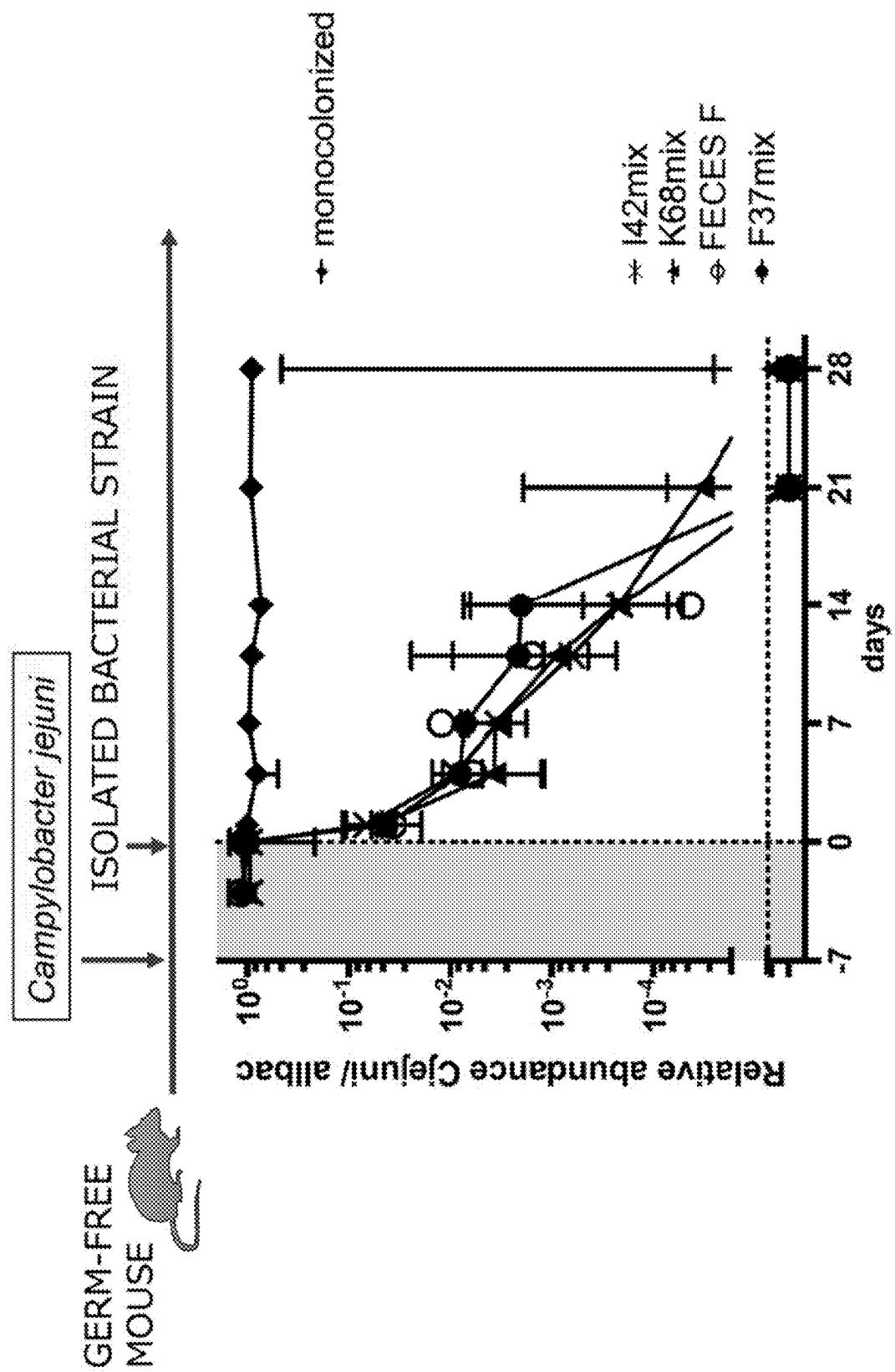


FIG.25

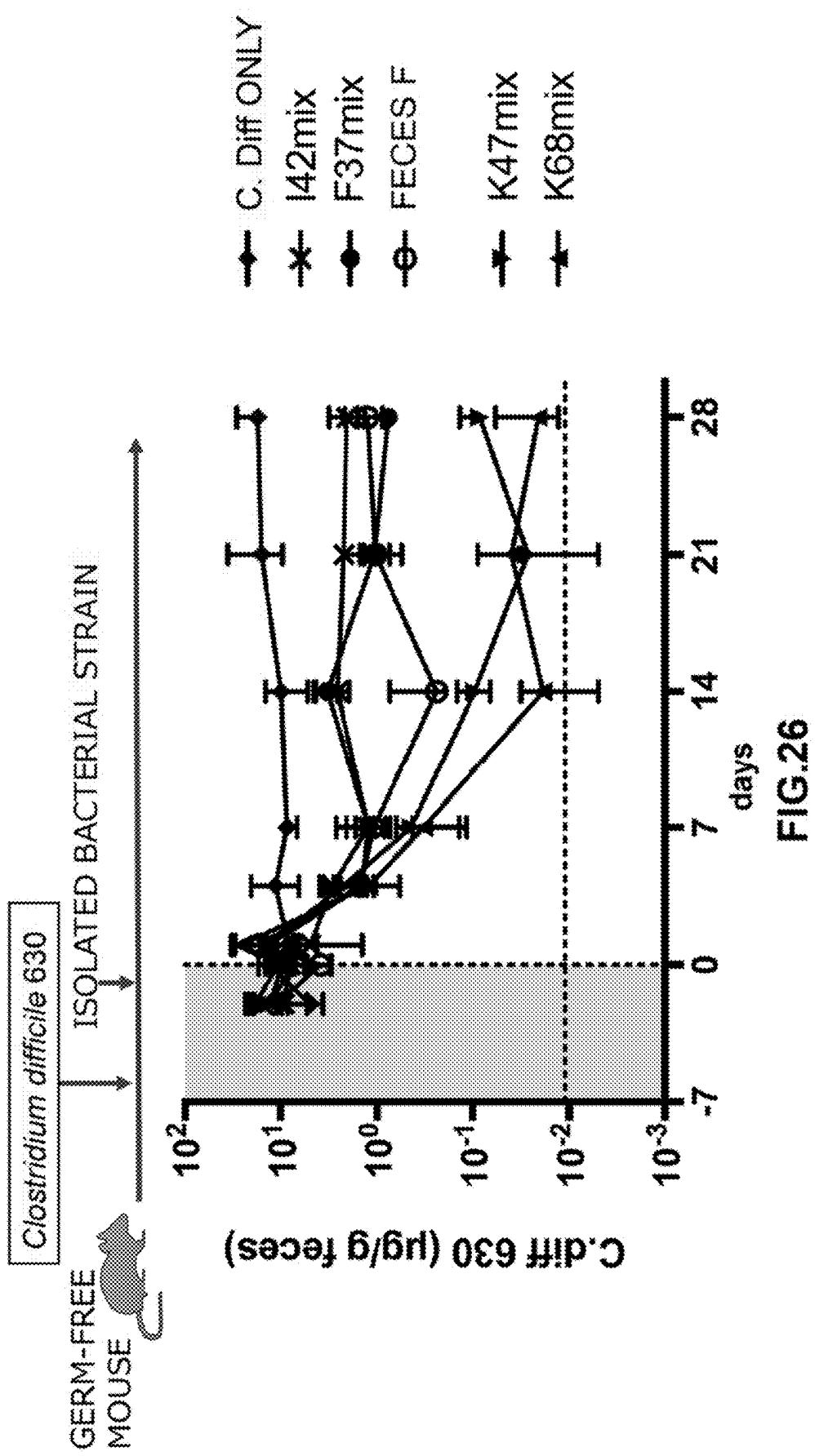


FIG.26

## ANTIBACTERIAL COMPOSITION AGAINST DRUG-RESISTANT BACTERIA OR PRO-INFLAMMATORY BACTERIA

### CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a Divisional of U.S. application Ser. No. 17/436,148, filed on Sep. 3, 2021, which is a National Stage of International Application No. PCT/JP2020/009423, filed on Mar. 5, 2020, which claims priority from U.S. Provisional Application No. 62/815,101, filed on Mar. 7, 2019, the contents of all of which are incorporated herein by reference in their entireties.

### INCORPORATION BY REFERENCE OF SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been filed electronically in xml format and is hereby incorporated by reference in its entirety. Said xml copy, created on Apr. 16, 2025, is named Q306447.xml and is 506,119 bytes in size.

### TECHNICAL FIELD

[0003] The present invention relates to an antibacterial composition against drug-resistant bacteria or pro-inflammatory bacteria. The present invention also relates to a pharmaceutical composition or method for treating, ameliorating, or preventing diseases caused by drug-resistant bacteria or pro-inflammatory bacteria.

### BACKGROUND ART

[0004] Various commensal bacteria are resident on mucous membranes such as the digestive tract and the oral cavity, forming a flora as a whole. The resident flora plays a very important role in the physiology and health maintenance of the host. A compositional abnormality of the resident flora is called dysbiosis, and has been gradually revealed to be a cause of various diseases. The advancement of the elucidation of the resident mucosal flora may have a high possibility of developing new disease countermeasures and treatments for various diseases, but the detailed mechanism of such flora has not been sufficiently clarified due to its complexity.

[0005] Humans produce and swallow about 1.5 liters of saliva every day. Normally, bacteria contained in saliva (oral bacteria) simply pass through the intestinal tract and do not colonize. However, in some situations, oral bacteria may colonize in the intestinal tract. Particularly in Crohn's disease, liver cirrhosis, and colorectal cancer, it has been reported that colonization of oral bacteria in the intestinal tract was observed even at the early stages of disease onset. In addition, it is known that the colonized oral bacteria affect the pathological conditions of the diseases (NPLs 1 to 6).

[0006] Meanwhile, by allowing oral bacteria of patients with Crohn's disease and the like to colonize in the intestinal tract to induce Th1 cells, the present inventors succeeded in isolating, culturing, and identifying the bacteria involved in the onset of the diseases (PTL 1). More specifically, the present inventors found that as a result of oral administration of saliva derived from a patient with Crohn's disease to germ-free mice, interferon gamma (IFN- $\gamma$ )-producing CD4-positive T-cells (Th1 cells) significantly increased in the large intestine. Then, the present inventors succeeded in

isolating and culturing the Kp2H7 strain, which is considered to belong to *Klebsiella pneumoniae*, from the intestines of the mice in which this increase in Th1 cells was observed. Furthermore, it was also clarified that the bacteria derived from the saliva of patients with Crohn's disease were involved in the development of enteritis by colonizing in the intestinal tract and inducing the proliferation or activation of Th1 cells.

[0007] Moreover, the present inventors found that when Kp2H7 strains were orally administered to SPF (specific-pathogen-free) mice, intestinal colonization of these bacterial strains was not observed, unlike the case of the germ-free mice. Furthermore, it was also clarified that by administering an antibiotic to the SPF mice, these bacterial strains might be able to colonize in the intestinal tracts of the mice. Then, from these results, the present inventors considered that the intestinal tract contains intestinal bacteria that inhibit the intestinal colonization of Th1 cell-inducible bacteria such as the Kp2H7 strain, and administration of the antibiotic eliminates the intestinal bacteria from the intestinal tract, making the intestinal colonization of the bacteria possible.

[0008] Therefore, the present inventors tried to identify the bacteria that suppress the intestinal colonization of Th1 cell-inducible bacteria among human intestinal bacteria. As a result, the present inventors succeeded in isolating and culturing 68 strains, 37 strains, and 42 strains of intestinal bacterial strains from fecal samples derived from 3 healthy subjects (#K, #F, and #I), respectively, and in determining the sequence of 16S rDNA of each bacterial strain. Furthermore, it was clarified that administration of these bacterial strains suppressed intestinal colonization of Th1 cell-inducible bacteria (PTL 2).

### CITATION LIST

#### Patent Literature

[0009] [PTL 1] International Publication No. WO2018/084172

[0010] [PTL 2] International Publication No. WO2019/017389

#### Non Patent Literature

[0011] [NPL 1] Y. Chen et al., *Scientific reports* 6, 34055 (2016)

[0012] [NPL 2] D. Gevers et al., *Cell host & microbe* 15, 382-392 (2014)

[0013] [NPL 3] C. A. Lozupone et al., *Cell host & microbe* 14, 329-339 (2013)

[0014] [NPL 4] I. Vujkovic-Cvijin et al., *Science translational medicine* 5, 193ra191 (2013)

[0015] [NPL 5] N. Qin et al., *Nature* 513, 59-64 (2014)

[0016] [NPL 6] C. L. Sears, W. S. Garrett, *Cell host & microbe* 15, 317-328 (2014)

### SUMMARY OF INVENTION

#### Technical Problem

[0017] The present invention has an object to find an intestinal bacterium having antibacterial activity against drug-resistant bacteria or pro-inflammatory bacteria, and to provide an antibacterial composition against drug-resistant bacteria or pro-inflammatory bacteria containing the intes-

tinal bacterium as an active ingredient as well as a pharmaceutical composition or method for treating, ameliorating, or preventing diseases caused by drug-resistant bacteria or pro-inflammatory bacteria.

#### Solution to Problem

[0018] The present inventors have made earnest studies to achieve the above object, and have clarified as a result that the above-mentioned bacteria that suppress the intestinal colonization of Th1 cell-inducible bacteria (68 strains of intestinal bacteria derived from healthy subject #K, 37 strains of intestinal bacteria derived from healthy subject #F, and 42 strains of intestinal bacteria derived from healthy subject #I) can suppress the intestinal colonization of multidrug-resistant bacteria (carbapenem-resistant Enterobacteriaceae, vancomycin-resistant enterococci, *Clostridium difficile*, *Campylobacter jejuni*) and pro-inflammatory bacteria (adherent-invasive *Escherichia coli*).

[0019] Furthermore, regarding the ability to suppress bacterial colonization in the intestine, the present inventors have succeeded in selecting 18 strains from the 37 strains of intestinal bacteria derived from healthy subject #F, which are capable of exerting the same level of suppression ability as the 37 strains. Thus, the present invention has been completed.

[0020] Specifically, the present invention provides the following.

[0021] [1] An antibacterial composition against drug-resistant bacteria or pro-inflammatory bacteria comprising: an intestinal bacterium as an active ingredient.

[0022] [2] The antibacterial composition according to [1], wherein the intestinal bacterium is at least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69 to 105 or a base sequence having at least 90% identity to the base sequence.

[0023] [3] The antibacterial composition according to [1], wherein the intestinal bacterium is at least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 or a base sequence having at least 90% identity to the base sequence.

[0024] [4] The antibacterial composition according to [1], wherein the intestinal bacterium is at least one bacterium specified by any of accession numbers NITE BP-03147 to 03164.

[0025] [5] The antibacterial composition according to [1], wherein the intestinal bacterium is at least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 147 or a base sequence having at least 90% identity to the base sequence.

[0026] [6] The antibacterial composition according to [1], wherein the intestinal bacterium is at least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 68 or a base sequence having at least 90% identity to the base sequence.

[0027] [7] The antibacterial composition according to [1], wherein the intestinal bacterium is at least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 106 to 147 or a base sequence having at least 90% identity to the base sequence.

[0028] [8] The antibacterial composition according to any one of [1] to [7], which is a pharmaceutical composition.

[0029] [9] The antibacterial composition according to any one of [1] to [7], which is a pharmaceutical composition for treating, ameliorating, or preventing an infectious disease or an inflammatory disease.

#### Advantageous Effects of Invention

[0030] According to the present invention, by suppressing the colonization and the like of drug-resistant bacteria or pro-inflammatory bacteria in the intestinal tract, it is possible to suppress the proliferation or activation of these bacteria, and it is possible to treat, ameliorate, or prevent diseases caused by these bacteria.

#### BRIEF DESCRIPTION OF DRAWINGS

[0031] The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

[0032] FIG. 1 is a graph in CFU showing changes over time in the bacterial amount of fecal *Klebsiella* when *Klebsiella* 2H7 strains (Kp2H7) were administered to germ-free mice, and one week later, fecal samples of healthy subjects were administered to the mice (FMT). Five types of feces were used, and *Klebsiella* was significantly reduced in all samples.

[0033] FIG. 2 is a bar graph showing the results of 16S meta-analysis of three types of feces derived from healthy donors F, I, and K. Each segment indicates one bacterial strain, and its size indicates the proportion of that bacterium to the total bacterial amount. The three types of feces were cultured in an anaerobic environment, and the strains that could be cultured and isolated there are shown in yellow in the adjacent graph (under color display). The total number of bacteria that could be isolated is shown below.

[0034] FIG. 3 is a graph in CFU showing changes over time in the bacterial amount of fecal Kp2H7 when Kp2H7 was colonized in germ-free mice and then the bacterial strains isolated from feces were mixed and administered. The 37 strains derived from the feces derived from healthy donor F (feces F) reduced *Klebsiella* as much as the fecal sample.

[0035] FIG. 4 is a graph in CFU showing changes over time in the bacterial amount of fecal Kp2H7 when Kp2H7 was colonized in germ-free mice and then the bacterial strains isolated from feces were mixed and administered. The 37 strains derived from feces F and 68 bacterial strains isolated from the feces derived from healthy donor K (feces K) reduced *Klebsiella* as much as the fecal sample.

[0036] FIG. 5 is a graph in CFU showing changes over time in the bacterial amount of fecal Kp2H7 when Kp2H7 was administered to germ-free mice, then F37mix (37 bacterial strains derived from feces F) was administered one week later, and ampicillin was further administered by drinking water one month later. *Klebsiella* transiently increased with ampicillin administration, but then decreased again.

[0037] FIGS. 6A1-6A4 are diagrams showing changes over time in the abundance ratio of each bacterial amount (F31, F22, F20, F32) in the total bacterial amount in the experiment shown in FIG. 5. Below the figure, the number of each bacterium, r (Spearman's rank correlation coefficient with *Klebsiella*), and the bacterium's name are shown.

[0038] FIGS. 6B1-6B4 are diagrams showing changes over time in the abundance ratio of each bacterial amount (F26, F28, F21, F30) in the total bacterial amount in the experiment shown in FIG. 5. Below the figure, the number of each bacterium, r (Spearman's rank correlation coefficient with *Klebsiella*), and the bacterium's name are shown.

[0039] FIGS. 6C1-6C4 are diagrams showing changes over time in the abundance ratio of each bacterial amount (F24, F23/F25, F35/F36, F09) in the total bacterial amount in the experiment shown in FIG. 5. Below the figure, the number of each bacterium, r (Spearman's rank correlation coefficient with *Klebsiella*), and the bacterium's name are shown.

[0040] FIGS. 6D1-6D4 are diagrams showing changes over time in the abundance ratio of each bacterial amount (F33, F12, F17/F19, F18) in the total bacterial amount in the experiment shown in FIG. 5. Below the figure, the number of each bacterium, r (Spearman's rank correlation coefficient with *Klebsiella*), and the bacterium's name are shown.

[0041] FIGS. 6E1-6E4 are diagrams showing changes over time in the abundance ratio of each bacterial amount (F34, F03/F08, F29, F13) in the total bacterial amount in the experiment shown in FIG. 5. Below the figure, the number of each bacterium, r (Spearman's rank correlation coefficient with *Klebsiella*), and the bacterium's name are shown.

[0042] FIGS. 6F1-6F4 are diagrams showing changes over time in the abundance ratio of each bacterial amount (F04/F08, F37, F01, F02) in the total bacterial amount in the experiment shown in FIG. 5. Below the figure, the number of each bacterium, r (Spearman's rank correlation coefficient with *Klebsiella*), and the bacterium's name are shown.

[0043] FIGS. 6G1-6G3 are diagrams showing changes over time in the abundance ratio of each bacterial amount (F05, F07, F14) in the total bacterial amount in the experiment shown in FIG. 5. Below the figure, the number of each bacterium, r (Spearman's rank correlation coefficient with *Klebsiella*), and the bacterium's name are shown.

[0044] FIGS. 6H1-6H3 are diagrams showing changes over time in the abundance ratio of each bacterial amount (F10/F15, F16, F11/F27) in the total bacterial amount in the experiment shown in FIG. 5. Below the figure, the number of each bacterium, r (Spearman's rank correlation coefficient with *Klebsiella*), and the bacterium's name are shown.

[0045] FIG. 7 is a diagram in which bacteria are arranged in the order of positive correlation in Spearman's rank correlation coefficient between Kp2H7 and each bacterium in terms of bacterial amount. Many of the *Bacteroides* are not related in movement to Kp2H7, and many of the negatively correlated ones are in the *Firmicutes* genus.

[0046] FIG. 8 is a graph in CFU showing changes over time in the bacterial amount of fecal Kp2H7 when Kp2H7 was administered to germ-free mice for colonization, and then the 37 strains shown in FIG. 7 (F37mix), 8 strains of the 37 strains belonging to the Bacteroidetes genus (F8mix), or the 29 other bacterial strains (F29mix) were mixed and administered. The 29 strains excluding *Bacteroides* also showed a decrease in *Klebsiella* that was almost the same as the 37 strains, and it is considered that *Bacteroides* is unnecessary for the elimination of *Klebsiella*.

[0047] FIG. 9 is a phylogenetic tree showing a breakdown of F37mix, F8mix, and F29mix used in the experiment shown in FIG. 8. The phylogenetic tree was prepared by the Neighbor-joining method using MEGA X with the DNA base sequence of the 16S rDNA analysis result of the

isolated bacteria by the Sanger method. The same applies to the preparation of the phylogenetic trees in FIGS. 10 and 12.

[0048] FIG. 10 is a phylogenetic tree showing a breakdown of 18 bacterial strains derived from feces F (F18mix).

[0049] FIG. 11 is a graph in CFU showing changes over time in the bacterial amount of fecal Kp2H7 when Kp2H7 was colonized in germ-free mice, and then 37 bacterial strains derived from feces F (F37mix described above), 18 bacterial strains derived from feces F (F18mix shown in FIG. 10), or 42 bacterial strains derived from the feces derived from healthy subject I (feces I) were mixed and administered. F18mix also successfully eliminated *Klebsiella* in the same way as F37mix.

[0050] FIG. 12 is a phylogenetic tree that classifies 18 bacterial strains derived from feces F (F18mix) into 4 groups and shows the breakdown thereof. These 4 groups were subtracted from the 18 bacterial strains (F18mix) to prepare bacterial strain groups of F15mix (F18mix-other phyla), F12mix (F18mix-Lachnolactridium), F14mix (F18mix-Blautia), and F13mix (F18mix-other Firmicutes), which were subjected to the experiment shown in FIG. 11.

[0051] FIG. 13 is a graph in CFU showing changes over time in the bacterial amount of fecal Kp2H7 when Kp2H7 was colonized in germ-free mice, and then the group excluding the duplicate strains and F18mix from F37mix (F31-18mix), F15mix described above, F12mix described above, F14mix described above, F13mix described above, or F18mix described above was mixed and administered. Note that FIG. 13 shows data from the experiments performed twice. Excluding any group shown in FIG. 12 from F18mix decreased the ability to eliminate *Klebsiella*, and it has become clear that every group is important for the elimination of *Klebsiella*.

[0052] FIG. 14 is a graph showing the CFU of fecal Kp2H7 in each group at the time of day 28 in the experiment shown in FIG. 13. The F18mix-administered group has a statistically significantly smaller bacterial amount of *Klebsiella* than the other administration groups excluding F37mix.

[0053] FIG. 15 is a dot plot diagram showing the results of flow cytometric analysis of immune cells in the lamina propria of the large intestine of mice in the F37mix-administered group, the F18mix-administered group, or the Kp2H7 alone administration group. The numerical value in each gate (square) in the figure shows the proportion of CD4+IFN $\gamma$ + cells. The induction of CD4+IFN $\gamma$ + cells is suppressed in the F37mix-administered group and the F18mix-administered group as compared with the Kp2H7 alone administration group.

[0054] FIG. 16 is a graph in CFU showing changes over time in the bacterial amount of fecal Kp2H7 when Kp2H7 was administered to germ-free mice, and one week later, each bacterial strain mix was administered. The "F15mix" in the figure shows the result of mice administered by removing three strains of *E. coli*, *Fusobacterium*, and *Bifidobacterium* from F18mix, and "F18mix-*E. coli*", "F18mix-*Fusobacterium*," and "F18mix-*Bifidobacterium*" each show the result of mice administered by removing one of the three strains from F18mix. The effects of all three strains diminished when removed from F18mix, indicating that each was involved in the elimination of *Klebsiella*.

[0055] FIG. 17 is a graph in CFU showing changes over time in the bacterial amount of fecal Kp2H7 when Kp2H7 was administered to a germ-free Rag2<sup>-/-</sup>γc<sup>-/-</sup> mouse,

*MvD88<sup>-/-</sup>*Trif<sup>-/-</sup> mouse, or wild-type mouse (WT), and one week later, mixed F37mix was administered. *Klebsiella* was equally eliminated in all types of mice. This suggests that the major innate immunity and acquired immunity of the host are not involved in the elimination of *Klebsiella*.

[0056] FIG. 18 is a graph in CFU showing changes over time in the bacterial amount of fecal CRE when *Klebsiella* (Kp-CRE) was administered to germ-free mice, and one week later, the isolated bacteria mixes (F37mix, K68mix, I42mix) were administered to the mice. F37mix and K68mix can also reduce CRE.

[0057] FIG. 19 is a photomicrograph showing the results of analyzing the large intestine of a mouse at the end of the experiment shown in FIG. 18 by HE staining. No inflammatory findings were observed in any of the isolated bacterium mix-administered mice.

[0058] FIG. 20 is a graph in CFU showing changes over time in the bacterial amount of fecal VRE when VRE (vancomycin-resistant enterococci) was administered to germ-free mice, and one week later, the isolated bacteria mixes (F37mix, K68mix, I42mix) were administered to the mice. For VRE, K68mix was able to reduce the bacterial amount more than F37mix.

[0059] FIG. 21 is a photomicrograph showing the results of analyzing the large intestine of a mouse at the end of the experiment shown in FIG. 18 by HE staining. No inflammatory findings were observed in any of the isolated bacterium mix-administered mice.

[0060] FIG. 22 is a graph in CFU showing changes over time in the bacterial amount of fecal AIEC when AIEC was administered to germ-free mice, and one week later, the isolated bacteria mixes (F37mix, K68mix, I42mix) were administered to the mice. For AIEC, F37mix was most effective in reducing the bacterial amount.

[0061] FIG. 23 is a graph in CFU showing changes over time in the bacterial amount of fecal ESBL-producing *Klebsiella* when ESBL-producing *Klebsiella* was administered to germ-free mice, and one week later, the isolated bacteria mixes (F37mix, K68mix, I42mix) were administered to the mice. F37mix and K68mix were able to eliminate ESBL-producing *Klebsiella* as much as F-derived feces.

[0062] FIG. 24 is a graph in CFU showing changes over time in the bacterial amount of fecal *Campylobacter* when *Campylobacter jejuni* was administered to germ-free mice, and one week later, fecal samples derived from the isolated bacteria mixes (F37mix, K68mix, I42mix) or healthy subject F were administered to the mice. Elimination of *Campylobacter jejuni* was observed to the same extent in all the isolated bacteria mix-administered groups.

[0063] FIG. 25 is a graph showing changes over time in the bacterial amount of fecal *Campylobacter* as a relative value divided by the total bacterial amount when *Campylobacter jejuni* was administered to germ-free mice, and one week later, fecal samples derived from the isolated bacteria mixes (F37mix, K68mix, I42mix) or healthy subject F were administered to the mice. Elimination of *Campylobacter jejuni* was observed to the same extent in all the isolated bacteria mix-administered groups.

[0064] FIG. 26 is a graph showing the results of qPCR analysis of changes over time in the bacterial amount of fecal *Clostridium difficile* when *Clostridium difficile* was administered to germ-free mice, and one week later, fecal samples derived from the isolated bacteria mixes (F37mix,

K68mix, I42mix, K47mix) or healthy subject F were administered to the mice. K68mix and K47mix were able to eliminate *Clostridium difficile* as compared with F-derived feces, but the elimination effect of F37mix was lower.

#### BIOLOGICAL MATERIAL DEPOSIT INFORMATION

[0065] Applicants made the following biological deposits under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure at NITE Patent Microorganisms Depository, National Institute of Technology and Evaluation, #122, 2-5-8 Kazusaka-matari, Kisarazu-shi, Chiba 292-0818, Japan.:

Depositor Identification Reference	International Depository Designation	Date of Deposit
<i>Klebsiella pneumonia</i> Kp-2H7 strain	NITE BP-04150	Sep. 3, 2024
<i>Klebsiella aeromobilis</i> Ka-11E12 strain	NITE BP-04151	Sep. 3, 2024

#### DESCRIPTION OF EMBODIMENTS

##### <Intestinal Bacteria>

[0066] In the present invention, the intestinal bacteria contained as an active ingredient of the antibacterial composition have an antibacterial action against drug-resistant bacteria or pro-inflammatory bacteria (hereinafter also referred to as "drug-resistant bacteria and the like") in the intestinal tract.

[0067] In the present invention, the "antibacterial activity" means an activity of suppressing the activity of bacteria, more specifically, an activity of suppressing the proliferation or colonization of bacteria or killing bacteria, and examples thereof include the activity of suppressing the colonization of bacteria in the intestines and the activity of eliminating bacteria from the intestines.

[0068] The "Intestinal bacteria" mean bacteria present in the intestinal tract of an animal. Examples of animals in which such bacteria are present include humans and non-human animals (such as mice, rats, monkeys, pigs, cattle, horses, sheep, goats, chickens, ducks, ostriches, domestic ducks, dogs, cats, rabbits, and hamsters), but among these animals, humans are preferable.

[0069] In the present invention, the "intestinal bacteria" may be a single strain of bacteria or a mixture of bacterial strains composed of multiple strains of bacteria. Note that when composed of multiple strains of bacteria, it is desirable that at least one of the bacterial strains has antibacterial activity against drug-resistant bacteria and the like. Further, in such a case, the multiple strains of bacteria may even include a bacterial strain that does not have the antibacterial activity, such as a bacterial strain having an action of enhancing the activity of a bacterial strain having the antibacterial activity, a bacterial strain having an action of maintaining the proliferation or colonization of a bacterial strain having antibacterial activity, and a bacterial strain having an action of suppressing the inhibitory activity of a bacterium that inhibits the antibacterial activity.

**[0070]** In the present invention, examples of the “intestinal bacteria” include at least one bacterium having a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 147 or a base sequence having at least 70% identity to the base sequence, at least one bacterium having a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 68 or a base sequence having at least 70% identity to the base sequence, at least one bacterium having a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69 to 105 or a base sequence having at least 70% identity to the base sequence (for example, at least one bacterium having a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 or a base sequence having at least 70% identity to the base sequence), and at least one bacterium having a DNA composed of a base sequence set forth in any of SEQ ID NOS: 106 to 147 or a base sequence having at least 70% identity to the base sequence.

**[0071]** The sequence indicated by each SEQ ID NO is the sequence of 16S rDNA of each bacterium K68, F37, and 143 in the attached document. Tables 1 to 4 below show the correspondence between each bacterium, the SEQ ID NO indicating the sequence of each 16S rDNA, and each bacterial species estimated from the sequence. In addition, K, F, and I represent intestinal bacteria isolated from the feces of three healthy subjects (Japanese) (see PTL 2).

TABLE 1

No.	Species	SEQ ID NO:	NCBI subject id	TAX ID	% identity
K01	<i>Drancourtella massiliensis</i>	1	NR_144722.1	1632013	99.57
K02	<i>Bacteroides ovatus</i>	2	NR_112940.1	28116	99.86
K03	<i>Blautia coccoides</i>	3	NR_104700.1	1532	99.86
K04	<i>Blautia hominis</i>	4	NR_163638.1	2025493	99.43
K05	<i>Desulfovibrio vulgaris</i>	5	NR_074446.1	882	91.58
K06	<i>Alistipes ondorronkii</i>	6	NR_043318.1	328813	99.86
K07	<i>Eisenbergiella massiliensis</i>	7	NR_144731.1	1720294	99.50
K08	<i>[Clostridium] innocuum</i>	8	NR_029164.1	1522	97.93
K09	<i>Bacteroides fragilis</i>	9	NR_112936.1	817	99.71
K10	<i>Eggerthella lenta</i>	10	NR_074377.1	84112	100.00
K11	<i>Dielma fastidiosa</i>	11	NR_125593.1	1034346	99.71
K12	<i>Erysipelatoclostridium ramosum</i>	12	NR_113243.1	1547	100.00
K13	<i>Enterococcus faecalis</i>	13	NR_115765.1	1351	99.93
K14	<i>Bacteroides intestinalis</i>	14	NR_041307.1	329854	99.35
K15	<i>[Clostridium] symbiosum</i>	15	NR_118730.1	1512	98.35
K16	<i>[Clostridium] hylemonae</i>	16	NR_024719.1	89153	99.50
K17	<i>Hungatella effluvii</i>	17	NR_133762.1	1096246	98.49
K18	<i>Bacteroides dorei</i>	18	NR_041351.1	357276	99.93
K19	<i>[Clostridium] clostridiiforme</i>	19	NR_044715.2	1531	98.99
K20	<i>Flavonifractor plautii</i>	20	NR_029356.1	292800	100.00
K21	<i>Bacteroides xylosovens</i>	21	NR_112947.1	657309	99.50
K22	<i>Bacteroides thetaiotaomicron</i>	22	NR_112944.1	818	99.93
K23	<i>Parabacteroides merdae</i>	23	NR_041343.1	46503	99.78
K24	<i>Bacteroides vulgatus</i>	24	NR_074515.1	435590	100.00
K25	<i>[Clostridium] aldenense</i>	25	NR_043680.1	358742	99.41

TABLE 1-continued

No.	Species	SEQ ID NO:	NCBI subject id	TAX ID	% identity
K26	<i>Bacteroides uniformis</i>	26	NR_112945.1	820	97.39
K27	<i>Gordonibacter urolithinfaciens</i>	27	NR_148261.1	1335613	99.56
K28	<i>Coprococcus comes</i>	28	NR_044048.1	470146	92.77
K29	<i>Anaerostipes caccae</i>	29	NR_028915.1	105841	98.78
K30	<i>[Ruminococcus] gravus</i>	30	NR_036800.1	411470	99.78
K31	<i>[Ruminococcus] gravus</i>	31	NR_036800.1	411470	98.71
K32	<i>Alistipes shahii</i>	32	NR_113153.1	328814	100.00
K33	<i>Bacteroides stercoris</i>	33	NR_112943.1	449673	98.77
K34	<i>Blautia hominis</i>	34	NR_163634.1	2025493	98.71

TABLE 2

No.	Species	SEQ ID NO:	NCBI subject id	TAX ID	% identity
K35	<i>Butyrivibacter faecihominis</i>	35	NR_152060.1	1712515	97.89
K36	<i>[Clostridium] bolteae</i>	36	NR_025567.1	208479	99.50
K37	<i>Phocaea massiliensis</i>	37	NR_144748.1	1841867	99.93
K38	<i>Holdemania massiliensis</i>	38	NR_125628.1	1211819	99.71
K39	<i>Escherichia coli</i>	39	NR_114042.1	582	99.79
K40	<i>Agathobaculum desmolans</i>	40	NR_044644.2	39484	96.68
K41	<i>[Eubacterium] rectale</i>	41	NR_074634.1	515619	100.00
K42	<i>Lactonifactor longoviformis</i>	42	NR_043551.1	341220	100.00
K43	<i>Oscillibacter ruminantium</i>	43	NR_118156.1	1007096	95.90
K44	<i>Pseudoflavoribacter phocaensis</i>	44	NR_147370.1	1870988	97.42
K45	<i>Streptococcus pasteurianus</i>	45	NR_043660.1	197614	100.00
K46	<i>Sutterella wadsworthensis</i>	46	NR_117778.1	40545	99.93
K47	<i>Bifidobacterium faecale</i>	47	NR_133982.1	1454229	99.35
K48	<i>Eisenbergiella massiliensis</i>	48	NR_144731.1	1720294	93.50
K49	<i>Fusicatenibacter saccharivorans</i>	49	NR_114326.1	1150298	99.78
K50	<i>Robinsoniella peoriensis</i>	50	NR_041882.1	180332	93.40
K51	<i>Massilimicrobiota timonensis</i>	51	NR_144738.1	1776392	99.93
K52	<i>Blautia faecis</i>	52	NR_109014.1	871665	99.92
K53	<i>Blautia wexlerae</i>	53	NR_044054.1	1121115	98.63
K54	<i>Phascolarctobacterium faecium</i>	54	NR_026111.1	33025	99.72
K55	<i>Odoribacter splanchnicus</i>	55	NR_113075.1	28118	99.71
K56	<i>Faecalibacterium prausnitzii</i>	56	NR_028961.1	853	97.29
K57	<i>Collidextrabacter massiliensis</i>	57	NR_147375.1	1870986	94.70
K58	<i>Emergencia timorensis</i>	58	NR_144737.1	1776384	91.61
K59	<i>Alistipes finegoldii</i>	59	NR_043064.1	214856	99.42
K60	<i>Ruthenibacterium lactatiformans</i>	60	NR_151900.1	1550024	99.93
K61	<i>Christensenella minuta</i>	61	NR_112900.1	626937	98.71
K62	<i>[Clostridium] scindens</i>	62	NR_028785.1	29347	98.49
K63	<i>Enterococcus faecalis</i>	63	NR_115765.1	1351	100.00
K64	<i>Blautia coccoides</i>	64	NR_104700.1	1532	99.93
K65	<i>Alistipes ihumii</i>	65	NR_144706.1	1211813	99.28

TABLE 2-continued

No.	Species	SEQ ID NO:	subject id	NCBI TAX ID	% identity
K66	<i>Intestinimonas butyriciproducens</i>	66	NR_118554.1	1297617	99.86
K67	<i>Bacteroides uniformis</i>	67	NR_112945.1	820	99.93
K68	<i>Akkermansia muciniphila</i>	68	NR_074436.1	239935	98.91

TABLE 3

No.	Species	SEQ ID NO:	subject id	NCBI TAX ID	% identity
F01	<i>Bifidobacterium longum</i>	69	NR_145535.1	1931217	99.60
F02	<i>Bacteroides xylosoxolvens</i>	70	NR_112947.1	657309	99.59
F03	<i>Bacteroides fragilis</i>	71	NR_074784.2	817	98.95
F04	<i>Bacteroides uniformis</i>	72	NR_112945.1	820	99.93
F05	<i>Bacteroides thetaiotaomicron</i>	73	NR_074277.1	818	99.80
F06	<i>Bacteroides uniformis</i>	74	NR_112945.1	820	99.93
F07	<i>Bacteroides acidifaciens</i>	75	NR_112931.1	85831	97.18
F08	<i>Bacteroides fragilis</i>	76	NR_074784.2	817	98.95
F09	<i>Parabacteroides goldsteinii</i>	77	NR_113076.1	927665	98.98
F10	[ <i>Ruminococcus</i> ] <i>gnavus</i>	78	NR_036800.1	411470	99.80
F11	<i>Blautia luti</i>	79	NR_114315.1	649762	97.57
F12	<i>Faecalimonas umbilikata</i>	80	NR_156907.1	1912855	99.87
F13	[ <i>Clostridium</i> ] <i>saccharolyticum</i>	81	NR_102852.1	84030	94.34
F14	<i>Tyzzerella nexilis</i>	82	NR_029248.1	500632	98.49
F15	[ <i>Ruminococcus</i> ] <i>gnavus</i>	83	NR_036800.1	411470	99.80
F16	<i>Anaerostipes hadrus</i>	84	NR_117138.2	649756	99.74
F17	<i>Blautia glucarasea</i>	85	NR_113231.1	536633	96.91
F18	[ <i>Clostridium</i> ] <i>bolteae</i>	86	NR_025567.1	208479	99.60
F19	<i>Blautia caecimuris</i>	87	NR_144607.1	1796615	99.13
F20	[ <i>Clostridium</i> ] <i>innocuum</i>	88	NR_029164.1	1522	98.71
F21	<i>Blautia marasmi</i>	89	NR_147395.1	1917868	98.20
F22	[ <i>Clostridium</i> ] <i>lavalense</i>	90	NR_044289.1	460384	98.97
F23	[ <i>Clostridium</i> ] <i>glycyrhizinilyticum</i>	91	NR_112553.1	342942	99.13
F24	<i>Eisenbergiella massiliensis</i>	92	NR_144731.1	1720294	97.73
F25	[ <i>Clostridium</i> ] <i>glycyrhizinilyticum</i>	93	NR_112553.1	342942	99.13
F26	<i>Flavonifractor plautii</i>	94	NR_029356.1	292800	100.00
F27	<i>Blautia luti</i>	95	NR_114315.1	649762	97.57
F28	<i>Intestinibacter bartlettii</i>	96	NR_027573.1	261299	99.93
F29	[ <i>Ruminococcus</i> ] <i>gnavus</i>	97	NR_036800.1	411470	98.85
F30	<i>Massilimicrobiota timonensis</i>	98	NR_144738.1	1776392	100.00
F31	<i>Anaerostipes caccae</i>	99	NR_028915.1	105841	97.32
F32	<i>Blautia coccoides</i>	100	NR_104700.1	1532	99.93
F33	<i>Eysipelatoclostridium ramosum</i>	101	NR_029247.1	1547	99.41
F34	<i>Veillonella parvula</i>	102	NR_074980.1	479436	99.16
F35	<i>Fusobacterium varium</i>	103	NR_113384.1	856	99.73
F36	<i>Fusobacterium varium</i>	104	NR_113384.1	856	99.73
F37	<i>Escherichia fergusonii</i>	105	NR_074902.1	585054	99.87

TABLE 4

No.	Species	SEQ ID NO:	subject id	NCBI TAX ID	% identity
I01	<i>Bifidobacterium faecale</i>	106	NR_133982.1	1454229	98.06
I02	<i>Bifidobacterium pseudocatenulatum</i>	107	NR_037117.1	28026	99.63
I03	<i>Bifidobacterium bifidum</i>	108	NR_044771.1	1681	100.00
I04	<i>Bifidobacterium longum</i>	100	NR_145535.1	1931217	99.70
I05	<i>Collinsella aerofaciens</i>	110	NR_113316.1	74426	99.92
I06	<i>Collinsella aerofaciens</i>	111	NR_113316.1	74426	99.72
I07	<i>Bifidobacterium longum</i>	112	NR_145535.1	1931217	99.70
I08	<i>Bacteroides stercoris</i>	113	NR_112943.1	449673	99.18
I09	<i>Bacteroides massiliensis</i>	114	NR_042745.1	204516	99.70
I10	<i>Bacteroides vulgatus</i>	115	NR_074515.1	435590	100.00
I11	<i>Bacteroides dorei</i>	116	NR_041351.1	357276	100.00
I12	<i>Parabacteroides merdae</i>	117	NR_041343.1	46503	99.85
I13	<i>Parabacteroides distasonis</i>	118	NR_041342.1	823	99.03
I14	<i>Alistipes putredinis</i>	119	NR_113152.1	28117	100.00
I15	<i>Bacteroides uniformis</i>	120	NR_040866.1	820	97.75
I16	<i>Bacteroides Koreensis</i>	121	NR_159117.1	1912896	99.26
I17	<i>Alistipes shahii</i>	122	NR_113153.1	328814	99.63
I18	<i>Odoribacter splanchnicus</i>	123	NR_113075.1	28118	99.77
I19	<i>Faecalibacterium prausnitzii</i>	124	NR_028961.1	853	97.24
I20	<i>Faecalibacterium prausnitzii</i>	125	NR_028961.1	853	97.24
I21	<i>Blautia wexlerae</i>	126	NR_044054.1	1121115	98.38
I22	<i>Ruminococcus lactaris</i>	127	NR_027579.1	471875	97.24
I23	<i>Ruminococcus albus</i>	128	NR_113032.1	1264	94.68
I24	<i>Faecalibacterium prausnitzii</i>	129	NR_028961.1	853	96.86
I25	<i>Dorea longicatena</i>	130	NR_028883.1	88431	99.47
I26	<i>Dorea formicigenerans</i>	131	NR_044645.2	39486	97.94
I27	<i>Anaerostipes hadrus</i>	132	NR_117138.2	649756	99.85
I28	<i>Intestinibacter bartlettii</i>	133	NR_027573.1	261299	99.55
I29	<i>Flavonifractor plautii</i>	134	NR_029356.1	292800	99.71
I30	<i>Pseudoflavonifractor phocaeensis</i>	135	NR_147370.1	1870988	97.86
I31	[ <i>Clostridium</i> ] <i>spiroforme</i>	136	NR_114393.1	29348	93.09
I32	<i>Megasphaera elsdenii</i>	137	NR_102980.1	1064535	99.35
I33	<i>Dialister succinatiphilus</i>	138	NR_041666.1	742743	97.02
I34	<i>Acidaminococcus intestini</i>	139	NR_041894.1	187327	99.93
I35	<i>Allisonella histaminiformans</i>	140	NR_028862.1	209880	99.50
I36	<i>Megasphaera massiliensis</i>	141	NR_133027.1	1232428	99.00
I37	<i>Sutterella wadsworthensis</i>	142	NR_104851.1	40545	99.78
I38	<i>Clostridium baratti</i>	143	NR_029229.1	1561	99.85
I39	<i>Anaeromassilibacillus senegalensis</i>	144	NR_144727.1	1673717	97.27
I40	<i>Colidextribacter massiliensis</i>	145	NR_147375.1	1870986	95.00
I41	<i>Flavonifractor plautii</i>	146	NR_029356.1	292800	97.96
I42	[ <i>Clostridium</i> ] <i>leptum</i>	147	NR_114789.1	1535	94.55

[0072] Tables 1 to 4 show the top-hit species names and RefSeq accessions as a result of a BLAST search for the sequences set forth in the SEQ ID NOs on the RefSeq 16s DNA sequence database (as of Jan. 8, 2020). Note that it is generally said % identity>97% can identify species, and >94% can identify genus. Therefore, it should be understood

that bacterial strains with a % identity of >94% are bacteria that can be identified at the genus level.

[0073] The “at least 70% identity” in the intestinal bacteria of the present invention means that the identity to each base sequence is preferably 80% or more, more preferably 85% or more, further preferably 90% or more (for example, 91% or more, 92% or more, 93% or more, and 94% or more), more preferably 94% or more (for example, 95% or more, 96% or more, 97% or more, and 98% or more), and particularly preferably 99% or more.

[0074] In addition, the homology or identity of a sequence (amino acid sequence or nucleotide (base) sequence) can be determined by using the BLAST (Basic Local Alignment Search) program (Altschul et al. J. Mol. Biol., 215:403-410, 1990). The program is based on the algorithm BLAST by Karlin and Altschul (Proc. Natl. Acad. Sci. USA, 87:2264-2268, 1990, Proc. Natl. Acad. Sci. USA, 90:5873-5877, 1993). When analyzing the homology or identity between sequences by BLAST, it can be determined by using, for example, the BLAST of the National Center for Biotechnology Information (NCBI) (for example, by using the default, that is, initially set parameters).

[0075] In the present invention, the “intestinal bacterium” which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 147 or a base sequence having at least 70% identity to the base sequence is preferably at least 15 bacteria in the intestinal bacterial group, more preferably at least 30 bacteria in the intestinal bacterial group, further preferably at least 75 bacteria in the intestinal bacterial group, more preferably at least 120 bacteria in the intestinal bacterial group, further preferably at least 135 bacteria in the intestinal bacterial group, more preferably at least 140 bacteria in the intestinal bacterial group, further preferably 147 intestinal bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 147 or a base sequence having at least 70% identity to the base sequence, and particularly preferably 147 bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 147.

[0076] In the present invention, the “intestinal bacterium” which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 68 or a base sequence having at least 70% identity to the base sequence is preferably at least 7 bacteria in the intestinal bacterial group, more preferably at least 15 bacteria in the intestinal bacterial group, further preferably at least 35 bacteria in the intestinal bacterial group, more preferably at least 60 bacteria in the intestinal bacterial group, further preferably at least 65 bacteria in the intestinal bacterial group, more preferably 68 intestinal bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 68 or a base sequence having at least 70% identity to the base sequence, and particularly preferably 68 bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 68. In addition, the “intestinal bacterium” which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 68 or a base sequence having at least 70% identity to the base sequence desirably has resistance to ampicillin. Also, the present invention uses 46 bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 46 or a base sequence having at least 70% identity to the base sequence.

[0077] In the present invention, the “intestinal bacterium” which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69 to 105 or a base sequence having at least 70% identity to the base sequence is preferably at least 4 bacteria in the intestinal bacterial group, more preferably at least 8 bacteria in the intestinal bacterial group, further preferably at least 18 bacteria in the intestinal bacterial group, more preferably at least 29 bacteria in the intestinal bacterial group, further preferably at least 33 bacteria in the intestinal bacterial group, more preferably at least 35 bacteria in the intestinal bacterial group, further preferably 37 intestinal bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69 to 105 or a base sequence having at least 70% identity to the base sequence, and particularly preferably 37 bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69 to 105. In addition, the “intestinal bacterium” which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69 to 105 or a base sequence having at least 70% identity to the base sequence desirably has sensitivity to ampicillin.

[0078] In the present invention, the “intestinal bacterium” which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 or a base sequence having at least 70% identity to the base sequence is preferably at least 2 bacteria in the intestinal bacterial group, more preferably at least 5 bacteria in the intestinal bacterial group, further preferably at least 10 bacteria in the intestinal bacterial group, more preferably at least 14 bacteria in the intestinal bacterial group, further preferably at least 15 bacteria in the intestinal bacterial group, more preferably at least 16 bacteria in the intestinal bacterial group, further preferably at least 17 bacteria in the intestinal bacterial group, more preferably 18 intestinal bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 or a base sequence having at least 70% identity to the base sequence, and particularly preferably 18 bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 (bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 69, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 80, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 85, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 86, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 87, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 88, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 89, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 90, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 91, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 92, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 94, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 96, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 98, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 99, bacteria which include a DNA composed of a base

sequence set forth in SEQ ID NO: 100, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 101, bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 103, and bacteria which include a DNA composed of a base sequence set forth in SEQ ID NO: 105).

[0079] Note that typical examples of 18 bacteria each of which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 are accession bacterial strains shown in Table 5 below. All of the bacterial strains were deposited with the National Institute of Technology and Evaluation (NITE, 2-5-8 Kazusakamata, Kisarazu City, Chiba Prefecture, Room 122) on Mar. 2, 2020.

TABLE 5

No.	16S rDNA (SEQ ID NO:)	Identification Indication	Receipt Number	Accession Number
F01	69	f01_42H6	NITE ABP-03147	NITE BP-03147
F12	80	f12_42H4	NITE ABP-03148	NITE BP-03148
F17	85	f17_42I7	NITE ABP-03149	NITE BP-03149
F18	86	f18_42I2	NITE ABP-03150	NITE BP-03150
F19	87	f19_43G2	NITE ABP-03151	NITE BP-03151
F20	88	f20_43G1	NITE ABP-03152	NITE BP-03152
F21	89	f21_42A8	NITE ABP-03153	NITE BP-03153
F22	90	f22_43C3	NITE ABP-03154	NITE BP-03154
F23	91	f23_42K4	NITE ABP-03155	NITE BP-03155
F24	92	f24_42I4	NITE ABP-03156	NITE BP-03156
F26	94	f26_42K2	NITE ABP-03157	NITE BP-03157
F28	96	f28_43A3	NITE ABP-03158	NITE BP-03158
F30	98	f30_43A5	NITE ABP-03159	NITE BP-03159
F31	99	f31_43I5	NITE ABP-03160	NITE BP-03160
F32	100	f32_42A7	NITE ABP-03161	NITE BP-03161
F33	101	f33_43N2	NITE ABP-03162	NITE BP-03162
F35	103	f35_42L8	NITE ABP-03163	NITE BP-03163
F37	105	f37_42G1	NITE ABP-03164	NITE BP-03164

which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 106 to 147. In addition, the “intestinal bacterium” which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 106 to 147 or a base sequence having at least 70% identity to the base sequence desirably has sensitivity to ampicillin.

[0080] Further, in the present invention, an aspect of the “intestinal bacterium” is an intestinal bacterium that exhibits resistance to at least one compound selected from the group consisting of spectinomycin, and/or sensitivity to at least one compound selected from the group consisting of ampicillin, tylosin, and chloroform. In addition, another aspect includes intestinal bacteria that exhibit resistance to metronidazole and/or sensitivity to at least one compound selected from the group consisting of vancomycin and tylosin.

[0081] In addition, as shown in Examples described later, the above-mentioned intestinal bacteria have been isolated by the present inventors and are useful because they exert an antibacterial action against drug-resistant bacteria, pro-inflammatory bacteria, and the like. Therefore, the present invention may also provide the following.

[0082] (1) At least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69 to 105 or a base sequence having at least 90% identity to the base sequence.

[0083] (2) At least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID

NOS: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 or a base sequence having at least 90% identity to the base sequence.

[0084] (3) At least one bacterium specified by any of accession numbers NITE BP-03147 to 03164.

[0085] (4) At least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 1 to 147 or a base sequence having at least 90% identity to the base sequence.

[0086] (5) At least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 69 to 105 or a base sequence having at least 90% identity to the base sequence.

[0087] (6) At least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOS: 106 to 147 or a base sequence having at least 90% identity to the base sequence.

[0088] (7) The bacterium according to any one of (1) to (6), which is a bacterium having an antibacterial action against drug-resistant bacteria, pro-inflammatory bacteria, or bacteria that induce proliferation or activation of Th1 cells in the intestinal tract.

#### <Antibacterial Composition and Pharmaceutical Composition>

[0089] The composition of the present invention may be any as long as it contains the above-mentioned intestinal bacterium, and the bacterium may be a live bacterium or a dead bacterium. In addition, when the compositions can be used in combination, and they are ingested or absorbed in combination as a result (in the case of combined compositions), the above-mentioned intestinal bacteria can also be present separately in two or more compositions.

[0090] The composition of the present invention can be in the form of a pharmaceutical composition, a quasi-drug composition, food and drink (including animal feed), or a reagent used for research purposes (such as in vitro or in vivo experiments).

[0091] Since the composition of the present invention exhibits antibacterial activity against drug-resistant bacteria and the like, it is preferably used as a pharmaceutical composition, a quasi-drug composition, or food or drink for treating, preventing, or ameliorating diseases caused by the bacterium.

[0092] The composition of the present invention can be formulated by a known pharmaceutical method. For example, it can be used in the form of capsules, tablets, pills, liquids, powders, granules, fine granules, film coating preparations, pellets, troches, sublingual preparations, chews, buccal preparations, pastes, syrups, suspensions, elixirs, emulsions, coating preparations, ointments, plasters, poultices, transdermal preparations, lotions, inhalants, aerosols, injections, suppositories, and the like, for the purpose of administration by oral, parenteral (for example, intestinal, intramuscular, intravenous, tracheal, intranasal, transdermal, intradermal, subcutaneous, intraocular, vaginal, intraperitoneal, rectal, or inhalation), or multiple combinations of these routes.

[0093] In these formulations, they can be appropriately combined with a pharmacologically or food and drink acceptable carrier, specifically, sterilized water, saline, buffer solution, medium, vegetable oil, solvent, base, emulsifier, suspension, surfactant, stabilizer, flavor agent, air freshener, excipient, vehicle, antiseptic, binder, diluent, isotonic

agent, soothing agent, bulking agent, disintegrant, buffer agent, coating agent, lubricant, colorant, sweetener, thickener, flavor modifier, solubilizer, or other additives.

[0094] In addition, in these formulations, from the viewpoint of e.g., more efficiently exerting antibacterial activity against drug-resistant bacteria and the like in the intestinal tract, particularly in a formulation intended for oral administration, the composition of the present invention may be combined with a composition that enables efficient delivery into the intestinal tract. The composition capable of such delivery into the intestinal tract is not particularly limited, and a known composition can be appropriately employed, and examples thereof include pH-sensitive compositions, compositions that suppress release to the intestinal tract (such as cellulosic polymers, acrylic acid polymers and copolymers, and vinyl acid polymers and copolymers), bioadhesive compositions that specifically adhere to the intestinal mucosa (such as polymers described in U.S. Pat. No. 6,368,586), protease inhibitor-containing compositions, and compositions specifically degraded by intestinal enzymes).

[0095] In addition, when the antibacterial composition of the present invention is used as a pharmaceutical composition, it may further contain a known substance used for treating, preventing, or ameliorating diseases caused by drug-resistant bacteria and the like (such as other antibacterial agents, anti-inflammatory agents, and immunosuppressants), or may be used in combination with such a substance.

[0096] When the composition of the present invention is used as food and drink, the food and drink may be, for example, a health food, a functional food, a food for specified health use, a food with nutrient function claims, a food with functional claims, a dietary supplement, a food for patients, or animal feed. Specific examples of the food and drink include liquid foods such as fermented beverages, oil-containing products, soups, milk beverages, refreshing beverages, tea beverages, alcoholic beverages, energy drinks, and jelly-like beverages, carbohydrate-containing foods, processed livestock foods, and processed fishery foods; and processed vegetable foods, semi-solid foods, fermented foods, confectionery, retort products, microwave-compatible foods, and the like. It is also possible to list healthy food and drink prepared in the form of powder, granules, tablets, capsules, liquid, paste, or jelly. The food and drink according to the present invention can be produced by a production technique known in the art. In the food and drink, components (such as nutrients) effective for ameliorating or preventing diseases caused by drug-resistant bacteria and the like may be added. In addition, it may be a multifunctional food and drink by combining it with other ingredients or other functional foods that exhibit functions other than the amelioration and the like.

[0097] The product (pharmaceutical product, quasi-drug, food and drink, reagent) of the composition of the present invention or the instruction manual thereof may be provided with an indication that it exhibits antibacterial activity against drug-resistant bacteria and the like, or is used for treating, ameliorating, or preventing diseases caused by the drug-resistant bacteria and the like. Further, in relation to the food and drink, the product or the like of the composition of the present invention may be labeled with a health function as a food with health claims (food for specified health use, food with nutrient function claims, food with functional

claims) so that the form, target, and the like can be distinguished from general foods. Here, “the product or the instruction manual is labeled” means that a label is attached to the main body, container, packaging, or the like of the product, or a label is attached to the instruction manual, package insert, promotional material, other printed matter, or the like that discloses product information. Further, the composition of the present invention may be in the form of a kit.

[0098] Further, as described above, a pharmaceutical composition can be produced by a known formulation technique using the intestinal bacterium and the like of the present invention. Therefore, the present invention also provides the use of the intestinal bacterium and the like of the present invention for producing a pharmaceutical composition for treating, ameliorating, or preventing diseases caused by drug-resistant bacteria and the like.

#### <Treatment Method and the Like>

[0099] The present invention also provides a method for treating, ameliorating, or preventing diseases caused by drug-resistant bacteria and the like in a target, wherein the target is allowed to ingest the above-mentioned antibacterial composition or pharmaceutical composition, or the above-mentioned intestinal bacteria as an active ingredient thereof (hereinafter also collectively referred to as “the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof”).

[0100] In the present invention, the “drug-resistant bacterium” means a bacterium that has resistance to antibacterial agents (such as antibiotics) and the drugs are ineffective or difficult to be effective. Further, the drug may be one drug or multiple drugs. That is, the drug-resistant bacteria according to the present invention also include multidrug-resistant bacteria. Such bacteria are not particularly limited, but examples thereof include carbapenem-resistant Enterobacteriaceae (CRE, KPC-2-producing *Klebsiella pneumoniae*, and the like), vancomycin-resistant enterococci (VRE, bacteria with vancomycin-resistant gene (vanA), and the like), *Clostridium difficile*, and *Campylobacter jejuni*. More specific examples include *Klebsiella pneumoniae* (ATCC BAA-1705), *Enterococcus faecium* (Orla-Jensen) Schleifer and Kilpper-Balz (ATCC 700221), *Clostridioides difficile* (Prevot) Lawson et al. (ATCC 43255, bacterial strain designation: VPI 10463), *Clostridioides difficile* (Prevot) Lawson et al. (ATCC BAA-1382, bacterial strain designation: 630), and *Campylobacter jejuni* 81-176 (ATCC BAA2151).

[0101] The “diseases caused by drug-resistant bacteria” include infectious diseases caused by drug-resistant bacteria. They also include diseases associated with the infection. Examples of such diseases include respiratory infectious diseases such as sepsis, peritonitis, meningitis, gastroenteritis, and pneumonia, urinary tract infectious diseases, surgical site infectious diseases, soft tissue infectious diseases, and medical device-related infectious diseases (such as medical device-related bloodstream infectious diseases).

[0102] In the present invention, the “pro-inflammatory bacterium” means a bacterium that induces inflammation in the intestinal tract, and examples thereof include adherent-invasive *Escherichia coli* (AIEC). More specifically, AIEC LF82 can be mentioned.

[0103] The “diseases caused by pro-inflammatory bacteria” include diseases caused or involved in inflammation caused by the bacteria. Examples of such diseases include

inflammatory bowel diseases (including chronic inflammatory bowel diseases such as Crohn's disease, ulcerative colitis, and inflammatory bowel disease).

[0104] The pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof can be used for animals including humans, but there are no particular restrictions on animals other than humans, and various domestic animals, poultry, pets, laboratory animals, and the like can be targeted.

[0105] In addition, the ingestion target of the intestinal bacterium and the like of the present invention includes animals carrying the drug-resistant bacteria and the like, regardless of the onset of diseases caused by the drug-resistant bacteria and the like. From the viewpoint of prevention, an animal that does not possess the bacteria or is suspected of possessing them may be allowed to ingest the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof.

[0106] The method for ingesting the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof is not particularly limited, and may be oral administration or parenteral administration (for example, administration into the intestinal tract), and in the case of oral administration, from the viewpoint of further improving the effects of the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof, it is preferable that the ingestion target of the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof has reduced production of gastric acid by ingestion of a proton pump inhibitor (PPI) or the like.

[0107] In addition, in the case of ingesting the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof, the amount ingested can be appropriately selected by those skilled in the art according to the target's age, weight, disease symptoms, health conditions, composition type (such as pharmaceutical product, and food and drink), ingestion method, and the like.

[0108] Preferable embodiments of the antibacterial composition and the pharmaceutical composition as well as the therapeutic method and the like of the present invention have been described above, but the present invention is not limited to the above embodiments.

[0109] As shown in Examples described later, regarding the ability to suppress intestinal colonization possessed by the Th1 cell-inducible bacterium *Klebsiella* 2H7 strain (Kp2H7), the present inventors have succeeded in selecting 18 strains capable of exerting the same level of suppression ability as the 37 strains of intestinal bacteria derived from healthy subject #F. Therefore, the present invention may also provide the following aspects with respect to antibacterial

compositions and pharmaceutical compositions as well as treatment methods and the like.

[0110] <1> An antibacterial composition against Th1 cell-inducible bacteria, containing an intestinal bacterium as an active ingredient, wherein the intestinal bacterium is at least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOs: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 or a base sequence having at least 90% identity to the base sequence.

[0111] <2> The antibacterial composition according to <1>, which is a pharmaceutical composition.

[0112] <3> The antibacterial composition according to <1> or <2>, which is a pharmaceutical composition for treating, ameliorating, or preventing diseases caused by Th1 cells.

[0113] <4> A method for suppressing proliferation or activation of Th1 cells in a target, a method for suppressing immunity in the target, or a method for treating, ameliorating, or preventing diseases caused by Th1 cells in the target, including allowing the target to ingest the antibacterial composition according to any one of <1> to <3> or at least one bacterium which includes a DNA composed of a base sequence set forth in any of SEQ ID NOs: 69, 80, 85 to 92, 94, 96, 98 to 101, 103, and 105 or a base sequence having at least 90% identity to the base sequence.

[0114] The "Th1 cell-inducible bacterium" according to the present invention is a bacterium that normally exists in the human oral cavity, and induces the proliferation or activation of Th1 cells by colonizing in the intestinal tract. It is preferably a bacterium that belongs to *Klebsiella*, more preferably belonging to *Klebsiella pneumoniae* or *Klebsiella aeromobilis*, and induces the proliferation or activation of Th1 cells in the intestinal tract. Further, the "Th1 cell-inducible bacterium" is preferably a bacterium that easily colonizes in an intestinal environment in which the diversity has changed as compared with the healthy state due to the administration of an antibacterial agent. It is also a bacterium that easily colonizes in an intestinal environment in which the diversity has changed as compared with the healthy state due to colitis or the like.

[0115] For an example of the "Th1 cell-inducible bacterium," PTL 1 can be referred to, and typical examples include Kp2H7 strain, Ka11E12 strain, 34E1 strain, BAA-1705 strain, 700603 strain, and 40B3 strain belonging to *Klebsiella*. Among these, the Kp2H7 strain or the Ka11E12 strain is more preferable, and the Kp2H7 strain is particularly preferable. See Table 6 for details of these bacteria.

TABLE 6

Bacterial Name	Supplier	Information from Supplier	Registry number
KCTC2242	KCTC	http://koto.kribb.re.kr/English/_NCBI Taxonomy ID: 1049565 SearchView.aspx?sn=2242	
2552	ATCC	https://www.atcc.org/Products/ All/BAA-2552.aspx	NCBI Taxonomy ID: 507522
KP-1	—	—	NCBI Taxonomy ID: 1365186
700721	ATCC	https://www.atcc.org/Products/ All/700721.aspx	NCBI Taxonomy ID: 272620
13882	JCM	https://www.atcc.org/Products/ All/13882.aspx	NCBI Taxonomy ID: 1913574

TABLE 6-continued

Bacterial Name	Supplier	Information from Supplier	Registry number
40B3	—	—	SAMD00083913
34E1	—	—	SAMD00083911
1705	ATCC	<a href="https://www.atcc.org/Products/">https://www.atcc.org/Products/</a> All/BAA-1705.aspx	NCBI Taxonomy ID: 1276652
11E12	—	—	SAMD00083912
700603	ATCC	<a href="https://www.atcc.org/Products/">https://www.atcc.org/Products/</a> All/700603.aspx	NCBI Taxonomy ID: 1276653
2H7	—	—	SAMD00083910

[0116] In addition, examples of the “Th1 cell-inducible bacterium” of the present invention include a bacterium which contains a DNA composed of a nucleotide sequence having 90% or more (91% or more, 92% or more, 93% or more, 94% or more, 95% or more, 96% or more, 97% or more, 98% or more, and 99% or more) identity to the nucleotide sequence encoding the 16S rRNA of Kp2H7 strain, Ka11E12 strain, 34E1 strain, BAA-1705 strain, 700603 strain, or 40B3 strain, and also include a bacterium which contains a DNA composed of a nucleotide sequence having 70% or more (preferably 80% or more, more preferably 85% or more, further preferably 90% or more, and more preferably 94% or more (for example, 95% or more, 96% or more, 97% or more, 98% or more, and 99% or more)) homology or identity to the nucleotide sequence specific to Kp2H7 strain, Ka11E12 strain, 34E1 strain, BAA-1705 strain, 700603 strain, or 40B3 strain.

[0117] In the present invention, the “Th1 cell” is a subgroup of CD4 positive helper T-cells (Th cells) and means a cell that enhances cell-mediated immunity. In addition, the meaning of “activation of Th1 cells” includes the production of Th1 cytokines (such as IFN- $\gamma$ ) by the cells, induction of macrophages by the cytokines, activation of cells such as cytotoxic T-cells (CTL), and enhancement of cell-mediated immunity by the activation. Further, the meaning of “induction of the proliferation or activation of Th1 cells” also includes induction of differentiation from naive T-cells to Th1 cells which leads to proliferation or activation of Th1 cells.

[0118] The effect of inducing proliferation or activation of Th1 cells in the intestinal tract can be evaluated by quantitatively detecting Th1 cell-specific markers (such as CD4 and IFN- $\gamma$ ). Such quantitative detection can be performed by a known method, and can be performed by methods for detection using antibodies (immunological methods) such as flow cytometry, imaging cytometry, ELISA method, radioimmunoassay, immunohistochemical staining, immunoprecipitation, immunoblotting, and antibody array analysis.

[0119] Regarding whether or not any bacterium or the like has an effect of inducing proliferation or activation of Th1 cells in the intestinal tract, for example, it can be determined that the bacterium or the like has an effect of inducing proliferation or activation of Th1 cells in the intestinal tract when the proportion of IFN- $\gamma^+$  cells in CD4 $^+$ TCR $\beta^+$  T-cells in the intestinal tract detected by flow cytometry is 10% or more (it is preferable to determine, when the proportion is 25% or more, that the bacterium or the like has an effect of inducing proliferation or activation of Th1 cells in the intestinal tract, and it is more preferable to determine, when the proportion is 30% or more, that the bacterium, substance, or the like has an effect of inducing proliferation or activation of Th1 cells in the intestinal tract).

[0120] In the present invention, the “diseases caused by Th1 cells” mean diseases induced by proliferation or activation of Th1 cells, and examples thereof include inflammatory bowel diseases (including chronic inflammatory bowel diseases such as Crohn’s disease, ulcerative colitis, and inflammatory bowel disease), type 1 diabetes, rheumatoid arthritis, experimental autoimmune encephalomyelitis (EAE), multiple sclerosis, autoimmune diseases such as systemic lupus erythematosus, and chronic inflammatory diseases. In addition, the “immunity” suppressed in the present invention includes not only mucosal immunity (such as intestinal immunity) but also systemic immunity. Furthermore, not only cell-mediated immunity but also humoral immunity is included.

[0121] In addition, when the antibacterial composition of the present invention is used as a pharmaceutical composition, it may further contain known substances (such as anti-inflammatory agents and immunosuppressants) used for the treatment, prevention, or amelioration of diseases caused by Th1 cells, or may be used in combination with such substances.

[0122] Note that for other phrases in <1> to <4>, refer as appropriate to the above-mentioned <Antibacterial Composition and Pharmaceutical Composition> and <Treatment Method and the Like>.

<Composition for Examining Diseases Caused by Drug-Resistant Bacteria and the Like>

[0123] In the present invention, the presence of intestinal bacteria that can suppress the colonization and the like of drug-resistant bacteria and the like in the intestinal tract has been clarified. Therefore, by detecting the presence of the intestinal bacteria, it becomes possible to examine diseases caused by drug-resistant bacteria and the like.

[0124] Therefore, the present invention provides a composition for examining diseases caused by the following drug-resistant bacteria and the like.

[0125] A composition for examining diseases caused by drug-resistant bacteria and the like, containing an antibody that specifically recognizes the intestinal bacterium and the like of the present invention.

[0126] A composition for examining diseases caused by drug-resistant bacteria and the like, containing a polynucleotide for detecting a nucleotide sequence specific to the drug-resistant bacteria and the like of the present invention.

[0127] In the present invention, the “antibody that specifically recognizes the intestinal bacterium and the like of the present invention” may be a polyclonal antibody, a monoclonal antibody, or a functional fragment of antibody (for example, Fab, Fab', F(ab')2, variable region fragment (Fv), disulfide bond Fv, single chain Fv (scFv), sc (Fv)2, diabody, multispecific antibody, or a polymer thereof) as long as it

can specifically recognize the bacterium. If the antibody of the present invention is a polyclonal antibody, it can be obtained by immunizing an host animal with an antigen (peptide, polynucleotide, sugar chain, lipid, or the like derived from the intestinal bacterium and the like of the present invention) and purifying it from its antiserum by a conventional means (such as salting-out, centrifugation, dialysis, or column chromatography). In addition, the monoclonal antibody can be produced by a hybridoma method or a recombinant DNA method.

[0128] Further, as the antibody used for the examination of the present invention, it is possible to use an antibody bound with a labeling substance. By detecting the labeling substance, it is possible to directly measure the amount of antibody bound to the intestinal bacterium and the like of the present invention or a substance derived from the bacterium. The labeling substance is not particularly limited as long as it can bind to an antibody and can be detected by a chemical or optical method, and examples thereof include fluorescent dyes (such as GFP), enzymes (such as HRP), and radioactive substances.

[0129] In addition to the antibody component, the examination composition of the present invention may contain additional components acceptable as a composition. Examples of the additional components include carriers, excipients, disintegrants, buffer agents, emulsifiers, suspensions, stabilizers, preservatives, antiseptics, saline, labeling substances, and secondary antibodies. In addition to the above examination compositions, it is possible to combine substrates required for detection of labeling substances, positive controls and negative controls, buffer solutions used for diluting or washing the sample, tubes or plates used for the reaction of the sample with the antibody of the present invention, and the like, or use as an examination kit for diseases caused by drug-resistant bacteria and the like is possible. In addition, when an unlabeled antibody is used as an antibody standard sample, it is possible to combine a labeled substance (such as secondary antibody, protein G, or protein A) that binds to the antibody. Further, the kit for examining diseases caused by drug-resistant bacteria and the like can include an instruction manual for use of the kit.

[0130] Further, the examination composition of the present invention can be combined with an apparatus for detecting the antibody of the present invention. Examples of the apparatus include a flow cytometry apparatus and a microplate reader.

[0131] In the present invention, the "polynucleotide for detecting a nucleotide sequence specific to the intestinal bacterium and the like of the present invention" is not particularly limited as long as the sequence specific to the bacterium is detected, and examples thereof include polynucleotides according to any of the following (a) and (b), each having a chain length of at least 15 nucleotides.

[0132] (a) A polynucleotide that is a pair of primers designed to sandwich the specific nucleotide sequence, and

[0133] (b) A polynucleotide that is a primer or probe that hybridizes to a nucleotide sequence containing the specific nucleotide sequence.

[0134] The polynucleotide of the present invention has a base sequence complementary to the nucleotide sequence of the intestinal bacterium and the like of the present invention. Here, "complementary" does not have to be perfectly complementary as long as it hybridizes. These polynucle-

otides usually have 80% or more, preferably 90% or more, more preferably 95% or more, and particularly preferably 100% homology to the nucleotide sequence.

[0135] The "chain length" of the polynucleotide of the present invention, when used as a primer, is usually 15 to 100 nucleotides, preferably 17 to 30 nucleotides, and more preferably 20 to 25 nucleotides. In addition, when used as a probe, it is usually 15 to 1000 nucleotides, and preferably 20 to 100 nucleotides.

[0136] The polynucleotide of the present invention may be a DNA or RNA, or may have its nucleotide replaced with an artificial nucleic acid such as LNA (registered trademark, crosslinked nucleic acid), ENA (registered trademark, 2'-O, 4'-C-Ethylene-bridged nucleic acids), GNA (glycerol nucleic acid), TNA (threose nucleic acid), or PNA (peptide nucleic acid) in part or all of it.

[0137] Note that the polynucleotide of the present invention can be chemically synthesized using a commercially available nucleotide automatic synthesizer or the like. Further, as the polynucleotide used for the examination of the present invention, it is possible to use a polynucleotide bound with a labeling substance. The labeling substance is not particularly limited as long as it can bind to a polynucleotide and can be detected by a chemical or optical method, and examples thereof include fluorescent dyes (such as DEAC, FITC, R6G, TexRed, and Cy5) as well as dyes such as DAB (chromogen), enzymes, and radioactive substances in addition to fluorescent dyes.

[0138] In addition to the above-mentioned polynucleotide, the examination composition of the present invention may contain additional pharmacologically acceptable components. Examples of the additional components include buffer agents, emulsifiers, suspensions, stabilizers, antiseptics, and saline.

[0139] In addition to the above examination compositions, it is possible to combine standard samples such as substrates required for detection of labeling substances added to the polynucleotide, positive controls and negative controls, and buffer solutions used for diluting or washing the sample, thereby combining tubes or plates used for the reaction of the sample with the polynucleotide of the present invention, or use as an examination kit for diseases caused by drug-resistant bacteria and the like is possible. Moreover, the kit for examining diseases caused by drug-resistant bacteria and the like can include an instruction manual for use of the kit.

[0140] In addition, the examination composition of the present invention can be combined with an apparatus for detecting a nucleotide sequence specific to the intestinal bacterium and the like of the present invention. Examples of the apparatus include a thermal cycler, a sequencer, and a microarray.

[0141] Furthermore, the present invention also provides a method examining diseases caused by drug-resistant bacteria and the like using the above-mentioned antibody, polynucleotide, or examination composition. Specifically, the present invention provides a method for examining diseases caused by drug-resistant bacteria and the like, including the steps of contacting the antibody, polynucleotide, or examination composition with a sample isolated from a subject, and detecting the presence or absence of an intestinal bacterium and the like of the present invention in the intestinal tract by the contact.

[0142] The subject is not particularly limited, and examples thereof include animals such as humans suspected

of suffering from a disease caused by drug-resistant bacteria and the like. Further, the sample isolated from the subject is not particularly limited, but a fecal sample of a subject, a culture thereof, or a polypeptide, polynucleotide, sugar chain, lipid or the like extracted therefrom is preferably used in the method of the present invention.

[0143] As the method for detecting the presence or absence of an intestinal bacterium and the like of the present invention by contacting the sample with the antibody of the present invention or an examination composition containing the same, examples thereof include methods for detection using antibodies (immunological methods) such as ELISA method, immunoblotting, antibody array analysis, immunohistochemical staining, flow cytometry, imaging cytometry, radioimmunoassay, and immunoprecipitation.

[0144] Further, as the method for detecting the presence or absence of an intestinal bacterium and the like of the present invention by contacting the sample with the polynucleotide of the present invention or an examination composition containing the same, it is possible to use PCR (RT-PCR, real-time PCR, and quantitative PCR), DNA microarray analysis, Northern blotting, 16s rRNA sequencing, next-generation sequencing (synthetic sequencing (sequencing-by-synthesis, for example, sequencing by Solexa Genome Analyzer or Hiseq (registered trademark) 2000 manufactured by Illumina), pyrosequencing (for example, sequencing by a sequencer GSLX or FLX manufactured by Roche Diagnostics (454) (so-called 454 sequencing)), and ligase reaction sequencing (for example, sequencing by Solid (registered trademark) or 5500x1 manufactured by Life Technologies)), bead array method, in situ hybridization, dot blotting, RNase protection assay, mass spectrometry, genomic PCR method, and Southern blotting.

[0145] In the present invention, the "examination" of a disease caused by drug-resistant bacteria and the like includes not only the presence or absence of the onset of the disease but also the risk of the onset of the disease, and if the presence of an intestinal bacterium and the like of the present invention is detected in the intestinal tract by the above-mentioned method, it can be determined that a disease caused by drug-resistant bacteria and the like has not developed or the risk of developing the disease is low.

[0146] Diagnosis of a disease caused by drug-resistant bacteria and the like in a subject is usually made by a doctor (including a person who has been instructed by a doctor), but the data obtained by the method of the present invention is useful for diagnosis by a doctor. Therefore, the method of the present invention can also be expressed as a method of collecting and presenting data useful for diagnosis by a doctor.

[0147] Further, the present invention can also provide a companion diagnostic method using the above-mentioned examination method and a drug thereof. That is, the present invention also provides the following.

[0148] A method for determining the effectiveness of the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof in the treatment, amelioration, or prevention of diseases caused by drug-resistant bacteria and the like, including the steps of contacting the antibody, polynucleotide, or examination composition with a sample isolated from a subject, and detecting the presence or absence of the intestinal bacteria and the like by the contact, wherein in the step, when the presence of the bacteria is not detected, it is determined that

the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof in the subject is highly effective in treating, ameliorating, or preventing the disease.

[0149] A method for treating, ameliorating, or preventing diseases caused by drug-resistant bacteria and the like, including a step of allowing a patient determined by the determination method to have high effectiveness of the pharmaceutical composition and the like of the present invention or the active ingredient and the like thereof to ingest the pharmaceutical composition and the like or the active ingredient and the like thereof.

[0150] A composition for treating, ameliorating, or preventing diseases caused by drug-resistant bacteria and the like, containing the intestinal bacterium and the like of the present invention as an active ingredient, wherein the composition is ingested by a subject determined to have high effectiveness by the determination method.

<Method for Screening Intestinal Bacteria Having Antibacterial Activity Against Drug-Resistant Bacteria and the Like in Intestinal Tract>

[0151] It has also been clarified for the first time by the present inventors that among intestinal bacteria, there are bacteria that suppress the colonization of drug-resistant bacteria and the like in the intestinal tract. Therefore, the present invention provides a method for screening intestinal bacteria having antibacterial activity against drug-resistant bacteria and the like, including the following steps.

[0152] A step of allowing a non-human germ-free animal to ingest drug-resistant bacteria and the like and test intestinal bacteria in the intestinal tract, a step of detecting the drug-resistant bacteria and the like in the intestinal tract of the non-human germ-free animal, and a step of determining the test intestinal bacteria as intestinal bacteria having antibacterial activity against the drug-resistant bacteria and the like when the number of bacteria detected in the step is reduced as compared with the case where the test intestinal bacteria are not ingested.

[0153] The "drug-resistant bacteria and the like" are as described above. The "non-human germ-free animal" means a non-human animal that is born and grown under germ-free conditions. Examples of non-human animals include, but are not limited to, mice, rats, monkeys, pigs, cows, horses, sheep, goats, chickens, ducks, ostriches, domestic ducks, dogs, cats, rabbits, and hamsters. Moreover, in these animals, mice are preferably used.

[0154] The test intestinal bacteria to be ingested by non-human germ-free animals may be any bacteria present in the intestines of animals, examples of such animals include humans and non-human animals (such as mice, rats, monkeys, pigs, cows, horses, sheep, goats, chickens, ducks, ostriches, domestic ducks, dogs, cats, rabbits, and hamsters). In addition, the test intestinal bacteria to be ingested by non-human germ-free animals may be isolated intestinal bacteria, and examples thereof include a sample containing intestinal bacteria (for example, a fecal sample of the animal or a culture thereof).

[0155] Further, the method for "ingesting" the test intestinal bacteria and drug-resistant bacteria and the like to a non-human animal is not particularly limited, and is usually performed by oral administration, but may be parenteral administration (for example, administration into the intestinal tract). In addition, the test intestinal bacteria and drug-

resistant bacteria and the like may be ingested at the same time, the drug-resistant bacteria and the like may be ingested by the non-human animal after the test intestinal bacteria are ingested by the animal, or the test intestinal bacteria may be ingested by the non-human animal after the drug-resistant bacteria and the like are ingested by the animal.

[0156] The “detection” of drug-resistant bacteria and the like in the intestinal tract can be performed by detecting a nucleotide sequence specific to the drug-resistant bacteria and the like. Examples of the detection method include PCR (RT-PCR, real-time PCR, and quantitative PCR), DNA microarray analysis, Northern blotting, 16s rRNA sequencing, next-generation sequencing (synthetic sequencing (sequencing-by-synthesis, for example, sequencing by Solexa Genome Analyzer or Hiseq (registered trademark) 2000 manufactured by Illumina), pyrosequencing (for example, sequencing by a sequencer GSLX or FLX manufactured by Roche Diagnostics (454) (so-called 454 sequencing)), and ligase reaction sequencing (for example, sequencing by SoliD (registered trademark) or 5500x1 manufactured by Life Technologies)), bead array method, in situ hybridization, dot blotting, RNase protection assay, mass spectrometry, genomic PCR method, and Southern blotting.

[0157] Further, the “detection” of drug-resistant bacteria and the like in the intestinal tract can be performed, for example, by detecting an amino acid sequence specific to the drug-resistant bacteria and the like. Examples of the detection method include methods for detection using antibodies (immunological methods) such as ELISA method, immunoblotting, antibody array analysis, immunohistochemical staining, flow cytometry, imaging cytometry, radioimmunoassay, and immunoprecipitation. The timing of detection is not particularly limited, and those skilled in the art can appropriately adjust the timing according to the type and the like of animal to be used.

[0158] Note that if the screening method of the present invention fails to select intestinal bacteria having antibacterial activity against drug-resistant bacteria and the like in a single trial, an intestinal sample containing the obtained bacteria is ingested by a new non-human germ-free animal as the next test intestinal bacteria, and the above-mentioned screening is performed multiple times, making it possible to isolate the intestinal bacteria having the antibacterial activity.

## EXAMPLES

### Example 1

[0159] As shown in the upper part of FIG. 1, germ-free mice were administered with *Klebsiella* 2H7 strains (Kp2H7), and one week later, fecal samples of healthy volunteers were administered.

[0160] Specifically, the germ-free mice used were C57BL/6N at 4 to 8 weeks of age (CLEA Japan, Inc.), which were kept in a rearing vinyl isolator (germ-free isolator) (manufactured by ICM Co., Ltd.; ICM-1B) under the conditions of free-drinking water and feeding for one week or longer to acclimate them to the environment. The age at the start of the experiment was 8 to 14 weeks of age. The same applies to the other Examples in the present specification.

[0161] A bacterial solution of *Klebsiella* was placed in an LB liquid medium and cultured overnight at 37° C. to adjust the OD value to 1.2 (equivalent to 1\*10^9 CFU/mL), and

200 µL/individual (equivalent to 2\*10^8 CFU/individual) of bacterial solution was administered into the stomach of mice using a sonde.

[0162] For the fecal samples, feces provided by Japanese healthy subject volunteers (#A, #F, #I, #J, and #K) were diluted 5-fold by weight with a glycerol PBS solution (final concentration of glycerol: 20% by volume), which was filtered through a 100 µm diameter filter, and the resultant was stored as a stock solution at -80° C. At the time of fecal administration, the stock solution was diluted 10-fold with PBS in an anaerobic chamber, and administered in an amount of 200 µL/individual into the stomach of each mouse using a sonde.

[0163] Mouse fecal samples were dissolved in a solution of glycerol (final concentration and 20%) EDTA (final concentration 10 mM) mixed in PBS at a proportion of 50 mg feces/mL. The fecal lysate was seeded after appropriate dilution in DHL medium containing 50 mg/L ampicillin and 50 mg/L spectinomycin, and after culturing at 37° C. overnight, the number of colonies was counted and the number of CFUs per 1 g of feces was calculated.

[0164] In the other Examples in the present specification, bacterial solution of *Klebsiella* and feces were administered in the same manner, and CFUs were counted in the same manner.

[0165] As a result, as shown in the lower part (graph) of FIG. 1, five types of feces were used, and a significant decrease in the bacterial amount of Kp2H7 was observed in all the samples.

### (Example 2) Isolation of Bacteria from Feces of Healthy Subject Volunteers

[0166] Each of the frozen fecal samples derived from feces of healthy subjects F, K, and I (feces F, feces K, and feces I) prepared in Example 1 was thawed at room temperature, diluted with PBS, and cultured in an agar plate of EG medium, modified GAM agar medium (Nissui Pharmaceutical Co., Ltd.; 05426), REINFORCED CLOSTRIDIAL AGAR (RCM AGAR) (Thermo Fisher Scientific Inc; CM0151), or Schaedler blood medium (manufactured by Wako; 517-45805) under an anaerobic environment of at 37° C. and 10% CO<sub>2</sub>, and the colonies formed were isolated. From feces F, 37 strains were isolated, 42 strains were isolated from feces I, and 47 strains were isolated from feces K. After that, the feces K was isolated again, and finally 68 strains were isolated from the feces K.

[0167] For the isolated bacteria, the gene sequence was analyzed and the bacterial species was estimated by 16S rDNA analysis by the Sanger method. Sequence analysis was performed using 3130 DNA Analyzer manufactured by Thermo Fisher Scientific and a primer set having the following sequences.

27 Forward-mod: 5'-AGRGTGATYMTGGCTCAG-3'  
(SEQ ID NO: 148)

1492 Reverse: 5'-GGYTACCTTGTACGACTT-3' (SEQ ID NO: 149)

[0168] Here, R: A or G, Y: C or T, and M: A or C.

[0169] Furthermore, the genome sequences of the 37 bacterial strains derived from feces F were determined using a next-generation sequencer. That is, genome sequencing was performed using MiSeq manufactured by Illumina and

Sequel manufactured by Pacific Biosciences, and all genome sequences were obtained by hybrid assembly using Unicycler. By extracting the 16S rRNA sequence using RNAmmer for each of these genome sequences, a more accurate sequence was obtained, including both terminal sequences that could not be determined by the 16S rDNA sequence determined by the Sanger method.

[0170] Tables 1 to 4 show the results of this analysis. In addition, FIG. 2 shows the results of 16S meta-analysis of three types of feces derived from donors F, I, and K.

#### Example 3

[0171] As shown in the upper part of FIG. 3, Kp2H7 was administered to germ-free mice, and one week later, mixed isolated bacteria (37 strains derived from feces F (F37mix), 42 strains derived from feces I (I42mix), and 47 strains derived from feces K (K47mix)) or feces I were administered.

[0172] The isolated bacteria were cultured in mMAG liquid medium, EG medium, or CM0149 medium at 37° C. in an anaerobic chamber for 24 to 48 hours, and mixed. The mixed solution was concentrated 5 times, and 200 µL/individual (equivalent to total bacterial amount 1\*10<sup>9</sup> CFU/animal) of bacterial solution was administered into the stomach using a sonde. The mixed isolated bacterial strains in the following Examples were also administered in the same manner.

[0173] As a result, as shown in the lower part (graph) of FIG. 3, it was clarified that the 37 strains derived from feces F had the same activity as feces I in terms of the ability to eliminate *Klebsiella* from the mouse intestinal tract.

#### Example 4

[0174] As shown in the upper part of FIG. 4, Kp2H7 was administered to germ-free mice, and one week later, the mixed isolated bacteria (37 strains derived from feces F and 68 strains derived from feces K) were administered. As a result, as shown in the lower part (graph) of FIG. 4, 37 strains derived from feces F and 68 strains derived from feces K equally eliminated *Klebsiella* from the mouse intestinal tract.

#### Example 5

[0175] As shown in the upper part of FIG. 5, Kp2H7 was administered to germ-free mice, and one week later, mixed isolated bacteria (F37mix) were administered, and 200 mg/L of ampicillin was administered by drinking water after the administration of the isolated bacteria. In order to investigate the change in the bacterial amount of each of the administered bacteria, PCR was performed using a specific primer of each of the bacteria. Table 7 shows the primers used in the analysis.

TABLE 7

Forward Primer Name	SEQ ID NO:	Reverse Primer Name	SEQ ID NO:
f01 f01_42H6_Fw1	150	f01_42H6_Rv1	151
f02 f02_42I8_Fw1	152	f02_42I8_Rv3	153
f05 f05_43D4_Fw4	154	f05_43D4_Rv2	155
f06 f06_42F4_Fw1	156	f06_42F4_Rv1	157
f07 f07_42J6_Fw1	158	f07_42J6_Rv1	159
f08 f08_42B5_Fw1	160	f08_42B5_Rv1	161

TABLE 7-continued

Forward Primer Name	SEQ ID NO:	Reverse Primer Name	SEQ ID NO:
f09 f09_43F1_Fw1	162	f09_43F1_Rv1	163
f10 f10_43J3_Fw1	164	f10_43J3_Rv1	165
f12 f12_42H4_Fw1	166	f12_42H4_Rv1	167
f13 f13_42H8_Fw1	168	f13_42H8_Rv1	169
f14 f14_42L4_Fw1	170	f14_42L4_Rv1	171
f16 f16_43M1_Fw2	172	f16_43M1_Rv2	173
f17 f17_42I7_Fw3	174	f17_42I7_Rv3	175
f18 f18_42I2_Fw5	176	f18_42I2_Rv5	177
f19 f19_43G2_Fw2	178	f19_43G2_Rv2	179
f20 f20_43G1_Fw2	180	f20_43G1_Rv2	181
f21 f21_42A8_Fw2	182	f21_42A8_Rv6	183
f22 f22_43C3_Fw2	184	f22_43C3_Rv2	185
f24 f24_42I4_Fw1	186	f24_42I4_Rv1	187
f25 f25_42J1_Fw2	188	f25_42J1_Rv2	189
f26 f26_42K2_Fw1	190	f26_42K2_Rv1	191
f27 f27_42J5_Fw2	192	f27_42J5_Rv2	193
f28 f28_43A3_Fw1	194	f28_43A3_Rv1	195
f29 f29_43J8_Fw2	196	f29_43J8_Rv2	197
f30 f30_43A5_Fw1	198	f30_43A5_Rv1	199
f31 f31_43J5_Fw1	200	f31_43J5_Rv2	201
f32 f32_42A7_Fw1	202	f32_42A7_Rv2	203
f33 f33_43N2_Fw1	204	f33_43N2_Rv1	205
f34 f34_43K4_Fw1	206	f34_43K4_Rv1	207
f35 f35_42L8_Fw2	208	f35_42L8_Rv2	209
f37 f37_42G1_Fw3	210	f37_42G1_Rv4	211

[0176] As a result, as shown in the lower part of FIG. 5, the bacterial amount of *Klebsiella* was transiently increased by the administration of ampicillin, but decreased again thereafter.

[0177] In addition, the change over time of the abundance ratio of each isolated bacterium in the total bacterial amount was analyzed together with that of Kp2H7. FIGS. 6A1-6A4, 6B1-6B4, 6C1-6C4, 6D1-6D4, 6E1-6E4, 6F1-6F4, 6G1-6G3, and 6H1-6H3 show the results obtained. Furthermore, the bacterial amount of *Klebsiella* and the Spearman's rank correlation coefficient of each bacterium were calculated and arranged in order of high positive correlation. FIG. 7 shows the results obtained.

[0178] As shown in FIG. 7, it was found that the strains belonging to Bacteroidetes moved regardless of the movement of *Klebsiella*. On the other hand, many of the strains having a negative correlation belonged to the genus *Firmicutes*.

#### Example 6

[0179] As shown in FIG. 9, 37 the strains derived from feces F were divided into 8 strains belonging to Bacteroidetes (F8mix) and the 29 other bacterial strains (F29mix), and mixed respectively, and after Kp2H7 was colonized in germ-free mice, the mixed isolated bacteria were administered. Note that the phylogenetic trees shown in FIGS. 9, 10, and 12 were prepared by the Neighbor-joining method using MEGA X with the DNA base sequence of the 16S rDNA analysis result of the isolated bacteria by the Sanger method.

[0180] As a result, as shown in FIG. 8, F37mix and F29mix equally eliminated *Klebsiella* from the mouse intestinal tract. On the other hand, in the F8mix administration group belonging to Bacteroidetes, the bacterial amount of *Klebsiella* did not change, suggesting that F8mix is not related to the elimination of *Klebsiella*.

#### Example 7

[0181] From the 37 strains, 18 strains were selected by excluding strains belonging to Bacteroidetes, strains dupli-

cate at the 16S rDNA level, strains disappeared by ampicillin administration, and strains showing behavior unrelated to *Klebsiella* (see FIG. 10).

[0182] Then, as shown in the upper part of FIG. 11, the Kp2H7 strains were administered to germ-free mice, and one week later, mixed isolated bacteria (37 strains derived from feces F (F37mix), 18 strains (F18mix), and 42 strains derived from feces I (I42mix)) were administered.

[0183] As a result, as shown in the lower part (graph) of FIG. 11, it was clarified that the 18 strains shown in FIG. 10 was also able to exhibit the ability to eliminate *Klebsiella* strains as much as the 37 strains.

#### Example 8

[0184] The 18 strains shown in FIG. 10 were divided into 4 groups based on the phylogenetic tree (*Blautia*, *Lachnoclostridium*, other *Firmicutes*, and other Phyla) (see FIG. 12). Furthermore, these 4 groups were subtracted from the 18 bacterial strains (F18mix) to prepare bacterial strain groups of F15mix (F18mix-other phyla), F12mix (F18mix-Lachnoclostridium), F14mix (F18mix-*Blautia*), F13mix (F18mix-other *Firmicutes*). In addition, a bacterial strain set was also prepared by mixing 13 strains (F13mix (F31-18mix)), which were obtained by removing the duplicated strains from the 37 strains and further removing the above-described 18 strains from the remaining 31 strains. Then, as shown in the upper part of FIG. 13, Kp2H7 was administered to germ-free mice, and one week later, each isolated bacterium mixed as described above was administered.

[0185] As a result, as shown in the lower part (graph) of FIG. 13, F18mix best eliminated *Klebsiella*. However, the bacterial amount of *Klebsiella* significantly increased regardless of which group was excluded. In addition, as shown in FIG. 14, also in terms of the CFU of fecal *Klebsiella* in each administration group at the time of day 28 in the experiment shown in FIG. 13, F18mix was able to reduce *Klebsiella* statistically significantly by more than any other group excluding F37mix.

[0186] From the above, it was suggested that all of the four groups shown in FIG. 10 were involved in the elimination of *Klebsiella*, and eliminated *Klebsiella* as a community.

[0187] Further, in the experiment shown in FIG. 13, lymphocytes in the lamina propria of the large intestine were extracted from mice in the F37mix, F18mix, and F31-18mix groups and subjected to analysis by flow cytometry.

[0188] As a result, as shown in FIG. 15, it was clarified that the proportion of CD4+IFN $\gamma$ + cells was high in the F13mix (F31-18mix) group, and that the induction of Th1 cells was suppressed in F37mix and F18mix.

#### Example 9

[0189] As shown in Example 8, in the experiment of removing the bacteria of each group from F18mix, F15mix obtained by removing the 3 strains of other Phyla had the lowest ability to eliminate *Klebsiella*. Therefore, paying attention to this group, the present inventors prepared groups each obtained by removing any one of these 3 strains (*E. coli*, *Bifidobacterium*, and *Fusobacterium*) from the 18 strains derived from feces F. Then, as shown in the upper part of FIG. 16, the Kp2H7 strains were administered to germ-free mice, and one week later, isolated bacteria mixed as described above, F18mix, or F15mix were administered.

[0190] As a result, as shown in the lower part (graph) of FIG. 16, by removing any of the above three strains, an increase of about 1 log in the bacterial amount of *Klebsiella* was observed, suggesting that all of the strains were involved in the elimination of *Klebsiella*.

#### Example 10

[0191] In order to explore the mechanism of eliminating *Klebsiella* of F37mix, the present inventors focused on whether host immunity was involved in this mechanism. Therefore, as shown in the upper part of FIG. 17, the *Klebsiella* 2H7 strain was administered to a germ-free Rag2<sup>-/-</sup>/yc<sup>-/-</sup> mouse, MyD88<sup>-/-</sup>/Trif<sup>-/-</sup> mouse, or wild-type mouse, and one week later, mixed F37mix was administered.

[0192] As a result, as shown in the lower part (graph) of FIG. 17, the same degree of elimination of the *Klebsiella* 2H7 strain by F37mix was observed in all types of mice. This suggests that the major innate immunity and acquired immunity of the host are not involved in the elimination of *Klebsiella*.

[0193] Next, the effect of eliminating the isolated bacterial strains on pathogens and drug-resistant bacteria other than the Kp2H7 strain was evaluated. Note that in the analysis, the primers shown in Table 8 were used as primers specific to the bacteria.

TABLE 8

Target Bacteria and the Like	Primer Name	SEQ ID NO:
CRE	KPC-F684	212
	KPC-R860	213
VRE(vanA)	VanABF_JCM1998	214
	VanAR_JCM1998	215
ESBL	ESBL-F_AAC2001	216
	ESBL-R_AAC2001	217
LF82-specific pMT gene	LF82-F	218
	LF82-R	219
<i>C. jejuni</i>	<i>C. jejuni</i> _F	220
	<i>C. jejuni</i> _R	221
Universal	Universal_Fw_1387	222
	Universal_Rv_1492	223
<i>C. diff</i>	tpi-F	224
	tpi-R	225
<i>C. upsaliensis</i>	Cupsaliensis_2F	226
	Cupsaliensis_2R	227
<i>C. upsaliensis</i>	Cupsaliensis_3F	228
	Cupsaliensis_3R	229
Kp-P1	khe-Fw	230
	khe -RV	231
<i>E. gallinarum</i>	Eg_2F	232
	Eg_2R	233
<i>P. mirabilis</i>	P.mirabilis_NatMicro_F	234
	P.mirabilis_NatMicro_R	235

#### Example 11

[0194] First, as shown in the upper part of FIG. 18, carbapenem-resistant *Klebsiella* (CRE) was administered to germ-free mice, and one week later, mixed F37mix, K68mix, or I42mix was administered. The results obtained are shown at the lower part of FIG. 18.

[0195] Note that a bacterial solution of CRE was placed in an LB liquid medium and cultured overnight at 37° C. to adjust the OD value to 1.2 (equivalent to 1\*10<sup>9</sup> CFU/mL), and 200 μL/individual (equivalent to 2\*10<sup>8</sup> CFU/individual) of bacterial solution was administered into the

stomach of mice using a sonde. Regarding the CFU count for CRE, DHL medium containing 30 mg/L ampicillin and 30 mg/L spectinomycin was used as a selective medium and cultured overnight at 37° C. under aerobic conditions.

[0196] In addition, the mice one month after administration of the mixed isolated bacteria were dissected, and the large intestine was fixed with 4% PFA and embedded in paraffin to prepare sliced sections. These sections were stained with hematoxylin solution and eosin solution to observe inflammatory images of the tissues. FIG. 9 shows the obtained results.

[0197] As shown in the lower part (graph) of FIG. 18, F37mix and K68mix showed equivalent CRE elimination ability, and I42mix was slightly inferior to them. In addition, as shown in FIG. 19, no inflammatory findings such as ulceration or infiltration of inflammatory cells were observed in any of the mice. From this, it was clarified that the induction of inflammation in the large intestine was suppressed by administering each of the isolated bacterial mixed groups.

#### Example 12

[0198] As shown in the upper part of FIG. 20, vancomycin-resistant *Enterococcus faecium* (VRE) was administered to germ-free mice, and one week later, mixed F37mix, K68mix, or I42mix was administered.

[0199] Note that a bacterial solution of VRE was placed in an LB liquid medium and cultured overnight at 37° C. to adjust the OD value to 1.2 (equivalent to  $1 \times 10^9$  CFU/mL), and 200 µL/individual (equivalent to  $2 \times 10^8$  CFU/individual) of bacterial solution was administered into the stomach of mice using a sonde. Regarding the CFU count for VRE, VRE medium (Nippon Becton) was used and cultured overnight at 37° C. under aerobic conditions.

[0200] As a result, as shown in the lower part (graph) of FIG. 20, K68mix exhibited the highest elimination ability on VRE. In addition, as shown in FIG. 21, no inflammatory findings such as ulceration or infiltration of inflammatory cells were observed in any of the mice. From this, it was clarified that the induction of inflammation in the large intestine was suppressed by administering each of the isolated bacterial mixed groups.

#### Example 13

[0201] As shown in the upper part of FIG. 22, adhesion-invasive *E. coli* (AIEC LF82) was administered to germ-free mice, and one week later, mixed F37mix, K68mix, and I42mix were administered.

[0202] Note that a bacterial solution of AIEC LF82 was placed in an LB liquid medium and cultured overnight at 37° C. to adjust the OD to 1.2 (equivalent to  $1 \times 10^9$  CFU/mL), and 200 µL/individual (equivalent to  $2 \times 10^8$  CFU/individual) of bacterial solution was administered into the stomach of mice using a sonde. Regarding the CFU count for AIEC LF82, MacConkey medium containing 1 mg/L cefotaxime was used as a selective medium and cultured overnight at 37° C. under aerobic conditions to calculate the CFU.

[0203] As a result, as shown in the lower part (graph) of FIG. 22, F37mix had the highest elimination ability on AIEC LF82.

#### Example 14

[0204] As shown in the upper part of FIG. 23, ESBL-producing *Klebsiella* (Kp-ESBL) (ATCC 700721) was administered to germ-free mice, and one week later, mixed F37mix, K68mix, I42mix, or feces F was administered.

[0205] Note that a bacterial solution of Kp-ESBL was placed in an LB liquid medium and cultured overnight at 37° C. to adjust the OD to 1.2 (equivalent to  $1 \times 10^9$  CFU/mL), and 200 µL/individual (equivalent to  $2 \times 10^8$  CFU/individual) of bacterial solution was administered into the stomach of mice using a sonde. Regarding the CFU count for Kp-ESBL, DHL medium containing 30 mg/L ampicillin and 30 mg/L spectinomycin was used as a selective medium and cultured overnight at 37° C. under aerobic conditions for calculation.

[0206] As a result, as shown in the lower part (graph) of FIG. 23, F37mix and K68mix showed the same Kp-ESBL elimination ability as feces F.

#### Example 15

[0207] As shown in the upper part of FIGS. 24 and 25, *Campylobacter jejuni* 81-176 (ATCC BAA2151) was administered to germ-free mice, and one week later, mixed F37mix, K68mix, I42mix, or feces F was administered.

[0208] The bacterial solution of *Campylobacter jejuni* was placed in a TS liquid medium, placed in an anaerobic jar together with a slightly aerobic AnaeroPack, and cultured at 42° C. for 48 hours, and the bacterial solution was administered into the stomachs of the mice using a sonde.

[0209] For *Campylobacter jejuni*, CFU and qPCR were used to show the bacterial amount.

[0210] CHROMagar *Campylobacter* was used for CFU counting, which was placed in an anaerobic jar together with a slightly aerobic AnaeroPack and cultured at 42° C. for 48 hours. FIG. 24 shows the obtained results.

[0211] The qPCR measurement was performed according to the following procedure.

[0212] LightCycler (registered trademark) 480II (Roche; 05015243001) and Thunderbird (registered trademark) SYBR (registered trademark) qPCR Mix (TOYOBO; QPS-201X5) were used to amplify and quantify with *Campylobacter jejuni* genome-specific primers and universal bacterial primers, and the calculated DNA concentration ratio was used as the abundance ratio of *Campylobacter jejuni*. FIG. 25 shows the obtained results.

[0213] Note that the primer sets set forth in SEQ ID NOS: 220 and 221 were used as *Campylobacter jejuni* genome-specific primers for qPCR, and the primer sets set forth in SEQ ID NOS: 222 and 223 were used as universal bacterial primers.

[0214] In addition, the bacterial genome was extracted by the following steps.

[0215] A PBS solution containing EDTA and glycerol (final concentration of EDTA: 10 mM, and final concentration of glycerol: 20% by volume) was added 5 times by weight to 10 mg of mouse feces, and the mixture was crushed and suspended with vigorous shaking and stirring. Added to 100 µL of sample solution was 800 µL of 10 mM Tris/10 mM EDTA buffer solution (pH 8.0, also referred to as "TE10" hereinafter) having 15 mg of lysozyme (manufactured by Sigma-Aldrich, Lysozyme from chicken egg white; L4919) and 5 µL of RNase (manufactured by Thermo Fisher Scientific, PureLink RNase A (20 mg/mL); 12091-

021) dissolved therein, and the mixture was shaken at 37° C. for 1 hour. Subsequently, 2,000 U of Achromopeptidase (registered trademark) (Wako; 015-09951) was added, and the mixture was shaken at 37° C. for 30 minutes for lysis. Then, 50 µL of a 20% SDS TE10 solution and 50 µL of a TE10 solution having Proteinase K (Roche, Proteinase K, recombinant, PCR Grade; 0311585.101) at a final concentration of 20 mg/ml dissolved therein were added, and the mixture was shaken at 55° C. for 60 minutes. Next, DNA was obtained from 400 µL of the solution using Maxwell (registered trademark) RSC Cultured Cells DNA Kit (Promega).

[0216] As shown in FIGS. 24 and 25, for *Campylobacter jejuni*, all the mixed bacteria had a good bacterial elimination ability equivalent to that of feces F.

#### Example 16

[0217] As shown in the upper part of FIG. 26, *Clostridium difficile* (St. 630) was administered to germ-free mice, and one week later, mixed F37mix, K68mix, I42mix, K47mix, or feces F was administered. Note that K47mix denotes 47 strains isolated from the fecal sample derived from #K, and is duplicated with the 68 bacterial strains (K1 to K46 shown in Tables 1 and 2) except for 1 bacterial strain.

[0218] The bacterial solution of *C. difficile* was subjected to spore formation, adjusted to around 1×10<sup>5</sup> cells, and administered into the stomachs of the mice using a sonde. The spore formation was performed by culturing in Clospore medium for 8 days in an anaerobic chamber at 37° C. and washing the medium with PBS, followed by treatment with sonication, addition of Lysozyme and trypsin, and treatment at 45° C. for 6 hours and then at 70° C. for 10 minutes.

[0219] For *C. difficile*, qPCR was used to quantify the bacterial amount. As the primers for qPCR, the primer set shown in SEQ ID NOS: 224 and 225 was used.

[0220] As a result, as shown in the lower part of FIG. 26, a high elimination ability was observed in K68mix and K47mix for *C. difficile*.

#### INDUSTRIAL APPLICABILITY

[0221] As described above, by suppressing the colonization of drug-resistant bacteria and pro-inflammatory bacteria in the intestinal tract, the present invention makes it possible to treat, ameliorate, or prevent diseases caused by these bacteria. Therefore, the present invention is extremely useful in the development, treatment, amelioration, prevention, and the like of pharmaceutical products relating to infectious diseases caused by drug-resistant bacteria or pro-inflammatory bacteria.

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caagtaaggc	ttggcactct	ggagagac	ccccggtaa	cgggggaggaa	gtgtggggac	1140
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SEQ ID NO: 6	moltype = DNA	length = 1383				
FEATURE	Location/Qualifiers					
misc_feature	1..1383					
source	note = Obtained from Intestinal Bacteria, K06					
	1..1383					
	mol_type = other DNA					
	organism = unidentified					
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organism = unidentified

**SEQUENCE: 9**

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cggttccat aggttgttgg tgaggtaacg gtcaccaag cttcgtatgg atagggttgc 180  
tgaggagaag gtccccccaca ttggaaactga gagacggcctc aaactctac gggaggcagc 240  
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**SEQ ID NO: 10**

moltype = DNA length = 1366

Location/Qualifiers

source 1..1366

note = Obtained from Intestinal Bacteria, K10

mol\_type = other DNA

organism = unidentified

**SEQUENCE: 10**

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ctggcccccc tcctgggggg ccggggaaag cccagacggc aagggtatggg gtcggggccc 180  
attagtagt aggcggggtaa acggccccc accggccgtc tagggccgcg tgggttagccg ggttggagaga 240  
ccgaccggcc acatggggac tgagataccg cccagactcc tacggggaggc agcagtgggg 300  
aatttgcgc aatggggaa accctgcgcg agcaacccggc ctgtggggac gacggcccttc 360  
gggttggtaaa cccgttccatc caggggaaatccatcggatggcc acctggggatccatcggatgg 420  
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ggcgtaaaga ggcgttaggc ggcctctaa gggatctc taatccggg gtcacacccc 540  
cgccggccatc cccgaaactggg aggcgttagt tcggtaggggg cggggggatccgggtgt 600  
gggttggaaat ggcgtatggat cggggaaagaa acggatggcg aaggcagatct gtcggccgc 660  
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ggatcggat gccgggggtg atacgttccc gggcccttgcg acacccccc gtcacaccac 1320  
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**SEQ ID NO: 11**

moltype = DNA length = 1395

Location/Qualifiers

source 1..1395

note = Obtained from Intestinal Bacteria, K11

mol\_type = other DNA

organism = unidentified

**SEQUENCE: 11**

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ggcggagagg aggcatctt tttctgtttaa agttggataa caacgcacaaat agatggatct 180  
ggcgtgttgcgtt agctgtttgg tgaggtaacg gcccaccaag gcatgtatgtc atagccggcc 240  
tgagggggcc aacggccaca ttggggactga gacacggccc aaactctac gggaggcagc 300  
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ttgtgtacggcc tacccatccaa gggggccaccc gtcataactcg tgccggccgc cggcggtataa 480  
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cattatgtca gggag 1395

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SEQ_ID NO: 12          moltype = DNA    length = 1383
FEATURE                Location/Qualifiers
misc_feature           1..1383
note = Obtained from Intestinal Bacteria, K12
source                 1..1383
                      mol_type = other DNA
                      organism = unidentified
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SEQ_ID NO: 13          moltype = DNA    length = 1423
FEATURE                Location/Qualifiers
misc_feature           1..1423
note = Obtained from Intestinal Bacteria, K13
source                 1..1423
                      mol_type = other DNA
                      organism = unidentified
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 tgcttatacc gcataacagt ttatgcggcc tcggatcataaaga gtgaaaggcg ctttccgggt 180  
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SEQ_ID NO: 19	moltype = DNA	length = 1393				
FEATURE	Location/Qualifiers					
misc_feature	1..1393					
	note = Obtained from Intestinal Bacteria, K19					
source	1..1393					
	mol_type = other DNA					
	organism = unidentified					
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FEATURE	Location/Qualifiers					
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	note = Obtained from Intestinal Bacteria, K20					
source	1..1394					
	mol_type = other DNA					
	organism = unidentified					
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ggccttgtac	acaccggcccc	tcacaccatg	agagtccgggaa	acacccgaag	tccgtaccc	1380
aaccgcagaagg	aggg					1394

SEQ ID NO: 21	moltype = DNA	length = 1385				
FEATURE	Location/Qualifiers					
misc_feature	1..1385					
	note = Obtained from Intestinal Bacteria, K21					
source	1..1385					
	mol_type = other DNA					
	organism = unidentified					
SEQUENCE: 21						
agtgcagggg	cagcattta	gtttgcattgc	aaactaaaga	tggcgaccgg	cgcacgggtg	60
agtaaacacgt	atccaacctg	ccgataactc	ggggatagcc	tttcgaaaga	aagattaata	120
tccgatgttta	tattaaaacc	gcatgtttt	actattaaag	aatttcgtt	atcgatgggg	180
atgcgttcca	ttagttgtt	ggcggggtaa	cggcccacca	agactacgt	ggatgggggt	240
tctgagagga	aggtcggccca	catttgaact	gagacacgg	ccaaactct	acgggaggca	300
gcagtggaga	atattggtca	atggacggaga	gtctgaacca	gccaagttagc	gtgaaggatg	360
actgccttat	gggttgtaaa	cttctttat	atggaaata	atgttccac	gtgtgggatt	420
ttgtatgtac	catatgaata	aggatcggt	aactccgtc	cagcagccgc	ggtataacgg	480
aggatcccgag	cgttatccgg	atttattggg	ttaaaaggaa	gcgttaggtgg	attgttaagt	540
cagtgtgaa	agtttgcggg	tcaaccgtaa	aatttgcgt	gaaactggca	gtcttgagta	600
cagttaggg	ggggcgaaatt	cgtgtgttag	cggtgaaatc	cttagatata	acgaagaact	660
ccgatttgcga	aggcagctca	ctgactgtca	actgacactg	atgctcgaaa	gtgtgggtat	720
caaacaggat	tagataccct	ggtagtccaa	acagttaaacg	atgaataactc	gtctttgcg	780
atatacgtaa	acggcccaag	cgaaaggccat	aatgttccaa	cctggggagt	acgcggccaa	840
cggtggaaact	caaaaggaaatt	gacggggccc	cgccacaacgg	gaggaaacatg	tggtttaatt	900
cgtatgtacg	cgagggaaac	tacccgggtt	taaatttgcatt	ttgaaataatc	tggaaacagg	960
ttagccgc	ggccaaatgt	aagggtctgc	atgggttgc	ttagctcg	ccgtgaggtg	1020
tcggcttaag	tgccataa	agcgcaccc	ttatctttat	ttactaaca	gtcatgtc	1080
ggactctaga	gagactggc	tcgtaaatg	tgtaggtgg	ggggatgacg	tcaaatacgc	1140
acggccctta	cgccggggcc	tacacacgt	ttacaatggg	gggtacagaa	ggcagctac	1200
tggcgcacagg	atgctaattcc	caaaaacctc	tctcagttcg	gatcgaagtc	tgcaacccga	1260
cttcgttgaag	ctggattcgc	tagtaatcg	gcatcagcc	tggcgccgtg	aatacgttcc	1320
cgggccttgc	acacaccg	cgtaagcc	tgaagccgg	gggtacctg	agtacgtaa	1380
cgcaaa						1385

SEQ ID NO: 22	moltype = DNA	length = 1385				
FEATURE	Location/Qualifiers					
misc_feature	1..1385					
	note = Obtained from Intestinal Bacteria, K22					
source	1..1385					
	mol_type = other DNA					
	organism = unidentified					
SEQUENCE: 22						
agtgcagggg	cagcattca	gtttgcattgc	aaactggaga	tggcgaccgg	cgcacgggtg	60
agtaaacacgt	atccaacctg	ccgataactc	ggggatagcc	tttcgaaaga	aagattaata	120
cccgatgttta	taatttagacc	gcatgtttt	tttattaaag	aatttcgtt	atcgatgggg	180
atgcgttcca	ttaggcgtt	ggtaggtaa	cggttcacca	aaccttcgt	ggatgggggt	240
tctgagagga	aggtcggccca	catttgcgt	gagacacgg	ccaaactct	acgggaggca	300
gcagtggaga	atattggtca	atggggcgc	gcctgaacca	gccaagttagc	gtgaaggatg	360
actgccttat	gggttgtaaa	cttctttat	atggaaata	atgttccac	gtgtgggatt	420
ttgtatgtac	catatgaata	aggatcggt	aactccgtc	cagcagccgc	ggtataacgg	480
aggatcccgag	cgttatccgg	atttattggg	ttaaaaggaa	gcgttaggtgg	acagtttaagt	540
cagtgtgaa	agtttgcggc	tcaaccgtaa	aatttgcgt	gatactggct	gtcttgagta	600
cagttaggg	ggggcgaaatt	cgtgtgttag	cggtgaaatc	cttagatata	acgaagaact	660
ccgatttgcga	aggcagctca	ctggactgtca	actgacactg	atgctcgaaa	gtgtgggtat	720
caaacaggat	tagataccct	ggtagtccac	acagttaaacg	atgaataactc	gtctttgcg	780
atatacgtaa	acggcccaag	cgaaaggccat	aatgttccaa	cctggggagt	acgcggccaa	840
cggtggaaact	caaaaggaaatt	gacggggccc	cgccacaacgg	gaggaaacatg	tggtttaatt	900
cgtatgtacg	cgagggaaac	tacccgggtt	taaatttgcatt	ttgaaataatc	tggaaacagt	960
atagccgtaa	ggccaaatgt	aagggtctgc	atgggttgc	ttagctgtg	ccgtgaggtg	1020
tcggcttaag	tgccataa	agcgcaccc	ttatctttat	ttactaaca	gtcatgtc	1080
ggactctaga	gagactggc	tcgtaaatg	tgtaggtgg	ggggatgacg	tcaaatacgc	1140
acggccctta	cgccggggcc	tacacacgt	ttacaatggg	gggtacagaa	ggcagctacc	1200
tggtgcacagg	atgctaattcc	caaaaacctc	tctcagttcg	gatcgaagtc	tgcaacccga	1260
cttcgttgaag	ctggattcgc	tagtaatcg	gcatcagcc	tggcgccgtg	aatacgttcc	1320
cgggccttgc	acacaccg	cgtaagcc	tgaagccgg	gggtacctg	agtacgtaa	1380
cgcaaa						1385

SEQ ID NO: 23	moltype = DNA	length = 1387
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<b>FEATURE</b>	<b>Location/Qualifiers</b>		
misc_feature	1..1387		
	note = Obtained from Intestinal Bacteria, K23		
source	1..1387		
	mol_type = other DNA		
	organism = unidentified		
<b>SEQUENCE: 23</b>			
agtgcgggg cagcatgatt	tgttagcaata cagattgatg	gcgacccggc cacgggttag	60
taacgcgtat gcaacttacc	tatcagaggg ggatagccgc	cgaaagtgc gattaatacc	120
ctataaaaaca ggggtcccgc	atgggaat ttgttaaagg	ttcategctg atagataggc	180
atgcgttca ttaggcgtt	cattggacta cggggggtaa	aaccgcgtt ggatagggg	240
tcttgagagga aggtccccca	catttgacta gagacacggc	ccaaactcct acgggaggca	300
gcagtggagga atattggtca	atggccgaga ggctgaacca	gccaagtgc gtgaaggaaag	360
aaggatctat ggtttgttaa	cttcttttta aggggaataa	agtgaggagc gtgtccctt	420
ttgtatgtac cctatgataa	agcatcggt aactccgtgc	cagcagccgc ggtataacgg	480
aggatgcgag cggttatccgg	attatttggg tttaaagggt	cgcttagtgg tgatttaagt	
cagcgggtaa agtttgtggc	tcaaccataa aatttgcgtt	gaaactgggt tacttgagt	600
tgtttgaggt aggccggat	cgtgtgttag cggtgaaatg	catagatatc acgcagaact	660
ccgattgcga aggacgtta	cttataaccata actgcacact	aagcacgaaa gcgtggggat	720
caaacaggat tagataccct	ggtgttccac gcatgttac	atgattacta ggagtttgcg	780
atacaatgtt agctctacag	cgaaaggcgtt aagtaatcca	cctggggagt acggccggca	840
cggtggaaact caaaggaaat	gacggggggcc cgacacggc	aggacatgtt ggtttaattc	900
gatgatacgc gaggaaacctt	accgggggtt gaacgttagt	tgaccggagt gaaacactc	960
tttctagcaa tagcagatta	cgagggtctg catgggttc	gtcagctctg gccgtgaggt	1020
gtcggcttaa gtgcataac	gagcgtcaacc cttatacta	gttactaaca ggtgaagctg	1080
aggactctgg tgagactgcc	agcgttaagct gtgaggaaagg	tggggatgac gtcaaatcag	1140
caaggccctt acatccgggg	cgacacacgtt gttacaatgg	catggacaaa gggcagctac	1200
ctgggtacag gatctaattc	tccaaaccat gtctcagttc	ggatcggagt ctgcaactcg	1260
actccgtgaa gttggattcg	cttagatactc cgcatcagc	atggcgggtt gaatacgtt	1320
ccgggccttg tacacaccgc	ccgtcaagcc atgggagccg	ggggtagctt aagtcgtt	1380
ccgcaag			1387
<b>SEQ ID NO: 24</b>			
<b>FEATURE</b>	<b>moltype = DNA length = 1384</b>		
misc_feature	Location/Qualifiers		
1..1384			
source	note = Obtained from Intestinal Bacteria, K24		
1..1384			
mol_type = other DNA			
organism = unidentified			
<b>SEQUENCE: 24</b>			
gtcgaggggc agcatggct	tagttgcta aggccgttgc	cgaccggcgc acgggttagt	60
aacacgtatc caacctgccc	tctactcttgc gacagccttc	tgaaaggaaat attaataacaa	120
gtatggcatca tgtagtgcgc	tgttccatcg attaaaggtag	ttccggtaga cgatggggat	180
gcgttccatt agatagtagg	cggggtaacg gcccacccat	tcttcgtatgg ataggggtt	240
tgagaggaaat gttcccccaca	ttggaaactga gacacggtcc	aaactccatc gggaggcagc	300
agtggggat attggtcaat	ggggcagago ctgaaccaggc	caagtagctg gaaggatgac	360
tgcctatgtt gttgttactt	tcttttataa aggaataaaag	tgggtatgg atacccttt	420
gcatgttactt tagttaaaatg	gtatgggtt ccctgtgc	gagccgggg taatacggag	480
gatcccgacgc ttatccggat	ttatgggtt taaaaggagc	gtatgttgc gtttaagtca	540
gttgtgaaat ttgcggctc	aaccgtaaaa ttgcagtta	tactggatat cttgagtgc	600
gttgaggccg gggggatctg	tgggtgtacg gtgaaatgtc	tagatatcga gaagaactcc	660
gattgtcgaatg cggccgtct	aaatgtcgtt gtcgaaaatg	gtgggtatca	720
aacaggatttata gataccctgg	tagtccacat ggtttaacat	gttgcgttactaactaacat	780
atactgtcaag cggccaagcg	aaagcgatcc gatattccacc	tgggggatgtc gccggcaacg	840
gtgaaacttca aaggaaatgt	cggggggcccg cacaacggca	ggaacatgtg gtttaatctc	900
atgatacgcg aggaaacctt	ccccgggtt aatttgcgtt	gaattacgtt gaaaggccgt	960
agccgcggaaat catctgtt	gggtgtcgat ggttgcgtc	actgtcgcc gtgagggtgc	1020
gggttaatgtt ccataacacg	cgcaaccctt gttgtcagt	actaacatgttccgttgc	1080
actctgtacaa gactccatc	gttgcgttgc gttgtcagt	actaacatgttccgttgc	1140
ggcccttacg tccggggctt	gttgcgttgc gttgtcagt	actaacatgttccgttgc	1200
ggcggtgtat gccaatcccc	acaatggggccgtt gttgtcgtt	actaacatgttccgttgc	1260
ccacgaaatgtt ggttgcgtt	gttgcgttgc gttgtcagt	actaacatgttccgttgc	1320
ggccttgcac acaccggcccg	tcaagccatg ggagccgggg	gttgcgttgc gttgtcagt	1380
cgatgttactt			1384
<b>SEQ ID NO: 25</b>			
<b>FEATURE</b>	<b>moltype = DNA length = 1396</b>		
misc_feature	Location/Qualifiers		
1..1396			
source	note = Obtained from Intestinal Bacteria, K25		
1..1396			
mol_type = other DNA			
organism = unidentified			
<b>SEQUENCE: 25</b>			
cgagtgcac gaaggatct	gggatgtt tttcggtt	attccctgtt gactgtgtt	60
cgacacgggtt agtaacgcgt	ggataaccctg ctcacactg	ggggataaca gttagaatg	120
gtctgttactt ccgcataa	ccgcataa gcatgttac	gtgtaaaaa cccagggtt	180

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gtgagatgga	tccgcgtctg	attagccagt	tggcggttta	acggccacc	aaagcgacga	240		
tca	ctgaccc	actgtggagg	gtgacggcc	acatgggac	tgagacacgg	ccc	aaactcc	300
ta	cggggc	agcgtgggg	aatattgcad	aatgggcgaa	agcctgtac	agc	gaccccg	360
cgt	gatgtaa	gaatgtatctc	ggatgtaaa	gctctatca	caggaaagaa	aat	gacggta	420
cct	gacta	aagccccggc	taactacgt	ccagcagccg	cgttaatacg	tagggggca	480	
ge	ttatccg	gatttactgg	gtgtaaagg	agcgttagac	gcgcacgca	tctggagt	ga	540
a	agcccg	cccaaccccg	ggactgttt	ggaaactgtg	ctgtggagt	gcaggagg	600	
ta	agtggat	tcctagtgt	gcccgtgaaat	gcgttagat	tagggaaac	acc	gtggcg	660
a	aggcg	actggactgt	aactgacgtt	gaggctcgaa	agcgtgggg	gcaaa	acagga	720
tt	agatacc	ttgttagtcca	cgccgttaaa	gatgaatgtc	aggtgtcg	ggcaaa	agcc	780
ctt	cgtgtcc	ccccgtaa	caataagcat	tcacactggg	gagtacgt	gcaaga	atga	840
a	aactcaa	agg	gacccgcaca	agcgggtgg	catgtgtt	aattc	gaagc	900
a	acgcga	aga	accttacca	gtcttgacat	ccccgtac	gnnc	ngcta	960
ctt	cgggaca	ggggagacag	gtgtgtcgat	gttgcgtca	gtcgtgtcg	tgagatgtt	g	1020
gg	ttaa	gttgcgtcc	gcacacgac	gcaaccccta	tccttagt	ccagcacgt	anggtgg	1080
ctt	taggg	actgc	ccccatgg	ataacctga	gaaagg	gtgacgtca	aat	1140
cc	cttatg	tttggctac	acacgtcta	caatggcgta	aacaagg	ggcgacc	ct	1200
c	gaagg	caag	aaatccaa	aaataacgtc	ccagttcg	ctgtgtct	caacccg	1260
ac	acg	gac	gaaatcg	gtaatcgcn	atcagaatgc	cgccgt	aat	1320
gt	ttgtt	taca	caccgcccgt	cacaccatgg	gagtacgca	cgcc	gaagt	1380
ac	cttaa	ca	gagg	1396				

SEQ ID NO: 26	moltype = DNA	length = 1382				
FEATURE	Location/Qualifiers					
misc_feature	1..1382					
note	= Obtained from Intestinal Bacteria, K26					
source	1..1382					
mol_type	= other DNA					
organism	= unidentified					
SEQUENCE: 26						
gtcgaggggc	atcaggaaga	aagcttgctt	tctttgctgg	cgaccggcgc	acgggtgagt	60
aacacgtatc	caacctgccc	atgactcggg	gatagcctt	cgaaagaag	attaataccc	120
gatggatata	ctgaaaggc	tctttcagct	attaaagaat	ttcggtatt	gatgggtatg	180
cgttccatta	gggttggc	ggggtaacgg	ccccaac	cgctcgatg	ta	240
gagaggaa	gggg	tttttt	ttggactg	acacgg	tttttt	300
gtgagga	tttgg	tttttt	ttggactg	aaactctac	ggggc	360
cccttatgg	tttttt	tttttt	ttggactg	tgaaacc	tttttt	420
tatgttaccgt	atgaa	atcggttt	tccgttcc	cagccgcgtt	aatacggagg	480
atcccgag	at	atccggatt	tatttttt	aaagg	gttgcgtt	540
tttgtt	aaat	tttgcgtt	tttttt	tttttt	tttttt	600
tagaggc	tttttt	tttttt	tttttt	tttttt	tttttt	660
attgcga	agg	tttttt	tttttt	tttttt	tttttt	720
acaggat	tttttt	tttttt	tttttt	tttttt	tttttt	780
tacagta	tttttt	tttttt	tttttt	tttttt	tttttt	840
tgaact	tttttt	tttttt	tttttt	tttttt	tttttt	900
tgatac	tttttt	tttttt	tttttt	tttttt	tttttt	960
gccc	tttttt	tttttt	tttttt	tttttt	tttttt	1020
getta	tttttt	tttttt	tttttt	tttttt	tttttt	1080
cttt	tttttt	tttttt	tttttt	tttttt	tttttt	1140
gccc	tttttt	tttttt	tttttt	tttttt	tttttt	1200
ttag	tttttt	tttttt	tttttt	tttttt	tttttt	1260
catga	tttttt	tttttt	tttttt	tttttt	tttttt	1320
gctt	tttttt	tttttt	tttttt	tttttt	tttttt	1380
ga						

SEQ ID NO: 27	moltype = DNA	length = 1370				
FEATURE	Location/Qualifiers					
misc_feature	1..1370					
note	= Obtained from Intestinal Bacteria, K27					
source	1..1370					
mol_type	= other DNA					
organism	= unidentified					
SEQUENCE: 27						
tgc	aa	gttgcgtt	ccggataga	gtggcgtt	gggtgttt	60
acgt	gac	cc	ccgttgg	ccggataga	gtggcgtt	120
act	cc	cc	ccgttgg	ccggataga	gtggcgtt	180
g	cc	cc	ccgttgg	ccggataga	gtggcgtt	240
g	ac	cc	ccgttgg	ccggataga	gtggcgtt	300
gg	gg	cc	ccgttgg	ccggataga	gtggcgtt	360
ttt	gg	cc	ccgttgg	ccggataga	gtggcgtt	420
ttt	gg	cc	ccgttgg	ccggataga	gtggcgtt	480
ttt	gg	cc	ccgttgg	ccggataga	gtggcgtt	540
ccc	gg	cc	ccgttgg	ccggataga	gtggcgtt	600
ttt	gg	cc	ccgttgg	ccggataga	gtggcgtt	660
cat	ca	cc	ccgttgg	ccggataga	gtggcgtt	720
cc	cc	cc	ccgttgg	ccggataga	gtggcgtt	780

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cgcattaagc	gccccgctg	gggagtagcg	ccgcaggct	aaaactcaa	ggaattgac	840
ggggcccgca	caagcagcgg	agcatgtgg	ttaattcgaa	gcaacgcgaa	gaaccttacc	900
agggcttgac	atgctnntga	agccggggaa	accgggtggc	cgagggagc	cagcgcagg	960
ggtgtcatggc	tgtcgtcagc	tcgtgtcg	agatgttgg	ttaagtccc	caacgagcgc	1020
aaccctgc	atatgtgcc	agcattcagt	tggggactca	tatgggactg	ccggcgtcaa	1080
gcgggaggaa	gttggggacg	acgtcaagtc	atcatgcct	ttatgcctg	ggctgcacac	1140
gtgtctacaat	ggccgtatac	acggggcgc	acctggcgc	aggaagcgaa	tccctcaag	1200
ccggcccccag	ttcggatcg	aggctgcaac	ccgcctcctg	gaagtcggag	ttgtctagta	1260
tcgcggatca	gcatgcgcg	gtatacgt	tcggggct	tgtacacacc	gcccgtcaca	1320
ccacccgagt	ctgtcgacc	cgaagccgc	ggccgaacc	gcaaggggcg		1370

SEQ ID NO: 28                    moltype = DNA length = 1394  
 FEATURE                        Location/Qualifiers  
 misc\_feature                1..1394  
                               note = Obtained from Intestinal Bacteria, K28  
 source                        1..1394  
                               mol\_type = other DNA  
                               organism = unidentified

SEQUENCE: 28  
 caagtcaac gaagcaactt cttccaaatc ttccgaagag gaggtattt actgagttgc 60  
 ggacgggtga gtaacgcgtg gggacactgc cccgtaccgg gggataacag tcagaatga 120  
 ctgtctaatac ccgcataaagcg cacaaaggcg catgccttt tggtaaaaac tccgggtgta 180  
 cgggatggtc ccgcgtctga tttagcagg tgggggttaa cggggccacca aagcgacgat 240  
 cagttagccg cttgtatggg tggacggca cattgggact gagacacggc ccagactcct 300  
 acggggaggca gcagtgggga atattgcaca atgggggaa ccctgtatgca gcgacgcgc 360  
 gttagcggcgg aagtatttcg gtatgtaaag ctctgtcagc agggaaagaaa atgacgggtac 420  
 ctgtaccaaga agcaccgggt aaatacgtgc cagcaggccg ggtataacgt atgtgcgaaag 480  
 cgttatccgg attacttgg tgtaaaggga gctgtacggc agggcaagt ctgaagtgaa 540  
 agccccgggc ccaaccccg gactgcctt gaaaactgtcc gtctggagtg cggagaggt 600  
 aagcggaaatt cccagtgtag cggtaaaatg cgttagatatt gggaggaaca ccagtggcga 660  
 aggccggatca ttggacggc actgtacgtt aggctcgaa gctgtggggag caaacaggat 720  
 tagataccct ggtatgtccac ggcgtaaacg atgactacta ggtgtcggtt ggcagagcca 780  
 ttccggcgcg cagccaaacgc agtaatgtt ccacctgggg agtacgttcg caagaatgaa 840  
 actcaaaggaa attgacgggg accccgcacaa gccgtggagc atgtggttt attcaagca 900  
 accgcggagnn ncttacactgg ccttgacatc cccctgaccgc ggcgcgtaaatg gtgcctttcc 960  
 ttccggcgcg agggcgtacac acgtgtacaa atggtcgtaaa cagagggaaag cgagccgcgc 1020  
 gtttaagtccc gcaacgagc caacccttta cttcgtatgc cagcattcag gatgggcact 1080  
 ctggagagac tgccaggggac aacctggagg aagggtgggaa tgacgtcaaa tcatatgccc 1140  
 ccttatggcc agggcgtacac acgtgtacaa atggtcgtaaa cagagggaaag cgagccgcgc 1200  
 agggggggca aatccaaaaa ataacgtccc agttcggact gcaaggctgc acccgccctc 1260  
 acaagctgg aatcgctgt aatcgcaat cagcatgtc cggtaatc gttccgggtt 1320  
 ttctgtacaca ccggccgtca caccatggg gtcggtaacg cccgaagtca gtgacccaaac 1380  
 ctccgggaggc gggc

SEQ ID NO: 29                    moltype = DNA length = 1387  
 FEATURE                        Location/Qualifiers  
 misc\_feature                1..1387  
                               note = Obtained from Intestinal Bacteria, K29  
 source                        1..1387  
                               mol\_type = other DNA  
                               organism = unidentified

SEQUENCE: 29  
 agtcgaacga agcatttagg attgaagtt tcggatggat ttcctttatc actgagttgc 60  
 ggacgggtga gtaacgcgtg gggacactgc cctatacagg gggataacag ctggaaacgg 120  
 ctgtctaatac ccgcataaagcg cacaaatcg catgattcg tggtaaaaac cctggcagta 180  
 taggtatggtc ccgcgtctga tttagtgggtt ggtggggatc cgggtacacca aagcgacgat 240  
 cagttagccg cttgtatggg tggacggca cattgggact gagacacggc cccaaactcct 300  
 acggggaggca gcagtgggga atattgcaca atgggggaa ccctgtatgca gcgacgcgc 360  
 gttagtggaaat ggtatgtaaag ctctatcagc agggaaagaaa acagacggta 420  
 cctgactaaag aagccccggc taactacgtt ccagcaggccg cggtaatcagc tagggggca 480  
 gctgtatccg gaattacttgg tggtaaaggga tgctgtatgg gcatgttgc tgaaatgt 540  
 aagccccggg cttaaaccccg ggactgtctt tggaaactgtc atgtggagtg gcaaggaggg 600  
 taagcggaaat ttctgtatgtc tgctgtatgc gctgtatggat tagggaggaaac accagtggcg 660  
 aaggccgggtt actggactgt cactgtacatc gatgcacca gacgtggggaa gcaaaacagga 720  
 tttagataccct ttgttagtcca cggccgtaaac gatgtatgtt aggtgtcggtt gccgttaggg 780  
 ctccggcgcg ctagaaatgtt tccacactgg ggtacgttc gcaaaatgt 840  
 aactcaaaggaa attgacgggg gaccgcaca acgggtggag catgtgggtt aattnnaagc 900  
 aacgcgtcaagn nncttacactgg gtcttgacat cccaaatgtc gnnnnnttaac cgnnttttc 960  
 ttccggacaca ttggatggacac gttgtcgatc gttgtcgatc tgatgttttgc 1020  
 ggttaagtcc cggcaacgc gcaaccccta tcttttagtgc ccagcattgc aggtggggcac 1080  
 ttcttagatggc ctggccaggaa taacccgtgg gaaagggtgggg aggacgtcaaa atcatatgtc 1140  
 cccttatggc cagggtatca cactgtatgc aatggcgtaa acaaaggaa gcaaggatgt 1200  
 gaggcgtacaa aataacgtt cagttcgatc tggatgttc aactcgacta 1260  
 catgtatggc gatgtatgc taatcgatca tcagaatgtc acgggtgtaa cgttccgggg 1320  
 ttctgtacaca accggccgtc acaccatggg agtcaatgtc gcccgtac ggtgacccaa 1380  
 ccgcgtacaa

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cgcgatgcgaa	acctaccat	aacaggggga	taacactgaa	aaattggta	taataccca	120
taacatcagg	acccgatcg	gttctggtg	aaaactccgg	tggttatgga	tgggcatcg	180
ttgttattgc	ttgggtgtg	ggttaacggct	caccaaggca	acgatacata	gggggactga	240
gaggttaacc	ccccacattg	gtactgagac	acggaccaa	ctccctacggg	aggcagcagt	300
gaggaatatt	ggtcaatgg	cgcaagtctg	aaccagccat	gcccgtgca	ggaagacggc	360
tctatgagg	gtaaaactgt	tttgtacgag	ggtaaacgcgt	tttacgtgt	agagcctgaa	420
agtatcgtac	gaataaggat	cggetaactc	cgtgcccag	gcccggtaa	tacggaggat	480
ccaaacgtta	tccggattt	ttgggtttaa	agggtgcgt	ggccgttta	taagtttagag	540
gtaaaatacc	ggtgcgttaac	accggaaactg	cctctaatac	tgttgaacta	gagagtagtt	600
ggcgtagggc	gaatgtatgg	tgtatcggtg	aaatgtctta	agatcataca	gaacaccgt	660
tgcgaaggca	gcttaccca	ctatactcg	cgttgaggca	cgaaggcg	gggagcaac	720
aggattagat	accctgttag	tccacgcgt	aaacgcgtat	aactcgctgt	cggcgatata	780
cagtcggccg	ctaagcgaa	gcpataagtt	atccacctgg	ggagtcgtt	cgcaagaatg	840
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atacgcgagg	aaccttaccc	ggggatggaa	gttactgttt	acggatgtt	caggatttcc	960
cttcggggca	gaaaaactgg	tgcgtcatgg	ttgtcgatcg	ctcgccgt	gagggtcg	1020
gttaagtccc	ataacgagcg	caacccctac	cggttagtgc	catcaggta	agctgggcac	1080
tctgggggca	ctgcgggt	aagccggag	gaaggtgggg	atgacgtca	atcagcacgg	1140
cccttacgtc	cggggttaca	cacgttttac	aatgggtat	acagggca	gttacccca	1200
gatggatgc	gaatctcgaa	agcttatctc	agttcgat	ggaggctgaa	acccgcctcc	1260
gtgaagttt	atcgctagt	aatcgcgat	cagccatgg	ggggtaata	cgttccccgg	1320
ccttgcac	accggccgtc	aagccatgg	agctgggggt	gcctgaagtt	cgtgaccgca	1380
agg						1383

SEQ ID NO: 33	moltype = DNA length = 1378
FEATURE	Location/Qualifiers
misc_feature	1..1378
note = Obtained from Intestinal Bacteria, K33	
source	1..1378
mol_type = other DNA	
organism = unidentified	

SEQUENCE: 33						
gaggggcagc	atcattaaag	cttgcgttga	tggatggcga	ccggcgcac	ggtgagtaac	60
acgtatccaa	cctggcaca	acactggat	agcccttcga	aagaaaggat	aataccggat	120
ggcatagttt	tcccgcatgg	gataattt	aaagaatttc	ggttgtcgat	ggggatgcgt	180
tccattaggc	agttggcg	gtaaacggcc	accaaaacca	cgtggatag	gggttctgag	240
aggaagggtcc	ccccatctgg	aactgagaca	cggtccaaac	tcctacggg	ggcagcagt	300
aggaatattg	gtcaatggac	gagagtctg	accagccaa	tagcgtgaag	gatgactgcc	360
ctatgggtt	taaacttctt	tttacggg	ataaaagttag	ccacgtgtt	ctttttgtat	420
gtaccgtatg	ataaggatc	ggctaaactcc	gtgcgcgt	ccgcgttata	acggaggatc	480
cgacgttatt	ccggattttat	ttgggtttaaa	ggggagctg	gggggttgg	aagtcaattt	540
tgaagttt	cggtcaacc	gtaaaattgc	agttgtatact	ggcgacctt	agtcaacag	600
aggttagggc	attcggtt	gttgcgttga	aatgcgttga	tatcaggaa	aactccgtt	660
gcaaggccg	cctactgtt	gttgcgttgc	gttgcgttgc	gaaagtgtt	gtatcaaaa	720
ggatttagata	ccctgtttagt	ccacacgt	aacgtat	actcgctt	ggcgatata	780
ggtcagccgc	caagcgaa	cattaagtat	tccacctgg	gatgtacgc	gcaacgggt	840
aactcaaa	attgtacggg	ggccggccaa	agccggaggaa	catgtgtt	aattcgat	900
tacccgttgc	acccttaccc	ggcttaattt	gcaactgtact	gaacggaaa	cggttctt	960
ttccggacgt	tgtgaagg	ctgtatgtt	gtgcgttgc	cggtgcgtt	gggtgcgtt	1020
taagtgcct	aaacgagcg	acccttatcg	atagttacta	gcaggtat	ctgaggactc	1080
tattgtatg	ggccgttgc	gtatgttgc	aggtggggat	gacgttataat	cacacggcc	1140
cttacgtcc	gggttacaca	cgtgttacaa	tgggggttac	agaaggc	tacacggca	1200
cgtgtgttgc	atcccgaa	cctcttctcg	ttccggatgtt	agttctca	ccgactccat	1260
gaagcttgc	tgcgtat	tcgcgcata	gccacggcc	ggttaata	ttccggggcc	1320
ttgtacac	cgcccgtaa	gcccgtt	ccgggggtt	ctgaagtac	taaccgcg	1378

SEQ ID NO: 34	moltype = DNA length = 1394
FEATURE	Location/Qualifiers
misc_feature	1..1394
note = Obtained from Intestinal Bacteria, K34	
source	1..1394
mol_type = other DNA	
organism = unidentified	

SEQUENCE: 34						
cagtgcgcg	aagactttaa	gtggatctct	tccgattgaa	acttattgt	actgagccgc	60
ggacgggtga	gtaaacgcgt	ggtaacctgc	ctcatacagg	gggataacag	tttggatgtt	120
ctgtataatc	cgccataagcg	cacaggacc	catgtgttgc	tgtaaaaac	tccgtgtt	180
tgagatggac	ccgcgtctg	tttagttagt	ggaggggtt	ccggccacca	aggcgacgt	240
cagtgcgcg	cctgatgtt	tgcgttgc	cattgggact	gagacacggc	ccagactcc	300
acggggaggca	gtcgtgggg	atattgcaca	atgggggaa	ccctgtat	gcgcacgc	360
gtgaaggaa	aagtatctcg	gtatgttac	tccat	aggaaagaaa	atgacgtt	420
ctgactaaga	agccccggct	aactacgtt	cagcagccgc	ggtataat	aggggcaag	480
cgttatccgg	atttactgg	tgtaaagg	cggtatgtt	aaagacgt	ctgtatgt	540
aggctggggc	ttaacccat	gactgcatt	gaaaactgtt	ttctatgtt	ccggagggat	600
aagcggaa	ctctgttgc	cggttataat	aggaggaa	ccat	ccatgttgc	660
aggccgtt	ctggacgtt	actgtacgtt	aggctcgaa	gctgtgggg	caaacaggat	720

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tagataaccct	ggtagtccac	gccgtaaacg	atgaataacta	ggtgtcgggt	ggcaaagcca	780
ttcggtgcg	cagcaacgc	aataagtatt	ccacctgggg	agtacgttcg	caagaatgaa	840
actcaaaggaa	attacgggg	acccgcacaa	gccccggc	atgtggtttta	attcgaagca	900
acccgaaagaa	cottaccaag	tcttgacato	cctctgaccc	gcccgtaaacg	gggccttccc	960
ttcggggcag	aggagacagg	tggtgcatgg	ttgtcgtca	ctcggtcgt	gagatgttgg	1020
gttaagtccc	gcaacgagcg	caaccctat	ccttagtgc	cagcagggtga	agctgggcac	1080
tcttagggaga	ctggcgggga	taacccggag	gaaggcgggg	acgacgtcaa	atcatcatgc	1140
cccttatgtat	ttgggttaca	cacgtgtac	aatggcgtaa	acaaaaggaaa	gcgagacagc	1200
gatgttgcgc	aaatcccaa	aataacgtcc	cagttcggac	tgcagtctgc	aactcgactg	1260
caccaaggt	gaatcgctag	taatcgcgaa	tcagaatgtc	gccccgttgg	1320	
tettgtacac	accgcggcgtc	acaccatggg	agtcgtaaac	gccccgttgg	1380	
ccttacagga	gggg					1394

SEQ ID NO: 35            moltype = DNA length = 1392  
 FEATURE                Location/Qualifiers  
 misc\_feature            1..1392  
 note = Obtained from Intestinal Bacteria, K35  
 source                1..1392  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 35  
 cagtgcgaaacg gagactcgagg ttggaaactt tcttcggggag tggatttctc gacttagtgg 60  
 cggacgggtgc agtaacgcgt gagaatctcg cctttaaggg ggggataaca gtggaaacg 120  
 gctgtctaata ccgcataaag catttgcattc gcatgttttc gatgcacaaag gagaatccg 180  
 cttttagatg acgtcgctc tgattagcta gttggcgggg taacggccca ccaaggcgac 240  
 gatcgttgcg aggactgtgaa gggttgcacgg ccacattttggg actggacacac ggcccacact 300  
 cttacggggg gcaatcggtt ggaatattcg gcaatggggg aaaccctgac gcagcaacgc 360  
 cgcgtgtattc aagaaggcc tcgggttgc aagatcttta atcaggacg aaacaatgaa 420  
 cggtacatgtc agaataagct ccggcttaact acgtgcgc gacggcggta atacgttggg 480  
 agcaaggctt atccggattt actgggtgtta aaggcgccgc acggcggccg gcaagtgg 540  
 agtggaaatct atggggcttaa cccatggatc gtttcaaaa ctgcgttgcgt tgagtgtatgg 600  
 agaggcggc ggaattccgt gtgtgggtt gaaatgcgtta gatatacgga ggaacacccag 660  
 tggcgaaggc ggcctgctgg acatataactg acgctgaggc gcgaaacggtt gggggacaaa 720  
 caggattaga taccctggta gtccacgcgc taaacatgttgc atactagggtg tggggaggat 780  
 tgacccttc cgtgcggcag ttaacacataa aagtatccca cctggggaggat acggccgcac 840  
 gggttgaactt caaaaggattt gacggggccc cgcacaagca gtggaggatg tgggttaatt 900  
 nagaaccaacg cgaagaaccc taccaggctt tgacatccgc atgaccgcct tagagataag 960  
 gcttttttc ggaacatcggtt tgacagggttgc tgcatgggttgc tggtcgttgcgttgc 1020  
 atgttgggtt aagtccgcg acgacgcgc cccttacggcgt tagtgcatac gcaagatcac 1080  
 tctagccgcg ctggcgttgc caaaaggatgg gaaagggtgggg acgacgtcaa atcatcatgc 1140  
 cccttatgtac ctgggttaca cacgtactac aatggcgatc atacagaggaa aagcaaaaacc 1200  
 gcgagggtggc gcaaaatccctt aaaagctgtc ccagttcaga ttgcaggctg caaccgcct 1260  
 gcatgaatgc gaaattgtca gtaatcgcggtt atcagcatgc cgcgggttgc acgttcccg 1320  
 gccttgcata cacccggcgtt cacaccatgtc gaggcgttcaaa taccggaaat ccgtactca 1380  
 accttcttgg ag 1392

SEQ ID NO: 36            moltype = DNA length = 1394  
 FEATURE                Location/Qualifiers  
 misc\_feature            1..1394  
 note = Obtained from Intestinal Bacteria, K36  
 source                1..1394  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 36  
 agtcgcgaaacg agcaattaaa atgaagttt cggatggatt tttgatttgc tgagtggcgg 60  
 acgggggtgagt aacgcgttgcgtaa acactcgccat cacactgggg gataacaggat agaaatgact 120  
 gctaataccgc cataacgcgc cagttacccgc tggtaacgggttgc tgaaaaaccc cggtgtgt 180  
 agatggatcc gctgtctgatt agccgttgcggggtaacccg gcccacaaa ggcacgtatca 240  
 gtacccgcacc tgagagggttgc accggccatca ttggactgttgc gacacggccc aaactccctac 300  
 gggaggcgcg acgtggggatatttgcacaaat gggcgaaaggcttgcgttgc gacggccgcgt 360  
 gactgttgcgttgc atgttgcgttgc atgttgcgttgc ggaagaaaat gacggatcc 420  
 gactaagaag ccccggttgc atcactgttgc gacccgcggtaatcgttgc gggcaacgc 480  
 ttatccggat ttactgggttgc taaaggggatgc tgacggcgc aacgttgcgttgc gaaatgggg 540  
 cccagggttgc aaccctggta ctgttttgc aactgttttgc cttagatgttgc gggaggatgg 600  
 gtggaaatccctc tagtgcgttgc tgtaatggatgc tagatattttgc gaggaaaccc acgtggcgttgc 660  
 gccgcgttactt ggcacatgc tgacgttgcgttgc gtcggaaacgc gtggggaggca aacaggatca 720  
 gataaccctgg tagtccacgc cgttaacatgc gatgttgcgttgc tggtgggggg caaaggccctt 780  
 cgggtccgcgc gcaaaacgcgc taagcattcc acctggggatgc acgttgcgttgc agaaatgggg 840  
 tcaaaaggatgc tgacggggatgc cccgcacatgc ggtggaggatgc tggtggggatgc acgttgcgttgc 900  
 gcgaaaggatgc ttaccaatgc ttgcacatgc ctgttgcgttgc gtcggaaacgc gccttccctt 960  
 cggggcgttgc gaggacggatgc tgacgttgcgttgc gtcggaaacgc gtggggaggca aacaggatca 1020  
 taagtccgcgc aacgcgttgc acccttacgc ttactgttgc gacgggttgc gtcggactc 1080  
 tagggggactt ggcaggatgc acctggggatgc aggtggggatgc acgttgcgttgc agaaatgggg 1140  
 cttagtgcgttgc gggctacaca tggtgttgc gtaatggggatgc aacaggatgc acgttgcgttgc 1200  
 tggtggggactt ggcaggatgc acctggggatgc aggtggggatgc acgttgcgttgc gtcggactc 1260  
 cgaaggatgc acgttgcgttgc agaaatggggatgc gtcggactc ttccgggttgc 1320

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ttgtacacac cgcccgtaac accatggag ttagcaacgc ccgaagtca gtagccaact 1380
cgcaagagag ggag 1394
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SEQ ID NO: 37 moltype = DNA length = 1371
FEATURE Location/Qualifiers
misc_feature 1..1371
note = Obtained from Intestinal Bacteria, K37
source 1..1371
mol_type = other DNA
organism = unidentified
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SEQUENCE: 37
cagtcaacgc agccgagggg agcttgcac ccagagctag tggcggacgg gtgagtaaca 60
cgtgagcaac ctgccttc aagggggata acgtttggaa acgaacgcata ataccgcata 120
acataccggg accgcgtat tctgtatca aaggagaac ccgcgtaaag atgggctcgc 180
gtccgattag ctatggcggc gggtaacgcg ccaccaaggc gacgtacgtt agccggactg 240
agaggttgat cggccacatc gggactgaga cacggcccg actcctacgg gaggcagcag 300
tgggggatat tgcacaatgg aggaaactct gatgcagcga cgccgcgtga gggagaacgg 360
tcttcgatt gtaaacctct gtcttgggg acgataatcga cggtaacccaa ggaggaagct 420
ccggctaaact acgtgcccgcg acggcggta atacgttaggg aacggcgtt gtccggatt 480
actcgggtta aaggagcgtt acggcgggtt tcaagtcgaa ttgttaaatct accggctcaa 540
cttgttagctt ctgtcgaaac tggggctt ggttggatc gaggcggcgtt gatggcttag 600
tgttagcgtt aaatgcgtt atatttaggaa gaaacaccgtt ggcgaaggcg gcctgctgg 660
cttttactga ctgtggggctt cggaaacgtgtt gggagcaaggc aggatagat accctggtag 720
tccacgcgtt aaacgtatgtt taatgggtt gggggactt accccctccg tgccggattt 780
aacacaataa gtaatcacc tggggatgtt gacccgtt gttgaaactca aaggaaatgtt 840
cggggccccc cacaaggatgtt ggatatgtt gtttatttcg aacgcacccg aagaacccta 900
ccaggcttgc acatcgatgtt acgggttgcgtt agatagatgtt ttcccttggg acacaaaggac 960
agggtgttgc tgggtgtcgtt cagtcgtgtt cgttggatgtt cccgcacacgtt 1020
ggccaaacctt tattttatgtt tgctacatcc tgggtgttgcac tcaatgttgc tgggtgttgc 1080
caaaacgggg gaaagggtttt atggatgttgc acatcatgttgc cccttgcgttca 1140
cacgtatgtt gatggatgtt aacagaggaa aacagaggaccc cgatgggtttt caaaccctta 1200
aaagtctctt cagttcgatgtt tggggatgttgc aacttcgttgc catggatgttgc gaatttgcgtt 1260
taatcgccgaa tcagcatgttgc gccgtgttgcata cgttggatgttgc accggccgtt 1320
acaccatggg agtcgttgcata accccgttgc agttagcgttgc cccgcacaggag 1371
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SEQ ID NO: 38 moltype = DNA length = 1396
FEATURE Location/Qualifiers
misc_feature 1..1396
note = Obtained from Intestinal Bacteria, K38
source 1..1396
mol_type = other DNA
organism = unidentified
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SEQUENCE: 38
tgcagtcgaa cgctttgtt aaggagttgc ttctttacg gtaggtggcgac acgggttgcgtt 60
aatacataag caatctgccc atcgccctgg gataacagt gggaaacgcact gctaataccg 120
gatagggttag ttcttggcat cagggactaa ttaaagtgg gataacaacac ggttggatgtt 180
gtcttatggcg tattatgtt taggtggatgtt gggggccac ccgtggatgtt atacgtatgtt 240
gacccgttgcg ggttggatgtt gggggccac ccgtggatgtt gggggccac ccgtggatgtt 300
cagcgttgcg gaaatttccg caatggggca aacgttgcgtt gggggccac ccgtggatgtt 360
agaaggccctt cgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 420
tatggggatgtt acgggttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 480
aatacgttgcg tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 540
gaaaaggatgtt aatgttgc gttgggttgc tgggtgttgc tgggtgttgc tgggtgttgc 600
agagttacagg agagggttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 660
ggaaacccagg tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 720
ggggggatgtt taggatgtt tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 780
ttggggaaatc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 840
aagtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 900
ttcgacgcaccc cggccggatgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 960
tagtggggatgtt tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 1020
gttgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 1080
gactcttagatgtt acgttgcgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 1140
tgcccccttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 1200
agcaatgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 1260
cttcatgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 1320
ggggccgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 1380
taaccctgttgc aagggttgc tgggtgttgc tgggtgttgc tgggtgttgc tgggtgttgc 1396
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SEQ ID NO: 39 moltype = DNA length = 1399
FEATURE Location/Qualifiers
misc_feature 1..1399
note = Obtained from Intestinal Bacteria, K39
source 1..1399
mol_type = other DNA
organism = unidentified
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SEQUENCE: 39
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cgtctgaacg	gtaacaggaa	gcagttgtc	gcttggctga	cgagtggcg	acgggtgagt	60
aatgtctgg	aaactgcctg	atggaggggg	ataactacty	gaaacggtag	ctaataccgc	120
ataaactgc	cggaaag	ggggggact	tagggctct	tgcctacgga	tgtggcccac	180
ttgggattagc	taggtgttg	ggtaacggct	cacctagcg	acgatcccta	gtgtggctgta	240
gaggatgacc	agccacactg	gaactgagac	acggttcaga	ctcctacggg	aggcagcagt	300
ggggaaatatt	gcacaatggg	cgcaacgctg	atgcggcat	gcggcgctgta	tgaagaaggc	360
cttcgggttg	taaagtact	tcagggggg	ggaaggggat	aaagtataa	cgttgcgtca	420
ttgtacgttac	ccgcagaaga	agcacggct	aactcctgtc	cagcagccgc	gttaataccgg	480
agggtgcaag	cgttaatcgg	aattactggg	cgttaaagcgc	acgcaggcg	ttttgttaagt	540
catatgtgaa	atccccggca	tcaacccctgg	aactgcatct	gatactggca	agcttgatgc	600
tctgtatagggy	gggttagatt	ccagggttgat	cgggtgaat	cgttagagatc	tggagaaata	660
ccgggtggcg	aggccggcccc	ctggacggag	actgcgc	atgtgcggaaa	gcgtggggag	720
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ccctttaggg	gtgggttcgg	ggactaaccg	gtaaactcg	ccgcctgggg	agtcacggccc	840
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agaatgtgc	ttcgggaaacc	gtgagacagg	tgctgcatt	ctgtcgctcg	ctcggttgtt	1020
gaaatgttg	gttaagtctcc	gcaacggacg	caacccctt	ccttgggttc	cagcggttcgg	1080
gcggggaaact	caaggagac	tgcccgat	aaactggagg	aagggtgggg	tgacgtcaag	1140
tcatatgtcc	ccttacggacc	agggtacac	acgtgcata	atggccatca	caaaagagaag	1200
cgacccctgcg	agagcaagcg	gacccatata	agtgcgtcg	agtccggatt	ggagtcgtca	1260
actcgacttc	atgaaatcg	aatcgctatg	aatcggtat	cagaatgc	cgggtaaat	1320
gttcccccggc	cttgcatac	ccggccgtca	caccatggg	gtgggttgca	aaagaagtag	1380
tgatgtttac	cttcggggag					1399

```
SEQ ID NO: 40          moltype = DNA    length = 1384
FEATURE                  Location/Qualifiers
misc_feature             1..1384
                           note = Obtained from Intestinal Bacteria, K40
source                   1..1384
                           mol_type = other DNA
                           organism = unidentified
```

```
SEQ ID NO: 41          moltype = DNA  length = 1392
FEATURE                  Location/Qualifiers
misc_feature             1..1392
note = Obtained from Intestinal Bacteria, K41
source                   1..1392
mol_type = other DNA
organism = unidentified
```

```

SEQUENCE: 41
          organism = unclassified

agtgcgaacgaa agcactttat ttgatttct tcggggactga ttattttgtg actgagtgcc 60
ggacgggtga gtaacgcgtg ggtaaccctcg cttgtacagg gggataaacg ttggaaacgg 120
ctgctataac cgcataaagcg cacggcatcg catgtatcg tggtaaaaac tccgggttga 180
taataggcgc cccgcgttggaa tttagcttagt ggtggaggtaa cggccccca aggccgacat 240
ccatagccgaa cctgagagggg tgaccggcca cattgggact gagacacggc cccaaactct 300
acgggaggcga gcagtggggaa atattgcaca atgggcgaaa gcctgtatgca gcgacgcccgc 360
gtgagcgaag aagtatttcgt gtatgtaaag ctctatcagc agggaaataga attgacgtac 420
ctgtatcaga agcacccggct aaatacgtgc cagcagccgc ggtaaatacgt atggtgcga 480
cggttatccgg atttactggg tgatggaggaa ggcggccggc tgccggcaactgt ctgtatggaa 540
agccccggggc tcaaccccggt tactgcattt gaaactgtcg tactagatgt tcgggggggt 600

```

-continued

aaggcggaaatt	cctagtgtag	cggtgaaaatg	cgttagatatt	agggagaaca	ccagtggcga	660
aggcggtta	ctggacgata	actgacgcgtg	aggctcgaaa	gcgtggggag	caaacaggat	720
tagataccctt	ggtagttccac	ggcgttaaacg	atgaatacta	ggtgttttttt	aggatcttttt	780
ctcggtgcgc	tcgcaaaacgc	agtaagtattt	ccacctgggg	agtagcttcg	caagaatgaa	840
actccaaaggaa	attqacgggg	accccacaaac	ggcggttgagc	atgttttttttta	attcqaaacga	900
acgcgaaagaa	ccttaccaag	tcttgacatc	cttctgaccg	gtacttaacc	gtaccccttc	960
ttcgagcacg	gagtgcacgg	ttgtgtatgg	ttgttgttcg	ctctgttgtt	gagatgttgg	1020
gttaatggcc	gcaacgcgcg	caacccttat	ctttagatgc	cagegggttcg	gecgggcaact	1080
cttagagagac	tgccggatgt	aaacctgggg	aaggcggggg	tgacgttttttt	ttcatcatgcc	1140
cctttagact	tgggttacac	acgtgttaca	atggcgtaaa	caaagggaag	caaagctgtg	1200
aagcccgagca	aatctaaaaa	ataacgttcc	agttccggact	gtatgtctgca	accccgactac	1260
aaacggatgc	aatcgcttagt	aatcgcaatg	cagaatgtctg	cggtgaaatac	gttccccgggt	1320
cttgcatacaca	ccggccgtca	cacccatggga	gttgggaatg	cccgaaagcca	gtgacttaac	1380
cgaaaggaaq	qa					1392

```
SEQ ID NO: 42          moltype = DNA    length = 1397
FEATURE                  Location/Qualifiers
misc_feature            1..1397
                        note = Obtained from Intestinal Bacteria, K42
source                   1..1397
                        mol_type = other DNA
                        organism = unidentified
```

```

SEQUENCE: 42
caagtcaaaacg aagcatatag agacgagttt tcgggtatgt aactatata gactgagtgg 60
cggaggcggtt agtaacgcgt ggataaccctt ctcatacag gggataaca tttagaaatg 120
actgtcaata cccataaaggc gcacagtgctt gatggcaca gtgtaaaaa ctccggcggt 180
atgagatggc tccgggtttt attagctgt tggtgggtt aaggccattt aaggcagcga 240
tcaatagccg acctggagggtt gtgaccggcc acattggcac tgagacacgg cccaaactcc 300
taatggggggc agcactggggg attatggcactt atggggggaa accctgtatgc agcgacggcc 360
ctgtggggaaa gaatgtttt ggtatgtaaa ctttcatcg caggggaaa aatgtacgtt 420
cctgactaaag aaggccccggc taattacgtt ccagcagccg cggtaatacgt taaggggcaa 480
ggcttatccg gattttactgg gtgttaaaggg agcgttagacg gcaagtcaag tctgtatgt 540
aaaggccccggg ctcaaccccg ggactgtttt ggaaatgtt cttttttttt gttttttttt 600
taatggat tccatagttgc ggggtttttt gctgtatgtt tagggggaaac accatggcg 660
aaggccgctt actggacgtt aactgtttttt ggggtttttt gcaaaacccgg 720
ttatgataccctt tggatgttcc cccggtaaaac gatgtttttt aggtgtccggg cggccaaaggc 780
gttccgggttcc gcaacaaaggc caataatgttcc ttccatctttt ggtttttttt gcaaaatgtt 840
aactcaaaaggc aatttgcggcc acggccggccca acggccggccca catgtttttt aatttgcggcc 900
aacggcaagaac acctttttttt gttttttttt ctggccgtttt ggtttttttt aggacccccc 960
cttcgggacca gggcaagacag gttttttttt gttttttttt gttttttttt tgatgtttt 1020
ggtaatggctt cccggccggcc gcaacccctt tttttttttt ccacggccgtt gacgtttttt 1080
ctctatggggacttggccgggg acacacccggg ggaatgggggg gatgtttttt aatcatcatg 1140
cccccttgcgtt tttttttttt acacacccggg ccacatgtttt caatggccgtt aacaaaggggg agccggaaagggg 1200
tgacctgtttt gaaatcccaaa aataatgtttt tcagttttttt ttgtttttttt caactctgtt 1260
acatgtttttt ggaatgtttt gtaatgtttt atcgtttttt cgccgtttt gatgtttttt acgtttttttt 1320
gttttttttccacccggccgtt cacacccatgg ggtttttttt tgccggaaac ccgttgcggcc 1380
accggaaaggggg gaaagggg 1397

```

```
SEQ ID NO: 43          moltype = DNA    length = 1388
FEATURE                  Location/Qualifiers
misc_feature             1..1388
note = Obtained from Intestinal Bacteria, K43
source                   1..1388
mol_type = other DNA
organism = unidentified
```

```

SEQUENCE: 43
agtccgaacgg agcacccctt actgagggtt cggccaaatg ataggaatgc ttagtgtggcg 60
acttgtgtat aacgcgttgag gaacctgtct tcacaggggg gacaacatgg gaaaacact 120
gtaatacccg catgacgcatt gaccggggca tcccccggat gtcaaaatgt ttatcgttgg 180
aagatggctt cgcgctgtat tagctatgtt gttgggtttaac ggccccccat ggccgacatc 240
agtagccgga ctgaggggtt gaccggccac attgggactg agataccggc cagactccta 300
cgggaggccgca cagtggggaa tattggggca tggacggcaag tctggcccgaa caacccggcg 360
ttaaggagaaga aggctttccgg tggttaaaat tcttttgc tggaaagatgaa gaagacgtt 420
cttgcacat aaggccacggc taactacgtt ccacgcggcc cgttataatcg tagttggcaa 480
gegttgtccg gatTTTactgg tgtaaaagg egtpcggccg ggccggcaag tcatgtga 540
aatctggagg cttaacccctt aaactgcatt tgaaaactgtt ggtcttggat accggagagg 600
ttatcggat tccttgttgc gccgttgaat gctgtat aaggaagaac accagtggcg 660
aaggccgttacttgcggc aactgcggg gaggccggaa agcgttgggg gcaaaacaggaa 720
ttatgatacc ttggtagtcca cgcgtttaac ggtgtatcatggatcatggatgttggcg 780
cttcgttgcg cgcgtttaaca caataatgtt cccacccctggg tgcgttccat gcaagggttga 840
aactcaaaagg aattgtacggg ggcggccaca agcgttggat tatgttggttt aattcgaagc 900
aacgcgttgc aacttttccatgg ggttgcgttcat cctactaaatc aagttagatg acatcggat 960
cccttcggggaa aagttagatgc cgggttgcgtt atgggttgcgtt tcagtcgttgc tggatgttggat 1020
ttgggttgcgtt aatccgcaccc agcgttgcgttcatggatgttgcgttgc aagacgttgcgtt 1080
agcgagactt cgcgttgcacca aacggggggaa ggtttttttttt acgttcaatc atcatgcggcc 1140
ttatgttgcgtt ggttgcgttgcacca gtaatcaat ggcgttgcgtt acgttcaatc atcatgcggcc 1200

```

-continued

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ggcagagcaa	cccccaaaa	gccgtccag	tccggatcg	aggctgcaac	ccgcctgcgt	1260
gaagtggaa	tcgctgtaa	tcgcccata	gcatggccgc	gtgaatacgt	tcccgccct	1320
tgtacacacc	ccccgtcaca	ccatgagagt	cggaaacacc	cgaagtcgt	agcctaaccg	1380
caaggagg						1388
 SEQ ID NO: 44						
FEATURE						
misc_feature						
1..1393						
note = Obtained from Intestinal Bacteria, K44						
 source						
1..1393						
mol_type = other DNA						
organism = unidentified						
 SEQUENCE: 44						
tgca	ggactggct	tagaaagagg	attcgtccaa	ttgataaagg	tacttagtg	60
cgac	ggat	ggaaac	ctcggag	ggaaataaca	gaccgaaagg	120
cctg	ctaa	cgc	gat	gttcc	gat	180
tctg	gat	ttcg	ttgg	atgg	caaggc	240
atca	gtac	ggact	ggat	ggcc	gccc	300
ctac	gggg	cagc	cat	gggg	ggcc	360
gcgt	gaag	aga	aat	gggg	aagg	420
gtac	ctgagg	aata	ggc	actt	tcagg	480
caag	cgttat	ccgg	tttt	ttgg	gatc	540
tgaaa	actat	gggt	at	ggaa	atgt	600
aggca	atcc	ttgt	ttgt	tttt	ttgt	660
gcca	aggc	attt	ttgt	tttt	ttgt	720
ggatt	ttgt	ttgt	ttgt	tttt	ttgt	780
acccc	ccct	ttgt	ttgt	tttt	ttgt	840
ttgaa	acttca	ttgt	ttgt	tttt	ttgt	900
aagca	aaac	ttgt	ttgt	tttt	ttgt	960
gg	gggg	ttgt	ttgt	tttt	ttgt	1020
gtat	ttgt	ttgt	ttgt	tttt	ttgt	1080
ctttag	ccat	ttgt	ttgt	tttt	ttgt	1140
cccctt	ttgt	ttgt	ttgt	tttt	ttgt	1200
gca	aaat	ttgt	ttgt	tttt	ttgt	1260
gtat	ttgt	ttgt	ttgt	tttt	ttgt	1320
gcct	ttgt	ttgt	ttgt	tttt	ttgt	1380
accg	ttgt	ttgt	ttgt	tttt	ttgt	1393
 SEQ ID NO: 45						
FEATURE						
misc_feature						
1..1409						
note = Obtained from Intestinal Bacteria, K45						
 source						
1..1409						
mol_type = other DNA						
organism = unidentified						
 SEQUENCE: 45						
caagt	aaac	gtgtact	ttagttgt	agat	gat	60
acgc	gttgt	tttt	ttgt	ttgt	ttgt	120
ataac	atgt	tttt	ttgt	ttgt	ttgt	180
acct	gttg	tttt	ttgt	ttgt	ttgt	240
gacct	ggat	tttt	ttgt	ttgt	ttgt	300
cagc	atcc	tttt	ttgt	ttgt	ttgt	360
aga	tttt	ttgt	ttgt	ttgt	ttgt	420
ttt	ttgt	ttgt	ttgt	ttgt	ttgt	480
taata	actt	ttgt	ttgt	ttgt	ttgt	540
taata	actt	ttgt	ttgt	ttgt	ttgt	600
ttt	ttgt	ttgt	ttgt	ttgt	ttgt	660
agga	accc	ttgt	ttgt	ttgt	ttgt	720
ttgg	ttgt	ttgt	ttgt	ttgt	ttgt	780
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	840
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	900
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	960
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	1020
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	1080
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	1140
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	1200
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	1260
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	1320
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	1380
tttt	ttgt	ttgt	ttgt	ttgt	ttgt	1409
 SEQ ID NO: 46						
FEATURE						
misc_feature						
1..1395						
note = Obtained from Intestinal Bacteria, K46						
 source						
1..1395						

-continued

**mol\_type** = other DNA  
**organism** = unidentified

**SEQUENCE: 46**

```

caatgcggac ggcagcgcgg ggagcttgc ccctggccg gagtggcgca cgggttagta 60
atacatcgga acgtgtcttc tagtggggaa taactcccg aaaggccgcg taataccgca 120
tgagaccta ggggtaaagc gggggatcgc aagacctcg gctggaaagag cggccatgt 180
ccgatttagt agtttgtgtg gtaaaggcgc accaaggcga cgatcgtag ctgtctggag 240
aggacgacca gcccacactgg ggttagagaca cggccggac tcctacggg ggcagactg 300
ggacattttg gacaatacggg gcaaccctga ttccacggat ccgcgtcgat gatgaaggc 360
ttccggattgt aaactgcatt tgcacggac gaaaaggat ggcataaacac cgcattccgc 420
tgacggtacc tgaagaataa gcaccggta actacgtcc agcggccgcg gtaatacgta 480
gggtggcgaag gttaatcgga attactggc gtaaaggctg cgcggccgtg tctgttaagat 540
agatgtgaaa tccccgggtt caacatggga attgcataat tgactgcagg atctgtatgtt 600
gtcagaggag ggttggattc cacgtgtac agtgaatgc gtagatatgtt ggaagaacac 660
cgatggcga ggcacggccctt tggggatcga ctgcacgcctca tgcaacggaa cgtggggagc 720
aaacaggattt agataccctgt gtatccacg ccctaaacgta tgcttactag ttgttgggaa 780
cgatgtccctt tggttaacgcg gctaaccgcgt gaagtagaccc gcctggggag tacgggtcgca 840
agattnaaac tcaaaaggat tgcacggggc cggcacaacg ggttgatgt tggttataat 900
tcgcgtcaac gcgaaaaacc ttacccatggc ttgacatgcc aggaaggcct gagagatcag 960
ggccgtccggc caaggggatc gggacacagg tgctgcattg ctgcgtcgat ctcgtcgct 1020
gagatgttgg gtttaagtccc gcaaggcggc caacccctgtt cattatggc tgacggagg 1080
cactctatgg agactgcggg tgacaaacccg gaggaaaggtg gggatgacgtt caagtcctca 1140
tggcccttat ggcttagggc tcacacgtca tacaatggtc ggaacagagg gaagcgaagc 1200
cgcgggttga agccaatccc agaaaaacgcg tgcgtatccg gatgcacgtc tgcaacatcga 1260
tcgcgtatggac tcgaaatcgc tagtaatcgc ggtacgtat ggcgcgtgtg atacgttccc 1320
gggttggtaa cacacccccc gtcacacatc gggagtgggg ttacccaga gacgtttggcc 1380
caacccggaa gaagg
  
```

**SEQ ID NO: 47**

```

moltype = DNA length = 1384
Location/Qualifiers
misc_feature 1..1384
note = Obtained from Intestinal Bacteria, K47
source 1..1384
mol_type = other DNA
organism = unidentified
  
```

**SEQUENCE: 47**

```

agtgcacccgg gatcccaagg gtttgcctt ggggttagatg ggcacccggg tgactaatgc 60
gtggccggacc tgccccatac accggaaatag ctcctggaaa cgggtggtaa tgccggatgc 120
ttccatgtac cgcatggccc ttggggaaatg attctatgg tatggatgg ggtcgccgtcc 180
tatcagcttg atggccgggtt aacggccac catggctcg acgggttagcc ggcttgagag 240
ggccggccggc cacatggggc ctgagatcgc gcccacatc ctacggggg cgcacgggg 300
gaatattggca caatggggc aacgctgtatc cgcacggcc ggtggccggg tgacggccctt 360
cggtggatggaa accgcgttttgc acggggacccg acggcccttcgg ggtgatgtatc ctttcgaat 420
aagcaccggc taactacgtg ccacgcgcg cgttaatcgc taggggtccaa cggttatacg 480
gaattatggc gctgtaaaggc ctgcgtatccg gttcgatccg tccgggtgtgaa aagtccatcg 540
cttacccgttgc gatccggccg gggtaatggc ggggttggat ggggttgggg agactggat 600
ttccgggtgttgc acgggtgtat gttatggatgg gggggaaaggc accaaatggc gggcggatc 660
tctggccgttgc cactgtatccg gggggatggc acgcgtgggg ggcacccaggat ttagatacc 720
tggtagtccaa cggccgttac ggttggatgtt ggtatgtggg accattccac ggttctccgt 780
tcggggccggc cgcgtttaaaggc atcccgccgtt gggatgtccgg ccgcacggat aaaactcaaa 840
gaaatttgcgc gggggccggc caacggccggc acgtatccgc ttaatccgt gcaacggaa 900
gaaaccttacc tggggatgtac atgttccgcg cagccgtatc gatacgttcc ctttcgggg 960
cggtgttccaca ggttggatccat ggtcgatccgc acgtcgatccg gttagatgtt ggggtttagatc 1020
ccggccacccgcg cgcaccccttgc gcccgtgtt ggcacccgcgt cgtgtggggg actccacggg 1080
gaccggccggc gtcaactcggtt aggaagggtgg ggtatgcgttcc agatcatcat gccccttacg 1140
ttccgggtgttgc acggcatgttca acaaattggcc gttacaacggg atgcacatcgt gtcgggggg 1200
ggggatccctt gggggatccatc gttcaatccgcg attggatgtt gcaacccgcg tccatggaa 1260
cggtgttgcgtt agtaatcgcc gtcacgttccg gccgcgggtgaa atgcgttccc gggcccttgc 1320
cacacccggcc gtcacgttccg gaaatggggt gacacccggaa gccgggtggcc caaccccttgc 1380
gggg
  
```

**SEQ ID NO: 48**

```

moltype = DNA length = 1387
Location/Qualifiers
misc_feature 1..1387
note = Obtained from Intestinal Bacteria, K48
source 1..1387
mol_type = other DNA
organism = unidentified
  
```

**SEQUENCE: 48**

```

gtcgaacggaa gtcgttttgc tgaagtttc ggttggatggaaa aacacgttttgc agtggggggac 60
gggttggatggaa cgcgtgggtt acctgcctca cactggggggaa taacaggatggaa aataatcgatc 120
taatacccgca taagcgcaca gttccgcatttgc gaaacgtgttggaaa aacccatccgc tggtgtgtg 180
atggacccgcg ctgtcgatgttccgcg ggttggatggggcc ccacccaaacgc gacgtatgtt 240
agccggccggc agggggatggaa cggccacatccgc gggactgaga cgcggcccaactccatcg 300
ggggccggcgttgc gggggatggatggggccatccgc gatgcacatcgttcc gtcggccgttgc 360
gttggatggatggaa gttccgcatttgc gaaacgtgttggaaa aacccatccgc tggtgtgtg 420
gttggatggatggaa gttccgcatttgc gaaacgtgttggaaa aacccatccgc tggtgtgtg
  
```

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ataagaagcc	ccggtaact	acgtgccago	agccgcggtta	atacgttaggg	ggcaagcgctt	480
atccggattt	actgggtgt	aagggagcgt	agacggcaag	gcaagtctga	agtgaaagcc	540
cggtgcttaa	cgccggact	gctttggaaa	ctgtttggct	ggatggcccgg	agaggttaagc	600
ggaattctta	gtgtagcggt	gaaatgcgt	gatatttagga	agaacaccag	tggcgaaggc	660
ggcttactgg	acggttaactg	acggttaggc	tcgaaagcgt	ggggagcaaa	caggattaga	720
taccctgtta	gtccacgccc	taaacatgta	ttgtcttaggtt	taggtgggtt	tggaccatc	780
ggtgcgcag	ctaaccgtat	aagaatcca	cctggggggat	tacgttcgca	agaatgaaac	840
tcaaaggaaat	tgacggggac	ccgcacaago	ggtggagcat	gtgggttaat	tcgaacgaaac	900
gcaagaacc	ttaccagggtc	ttgacatccc	gatgaaaaac	ccgttaacggg	gttccctt	960
cgaggatcg	gagacagggt	gtgcgtatgtt	gtcgtcaagct	cgtgtcgta	gatgttgggt	1020
taagtccccg	aacgacggca	acccttattt	tttagtagcca	gcaggtaaaag	ctgggcactc	1080
taaggagact	gccccggata	acccggggat	agggtggggat	gacgtcaaat	catcatgccc	1140
cttatgtatct	gggctacaca	cgtgtacaa	tggcgtaaaca	aagggaagcg	agcctgcccgg	1200
ggtgagcgaa	tcccaaaaat	aacgtccccag	ttcggactgt	agtctgcaac	ccgactacac	1260
gaagctgtgg	tcgtctgtt	tcgcaatca	gaatgtcgcc	gtgaatact	tccgggtct	1320
tgtacacacc	gccccgtcaca	ccatgggat	cgaaaaatgcc	cgaagtctgt	gactcaacccg	1380
caaggag						1387

SEQ ID NO: 49                    moltype = DNA length = 1368

FEATURE                        Location/Qualifiers

misc\_feature

1..1368

note = Obtained from Intestinal Bacteria, K49

source

1..1368

mol\_type = other DNA

organism = unidentified

SEQUENCE: 49

ttaaggagat	tcttcggat	attcttgcgt	gactgaggg	cgacgggtt	agtaacgcgt	60
gggtgaccc	ccccataccg	ggggataaca	gctggaaaacg	gctgtctata	ccgcataagc	120
gcacagacgt	gcatggctcg	gtgtaaaaaa	ctccgggtgt	atgggtatggg	cccgctgtcg	180
attaggcagt	ttggcggggta	acggccacc	aaaccgcgt	tcaatggccg	gcctgagagg	240
gacccggccc	acatggggac	tgagatggac	ccccaaactcc	tacggggggc	agcagtgggg	300
aatattgcac	aatggggaa	acccatgtgc	agcgcacggc	cgtgagcgaa	gaagtatttc	360
gttatgtaaa	gtctatcgt	cagggaaat	aatgacggta	cctgtactaag	aagccccggc	420
taactacgtg	ccagcagccg	cggtaatac	tagggggca	gcgttatccg	gatttactgg	480
gtgttaaagg	acgcgtacgt	gcaaggcgt	tctgtatgt	aaacccagg	cttaaacctg	540
ggactgcatt	ggaaactgtc	tggctcgat	ggccggggat	taaggcgtat	tcctagtgta	600
gccccgtaaat	gogtagat	taggaagaa	accagtggc	aaaggcgctt	actggacgg	660
aactgacgtt	gagggtcgaa	agcgtgggaa	gcaaacagg	ttagataccc	ttgttagtcca	720
cgcgcgtaaac	gtatgtat	agggttgtgg	gaggcaatgt	cttcgggtcc	ccgcacaaacg	780
cattaaggat	tccacccgtt	gatgtatgt	gcaagaatgt	aactcaaaagg	aattgacggg	840
gaccgcaca	acgggtggag	catgtggtt	aattcgtac	aacgcgtaaa	accttaccc	900
gtcttgacat	cccgatgacc	ggccgttaac	ggggccttct	cttcggagca	ttggagacag	960
gtgtgtcatg	gttgcgtcg	gtctgtgtcg	tgagatgtt	gggttaagtcc	cgcaacgcgt	1020
gcaaccctta	tcttcgtat	ccaggatgt	aaatgtggca	ctctgtggat	actggccagg	1080
ataaccctgt	ggaagggtgg	gatgtatgt	cccttata	tctgtggctac	1140	
acacgtgt	caatggcgta	aacaaaggga	ggcaagccg	cgagggtgg	caaatccaa	1200
aaataacgtc	tcaatggcgta	ctcgatgt	caactcgact	gcacgtact	ggaatcgct	1260
gtataatcgca	atcagaatgt	cgccgtat	acgttccgg	gtcttgta	caccggccgt	1320
cacaccatgt	cgccggaaatgt	cgtgtaccc	acccatcc			1368

SEQ ID NO: 50                    moltype = DNA length = 1390

FEATURE                        Location/Qualifiers

misc\_feature

1..1390

note = Obtained from Intestinal Bacteria, K50

source

1..1390

mol\_type = other DNA

organism = unidentified

SEQUENCE: 50

gtcgagcgaa	gcacttatgt	tgatgtatgt	ttgtgtactgt	gccccggacg	60	
ggtgagtaac	cgctgtat	cctgcgtat	acaggggat	aacagttaga	aatgtactgt	120
aatgcgcata	aacgcacag	ggccgcata	cccggtgt	aaaactccg	tggatgtata	180
tggactcgcg	tctgtatgt	tagttggcg	ggtaacggcc	taccaaggcc	acgtatgt	240
gccccgtcg	gagggtgtaa	ggccacattt	ggactgtgg	acggccaaa	ctccatccgg	300
aggcgcgt	ggggatattt	gcacatgtgg	ggaaacccctt	atgcacggc	ccgcgtgtgg	360
tgaagaatgt	tttcggatgt	taatgtctat	tcagcagggtt	agaaaaatgt	ggtacatgt	420
taagaagcc	cggtactata	cgtgtatgt	gccccgtata	tacgttaggg	gcaagcgtt	480
tcgggatata	ctgggtgtaa	aggggatgt	gacggcttt	caagtctgt	gtgaaactcc	540
ggggctcaac	tccggaaactg	cggtggaaac	tgtaggctt	gagtgtccgt	gaggtaagcg	600
gaattccat	tgtatgtatgt	aatatgtatgt	gaaacccatgt	ggcgtaaagg	660	
gttactgtt	cggtatgtt	cggttggatgt	cgaaagcggt	ggggacaaac	aggattatgt	720
accctgtatgt	tccacccgtt	aaacgtatgt	tacttaggtt	tggggatcaa	agtcttccgt	780
tgccgcgcgt	aaacgtatgt	gtattccat	tggggatgt	cggtcgatgt	aatgtaaatc	840
aaaggtatgt	acggggatcc	gcacaaggcg	tggatgtatgt	gtttaatgt	gaagcaacgc	900
gaagaacacctt	accaatgtt	gacatgtatgt	cgacgggtat	cttcccttcc	960	
ggggacgtatgt	aaacgtatgt	gtatgtatgt	cggtatgtatgt	gtatgtatgt	1020	
taagtccccgt	aaacgtatgt	acccttatgt	tcaatgtatgt	gccccgtatgt	1080	

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```
tggagagact gccaggaca acctggagga aggtggggat gacgtcaa atcatatgccc 1140
cttatgactt gggcacaca cgtgtacaaa tggcgtaaac aaaggaaagc gaacctgtga 1200
gggtggcaaa atcccaaaaa taacgtctca ttccggattt tagtgcataa ctgcactaca 1260
tgaagctgga atcgttagta atcgcatac agcatgtcgc ggtgaataacg ttccgggtc 1320
ttgtacacac cgccgtcac accatggag tcggtaacgc ccgaagtca tgaccacacc 1380
gcaaggagg 1390
```

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SEQ ID NO: 51 moltype = DNA length = 1382
FEATURE Location/Qualifiers
misc_feature 1..1382
note = Obtained from Intestinal Bacteria, K51
source 1..1382
mol_type = other DNA
organism = unidentified
```

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SEQUENCE: 51
gcagtcggac qcaatgcttc ggcattgagt qgcgaacggg ttagtaagac ataagcaacc 60
tgcctctgtg agggggataa ctgctggaaa cggcagctaa gaccgcata gcatagagga 120
cgcatgtca ctatgttaa tateccacgg gatagcacag ggatgggctt atgacgcatt 180
agccagctgg tgaggtaacg gtcaccagg gcgacgatgc ttagccggcc tgagagggtg 240
gacggccaca ctgggactga gacacggccc agactctac gggaggcagc agtagggat 300
tttcggcaat gggcgaagc ctgaccggago aacggcgctg gaaggaagaa gtcattctgt 360
atgttaactt ctgttatgaa ggaagaacgg cagatggagg gaatgccatg tgcgtgacgg 420
tacttcatgaa ggaaggcacg gctaactcg tgcgcacgc cgcgttataa cgttaggtgc 480
gagcgttatac cggaaatcatt gggctttaaag aggaggacgg cggcgttca ggttgcgggt 540
gaaagacccg actaaactt cggtaagccg tggaaaccgc acagcttagag agcatcagag 600
gatcgcggaa ttccatgtgt acgggtgaaa tgcgtataga tatggagggaa caccagtggc 660
gaaggcggcg ctctgggggt cagtcgacgc tcagtcggca aagcgtgggg agcaaatagg 720
atttagatacc cttagtagtcc acggcgtaaa cgtatgttc taatgttgg gggtcagacc 780
tcagtgtgg agttaacgcg ataagcactc cgcctgtata gtacgttgc aagaatgaaa 840
ctcaaaggaa ttgacggggg cccgcacaaa gcggtggagc atgtgttta attcgaagca 900
acgcgacaaacg ctttaccagg tcttcgtatg gagataaaagg ccctggagac agggagatag 960
atatatctca cacagggtt gcatgttgtt cgtcagctcg tgcgtgaga tttttttttt 1020
agtccgcacaa cgagcgcaac ccctgttgc agttgcacg attaggttgg ggactctggc 1080
gagactgctt ctgcaaggag gaggaaaggcg gggatgcacg caaatcatca tgccccttat 1140
gacctgggtt acacacgtgc tacaatggd ggatcagagg gaggccaaagc cggcgggtgg 1200
agcgaacacc cttttttttt ttcacatgtc gactgcacgc tgcaactcga ctgcaccaag 1260
cttgcacatgc tagtaatcgc gaatcagcat gtcgcgggtt atacgttctc gggcccttta 1320
cacacccgccc gtcacacccat gagagttgtt aacacccgaa gccgggtggcc caaccgc 1380
ga 1382
```

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SEQ ID NO: 52 moltype = DNA length = 1388
FEATURE Location/Qualifiers
misc_feature 1..1388
note = Obtained from Intestinal Bacteria, K52
source 1..1388
mol_type = other DNA
organism = unidentified
```

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SEQUENCE: 52
agtccgaacgg gaaatattttt attgaaactt cggtgattt aattttttt tagtggccg 60
cggtgtgatc acgcgtgggt aacctgcctt atactggggg ataaacgcac gaaatgactg 120
ctaatccgc ataaacgcac agaaccgcac ggttcgggtt gaaaaactcc ggtgttataa 180
gatggacccg ctttggatc gttgttgcg agggcagcgg ctttccaaagg cgcacatcca 240
tagccggctt gaggagggtt gacccgcacat tggactgtt acacggccca gactcctacg 300
ggaggccgca gtggggataa ttgcacaatg gggggaaacc ttatgtccggc acggccgtg 360
aaggaaagaaat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 420
actaagaacgc cccggcttac acgttgcacgc cggccgggtt aataacgttgg gggcaacgcgt 480
tatccggatt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 540
caggggctta aaccctggac tgcattttttt tttttttttt tttttttttt tttttttttt 600
cgaaattttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 660
cggtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 720
ataccctgtt atgcacatgc gttttttttt tttttttttt tttttttttt tttttttttt 780
gggtggccggc cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 840
caaaacgcatt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 900
caaaaggaaat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 960
cgaaacccctt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1020
ggggacggggg agacagggtgg tttttttttt tttttttttt tttttttttt tttttttttt 1080
aagtccgcac acggccggca cccctttttt tttttttttt tttttttttt tttttttttt 1140
gaggaggactt ccagggtttttt tttttttttt tttttttttt tttttttttt tttttttttt 1200
ttatgattttt ggcttacacac tttttttttt tttttttttt tttttttttt tttttttttt 1260
gggtggccaaat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1320
gaagctggaa tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1380
ttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1388
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SEQ ID NO: 53 moltype = DNA length = 1385
FEATURE Location/Qualifiers
misc_feature 1..1385
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source          note = Obtained from Intestinal Bacteria, K53
                1..1385
                mol_type = other DNA
                organism = unidentified

SEQUENCE: 53
cgaacggaa ttatttcatt gagacttcgg tggatttgat ctatttctag tggcgacgg 60
gtgagtaacg cttgggtaaac ctgccttata caggggataa agactcagaat atggctgcta 120
ataccgcata agcgcacaga gctgcattgg tcagtgtgaa aaactccgtt ggtataagat 180
ggaccgcgt tggatttagct tgggttggg gtaacggccc accaaggcga cgatccatag 240
ccggcctgag agggttgcacg gccacattgg gactgagacca cggcccgac tcctacggg 300
ggcggcgtt gggaaatgg cacaatgggg gaaaccctgaa tgccggacg ccggctgaaag 360
gaagaagttt atccgttatgt aaacttctat cgcggggaa gatagtgcacg gtacctgact 420
aagaagcccc ggcttaactac gtgcgcacg cccggtaat acgttaggggg caagcggtat 480
ccggattttc tgggttgcac gggggcgtt acgggtgtggc aagtctgtat tgaaaaggcat 540
gggctcaacc ttgtggacttc attggaaactt gtcataacttgg aatggccgggg gggtaaggcgg 600
aattccatgtt gtacgggtt aatgcgttata tatttagggg aacaccatgtt qcgaaaggcgg 660
cttactggac ggttaacttgc gttggggctt gaaagcgtgg ggagcaaaaca ggatttagata 720
ccctggtagt ccacggcgtaa aacgtatgtt actagggttc gggggacatg gctttccgtt 780
gcccgtccaa acgcgcataaatttccatgtt gggggatgtt gttccgtcaaga atgaaactca 840
aaggaaatgg cggggacccg cacaacgggtt ggacatgtt gtttaatttgc aagcaacccg 900
aagaacccca ccaagtcttgc acatccgcctt gaccgtatctt taatcggttcc tttttccgtt 960
gacagacggg acagggttgcg catgggttgc gtcagctgtt gtcgttgcgat gttgggttaa 1020
gtcccgcaac acgcgcaccc ccttacttgc gtagccggatc tttaagggtgg gcaactctggg 1080
gagactgcac gggataacccctt gggggatgtt gttccgttgc tcaaatcata atgcccctta 1140
tgattttggc tacacacgtt ctacaatggc gtaaacaatgg ggaageggaga tcgttgcgat 1200
gagcaaatcc caaaaataac gttcccgatgc ggaactgttgc ctgcacccgg actacacggaa 1260
gtctggatcc ctgtatcccg cggatcgatc tgccgggtt aataacttgc cgggttctgtt 1320
acacacccgc cgtcacacca tggggatgttgc taacccggc agtcgttgc ctaacttgc 1380
agaag 1385

SEQ ID NO: 54      moltype = DNA length = 1415
FEATURE          Location/Qualifiers
misc_feature    1..1415
source          note = Obtained from Intestinal Bacteria, K54
                1..1415
                mol_type = other DNA
                organism = unidentified

SEQUENCE: 54
gtcgaacggaa gaattttattt tcggtagaaat tcttagtggc gaacgggttgc gtaacgcgtt 60
ggcaacccgtc ctttttagacg gggacaacat tccgaaaggaa tgctaaatc cggatgtgtat 120
catcgtgcgc catggcaggaa tgaagaaaga tggctcttac aagtaactca tcgctaaagg 180
atggggcctgc gtctgattttt ctatgttgc gttgttgcgatc tttaagggtgg gcaactctggg 240
agccggcttc agagggttgc cggggacttgc gggactgttgc cacggcccaa actcttacgg 300
gaggccgcacg tggggatctt ctcgcattttt gggaaatgtt gacggatggaa cggccgtgtt 360
gtgtatgggg atttccgttgc gtaaacttgc gttgttgc gttgttgcgatc atgtgttgc 420
caatgcatttgc atatgcgtt gttttttttt gttttttttt gttttttttt gttttttttt 480
ggccgttataatc gttaggttgcg acggctgttgc ggaactgttgc gttgttgcgatc 540
gtgtttaataatc gtcgcgttgcg aaaaatgggg gttttttttt gttttttttt gttttttttt 600
aggcttgcgtt gtcgcgttgcg aaaaatgggg gttttttttt gttttttttt gttttttttt 660
tggggagggatcc accgttgcgtt gttttttttt gttttttttt gttttttttt gttttttttt 720
agcccgatggatcc gtcgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt 780
aggtgttgcgtt ggtatccgc ctttctgttgc cggatgttgc gttttttttt gttttttttt 840
ggatgttgcgtt gtcgcgttgcg aaaaatgggg gttttttttt gttttttttt gttttttttt 900
gtatgttgcgtt taatttgcgtt gtcgcgttgcg aaaaatgggg gttttttttt gttttttttt 960
gtctcttgcgtt tagatgttgc ctttctgttgc cggatgttgc gttttttttt gttttttttt 1020
agctctgttgc gtcgcgttgc gttttttttt gttttttttt gttttttttt gttttttttt 1080
accaggcaatgtt aatgttgcgtt gttttttttt gttttttttt gttttttttt gttttttttt 1140
ggatgttgcgtt aatgttgcgtt gttttttttt gttttttttt gttttttttt gttttttttt 1200
gaaacacgggg gaaatgttgcgtt gttttttttt gttttttttt gttttttttt gttttttttt 1260
gatcgccgcgtt gtcgcgttgc ctttctgttgc cggatgttgc gttttttttt gttttttttt 1320
actcgccgttgc gtcgcgttgc gttttttttt gttttttttt gttttttttt gttttttttt 1380
aacacccggaa gtcgcgttgc gttttttttt gttttttttt gttttttttt gttttttttt 1415

SEQ ID NO: 55      moltype = DNA length = 1366
FEATURE          Location/Qualifiers
misc_feature    1..1366
source          note = Obtained from Intestinal Bacteria, K55
                1..1366
                mol_type = other DNA
                organism = unidentified

SEQUENCE: 55
atggggatgtt gataacttgc tggcgacccg cgcacgggtt gttttttttt gttttttttt 60
cctgtatccgc ggggtatagcc catggaaacg tggatataaca ccccatagttt cttttttttt 120
gcgtggatgtt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 180
ggccgggttgc gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 240
cattggaaacttgc gtcgcgttgc gttttttttt gttttttttt gttttttttt gttttttttt 300

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atggacgaga	gtctgaacca	gccaaagtgcg	gtgagggaaag	actgccttat	gggtttaaaa	360
cctcttttat	aaggaaagaa	taagtctac	gtgtagaatg	atgcctgtac	ctttagataa	420
agcatcggtc	aactccgtgc	cagcagccg	ggtataatcgg	aggatcgcg	cgttataccgg	480
atttatttggg	ttaaagggt	gcttaggcgg	tttataatgt	tagtggtaa	atatttgac	540
taaactcaat	tgtgccatta	atactggtaa	actggagta	agacgaggta	ggcggaaataa	600
gttaaagtgc	ggtaaatgc	atagatataa	cttagaactic	cgatagcgaa	ggcagcttac	660
cagactgtaa	ctgacgctga	tgcacgagag	cgtgggtage	gaacaggatt	agataaccctg	720
gtatgtccacg	cgtaaacgt	tgctactgg	ttctgtgega	tatattgtac	gggattaagc	780
gaaagtattt	agtgagccac	ctggggagta	cgtcgccaa	gatgaaactc	aaaggaattt	840
acggggggcc	gcacaagcg	aggaaacatgt	ggttaatattc	gatgatacgc	gaggaaacct	900
acctgggtt	aatggggaa	tgtcgattt	ggaaacagat	attcttcg	gagggtttt	960
caagggtgtc	catgggtgtc	gtcagctgt	gcccgtgaggt	gtcgggtttaa	gtccccataac	1020
gagcgcAAC	cttaccgtt	gttcttagca	tgtatgtat	agcactctaa	cgggactgc	1080
accgtaaagg	gagggaaagg	cggggatggc	gtcaaatcag	cacggccctt	acacccagg	1140
cttacacacgt	gttacaatgg	ccggtagaca	ggggcgtctac	cagggtgactg	gtatccaaatc	1200
tcaaaagccg	gtcgtatgc	ggatggag	ctgtaaatccg	actccatgaa	gttggatcc	1260
ctagtaatcg	cgcatcagcc	atggcgcgtt	gaatacgttc	ccgggcctt	tacacaccgc	1320
ccgtcaagcc	atggaaagccg	gggggccttg	aagtccgtaa	ccgcgca		1366

SEQ ID NO: 56	moltype = DNA	length = 1364
FEATURE	Location/Qualifiers	
misc_feature	1..1364	
	note = Obtained from Intestinal Bacteria, K56	
source	1..1364	
	mol_type = other DNA	
	organism = unidentified	

SEQUENCE: 56						
tcgaacgagc	gagagagagc	ttgccttctc	gagcgagtgg	cgaacgggtg	agtaacgcgt	60
gaggaaacctg	cctcaagag	ggggacaaca	gttggaaacg	actgctaata	ccgcataa	120
ccacgggtcg	gatcgcacca	gagggaaaag	gagcaatccg	ctttagatg	gcctcgctc	180
cgatttagtgc	gttgggtggg	taacggccca	ccaaggcgac	gatcggtacg	cggactgaga	240
gggtgaacgg	ccacatggg	actagacac	ggcccgacat	cctacgggag	gcagcgttgg	300
ggaatattgc	acaatgggg	aaaccctgt	gcagcgcac	cgcgtggagg	aagaaggct	360
tcggattgt	aactctgtt	gttggggaa	ataatgcacg	tacccaaacaa	ggaagtgc	420
gctaactacg	tgcccaagc	cgcggtaaaa	cgtaggttc	aacgcgttgc	cggaattact	480
gggtgttaaag	ggagcgcagg	cgggagaca	atgtggaaat	gaaatctatg	ggctcaaccc	540
ataaactct	tccaaact	ttttctgt	gtatgtcaga	ggtagggcga	attccgggt	600
tagcgggtga	atgcgtat	atcggggaa	acaccagtgg	cgaaggcg	ctactggca	660
ccaaactgac	ctggggctcg	aaatgtgtgg	tagcaaacac	gatttagatc	cctgttagt	720
cacaccgtaa	acatgtat	ctagggttt	gaggattgac	cccttcgt	ccgcgttta	780
cacaataatg	aatccac	ggggatcga	ccgcgtat	gaaactcaaa	ggaattgc	840
ggggcccgca	caagcgttgc	agttatgtgt	ttaattcgc	gcaacgc	gaaccttacc	900
aagtctgtac	atccctgtac	agnnataagaa	atatgtttt	tcttcggac	aaggagac	960
gtgggtgc	catgtgtca	gtctgtgt	tgatgtttt	ggtaatgtcc	cgcaacgc	1020
gcacccctta	ttgttcgtt	ctacggca	ggactcttgc	cagactgc	ttgacaaac	1080
ggaggaagg	ggggatgac	tcaatatc	atgccttta	tgacttggc	tacacacgt	1140
ctacaatggc	gtttaaaca	gagaacg	accgcgtat	gggacaaac	tcaaaacaa	1200
cgtcccaat	cggtactgc	gtctgcac	gtctgcac	agtcgttac	gtctgttt	1260
gttggatc	atgcac	gttacgtt	ccgggcctt	tacacaccgc	ccgtcacacc	1320
atgagagccg	gggggacccg	aagtccgtng	nntaaccgc	agga		1364

SEQ ID NO: 57	moltype = DNA	length = 1391
FEATURE	Location/Qualifiers	
misc_feature	1..1391	
	note = Obtained from Intestinal Bacteria, K57	
source	1..1391	
	mol_type = other DNA	
	organism = unidentified	

SEQUENCE: 57						
tgcagtcgaa	cgaggatgtc	atgacagagg	attcgtccaa	tggagtgt	tacttagtgg	60
cgggacgggt	agtaacgcgt	gagtaac	cttggagt	gggataaca	ggtggaaaca	120
tctgctaata	ccgcacatgt	cagttggtc	gcatggctc	gactgc	aaaaatgc	180
tctgagatgg	actcgcgtc	gattagctgg	ttgggggg	aacggccac	caaggcgac	240
atcagtgac	ggactgtat	gttggccgg	acatattgg	ctgagacac	gcccacact	300
ctacgggg	cagcgttgg	gaatattgg	caatgggc	aacgcgtt	ccgcaacgc	360
gcgtgaagg	agaaggctt	cggttggtaa	acttctt	tcagggtac	agcaatgt	420
ggtagctgt	gtataagcc	cggtacta	cgtgcac	gcccgcgt	tacgttagt	480
gcgagcgtt	tccggat	ctgggtgt	aggcgtgt	ggcgggact	caagtca	540
gtgaaaacca	tgggtcaac	ctgtggct	catttgc	tgtatgtt	gagtactgg	600
gaggcagac	gaatttctat	tgtatgtt	aaatgcgt	atatttagg	gaaacaccgt	660
ggcggaaagg	gtctgttgc	cagcaact	cgtgtggc	cgaaagcgt	ggggacaa	720
aggattagat	acccttgt	tccacgtt	aaacgtat	tacttaggt	gggggtct	780
accccccctcg	tgccgcgtt	aacacaataa	gtatcccacc	tggggat	gatcgcaagg	840
ttgaaactca	aaggaaattt	ccccggcc	cacaacgg	ggagatgtt	gtttaat	900
aagcaacgc	aagaacctt	ccagggtt	acatcccgt	gaccgtgt	gagatacacc	960
tttttcttc	gaagcgcgg	tgacaggtt	tgcgtat	tggtcg	tgatgttgc	1020

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atgttgggtt aagtcccgca acgagcgcac cccttattgt tagttgtac gcaagagcac 1080
tc tagc gaga ctgc cggta caaaacggag gaagggtggg acgacgtcaa atcatcatgc 1140
ccctttagtc ctggggcaca cacgtactaa aatggtggtc aacagaggga agcaagaccg 1200
cgaggtggag caaaccccta aaaggccatcc cagttcggt tgcaggctgc aactcgctg 1260
tatgaagttg gaatcgctag taatcgccga tcagcatgcc gcgggtaaata cggtccggg 1320
ccttgtacac accgcccgtc acaccatgag agtccccggaa acccgaagtc cgtagcctaa 1380
ccgcaagggg g 1391
```

SEQ ID NO: 58 moltype = DNA length = 1377

FEATURE Location/Qualifiers  
misc\_feature 1..1377  
note = Obtained from Intestinal Bacteria, K58  
source 1..1377  
mol\_type = other DNA  
organism = unidentified

SEQUENCE: 58

```
gcaagtcgag cgagaagctt tgaactgacg cttcggtta tgatcaaagt ggaaaggccg 60
ggacgggttca gtaacgcgtg ggcacactcg ccttgcaga gggatagct cgggaaaccg 120
ggataaaaac ctcataacgc acaactgaga catcttggat gtgccaaga tttatcgca 180
gaggatggc ctgcgtctga ttatgttagtt ggtgggtaa cggccatcca aggccgacat 240
cagtagccg cttgagaggg tgatoggca cattggaaact gagacacggt ccaactcct 300
acggggggca gcaatggggg atatggcaca atggggggaa ccctgtatgca gcaacgcgc 360
gtgaaggatg aaggatccctt ggtcgtaaac ttctgttcta gggggagata gtgcggatc 420
cttagggaca agtccccgtc aactactgtc cagcagccgc ggtataactgt agggggcaag 480
cgttatccgg aattattggg cgtaaagagt aegtaggtgg ttacctaagc aagggttta 540
aggcaatggc ttaactattt ttcgcccctt gaactgggct acttggatgc aggagaggaa 600
agoggaaatc ctatgttgc ggtggaaatgc gtatgatatta ggaggaaac cagtgccgaa 660
ggcggcttc tggactgtaa ctgcacatcg ggtacgaaatc cgtggggagc aaacaggatt 720
agataccctg gtatgtccacg ccgtaaacgc tgacgactag gtgtcggttgc cgcaagactt 780
cggtccgcga gttaaacgca taatgtcttgc gcttggggat tacgttgcgca agaatgaaac 840
tcaaaggatc tgacccggc ccgcacacaatc aegggagcat gtgggttaat tgcgacaaac 900
gcaagaaacc ttaccaggc ttgacatctt cttgcacagc cttaaacgg gtccttcttc 960
ggacaggaaa gacagggtgt gcatgttgt cgtcagctc tgctgtgaga tgggggtta 1020
agtcccgcaac cgacgcacac cctgtcttgc agtgcacatc attaagtgg gcactctaa 1080
gggactcgccg gggatcaactc ggagggaaatc ggggatgacg tcaaatcattt atgcccctt 1140
tggcttgcgc tcacacatgtc tacaatggc cgttacaaatc aggaaggcag accggcggat 1200
ggagcgaatc taaaaggccg gtcggatctt ggttgcggc ctgcacactcg cttgcataaa 1260
gtcggagttt ctatgtatcg cgaatcggaa tggccgggtt aatgcgttcc cgggtcttgt 1320
acacccggcc cgtcacaacca tggaaatggg gggccggccg agttggcagg caaatat 1377
```

SEQ ID NO: 59 moltype = DNA length = 1373

FEATURE Location/Qualifiers  
misc\_feature 1..1373  
note = Obtained from Intestinal Bacteria, K59  
source 1..1373  
mol\_type = other DNA  
organism = unidentified

SEQUENCE: 59

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cgagggggcag cgcggagagt agcaatactt tggagggcagc cggcgcacgg gtgcgttaacg 60
cgtatgcac ctacctttaa caggggcata acactgagaa attggacta attccctata 120
acattcgaga aggcatctt ttgggttaaa aactccgggtt gttaaatggat ggcatgcgtt 180
gtattagctt gttgggtggg taacggctt ccaaggccgac gatacatagg gggactgaga 240
ggtaaaccctt ccacatgtt actgagacac qgaccaaaatc cttacgggag gcaacgtgt 300
ggaatattgg tcaatggacg caagtcttgc ccagccatgc cgcgtcagg aagacggctc 360
tatgagttt aaactctttt tttatgttgcg taaaatggatc tacgttgcagg agtctgaaag 420
tatagtcgca ataaaggatcg gtaactatcg tggccacgc ggcgttataa cggggatcc 480
aagcgttac tggattttt ggggtttaaatc ggtgcgttgc cgggttgcgat agttggatgt 540
gaaataccgg ggctcaactc cggaaactgc tctaatactg ttgaaactaga gagtagtgc 600
ggtagggcga atgtatggt tagccgttgc atgcttagag atcatacaga acacccattt 660
cgaaggccgcg atatccatgc ttggccacgc aaacgcgtggg gagcaaaacag 720
gattatgtac cttggtagtc cacgcacgtaa acgtatgttgc cttcgatgtc ggcataacaca 780
gtcgggtact aagcgttac gataagttt ccacccggggt agtacgttgc caagaatgaa 840
actcaaaggaa attgacgggg gcccgcacaa gcccggggac atgtgggttta attcgatgt 900
acccggggaa ctttacccgg gcttggaaatc tagtgcgttgc tctggaaaca ggatccct 960
tcggggccacg aacttaggtt ctgcgtatgtt gtcgtcgatc cttcggttgc ggtgtcggtt 1020
taatgtccat aacgacgcga accccttccgg ttagttgcata cttcggttgc cttccgtt 1080
tggccggact gcccgtttaa gcccggggac aggtggggat gacgttcaat cggccgttgc 1140
cttacgttgc gggctacaca cttcggttgc tttttttttt tttttttttt 1200
ggggatgcac atctcgaaatc cttccgttgc gggccgttgc accgttcaat cggccgttgc 1260
gaatgtttttt tttttttttt tttttttttt tttttttttt 1320
ttgtacacac cggccgttgc gccatgttgc tttttttttt tttttttttt 1373
```

SEQ ID NO: 60 moltype = DNA length = 1384

FEATURE Location/Qualifiers  
misc\_feature 1..1384  
note = Obtained from Intestinal Bacteria, K60

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aaggatgaag tatttcggta	tgtaaacttctatcagcagg	gaagaagatg acggtaactg	420
actaagaacccggctaac	taactgcggcag cagocgcgggt	aatacgttagg gggcaagcgt	480
tatccggatt tactgggtgt	aaaggagcg tagacggoga	tgcaagcccg atgtgaaagc	540
ccggggctca accccgggac	tgcatttga actgcgtggc	tggagtgtcg gagaggcagg	600
cggattctc agtgtacgg	tgaaaatgcgt	agaatattag gaggaacacc agtggcgaag	660
geggcctgtc ggacgtac	tgacgtttag gctcgaaaagc	gtggggagca aacaggatta	720
gataccctgg tagtccacgc	cgtaaacatgactactagg	tgtcggttgc caaggccatt	780
cggtgccgca gcaaaccgaa	taatgttcc acctggggga	gtacgttgc aagaatgaaa	840
ctcaaaaggaa ttgacgggaa	ccgcacaag cggtggagca	tgtggttaa ttcaagccaa	900
cgcgaqaacatccatgt	cttgacatcc cgatgcacaa	gcccgttaacg cgctttct	960
tccgaacatc ggtgacagg	ggtgcatgtt tgcgtcage	tgcgtcgtagt agatgttggg	1020
ttaagtcccg caacgacgc	ttcagtagcc aacattccgg	atgggactc 1080	
tggagagact gccaggaca	acctggggaa aggtggggat	gacgtcaat catcatgcc	1140
cttatgacca gggcacaca	cgtgttacaa tggcgttaac	tggcgttaac aaaggagggc gaacccgcga	1200
gggtggggaa atccccaaa	taatgtctc gttcggttgc	tagtgcacaa ctgcgactaca	1260
tgaagctgaa atcgtagta	atcgcaatc agaardtgc	ggtgaaatcg ttccgggtc	1320
ttgtacacac ccggcgtcac	accatggag tcaatgcgc	ccgaagccgg tgacccaacc	1380
cgcaagg			1388

SEQ_ID NO: 63	moltype = DNA length = 1415		
FEATURE	Location/Qualifiers		
misc_feature	1..1415		
	note = Obtained from Intestinal Bacteria, K63		
source	1..1415		
	mol_type = other DNA		
	organism = unidentified		
SEQUENCE: 63			
agtgcgaacgc ttctttctc	ccgagtgttgc gcactcaattt	ggaaagagga gtggcggacg	60
ggtgagtaac acgtggtaa	cctaccatc agagggggat	aacacttggaa aacagggtgt	120
aataccgcatt aacagtttat	gcccgtatgc ataagagtga	aaggcgcttt cgggtgtcgc	180
tgatcatggc gacctggag	cattatgttgc tttggtaggtt	aacggctcac caaggccacg	240
atgcatacgcc gacctggag	gggtatcgcc	caactggggaa ctgagacacg gcccagactc	300
ctacgggagg cagcaatgg	gaatcttcgg	caatggggca aagtctgacc gagaacgc	360
gcgtgagtga agaaggtttt	cggatcgtaa aactctgttgc	ttagagaaga acaaggacgt	420
tagtaactga acgtccccctg	acggatctatc accagaaaacg	cacggctaac tacgtgcac	480
cagcccggtt aatacgtagg	tggcaagcgt	tgtccggatt tattgggtgt aaagcgacgt	540
caggcgggtt ctaatgttgc	atgtgaaagc	ccccggctca accggggagg gtcattggaa	600
actggggagac ttgagtgcag	aagaggagag tggaaatttca	tgtgttagcgg tgaaatgcgt	660
agatataatgg aggaacacca	gtggcgaagg	cggtctcttggt ctgtgtact gacgtgtgagg	720
ctcggaaacgc gggggggca	acaggatgttgc	ataccctgtt agtccacggc gtaaacgtat	780
agtgctaattgt gtgggggggt	ttccggccctt	cagtgtgtca gcaaaacgtat taagcactcc	840
gcctggggag tacgaccgc	agggtgaaac tcaaaaggaa	tgcacggggc ccgcacaacg	900
gtggggggat gtggggat	tcgacggcaac	tcgacggggc ttaccaggc ttgacatcc	960
ttgaccactc tagatagata	gtttccctt	cggggacaaa gtgacagggt gtgcgttgt	1020
gtcgtcactg cgtgtgtga	gatgtgggt	taatgtccgc aacgacgcgt acccttatttgc	1080
ttagttgcac tcattttat	gggcactcta	gcaacgcgtat gtaacactcc	1140
gtggggatgtt ggtggatgtt	tcatgtccctt	tatgtccctt gtcacacacg tgcataatgc	1200
ggaagtacaa cggatgttgc	gacccggagg	tcatgtccat ttccttcaatgc	1260
tcggatgtca ggtgtcaact	cgccgtatgc	aaaggccgtt cgtagtataatgcgtat	1320
cacccgggg tgaatacggtt	ccccggctt	gtacacaccc cccgtcacac cacgaggtt	1380
tgtacacccca gaaatcggtt	aggtaacattt	tttgg	1415

SEQ_ID NO: 64	moltype = DNA length = 1392		
FEATURE	Location/Qualifiers		
misc_feature	1..1392		
	note = Obtained from Intestinal Bacteria, K64		
source	1..1392		
	mol_type = other DNA		
	organism = unidentified		
SEQUENCE: 64			
agtgcggcga agcgcataaa	caggattttct tcggattggaa	gtctttgtga ctgagcggcg	60
gacgggttaga taacgcgtgg	gtaaacctgc tcatacagggg	ggataacagt tagaaatgac	120
tgctaatacc gcataagcgc	acaggaccgc atggctctgtt	gtggaaaactt ccgggtgttat	180
gagatggacc cgcgttgcgt	tagatgttgc	gaggggttacccggccaa ggcgcacgt	240
agtgcggcgc ctggatgggt	gaacggccac	atggggactt agacacggcc cagactctta	300
cggggaggcgt cagtggggaa	tattgcacaa	tggggggaaac cttgtatgcac ccgcgcgc	360
tgaaggaaga agtatctgg	tatgtaaact	tctatcgac gggaaagaaaa tgacggtacc	420
tgactaaagaa gccccggcta	actacgtgc	agcagccgcgt gtaatacgta gggggcaacg	480
gttattccggta ttactgggtt	gtaaaaggag	cgttagacggaa agacaaatgcgtatgtgaaa	540
ggctggggct taacccccc	actgcatttgc	aaactgtttgtt tcttagtgc cggagaggta	600
agcggaaatcc tcaatgttgc	gggtttatgc	gtagatattttaa ggagggacac cagtgcgtt	660
ggcggtttac tggacggtaa	ctgacgttgc	ggctcgaaag cgtggggagc aaacaggatt	720
agataccctgt gtagtccacg	ccgttaaacgc	tgaataacttag gtgtcggttgc gcaaaacgc	780
tcggtgccgc agcaaaacgc	ataagtatttgc	cacctggggaa gtacgttgc aagaatgaaa	840
ctcaaaaggaa ttgacgggaa	ccgcacaag	cggtggagca tggggttaa ttcaagccaa	900
cgcgaagaac ctatccaaat	tttgacatcc	ctctgaccgtt cccgttaacgc gggctccct	960

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tcggggcaga ggagacaggt ggtgcattgt tgctgtcagg tcgtgtcggt agatgttggg 1020
ttaaatcccg caacgagcgc aacccttata cttagtagcc agcacatgt ggtggcaact 1080
cttagggac tgcggggat aaccggggg aaggcggggg cgaatgtcaaa tcatcatgcc 1140
ccttatgatt tgggtacac acgtgtaca atggcgtaaa caaaggaaag cgagacagcg 1200
atgttgagcg aatccaaaaa ataacgtccc agttcggact gcagtctgca actcgactgc 1260
acgaagctgg aatcgctagt aatcgccgt cagaatgccc cggtaatc gttccgggt 1320
cttgcacaca ccggccgtca caccatggg gtcagtaacg ccgaatgtca gtgacctaacc 1380
cgaaggaaag ga 1392

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SEQ ID NO: 65 moltype = DNA length = 1388
FEATURE Location/Qualifiers
misc_feature 1..1388
note = Obtained from Intestinal Bacteria, K65
source 1..1388
mol_type = other DNA
organism = unidentified
SEQUENCE: 65

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aagtgcgggg gcagcggatg gagtgcattcg gtactcctgc cggcgaccgg cggacgggtg 60
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ccccataata ttccgcacagg catctgtcg agttgaaacg ttccgtgtt ggagatggc 180
atgcgttgta ttagctggat ggtgaggtaa cggctcacca tggcgatgtat acataggggg 240
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gcagtggagga atattgttca atggacgggaa gtcgtggatc cccatgcggc gtgcaggatg 360
aatgtgttat gtatgttaaa ctgtttgtt acgagggttac acccgatatac gcgtatctgc 420
ttgaaatgtt cgtacgataa aggtatgggt aactccgtgc cagcagccgc ggtataacgg 480
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tagagggttca aactcgacgc tcaacgttca aattgcgttca gatctggaga gactagatg 600
tagttgcggg aaggcggatg tggtgtttag cgggtgaaatg cttagatatac acacagaaca 660
ccgatttgcg aggcaacctt ccaagctatt actgacgtctg aggcaegaaa gcgtggggag 720
cgaacaggat tagataccctt ggtgttccac gcaatgttacg atgtataactc gttccggcg 780
atacagatc ggtgtttagt cggaaatggc aatgttaccca cctggggggatc tacgttgcga 840
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tcgtatgatac gcgaggaaacc ttacccggg ttgaaatgtt gcgacggatc gagaatccg 960
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ggggacttca gggggacttc cgggttcaatc cggggggatc gttggggatc cgtcaatca 1140
gcacggccct taatgtccggg ggcacacacg tggttacatg gccggatcag agggtagcta 1200
cctgggtaca ggtatggcaat ctcgaaagcc ggtcttgcgtt cggattggag gctgaaactc 1260
gcctccatgtt aatggggatc gctgttacatc ggcacatcgc catggggccgg tgaataatgtt 1320
cccgccctt taatgtccggg ggcacacacg tggttacatg ggggggttgcgtt gaaatgtt 1380
acccgaag 1388

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SEQ ID NO: 66 moltype = DNA length = 1388
FEATURE Location/Qualifiers
misc_feature 1..1388
note = Obtained from Intestinal Bacteria, K66
source 1..1388
mol_type = other DNA
organism = unidentified
SEQUENCE: 66

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gtcgaacggc gcacccctga cggagttttc ggacaacacggaa agggaaatgt tagtggccga 60
cgggtggatc acgcgtgtt aacctgcctt ggagtggggaa ataacacggc gaaacggctg 120
cttaataccgc atatgttata tggatgcata qgttcttgcgtt accaaaggatt tatecgctcg 180
agatggactc gctgtgttgc agttagttgg tgaggtaatg gtcacccaag ggcacgtatca 240
gtagccggac tgatgggttgc gccggccaca ttggggacttc gacacggccc agactccctac 300
ggggaggcgcg agtggggatc atggggcaat gggggcaaaatc ctggccacgc aacggccgcgt 360
gaaggaaagaa ggccctccggg ttgttacatc cttttgttgc ggcacggaaatc agtgcgttgc 420
cctgacgat aagccacggc taactacgtg ccagcagccg cggtaatcag taggtggca 480
gcgttataatc gatgggttgc ttgttacatc cttttgttgc ggcacggaaatc agtgcgttgc 540
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caggccgaaat tccatgttgc gccgttgcgttgc gtcgttgcgttgc gtcgttgcgttgc 660
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cctccgttgc gcaatgttaca caataatgtt cccacccatc ggcacggaaatc agtgcgttgc 840
aactcaatggg aatgttgcgttgc ggcacccatc agtgcgttgc gtcgttgcgttgc gtcgttgcgttgc 900
aacgcgttgc gtcgttgcgttgc aactgttgcgttgc gtcgttgcgttgc gtcgttgcgttgc 960
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gaaggccgcct gtcgttgcgttgc gtcgttgcgttgc gtcgttgcgttgc gtcgttgcgttgc 1320
tgttacatc gtcgttgcgttgc gtcgttgcgttgc gtcgttgcgttgc gtcgttgcgttgc 1380
caatgggg 1388

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SEQ ID NO: 67 moltype = DNA length = 1380

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-continued

**FEATURE** Location/Qualifiers  
**misc\_feature** 1..1380  
**source** note = Obtained from Intestinal Bacteria, K67  
**mol\_type** = other DNA  
**organism** = unidentified

**SEQUENCE:** 67

tgcggggcgc	gcatgaactt	agcttgcata	gtttatggc	gaccggcgca	cgggttagta	60
acacgttatcc	aacctgcgcg	tgactcgcccc	atagccttc	aaaagaaga	ttaatacccg	120
atggcataat	tcttcgcatt	ggtagaaacta	ttaaaagaatt	tcggatcatcg	atggggatgc	180
gttccattag	gttggggcgc	ggtaacggc	ccaccaagcc	ttcgatggat	aggggatctg	240
agaggaaatgc	ccccccatc	ggaaactgaga	cacggccaa	actcttacgg	ggggcagcag	300
tgagaaatat	tggatcgatgg	acagactgt	ggaccggca	atagtcgtga	aggatgactg	360
ccctatgggt	tgtaaacttc	ttttataccg	gaataaaagt	aggcacgtgt	gccttttgt	420
atgtaccgtt	tgaataagg	tcggctactt	ccgtgcccag	agccgcggta	atacggagga	480
tccgagcgtt	atccggattt	atgggggtt	aaggggagcg	aggccggacgc	ttaaqtcgt	540
tgtgaaatgtt	tgccgctca	cctgtaaa	cgatgtgata	ctgggtct	tgatgtacat	600
agaggcggc	ggatctcggt	gtgtacggt	gaaatgttca	gatcatcaga	agaacttcga	660
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gatacgcgag	gaaccttacc	cggggcttga	ttgcaactga	atgtatgtt	gacatgtcag	960
ccgcaaggc	gttggtaagg	tgtgtatcg	ttgtcgctcg	ctcgccgtt	gagggtgtcg	1020
cttaagtgc	ataacgcagc	caaccctt	cgatgtatc	catcaggta	tcgtggggac	1080
tgtgtcgaga	ctggcgctgt	aatagtgta	ggggatgggg	atagctgttt	aaatcagacgg	1140
cccttacgtc	cggggctaca	cacgtgttac	aatgggggtt	acagaaggca	gctacacggc	1200
gacgtatgc	taatccctaa	agcctcttctc	agttcggatt	ggagtctgc	acccgactcc	1260
atgaatgcgtt	atccgtatgt	aatcgcgtat	cagccacggc	ggcgtgttata	cgttccggg	1320
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aaaatcgca	gattaaage	geatgcgt	ttggggatgg	ctcgccgtct	attagttagt	180
ttgtgaggta	acggcttacc	aaggcgat	cgggtagcc	gtctgaggg	atgtccggcc	240
acactggaa	tgagacacgg	tccagacacc	tacgggttgc	agcagtgcgt	aatcattcac	300
aatgggggg	accctgtatc	tgccgacgcg	cgtgggggaa	tgaagggttt	oggatgtttaa	360
acccttgc	tgtggggaga	aattaaaaag	atagtcacac	aaagggaga	gacgggtacaa	420
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tggaaatgc	agatatacg	aggaacactc	gttggcgaa	cggttctctg	gacattact	660
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gtaaacgggt	cacgttgcgt	gtggggggaa	tcgccccct	gctgtccgg	gctaaccgcgt	780
taagcggtc	gcctggggg	gtacgggtc	aagattaaaa	ctcaaagaaa	ttgacgggg	840
cccgacaca	cgggtggaga	tgtgtttaa	ttcgtatgc	cgccgaa	acttacgttgg	900
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ctgtcgcc	tgtgtcgatgt	cggtcgta	gtatgtttt	taatgtccac	aacagacgc	1020
accctgtt	ccagttacca	gcacgtaa	gtggggactc	tggcgagat	gcccagatca	1080
actgggggg	agggtgggg	gacgtcgatgt	cagtatgc	ttatgc	gggtcgacca	1140
cgtactacaa	tgccccatgt	agggggggcc	aaacggccga	ggggggggaa	atccaaaa	1200
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gggatccatc	aggcttgcgt	tgggtggag	agtggcgac	gggtgtgat	tgcgtgaccg	120
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atgtcgtat	tcttcggaa	aaacgttccgc	gggtatggat	gggggtcg	cttatacgat	240
tgacggcg	gtacggccc	accgtggctt	cgacgggt	ccggctcg	agggcgaccg	300

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gcccacattgg	gacttagagata	cggcccgagac	tcctacggga	ggcagcagtg	ggaaatattg	360
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caagtcatga	aagtggggcg	cacccgaacg	cggtggccct	acccctgtg	ggatggagcc	1440
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cggtggatc	acct					1514

SEQ ID NO: 70	moltype = DNA	length = 1517				
FEATURE	Location/Qualifiers					
misc_feature	1..1517					
note	= Obtained from Intestinal Bacteria, F02					
source	1..1517					
mol_type	= other DNA					
organism	= unidentified					
SEQUENCE: 70						
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gtatccaacc	tgccgataac	tcggggatag	ccttcgaaa	gaaagattaa	tatccgatag	180
tatattaaaa	cogcatgg	ttactattaa	agaatttcg	ttatcgatgg	ggatgcgttc	240
cattagtttgc	ttggcgccgg	aacggcccac	caagactacg	atggatagg	gttctgagag	300
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gtgcgttcc	aacacct					1517

SEQ ID NO: 71	moltype = DNA	length = 1517				
FEATURE	Location/Qualifiers					
misc_feature	1..1517					
note	= Obtained from Intestinal Bacteria, F03					
source	1..1517					
mol_type	= other DNA					
organism	= unidentified					
SEQUENCE: 71						
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cgttatccgg	atttattggg	tttaaagggtt	cgcttaggttgc	actggtaatgt	cgttgcgaa	600
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caaaggaaatt	gacggggcc	cgcacaagcg	gaggaacatg	tggttaatt	cgatgatacg	960
cgaggaaacct	tacccggct	taaatgcag	tggaatatgat	tggaaacatg	tcagtgagca	1020
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agtgcataaa	cgagcgcaac	ccttatctt	agtactaac	aggtcatgt	gaggactctg	1140
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gtatgtcaat	ccaaaagcc	tcttcgtt	cgatcgaaat	tctgcacccc	gacttcgtga	1320
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gtcgccgttgg	aacacct					1517

SEQ ID NO: 72	moltype = DNA	length = 1515				
FEATURE	Location/Qualifiers					
misc_feature	1..1515					
note = Obtained from Intestinal Bacteria, F04						
source	1..1515					
mol_type = other DNA						
organism = unidentified						
SEQUENCE: 72						
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cgccgttggaa	cacct					1515

SEQ ID NO: 73	moltype = DNA	length = 1517				
FEATURE	Location/Qualifiers					
misc_feature	1..1517					
note = Obtained from Intestinal Bacteria, F05						
source	1..1517					
mol_type = other DNA						
organism = unidentified						
SEQUENCE: 73						
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tataatcgttgc	ccggatgttgc	tttgcgttgc	ttatgcgttgc	ttatgcgttgc	ggatgcgttgc	240
cattaggcg	tttgcgttgc	aacgcgttgc	caaaacccgt	atggatagg	tttgcgttgc	300
gaagggttgc	cacatttttttgc	cttgcgttgc	gtccaaactc	stacccgggg	cagcgttgc	360
gaatattttgt	caatggggc	aggcttgc	cagccaaatgt	cggttgcgttgc	tgactgcctt	420
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gtgcggctgg	aacacct					1517

SEQ ID NO: 74                    moltype = DNA length = 1515  
 FEATURE                         Location/Qualifiers  
 misc\_feature                 1..1515  
 note = Obtained from Intestinal Bacteria, F06  
 source                        1..1515  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 74

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atccaacctt	ccgatgactc	ggggatagcc	tttcggaaaga	aagattaata	cccgatggca	180
tagttcttcc	gatgtttaga	actttaaaag	aatttcggtc	atcgatgggg	atgcgttcca	240
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cgccgtggaa	cacct					1515

SEQ ID NO: 75                    moltype = DNA length = 1518  
 FEATURE                         Location/Qualifiers  
 misc\_feature                 1..1518  
 note = Obtained from Intestinal Bacteria, F07  
 source                        1..1518  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 75

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aggatgcata	tcccaaaaac	ctctctcgt	tcggatgtca	gtctgtcaacc	cgacttcgt	1320
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ggtgccggctg gaacacct

SEQ ID NO: 76 moltype = DNA length = 1517  
FEATURE Location/Qualifiers  
misc\_feature 1..1517  
note = Obtained from Intestinal Bacteria, F08  
source 1..1517  
mol\_type = other DNA  
organism = unidentified

SEQUENCE: 76  
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atccaacccgtt ccctttactc ggggatagcc ttgcgaaaga aagatataa cccgatggta 180  
taattatttc gcatgggtt attataaag gattccgtt aaggatgggg atggcttcca 240  
tttaggtgtt ggtgggtt aa cggcttccatc agcgttccatg ggatgggggt tctyagaggg 300  
aggccccccca cattggaaact gagacacggt cccaaactcc acgggaggca gcagtgaggaa 360  
atattggtca atgggcgtat gcttgcgaa gccaaggtagc gtgaaggatg aaggcttat 420  
gggtcgatataa ctctttttat attagataaa agtgcatgt gtatgtt ttgtatgt 480  
aatatgaaata aggtacgggtt aactccgttc cggcggccg ggttataacgg aggtccggag 540  
cggttacccggtt atttttggg tttaaaggga cgcttaggtt actgtttaact cagttgttcaa 600  
agtttgcggc tcaaccgtt aatttgcattt gataactgttca gtcttgcgtt cagtagaggt 660  
ggggcgaattt cgtgggtttagt cgggttcaatg ctttagatatac acggaaactt ccgttgcgtt 720  
aggccgttccatc ctggactgttca acgtacacatg atgtccgtaaa gtgtgggttataa ccaacaggat 780  
tagataccctt ggttgcgttccatc acagtaaaacg atgttacttgc tctgttgcgtt atatacgtt 840  
agcggccaaatg cgaaaggattt aagtatttca cctggggatg acggccggaa cgggttggaaact 900  
caaaggaaat tttttttttt gacggggggcc cgcacaacggc gaggaaacatg tggtttaat cgtatgttacg 960  
cgaggaaactt taccgggttca atttttgcgtt gttttttttt gggggatgttca tttttttttt 1020  
ataccggctgtt gtaagggttgcgtt gcatgttgcgtt cttttttttt tttttttttt 1080  
agtttgcataatc cgagccgttccatc acgttacttgc tttttttttt tttttttttt 1140  
gagagactgc cttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1200  
tacgtccggcc gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1260  
ggatgttcaatc cccaaaggcc tttttttttt tttttttttt tttttttttt tttttttttt 1320  
atgttggattt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1380  
gttacacaccg cccgttcaatc tttttttttt tttttttttt tttttttttt tttttttttt 1440  
gggtccctagg gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 1500  
gttccggctgg aacacctt

SEQ ID NO: 77 moltype = DNA length = 1515  
FEATURE Location/Qualifiers  
misc\_feature 1..1515  
note = Obtained from Intestinal Bacteria, F09  
source 1..1515  
mol\_type = other DNA  
organism = unidentified

SEQUENCE: 77  
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ggcagcacgat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 120  
aaccttccatc tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 180  
ggttcccatat tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 240  
agtagttttt gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 300  
gtttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 360  
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misc\_feature                1..1519  
                         note = Obtained from Intestinal Bacteria, F10  
 source                1..1519  
                         mol\_type = other DNA  
                         organism = unidentified

SEQUENCE: 78

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gaagcacccc gacggatttc ttccgattta agcccttggtg acttgaggcgc ggacgggtga 120
gtaacgcgtg ggttaacactgc ctcatacagg gggataaacat ttggaaacgg ctgctaatac 180
cgatatacgcg cacatgtaccgc catggatccgg tggaaaaaacat ccgggttgta tgagatggac 240
ccgcgtctgat tttagttagtt ggtgggttaa cggccatccca agccgacgat cagtagccga 300
cctggagaggg tgacccggcca catttggact gagacacggc ccaaaactcc acgggaggca 360
gcagtggggaa atattgcaca atggggggaaa ccctgatgc gcgacggccg gtgagcgat 420
aagtatttcg gtatgtaaag ctctatcago agggaaagaaa atgacggatc ctgactaaga 480
ageccccggct aatactcgatc cagcagccgc ggtataatcgat agggggcaag cgttataccgg 540
atttacttgg tggtaaaggga gctgtacgcg catggcaacg cagatgtgaa agccccgggc 600
tcaacccccc gactgcattt ggaactgtca ggctagatgg tcggagaggaa aagcgaaatt 660
cctagtgtatc cggtgaaaatcg cgtagatattt agggagaaaca ccagtggccg aggcggctt 720
ctggacgatg actgacgttgc aggtggatccgg gctgtggggaa caaacaggat tagataccct 780
ggtagtccac gccgttaaaccg atgaataacta ttgttgcgggat ggcggaaacca ttccggccg 840
cagccaaacgc aataagtattt ccacccgggat agtacgttgc caagaatgaa actcaaagga 900
atttgacccggg accccgcacaa gccgtggggat atgtgggttta attcgaacgca acggcaagaa 960
ccttacccccc ttttgcaccc cctctgaccc ctctttatc ggatctttcc ttccggacag 1020
aggagacagg ttgttgcattttt ctccgtgtcgat gagatgttgg gttaaatccc 1080
gcacacggcc caaccccttat cttagtgcac cagcattttt gatggggact cttagagagac 1140
tgcggggat aacccgtgggg aagggtggggat tgacgttaaa tcatcatgcc ccttatgacc 1200
agggtctacac acgtgtatca atgggtttttttaa caaaggggaaac ccggccggccg agggggagca 1260
aattccccaaa ataacgttctc atttccggat ttgttgcata actcgactac atgaagctgg 1320
aatcgctatg aatcgcaat cagaatgttc cgggtgaatac gttccggggat ttgttacaca 1380
ccgccccgtca caccatggga gtcagtaacg cccggaaatc gtgaccacac ccggaaaggagg 1440
gagctggccca aggtggggacc gataacttggg gtgaagtcgtaa aacaaggtag ccgtatccgg 1500
agggtcgccgtt ggtatcaccc 1519
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SEQ ID NO: 79                moltype = DNA length = 1519  
 FEATURE                Location/Qualifiers  
 misc\_feature                1..1519  
                         note = Obtained from Intestinal Bacteria, F11  
 source                1..1519  
                         mol\_type = other DNA  
                         organism = unidentified

SEQUENCE: 79

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ggaaatcaact tcatttgcaccc ttccgatggat ttgattttgat tctatgtggcc gacgggttgat 120
taacgcgtgg gtaacactgc ttatccagggg ggataaacatc cagaatgcgat tggtaatacc 180
gcataagccgc acaggacccgc atggccgttgc ttggggat aacttgcatacc ccgggttgtat aagatggac 240
cgcggttggat tagcttgcgg tggggatggaaatccca ggcggacgatc catagccgc 300
ctggagggatggat gaaacggccac atttggacttgc agacacggccg cagactccca cggggaggac 360
caatggggaaat tattttgcacaa cttgttgcggat cttgttgcggc tggatggaa 420
agttatctccgg ttttgcaccc tctatcggat gggaaatgtatc tttttttttccggat tggatggaa 480
gcggccgtca actacgttgc ggcggccggc gtaataacgttcc gggggcaacg gttatccgg 540
tttactctgggt gtaaaaggggat cttgttgcggat ttggcaatgttcc gttatgtggat 600
caacctgtgg atctcgatccg aaactgtcat actttgcgttgc cggggggatcc acggaaattc 660
ctatgtttgcgtt ggttgcaccc ttttgcaccc ttttttttttttccggat tggatggaa 720
tggacgggttttttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc 780
gtatgttgcggcccg ccggtaacacgca gtaatgttgc ttttgcaccc ttttgcaccc ttttgcaccc 840
cgccaaacggca gtaatgttgc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc 900
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caacggccgc aaccccttcc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc 1140
tgcggggat aacccgtgggg aaggccggggat ttgttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc 1200
tgggttttttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc ttttgcaccc 1260
aattccccaaa ataacgttccc atttccggat ttgttgcata actcgactac acggaaatccc 1320
aatcgctatg aatcgcaat cagaatgttc cgggtgaatac gttccggggat ttgttacaca 1380
ccgccccgtca caccatggga gtcagtaacg cccggaaatc gtgaccacac ccggaaaggagg 1440
gagctggccca aggtggggacc gataacttggg gtgaagtcgtaa aacaaggtag ccgtatccgg 1500
agggtcgccgtt ggtatcaccc 1519
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SEQ ID NO: 80                moltype = DNA length = 1519  
 FEATURE                Location/Qualifiers  
 misc\_feature                1..1519  
                         note = Obtained from Intestinal Bacteria, F12  
 source                1..1519  
                         mol\_type = other DNA  
                         organism = unidentified

SEQUENCE: 80

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gaagcacttg	aatggaaattc	ttcgaaagg	agtcacatgc	actgagtcgc	ggacgggtga	120
gtaacgcgtg	ggtaacctgc	ctcatacagg	gggataacag	ttagaaatga	ctgctaatac	180
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cagccaaacgc	aataagtat	ccacgtgggg	agttacgttgc	caagaatgaa	actcaaaggaa	900
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ccttacatgc	tcttgacatc	cctctgacc	ctctttaatc	ggagctttc	tccgggacag	1020
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agggtctcac	acgtgttaca	atgggtttaa	caaaggaa	caggtgtgc	aggccgagca	1260
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ccgcggctca	caccatggg	gtcgtatc	cccgaaatgc	gtgaaatc	cgcaaggagg	1440
gagctgcgcg	agggtggacc	gataactggg	gtgaaatgtt	aacaaggtag	ccgtatcgga	1500
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SEQ ID NO: 81 moltype = DNA length = 1518  
 FEATURE Location/Qualifiers  
 misc\_feature 1..1518  
 note = Obtained from Intestinal Bacteria, F13  
 source 1..1518  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 81  

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gtaacgcgtg	ggtaacctgc	ctcatacagg	gggataacag	ttagaaatgg	ctgctaatac	180
cgcataacgc	cacagtgc	catggagac	tgtgaaaaac	tccgggtgt	tgagatggac	240
ccgcgtctga	ttagctgg	ggtaatggta	cgggttacca	aggcgcacat	cagtagccgg	300
cctgagaggg	tgacccggca	cattggact	gagacacggc	ccaaactcct	acgggaggca	360
gcagtgggg	atattgcaca	atggggaaa	ccctgatgca	gwgacgcgc	gtgagtgaag	420
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agccccggct	aactacgtc	cageageccg	ggtataatgc	agggggcaag	cgttatccgg	540
atttactgg	tgtaaagg	gctgtagacgg	catagacta	tccggatgg	agccggggc	600
tcaacccccc	tactgttt	gaaactgttta	agtagatgt	tccggaggg	aaggtaatt	660
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ctggacagata	actgtacgt	agggtcgaaa	gctgtgggg	aaacaggat	tagataccct	780
ggtagtccac	gocgttaaac	atgtacta	ttgttgcatt	ggcaaaagccc	atcgggtccg	840
ccgcataacgc	aataagtatt	ccacctgggg	atgtgttgc	caagaatgaa	actcaaaggaa	900
atttacgggg	acccgcacaa	gcccgggg	atgtgttta	attcqaacga	acgcgaaggaa	960
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cccgaggata	acgtgggg	agggtgggg	gacgtcaat	catcatgcc	ttatgattt	1200
ggggctacata	cgtgttacaa	tgggtttacaa	aaaggatgg	gacgtcgca	ggggggaggca	1260
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gggtcgccgt	gatcacct					1518

SEQ ID NO: 82 moltype = DNA length = 1519  
 FEATURE Location/Qualifiers  
 misc\_feature 1..1519  
 note = Obtained from Intestinal Bacteria, F14  
 source 1..1519  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 82  

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gtaacgcgtg	ggtaacctgc	ctcatacagg	gggataacag	ttagaaatga	ctgctaatac	180
cgcataacgc	cacagtgc	catggacac	tgtgaaaaac	tccgggtgt	tgagatggac	240
ccgcgtctga	ttagctgg	ggtaatggta	cgggttacca	aggcgcacat	cagtagccgg	300
cctgagaggg	tgacccggca	cattggact	gagacacggc	ccaaactcct	acgggaggca	360

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gcagtgggaa	atattgcaca	atggggaaa	ccctgatgca	gcgacgccgc	gtgagcgaag	420
aagtatttcg	gtatgtaaag	ctctatcago	aggaaagaaa	atgacggtac	ctgactaaga	480
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aggtgcggct	ggatcacct					1519

SEQ ID NO: 83	moltype = DNA length = 1519
FEATURE	Location/Qualifiers
misc_feature	1..1519
	note = Obtained from Intestinal Bacteria, F15
source	1..1519
	mol_type = other DNA
	organism = unidentified

SEQUENCE: 83						
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cagcaaaacgc	aataagtat	ccacctgggg	agtacgttgc	caagaatgaa	actcaaagga	900
attgacgggg	acccgcacaa	gcccgggg	atgtgggtt	attcgaagca	acgcgaagaa	960
cettacccgg	tcttgacatc	cctctgacc	ctctttaatc	ggagcttcc	ttcgggacag	1020
aggagacagg	ttgtgtatgg	ctctgtcg	ctctgtcg	gagatgttgg	gttaagtccc	1080
gcaacgcgc	caacccctat	ctttagtgc	cagcattttg	gatggcact	ctagagagac	1140
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aatcccaaaa	ataacgtctc	atgtcgat	gtatgttgc	actcgcactac	atgaaatcg	1320
aatcgctatg	aatcgcaat	cagaatgtcg	cggtgaatac	gttcccggt	tttgtacaca	1380
ccgcgcgtca	caccatggga	gtcagtaacg	cccgaagtc	gtgacccaa	cgcgaaggagg	1440
gagctgcgca	aggtggggacc	gataactggg	gtgaagtctg	aacaaggtag	ccgtatcgga	1500
aggtgcggct	ggatcacct					1519

SEQ ID NO: 84	moltype = DNA length = 1521
FEATURE	Location/Qualifiers
misc_feature	1..1521
	note = Obtained from Intestinal Bacteria, F16
source	1..1521
	mol_type = other DNA
	organism = unidentified

SEQUENCE: 84						
agagtttcat	cctggcttag	gatgaacgt	ggccggcgtgc	ttaacacatg	caagtgcac	60
aaaaacaccc	atttgat	tttgcgaa	acttgcgttgc	gaaatgg	tgatttgcgt	120
gagtaacgcg	tgggttac	gcccgtaca	ggggataac	agtcaat	gactgtctat	180
accgcataag	accacacgcac	cgcgttgc	agggttaaa	actccgttgc	tacaggatgg	240
acccgcgtt	gattatgttgc	ttgggtgggt	aacggctcac	caaggccac	atcgtatgc	300
ggcttggat	agtgaaacggc	cacattgggg	ctgagacacg	gcccacactc	ctacgggagg	360
cacgcgttgc	gatattgtca	caatgggg	aaccctgtat	cagcgttgc	gctgtgtat	420
agaagtattt	cggtatgtaa	agcttatac	gcagggaa	aatgcgttgc	acctgtactaa	480
gaagccccgg	ctaactacgt	gccagcagcc	gggttaat	gtagggggca	agcgttatcc	540
ggaattactg	ggtgtaaagg	gtgcgtatgt	ggtatggca	gtcagaatgt	aaaacccagg	600
gtttaactct	gggactgtt	ttgaaactgt	cagactagag	tgcaggag	gtaaacgcgaa	660
ttcctgtatgt	agcggtgaaa	tgcgtagata	ttaggaggaa	catcgttgc	gaaggccggt	720

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ctcgtagtcc	acgcggtaaa	cgtatgaatac	taggtgtcgg	ggccgttagag	gcttcgggtgc	840
cgcagccaac	gcagtaagta	ttccacettgg	ggagtacgtt	cgcaagaatg	aaactcaaag	900
gaattgacgg	ggaccggcac	aagcgggtga	gcatgtggtt	taattcgaag	caacgcgaag	960
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aggagtgaca	ggtggtgcac	ggtgtgcgc	agetcgtgtc	gtgagatgtt	gggttaagt	1080
ccgcacacgag	cgcaaccct	atctttagta	gccagcatat	aaggatggca	ctctagagag	1140
actgcccagg	ataacctgg	ggaagggtgg	gacgacgtca	aatcatcatg	ccccttatga	1200
ccagggtac	acacgtcta	caatggcgt	aacagaggga	agcagectcg	tgagagtgg	1260
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gggagctgc	gaaggcggga	ccgataactg	gggtgaagtc	gtaacaagg	agccgtatcg	1500
gaaggtgcgg	ctggatcacc	t				1521

SEQ ID NO: 85	moltype = DNA length = 1518					
FEATURE	Location/Qualifiers					
misc_feature	1..1518					
	note = Obtained from Intestinal Bacteria, F17					
source	1..1518					
	mol_type = other DNA					
	organism = unidentified					
SEQUENCE: 85						
agagtttgat	cctggctcag	gatgaacgt	ggccgcgtgc	ttaacacatg	caagtgcac	60
gggaaacatt	ttatggaa	gc	ttcgtggaa	atagcttgc	tctagtggcg	120
taacgcgtgg	gtaacctgcc	tcacactgg	ggataacagt	cagaaatgac	tgctaatacc	180
gcataaggcgc	acggggatgg	atgtccatgt	gtgaaaaaaact	ccgggtgggt	gagatggacc	240
cgcggtggat	tagccatgt	gcagggtaac	ggccttaccaa	agcgacgtc	catagccggc	300
ctgagagggt	ggacggccac	attggggactg	agacacggcc	cagactcc	cgggaggcag	360
cagtggggaa	tatttcacaa	ttggggaaac	cctgtatcg	cgacgcggc	tgaaggaaga	420
agtatctccg	tatgtaaact	tctatcagca	gggaaagaaa	tgacggtacc	tgactaagaa	480
gcccggcgt	actacgtcc	agcagcgcg	gtaaatcgt	ggggcaagc	gttatccgg	540
tttactgggt	gtaaaaggag	cgtagacgg	gcagcaagt	tgatgtaaa	ggccgggggt	600
caaccccccgg	actgcattgg	aaactgttga	tcttgagtac	cgagagaggta	agcggaaattc	660
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tttgacgggg	cccgacaca	cggtgagca	tgtggttaa	ttcgaagcaa	cgcaagaaac	960
cttaccaatc	cttgacatcc	ctctgacccg	tgtgttcgt	caccccttc	tcgggacaga	1020
ggagacaggt	gttgcattgt	tgtgttcgt	tcgtgtcggt	agatgtggg	ttaagtcccg	1080
caacgagcgc	aaaccctatc	cttagtagcc	agcggttgg	ccgggactc	tgaggagact	1140
gccaggatcac	acctgggg	aggcggggat	gacgtcaat	catcatgc	ccattatgatt	1200
gggtcacaca	cgtgtcaaa	tggcgtaaaa	aaaggaaagc	gagagtgtga	gettaagcaa	1260
atcccaaaaa	taacgtccca	tttccggactg	cagtctc	ctcgactc	cgaagcttgg	1320
atcgtctaga	atcgccgatc	agaatgccg	ggtgaat	tc	ttgtacacac	1380
cgcgcgtcac	accatgggg	tcgataacgc	ccgaatgt	tgaccgaacc	gaaaggacgg	1440
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gggtcggtgt	gatcacatc					1518

SEQ ID NO: 86	moltype = DNA length = 1522					
FEATURE	Location/Qualifiers					
misc_feature	1..1522					
	note = Obtained from Intestinal Bacteria, F18					
source	1..1522					
	mol_type = other DNA					
	organism = unidentified					
SEQUENCE: 86						
agagtttgat	cctggctcag	gatgaacgt	ggccgcgtgc	ctaacacatg	caagtgcac	60
gaagcaatta	aaatgaagtt	ttccgtatt	tttttattgg	actgagtgg	ggacgggg	120
gttaacgcgtg	gataacctgc	tcacactgg	gggataacag	ttagaaatga	ctgctaatac	180
cgcataaggcgc	cacagtaccg	catggtaacgg	tgtggaaaac	tccgggtgg	tgagatggat	240
ccgcgtctga	ttagccagtt	ggccgggtaa	cgcccacca	aagcgcacat	cagtagccg	300
cctcgaggagg	tgacccggcc	cattgggt	gagacacggc	ccaaactcct	acggggaggca	360
gcagtgggg	atattgcaca	atggcgaaa	gcctgtatgc	gcgcggccgc	gtgagtggaa	420
aagtatttcg	gtatgtaaag	ctctatc	agggaaagaa	atgacgttgc	ctgactaaga	480
agccccggct	aactacgtc	cagcagccgc	ggtataatc	agggggcaag	cggttatccgg	540
atttacttgg	tgtaaaggga	gcgttagacgg	cgaagcaat	ctgaatgt	aacccagg	600
tcaaccctgg	gactgttgc	gaaatgttgc	tgatgtatgt	tcggagagg	aagtgtgt	660
cctatgttgc	cggttgcatt	cgtagatatt	aggaggaa	ccagtgccgc	aggcggctta	720
cttgcgtacata	actgcattgc	aggctcgaaa	cgctgggg	caaaacaggat	tagataccct	780
ggtagtccac	ccgtaaacgc	atgaatgt	gggtgtgggg	ggcaaaagcc	tccgggtcc	840
tcgcacaa	actaaggatc	ccacatgggg	agtacgttgc	caagaatgaa	actcaaaggaa	900
attgacgggg	acccgcacaa	ggccgtgggg	atgtgtttt	attcgaagca	acgcgaagaa	960
ctttaccaag	tcttgacatc	ctcttgcac	gctgtgttgc	gcgccttccc	ttcggggca	1020
gagagacagg	ttgtgtcatgg	ctcggtcg	gagatgttg	ttaagtccc		1080

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gaaacgagcg caacccttat ccttagtago cagcaggtag agctggcac tctagggaga	1140
ctggccggga taacctggag gaagggtgggg atgacgtcaa atcatcatgc cccttatgat	1200
ttggggctaca cacgtgtac aatggcgtaa acaaaggaga gcaagacagt gatgtggagc	1260
aaatccaaa aataacgtcc cagttcgac ttagtgc aaccgcacta cacgaactg	1320
gaatcgtag taatcgca a tcagaatgtc gcggtgaata cggtccggg tcttgatcac	1380
accggccgtc acaccatggg agtcagcaad gcccgaagtc agtgacccaa ctgcgaagag	1440
aggggagctgc cgaaggcggg gcaggttaact ggggtgaagt cgtaacaagg tagccgtatc	1500
ggaggagtgcg gtcgatcac ct	1522

SEQ ID NO: 87	moltype = DNA length = 1520
FEATURE	Location/Qualifiers
misc_feature	1..1520
	note = Obtained from Intestinal Bacteria, F19
source	1..1520
	mol_type = other DNA
	organism = unidentified

SEQUENCE: 87	
agagtttgat cctggctca gatgaacgct ggccgcgtgc ttaacacatg caagtcaac	60
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agtaacgcgt gggtaacactg cctcacaactg gggataaca gtcagaaatg actgtataa	180
ccgcataaagc gcacgggatt gcatgatcca gtgtaaaaaa ctccgggtgt gtgagatgga	240
cccgccgtgg attagccgtg tggcaggta acggccatca aaagcgacga tccataggcg	300
gcctgagagg gtggacggcc acatggggac tgagacacgg cccagactcc tacgggaggc	360
agcagtgggg aatattgcac aatggggaa accctgtgc acgcacgcg cgtgaaggaa	420
gaagttatctc ggtatgtaaa ctctatcag cagggaaagaa aatgacggta cctgactaa	480
aaggccccgc taactacgtg ccagcagccg cgtaatac tagggggcaa gcgttatccg	540
gattttactgg gtgttaaaggg agcgttagacgg gacgcgaagg totgtatgta aaggccgggg	600
ctcaacccccc ggactgcatt ggaaaatgtt gatcttggat accggagagg taagcggaaat	660
tccctagtta gccggtaaat gctgtatgat taggaggaaac accagtggcg aaggccgtt	720
actggacggt aactgcgtt gaggctcgaa agcgtgggaa gcaaacagga ttatgatcccc	780
tggtagtcca cggcgtaac gatgaaatctt aggtgtccggg tggcagaggcc attcgggtcc	840
gcacggaaacg cagaatgtat tccacactgg gtagtcgtt gcaagaatgaa aactcaaagg	900
aattgacggg gacccgcaca agcgggtggag catgtggttt aattcgaagc aacgcgaaga	960
accttaccaa gtcttgcatt ccctctgacc ggtgagtaac gtcaccccttc cttcgggaca	1020
gaggagacag gtgggtcgat gttgtcgatca gtcgtgtcg tgagatgtg ggttaagtcc	1080
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ctggccaggaa taacctggag gaaggccgggg atgacgtcaa atcatcatgc cccttatgat	1200
ttggggctaca cacgtgtac aatggcgtaa acaaaggaga gcgagatgt gagcttaac	1260
aaatccaaa aataacgtcc cagttcgacg tgcgtctgc aactcgactc cacgaactg	1320
gaatcgtag taatcgca a tcagaatgtc gcggtgaata cggtccggg tcttgatcac	1380
accggccgtc acaccatggg agtcgtaccc gcccgaagtc agtgacccaa ccgaaggac	1440
ggaggtgcgc aaggcgggac ggatgactgg ggtgaagtgc taacaaggta gccgtatcc	1500
aaagggtgcgc tggatcacct	1520

SEQ ID NO: 88	moltype = DNA length = 1528
FEATURE	Location/Qualifiers
misc_feature	1..1528
	note = Obtained from Intestinal Bacteria, F20
source	1..1528
	mol_type = other DNA
	organism = unidentified

SEQUENCE: 88	
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gaagtttgcg ggaagcttgc ttccaaagag acttagtggc gaacgggtga gtaacacgt	120
ggtaacactgc ccatgtgtcc gggtaacttg ctggaaaccc tagctaaaac cggataggta	180
tacagagcgc atgctagta tattaaacgc cccatcaagg cgtgaacatg gatggactg	240
cggcgcattta gtagttgtt gaggtaacgg cccaccaagg cgatgtgcg tagccggct	300
gagagggtaa acggccacat tgggacttag acacggccca aactcctacg ggaggcagca	360
gtagggaaat ttcgtcaatg gggggaaaccc tgaacgacca atgcccgtg agtgaaggaa	420
gttctccggat ctgttgcgtc ttgttgcgtt aactgcactt gaggacacgg aacgcgtgggg	480
gagtgcgtt agcttacccag aacggccacgg ctaactacgtt ccacggcc gccgtataac	540
gttaggtggca agcgttatcc ggaatcattt ggcgtaaagg gtgcgttagt ggcgtactaa	600
gtctgtatgaa aagggtcaatg gtcacccat tgcgtatgtt ggtaaactgtt atgctggat	660
gcagaagagg ggcgttgcatt tccatgttgc ggcgtatgtt atggaggaaac	720
accagtggcg aaggccgtcg cctgggtgtt aactgcactt gaggacacgg aacgcgtgggg	780
gcaaatatgg ttagataccct tagtgtca ccgggttac gatgaaactt aatgttttgc	840
ggaatttgcgtt gtcgtatgtt acgcataatgg ttctccgcctt gggggatgtt caccgtatgt	900
tggaaactcaaa aggaaatgtac gggggcccgca acaagcggtt ggtatgtt tttatccgt	960
agcaacgcgc aacaccatcc caggccgttca catggaaacca aataccctag agatagggggg	1020
ataattatgg atcacacagg tggtgcattt ttcgtgtcgat aactgcactt gaggatgttgc	1080
gttaagtcc gcaacgcgcg caaccctgtt cgcgtatgttcc caccatcaag ttggggactc	1140
atgcgtatgtt gccgttgcaca aacggggatgg aggtggggat gacgtcaat catcatggcc	1200
cttcatggctt gggcttacca cgtactacaa tggcgttcc accagacggc gacacgttgc	1260
tgtgaaggcgaa atctcataaa ggtcgatctca gttcggtttt aactgcgttcc ctgcgttcc	1320
tgaaggcgaa atcgtatgtt atcgcgtatgtt acgcgtatgtt ggtatgttcc ttctccggcc	1380
ttgtacacac cggccgttca accatggggatcc tcaatatacc ccgaaggccggg tggcataacc	1440

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note = Obtained from Intestinal Bacteria, F23  
source 1..1519  
mol\_type = other DNA  
organism = unidentified

SEQUENCE: 91

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agagtttgat cctggctca gatgaacgct ggcggcgtgc ttaacacatg caagtgcAAC 60
gaaggactt acgggattt ttccggatgaa aagtttttgc actgatgtgc ggacgggtGA 120
gtaaacgcgtg ggttaacctgc ctctatacagg gggataaacAG tttagaaatgA ctgtataatC 180
ccgcataagac cacaggatG catgatcccc ttgtaaaaAC tcgggtgttA tgatgtggAC 300
ccgcgtctGA tttaggtAGtt ggtgggttAA cggtctacCA agccgacgAT cagttagCCGA 360
cctggagggG tgaccggCCA cattgggact gagacacGGC ccaaaACTC acggaggGCA 420
gcagtgggggA atattgtcaca atggggggAA ccctgtatGCA gcgcacGCGC gtgacGgtG 480
aagtatttGC ttatgttaAGG ctctatacAG gggagaAGAA atgcgttcAG ctgtactAGA 540
agcaccggGT aaatacgtGC cagcagcCGC ggttaatacgt atgggtcaAG cgttatCCGG 600
attactgtGG ttgtaaaggGA gctgtacAGC agggacAGt ctgtatgtGA aaccggggGC 660
tcaaccGGG gactgtcatG gaaaactttt ttcttagatGt tcggaggAGt aagtggAA 720
cctagtgtAG cggtaaaaAT ctgtatGAtt aggaggAAca ccaagtggCga aggccgCCTA 780
ctggacgtG actgtacgtG aggctegAAA gcgttggggAG caaacaggat tagataccCT 840
ggtagtccAC gccgttaaaCG atgactgtCA ggtgttggGA ggcAAAGCCT ttccgtGCCG 900
cagcaacACG aataaGcAGt ccacccGGG agtaacgttG caaagaatGAA actcaaaggGA 960
attggcgggg ACCCGCACAA ggggttggAC atgtgggttA attcgaAGCA acgcgaaAGA 1020
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gcaacgaggC caacccttA cttagtAGC cagcatCtG gatggcCt atcagagAG 1200
ccggcaggAG aacctgggg AGGGTGGGG tgacgttcaAA tcatatGcc ccttatGGG 1260
agggtacac AGTGTcAta atggcgttAA caaaggGAGG caacGtGCG aggggtGAGA 1320
aatccccAAA ataacgttC AGTtCggatt gtatgtcGA actcgactAC atgaagctGG 1380
aatcgctAGt aatcgcGAat cagaatgtCG cggtaataAC gttcccccgt ctgtacaca 1440
ccggccgtGA caccatGGGA gttgttAAcG cccgaAGtCA gtgacccaAC cgttaaggAGG 1500
gagctggcGA aggtgggACG gataactGGG gtgaagtCtG aacaaggTAG cctgtatCggA 1560
aggtgccggtt ggatcacct
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SEQ ID NO: 92 moltype = DNA length = 1520  
FEATURE Location/Qualifiers  
misc\_feature 1..1520  
source note = Obtained from Intestinal Bacteria, F24  
1..1520  
mol\_type = other DNA  
organism = unidentified

SEQUENCE: 92

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agagtttgat cctggctca gatgaacgct ggcggcgtgc ctaacacatg caagtgcAAC 60
gaaggactt acgggattt ttccggatgaa atcggtataa cttagtggcG gacgggttag 120
taacgcgtG gaaacGtCC ctgtacCCGG ggataaacACT tagaaatAGG tgtaataACC 180
gcataaGcGC acggAACGc atgggttGtG tgaaaaAACT ccgggtgtAC aggatggtCC 240
ccgcgtctGA tagccagtgC gcaagggttAC ggccttacAA acgcacGACt agtacGGCG 300
cagtggggAA tattgtcacaA tggggacttG agacacGGC caaacttCtA cgggaggCAG 360
cgttggggAA tattgtcacaA tggggacttG cttgtatGCA cggcgcCAG tgatgtggAA 420
agtatttGCG tattgttAAAGC tctatcAGCA gggaaAGAAA tgacGgttAC tgactaAGGA 480
gccccggGtA actacgtGtCC agcacGGCGC gtaatcAGtA gggggcAAGC gttatccGG 540
tttagtgggtG ttgtaaaggAG cgttagacGGC atggcaAGGC agatgtGAA acccaggGt 600
caacccGGG attcgttGtG gaaACTGCGC gctgggttGc agggaggta accgggattC 660
ctagtgtAGC ggtgaaatGt gtatgtatTA ggaggAAAC acgtggcGAa ggcggcttAC 720
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gtatgtccAG cggtaaaAGCA ttatgttGtG tgatgttGtG gtatgttGtC atcggttCCG 840
cgactaacGC aataaGcAA ccacccGGG agtaacgttG caagaatGAA actcaaaggGA 900
attggcgggg ACCCGCACAA ggggttggAC atgtgggttA attcgaAGCA acgcgaaAGA 960
ccttaccaAG tcttgacatC ccattGacGt gcctgttAA aggcatCCC ttccgggCAA 1020
tggagacAGG tgggttGtG cttgtatGtG gatgttGtG gttaaGtccc 1080
gcaacgaggC caacccttA cttagtAGC cagcatCtG gatggcCt atcagatGc cccttGt 1140
ctggccggGA taacccGGGAG gaaggcGGGAG atggcgttAA acatcatGc tctaaggAG 1200
tttgggttGtA cactgttGtAC aatggcgttAA acaaaggGAA gcgagacAGt gatgtggAGC 1260
aaatcccaGA aataacgttC cttgttGtG tgatgttGtG aactcgactA catgaaGtG 1320
gaatcgctGA taatcgcGA tttgtatGtG ggggttGtA cgttcccccGGG tttgttac 1380
acccggccGtC acaccatGGGAG aggtggaaat gcccgaAGtC tttgttacAA ccggaaaggGA 1440
ggagcaggCCG aaggcaggGtC tgataactGGG ggtgaagtCtG taacaaggTA gccgtatCggA 1500
aagggttGtG tggatcacct
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SEQ ID NO: 93 moltype = DNA length = 1519  
FEATURE Location/Qualifiers  
misc\_feature 1..1519  
source note = Obtained from Intestinal Bacteria, F25  
1..1519  
mol\_type = other DNA  
organism = unidentified

SEQUENCE: 93

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agagtttgat cctggctca gatgaacgct ggcggcgtgc ttaacacatg caagtgcAAC 60
gaaggactt acgggattt ttccggatgaa aatggggAA ccctgtatGCA ggcgggttG 120
gtaaacgcgtG ggttaacctGC ctctatacAGG gggataaacAG tttagaaatGCA ctgtataatC 180
ccgcataagAC cacaggatG catgatcccc ttgtaaaaAC tcgggtgttA tgatgtggAC 300
ccgcgtctGA tttaggtAGtt ggtgggttAA cggtctacCA agccgacgAT cagttagCCGA 360
cctggagggG tgaccGGCCA cattgggactt gagacacGGC ccaaaACTC acggaggGCA 420
gcagtgggggA atattgtcaca atggggggAA ccctgtatGCA ggcgggttG 480
aagtatttGC ttatgttAAAGC ctgtatGAtt aggaggAAca ccaagtggCga aggccgCCTA 540
ctggacgtG actgtacgtG aggctegAAA gcgttggggAG caaacaggat tagataccCT 600
ggtagtccAC gccgttaaaCG atgactgtCA ggtgttggGA ggcAAAGCCT ttccgtGCCG 660
cagcaacACG aataaGcAGt ccacccGGG agtaacgttG caaagaatGAA actcaaaggGA 720
attggcgggg ACCCGCACAA ggggttggAC atgtgggttA attcgaAGCA acgcgaaAGA 780
ccttacGTC ccttgacatC cggctgacCC gcgactatG tcgccttC ttccggacAG 840
ccgagacagg tggtgtcatGG ttgtcgtcAG ctctgttcgt GAGATGTTG gttaaGtccc 900
gcaacgaggC caacccttA cttagtAGC cagcatCtG gatggcCt atcagatGc cccttGt 960
ctggccggGA taacccGGGAG gaaggcGGGAG atggcgttAA acatcatGc tctaaggAG 1020
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aaatcccaGA aataacgttC cttgttGtG tgatgttGtG aactcgactA catgaaGtG 1140
gaatcgctGA taatcgcGA tttgtatGtG ggggttGtA cgttcccccGGG tttgttac 1200
acccggccGtC acaccatGGGAG aggtggaaat gcccgaAGtC tttgttacAA ccggaaaggGA 1260
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aagggttGtG tggatcacct
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cgcataagac cacaggattc catgatccgg tggtaaaaac tccgggttga tgagatggac	240
ccgcgtctga ttaggttagt ggtgggtaa cggotcacca agccgacgt cagtagccg	300
cctgagaggg tgaccggcca cattgggact gagacacggc ccaaactct acgggaggca	360
gcagtgggaa atattgcaca atggggaaa ccctgtatcga gcgcacgcgc gtgagcgatg	420
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agcaccgcgt aaatacgtgc cagcagccgc ggtataactgt atggtgcaag cggtatccg	540
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taacccccc gactgatctt gaaactgtt ttcttagatgt tccggagatg aagtgtatt	660
cctagtgtatc cgggtaaatc cgtatgatatt agggagaaca ccagtggcga aggccgtt	720
ctggacgatc atgcacgtt aggtcgaaa gcgtggggag caaacaggat tagataccct	780
ggtagtccac ggcgttaacg atgactgcta ggtgtcgaaa ggcaaaagct ttcgggtccg	840
caccaaaacgc aataaggat ccacccgggg agtacgttcg caagaatgaa actcaaaggaa	900
attgacgggg accccgcacaa ggggtgggg atgtgggttta attcgaagca acgcgaagaa	960
ccttacccgc ccttacatc cgggtacccgc gggatgtatg tccgccttcc ttccggacag	1020
ccgagacagg tgggtcatgg ttgtgtcatg ctgcgtgtcg gagatgttgg gttaaatccc	1080
gcacacgcgc caacccttat cttagtgcg cgcatttcg gatgggact cttagagagac	1140
tgcggggat aacctggggg aagggtgggg tgacgtcaaa tcatgtccgc ctttatgggc	1200
agggtctacac acgtgttaca atggcgtaaa caaaggaggaa caagctgcg agggtgagca	1260
aatccccaaa ataacgtctc agtttggatt gtatgtatcga actcgactac atgaagctgg	1320
aatcgcgtat aatcgcgaat cagaatgtcg cggtaatac gttcccggtt cttgtacaca	1380
cgcggccgtca caccatggga gttggtaacg cccgaagtca gtgacccaaac cgtaaaggagg	1440
gagctgcgcg aggtggggacc gataactggg gtgaagtctg aacaaggtag ccgtatcgga	1500
agggtgcgcgtt ggtatcacct	1519

SEQ ID NO: 94                    moltype = DNA length = 1520  
 FEATURE                         Location/Qualifiers  
 misc\_feature                 1..1520  
 note = Obtained from Intestinal Bacteria, F26  
 source                         1..1520  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 94  
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 gttaacgcgtg aggaacctgc cttggagagg ggaataaacac tccgaaaggaa gtgctaatac 180  
 cgcatgtgc agttgggtcg catggctcg actgccaag atttacgtct ctgagatggc 240  
 ctgcgtctgc attagttagt agggccggta acggcccccact taggcacgca tcagtagccg 300  
 gactgagagg ttgaccggcc acatggggat tgagacacgg cccagactcc tacggggaggc 360  
 agcagtgggg aatattgggc aatggcgca agcgtgaccc agcaacgcgc cgtaaaggaa 420  
 gaaggcttc ggggtgtaaa cttctttgt cggggacgaa acaaatacg gtaccgcacg 480  
 aataaaggcc acgttacact gtgcggcggcggtaat acgttaggtgg caagcgat 540  
 cccgattttac tgggtgtaaa gggcggtgtac gggggattgc aagtcatgt tgaaaactgg 600  
 gggctcaacc tccagctgc aatggggatgt tgatgttgcg aatggggatgt tgaaaactgg 660  
 aatccgtgt gtatgtgtaa aatgcgtaga tatacgggg aacaccatgt gcgaaaggccg 720  
 attgtggac agtaactgtac gtcgtggcggd gaaaggctgtt ggagcaaaaatggatgtat 780  
 ccttggatgtt acacccgcgaa aacgtatggat acttaggtgtg ggggggtctga ccccttcgt 840  
 gccgcgttta acacaataag tateccaccgtt gggggatgtacg atcgcacgtt tgaaaactcaa 900  
 aggaattgtac gggggccgcg acaagggtgt gaggatgtgg ttaattcga agcaacgcga 960  
 agaacccatcc cagggtgttgc categtccacta acgaaggcaga gatgtatgtatgt tgcccttcg 1020  
 gggaaaatgttgg agacagggtgg tgcgtatgtt tgcatgttgc tggtcgttgc atgtgggtt 1080  
 aagtcccgca acggccgcac ccctttatgt tagttgtatc gcaagacgcac tctatcgaga 1140  
 ctggcgttgc aaaaacggag gaagggtgggg acgacgttcaaa atcatatgtc cccttgcgt 1200  
 ctggccaca cactgttactt aatgtgtttt aacagaggaa ggcataatccg cgagggtggag 1260  
 caaatccca aacggccatcc caggtggat tgcagggttgc aacccgcctg tatgaatgtt 1320  
 gaatcgtag taatcgccga tcagcatgc gccgttataa cttgttgcac 1380  
 accggccgtc acaccatgtac agtcgggaaac acccgaaatgtc cgtatgtatccaa ccgcacaggag 1440  
 ggccggccgcg aagggtgggtt cgtataattgg ggtgaagtctg taacaaggta gccgtatcgga 1500  
 aagggtgcgcg tggatcacct

SEQ ID NO: 95                    moltype = DNA length = 1519  
 FEATURE                         Location/Qualifiers  
 misc\_feature                 1..1519  
 note = Obtained from Intestinal Bacteria, F27  
 source                         1..1519  
 mol\_type = other DNA  
 organism = unidentified

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 taacgcgtgg gtaacctgc ttatcaggg ggataacatgt cagaaatgtac tgctatacc 180  
 gcataaggcgc acaggaccgc atggccgttgc gtaaaaactt ccgggtgtat aagatggacc 240  
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 ctgtggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 360  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 420  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 480  
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 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 660  
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 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 780  
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 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 900  
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 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1020  
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 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1140  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1200  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1260  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1320  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1380  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1440  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1500  
 cgttggggatgttggatgttgc gttgggttgc aacccgcctt cttgttgcac 1560

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tttactgggt	gttaaaggag	cgttagacgt	gtggcaagtc	tgatgtgaaa	ggatgggd	600
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cgccaaacgc	gtaatgttac	cacctggga	gtacgttcgc	aagaatgaaa	ctcaaaaggaa	900
ttgtacgggaa	cccgcaaca	cggtgtggac	tgtgttta	ttcgaacaa	cgcgaaagaa	960
cttaccaagt	cttgacatcc	ctctgacccg	ctcttaacccg	agttttctt	tcgggacaga	1020
ggagacagg	gggtgcgtgt	tgtcgtcagc	tcgtgtcg	agatgttggg	ttaagtcccg	1080
caacgacgc	aaccctata	ctcagtagcc	agcaaggtaa	gttgggcact	ctgtggagac	1140
tgccaggat	aacctggat	aagggggg	tgacgtcaaa	tcatatgc	ctttatgat	1200
ttggccatcac	acgtgttca	atggcgttaa	caaaggaaag	cgjaggatgt	agatggagca	1260
aatccaaaaa	ataacgtccc	agttcggaact	gtagtctgca	acccgactac	acgaagctgg	1320
aatcgctagt	aatcgcggat	cagaatggcg	cggtaatac	gttcccggt	cttgtacaca	1380
ceggcccgta	caccatggg	gtcagtaac	cccgaagtc	tgacactaac	tgcaaaagaag	1440
gagctgccg	aggcgggacc	gatgacttggg	gtgaagtctg	aacaaggtag	ccgtatccgaa	1500
aggtgcggct	ggatcacct					1519

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SEQ ID NO: 96          moltype = DNA    length = 1491
FEATURE                  Location/Qualifiers
misc_feature             1..1491
note = Obtained from Intestinal Bacteria, F28
source                   1..1491
mol_type = other DNA
organism = unidentified
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SEQ ID NO: 97 moltype = DNA length = 1519
FEATURE Location/Qualifiers
misc_feature 1..1519
note = Obtained from Intestinal Bacteria, F29
source 1..1519
mol_type = other DNA
organism = unidentified
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SEQUENCE: 97

	organism = unclassified					
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gtaacgcgt	ggtaacc	tcatacagg	ggataaacag	ttggaaacgg	ctgctaatac	180
cgccataacg	cacagtacc	catgtacc	tgtaaaac	tccgggtgt	ttagatggac	240
cggcgct	tttagctagg	ggtggggtaa	cgccctacca	aggcgacgt	cagttagccg	300
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ctggacatg	actgcacgtt	aggctcgaaa	gcgtggggag	caaacaggat	tagataccct	780
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attgacgggg	accgcacaa	gccccgggg	atgtgggttta	attcgaagca	acgcgaaggaa	960
ccttacccgg	tcttgacatc	cctctgaccg	ctctttaaatc	ggagcttcc	ttcgggacag	1020
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aatccaaaa	ataacgtctc	agttcgatt	gtagtctgc	actcgactac	atgaagctgg	1320
aatcgctagt	aatcgcaat	cagaatgtcg	cggtaaac	gttccgggt	cttgtacaca	1380
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gagctgcca	agggtgggg	gataactggg	gtgaagtctg	aacaaggtag	ccgtatcgga	1500
agggtcgcc	ggatcacct					1519

SEQ ID NO: 98	moltype = DNA	length = 1512
FEATURE	Location/Qualifiers	
misc_feature	1..1512	
	note = Obtained from Intestinal Bacteria, F30	
source	1..1512	
	mol_type = other DNA	
	organism = unidentified	

SEQUENCE: 98						
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agggggataa	ctgctggaaa	cggcgtctaa	ggccgtatag	gtatagagga	cgcattgtcg	180
ctatgttaaa	tatccacgg	gatagcacag	ggatgggctt	atgacgcatt	agccagctgg	240
tgaggtaacg	gtcaccagg	gchgacatgc	gtacccggcc	tgagagggtg	gacggccaca	300
ctgggactga	gacacggccc	agactctca	ggggaggcgc	agttagggat	tttgcgcatt	360
ggggcggaa	ctgaccggc	aacgcgcgt	gaagggaa	gtcattcg	atgtaaactt	420
ctgttatgaa	ggaagaaacgg	cagatgggg	gaatgccc	tgcgtgacgg	tacttcatga	480
ggaagccacg	gctaactacg	tgccagcago	cgcgttaata	cgttagtgcc	gagcgttac	540
cggaaatcatt	ggcgttaaag	agggtgggg	cgccagtc	ggtctgggt	gaaagacccg	600
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cttaccagg	cttgacatgg	agataaaggc	cctggagaca	gggagataga	tatatctac	1020
acaggtgtt	gtcgtgttgc	gtcgtgtgt	gtcgtgtgt	gttgggtttaa	gtcccgcaac	1080
gagcgc	ccgttgc	gttgcagca	ttaggttgg	gacttgcgc	agactgcctc	1140
tgcgaaagg	aggaaaggcc	ggatgtac	aaatcatcat	gccccttatg	acctggct	1200
cacacgtgt	acaatggacg	gatcggaggg	aggcgaagc	gcggagggtg	gcaaaaccca	1260
gaaaacccgtt	cacagtccgg	actgtacgt	gcaactcgac	tgcacgaa	tggaaatcgct	1320
agtaatcg	aatcgtat	tcgcggat	taatgttgc	ggcccttgc	acaccgccc	1380
tcacaccat	agatgttgc	acaccgc	ccgggtggcc	aaccgtca	agggtgt	1440
ctaagggtgg	actgtatgtt	gggggtga	gtgttgc	atccctacg	ggaacgtgg	1500
gtatggatc	ct					1512

SEQ ID NO: 99	moltype = DNA	length = 1523
FEATURE	Location/Qualifiers	
misc_feature	1..1523	
	note = Obtained from Intestinal Bacteria, F31	
source	1..1523	
	mol_type = other DNA	
	organism = unidentified	

SEQUENCE: 99						
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tcccgctt	gattagctgg	ttgggggg	aacggccccc	caaggcgcac	atcaggatcc	300
ggcttgag	atgtggcc	cacattggg	ctgagacacg	gccccaaactc	ctacgggagg	360
cagcagtgg	aatatttgc	caatgggggg	aaccctgtat	cagcgcaccc	gcgtgagtg	420
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ggaatttgac	gggacccgca	caagcgttgc	agcatgttgc	ttaatttgc	gcaacgcgaa	960
gaaccttacc	ttgttctgac	atctaact	ccgggttgc	atgggaccc	tccttcggg	1020
cagttaagac	agggtgtgc	tgggtgttgc	cagctgttgc	cgttagatgt	tgggttaat	1080
ccgcacaa	gcaaccccc	tatctttagt	agccgtat	taagggtggc	actctagaga	1140
gactgc	caggatgttgc	ggatccatgtt	ggacgtatgt	aaatcatcat	gcccccttat	1200

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cggaagggtgc	ggctggatca	cct				1523

SEQ ID NO: 100	moltype = DNA length = 1520					
FEATURE	Location/Qualifiers					
misc_feature	1..1520					
note	= Obtained from Intestinal Bacteria, F32					
source	1..1520					
mol_type	other DNA					
organism	unidentified					
SEQUENCE: 100						
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cagcaaaacgc	aataagtatt	ccacctgggg	agtagcttc	caagaatgaa	actcaaagga	900
attgacgggg	gcccgtacaa	gcccgtgggg	atgtgggttta	attcgaagca	acgcaagaaa	960
ccttaccaacg	tcttgacatc	cctctgaccg	tccctgttttt	ggggcttccc	ttcggggcag	1020
aggagacagg	ttgtgtatgg	tttgtgtcgt	ctctgtgtgt	gagatgttgg	gttaagtccc	1080
gcaacgagcg	caacccttat	ccttagttago	cagcacatga	ttgtgggcac	tcttagggaga	1140
ctggccgggg	taaccgggg	gaaggccgggg	acgacgttca	ccctttatgt	atccatcg	1200
tttgggttata	cacgtgtac	aatggcgtaa	acaaaggggaa	gctgtacgg	gatgttgagc	1260
gaatccaaa	aataacgtcc	cgttccggac	tgctgttc	aactcgact	cacaaactgt	1320
gaatcgtag	taatcgccg	tcagaatgc	gcccgttata	cggtttccgg	tcttgcac	1380
acccggccgtc	acaccatggg	agtctgttttgc	gcccgtttttc	gttgcacca	ccgaaaggaa	1440
ggagctgcgg	aaggcgggac	cgataactgg	ggtgttttttgc	taacaaggta	gcccgtatcg	1500
agggtgcggc	ttgtatcacct					1520

SEQ ID NO: 101	moltype = DNA length = 1515					
FEATURE	Location/Qualifiers					
misc_feature	1..1515					
note	= Obtained from Intestinal Bacteria, F33					
source	1..1515					
mol_type	other DNA					
organism	unidentified					
SEQUENCE: 101						
agagtttgat	cctggctcag	gatgaacgct	ggccggcgtgc	ctaatacatg	caagtcgac	60
gcgagcactt	gtgtcgatgt	ggcgaacggg	tgtgtatcac	ataagtaacc	tgcctatagc	120
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cctgttttttt	atgtgttca	agcactggta	gaggatggc	ttatggcgc	ttatgtgtt	240
ggccgggttaa	ccggccacca	aggccgttat	gcgttgcgc	cctgttttttgc	tgacggggca	300
cactggggact	gagacacggc	ccactgttttgc	acggggggca	gttgcgttgc	attttgcgc	360
atggggggaaa	ccctgttgc	gcaacggccgc	gtgtttttttgc	aaagggttttgc	ttttgttaac	420
ttctgttata	aaaggaaac	ggccgttaca	ggaaatggta	gcccgtgt	gttactttat	480
tagaaagcoca	ccggcttacta	cgtgtccgg	gcccgttata	ttatgtgttgc	gcaaggcgtt	540
tccggatata	ttggggcgat	agagggttttt	ggccgttgc	agggttttttgc	gttgcgttgc	600
gaagcttac	tccgttacgc	catatgttttt	ggccgttgc	agggttttttgc	gttgcgttgc	660
aattccatgt	gtatgttgc	aatgtgttgc	tatatgggg	aacaccatgt	gcaaggcgtt	720
cgtatctggcc	tgcaacttgc	gtctgttgc	gaaaggcgttgc	ggagcaataa	ggattttat	780
ccctgttttttgc	ccacgtatgt	actaagggttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	840
gcgttacacg	caataatgttgc	tccgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	900
aattgtacgg	ggccggccaca	agccgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	960
acccgttac	gttttgc	actatgttttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1020
atacagggttgc	tcgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1080
acccgttac	cccttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1140
agtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1200
cttacacatgt	gttacatgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1260
ccataaaacc	atcttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1320
gctgttttttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1380
ccgttacacc	acggatgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1440
tgttcaatgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	ttatgtgttgc	1500
ggggatgttgc	caccc					1515

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SEQ ID NO: 102      moltype = DNA  length = 1552
FEATURE             Location/Qualifiers
misc_feature        1..1552
                      note = Obtained from Intestinal Bacteria, F34
source              1..1552
                      mol_type = other DNA
                      organism = unidentified

SEQUENCE: 102
agagttttagt cctgggttcag gacgaacgtt ggccggcgtgc ttaacacatg caagtcaac 60
gaagagggat ggaaggatgtc ttctatcaat cttagtggcg aacgggttagt taacgcgtaa 120
tcaaccgtcc cttcaaggggg ggacaacagt tggtaaacgcgat tgtaatacc gcatacgatc 180
taatctcgcc atcgaggata gatgaaagggt ggccctctaca tgtaagctat cactgaagga 240
ggggatttgcg tctgtttagtc tagtgggggg ggttaacggccg caccgaaggccg atgtacatgt 300
gcccgttgcg gaggatgaaac ggccacatggg gggactggagac acggcccaaga ctcctacggg 360
aggcagcgtt ggggtatctt ccgcgttgcg cggaaatcttgcgatggatc acggagcaac gccgcgttgcg 420
tgatgacggc ctccgggtt gaaagcttgcg ttaatcggtt cggaaaggctt tcttcgttgcg 480
agtggaaaagg attgacggta ccggaaataga aagccacggccg taactacgtt ccagcaggccg 540
cggttaatccg taggttgcgaa gctgttgcg gaaattttggg ggttaaaggccg cggccggccg 600
gataggtagt cttgttctt aagttttttttt gttttttttt gttttttttt gttttttttt 660
atcttagatgtt tcggagaggg aagtggaaatt cctgttgcg tttttttttt gttttttttt 720
aggaagaaaca ccaggatggcg agggacttgcg cttggacggaaa actgtacgtt ccggccggaaa 780
cccaagggggg ccggatggatgtt tagataccggg ggttgcgttgcg ggttgcgttgcg 840
gggtttagggat gtatcgaccctt cttctgttgcg ggttgcgttgcg ggttgcgttgcg 900
gagtagcacc gcaagggttga aactcaaagg aatttgcgggg gggccggccaca acgggttgcg 960
tatgttgcgtt aatcgacgc aacgcgttgcg accttaccatgttgcg tttttttttt 1020
aaccaggatgtt gtttccgtt cttccggatc cggaaatccatgttgcg gtttgcgttgcg 1080
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ccaggatcgatc tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1200
gtatgacgttca aatcatcgatc ccccttgcgttgcg gtttgcgttgcg gtttgcgttgcg 1260
taatcgatcg aacgcgttgcg gtttgcgttgcg gtttgcgttgcg gtttgcgttgcg 1320
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ctcgatcgatc tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1440
gtgtccaaagg cccgttgcgttgcg aaccttgcgttgcg gtttgcgttgcg gtttgcgttgcg 1500
gggttgcgttgcg gtttgcgttgcg gtttgcgttgcg gtttgcgttgcg gtttgcgttgcg 1552

SEQ ID NO: 103      moltype = DNA  length = 1496
FEATURE             Location/Qualifiers
misc_feature        1..1496
                      note = Obtained from Intestinal Bacteria, F35
source              1..1496
                      mol_type = other DNA
                      organism = unidentified

SEQUENCE: 103
agagttttagt cctgggttcag gatgaacgtt gacagaatgc ttaacacatg caagtctact 60
tgatccttcg ggttgcgttgcg gggccgggtt ggttgcgttgcg taaagaacctt gccttacaga 120
ctgggacacatttggaaatc gatgttgcgttgcg tttttttttt gttttttttt gttttttttt 180
gtttatggatgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 240
taacggctca ccaagacgtt gatgggttgcg cggccgttgcg ggttgcgttgcg ccacaaggggg 300
actggatgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 360
aaaatgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 420
cagttggaaatc gatgttgcgttgcg gtttgcgttgcg gtttgcgttgcg gtttgcgttgcg 480
cagccgcgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 540
tagggcggttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 600
ctgtcttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 660
gatattttgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 720
ggccaaaggcttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 780
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agcatgttgcgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 960
gtttacacatgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1020
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atgttaccatgttgcgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1140
tggggatgttgcgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1200
gtgttacatgttgcgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1260
cggttgcgttgcgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1320
tatgttgcgttgcgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1380
gggttgcgttgcgttgcgttgcg tttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1440
gattttttttt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt gttttttttt 1496

SEQ ID NO: 104      moltype = DNA  length = 1496
FEATURE             Location/Qualifiers
misc_feature        1..1496
                      note = Obtained from Intestinal Bacteria, F36
source              1..1496
                      mol_type = other DNA

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	organism = unidentified
SEQUENCE: 104	
agagttttag cctggctca gatgaacgct gacagaatgc ttaacacatg caagtctact	60
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ctgggacaac atttggaaaac gaatgctaatt accggatatt atgattgggt cgcatgatct	180
ggttatgaaa gctatatgcg ctgtgagaga gctttgcgc ccattagttt gtgggtgagg	240
taacggctca ccaaaacgacat gatgggtacg cggccgtaga gggtaacgg ccacaagggg	300
atagacac gggcccttact cctacgggg acgacgttgg ggaatattgg aataatggacc	360
aaaagtctga tccacaaat ctgtgtgcac gatgaagggtt ttccgaatgt aaagtgtttt	420
cagttggaa gaagtctggg acggtaacaa cagaagaacg gacggctaa tacgtgccag	480
cagccgggtt aatacgtat tcggcaagct tatccggatt tattgggggtt aaagcggcgtt	540
tagccggctt agtaagtctg atgtggaaaat ggccgggtca accccgtatt gcgttgaaa	600
ctgtttaactt agatgtactgg agaggttgcg ggaactacaaat gtgttagatgtt gaaattctgt	660
gatatttgcg ggaatggccg tggggaaagcc aecctactgg acagatactg acgcttaaagc	720
gcgaaaaggctt gggtagcaaa caggattaga taacctgtt gtcacccggc taaacgtatg	780
ttacttaggtt tgggggtgtt aacccctggc cccaaactgtt cggcgtatgtt aatccgtctg	840
ggggatgtatc acgcaaatgtt aacaaatggaa gaaatgttgcg gggacccgcgca caagcggctgg	900
agcatgtgtt ttaatttcgac gcaacgcgag gaaccattacc agcggttgcg atcccaagaa	960
gttaacagag atgttttgcg gctcttccgg aggaaatctgg tgacagggtt tgcatgttgc	1020
tgttgcgttgc gttgtgtgtt atgttggggt aagtccgcgca acgacggcga coccttttgtt	1080
atgttaccat cattaatgtt gggactcatg cggactgttgc tgccgtatgtt aggaggaaagg	1140
tggggatgtac gtciaatgtt catggccctt atacgttggg ctacacatgtt gctacaatgg	1200
gttagtacaga gagctgcggaa cctgcgaggg taagctatac tcataaaaactt attctttgtt	1260
cggttgcgttgc tctgcgttgc gactatcgtt agttggaaat gcttagtatac gcaaatcgac	1320
tatgttgcgg tgaatacgtt ctgcgggttgc gacacacccg cccgttcacac caccggatgtt	1380
gatttgcgttgc gaaatgttgc gcttacccgtt aaggagggtt gttccggaccc gttgttggatgtt	1440
gattttgggtt aaggtcgtaac aaggtatccg tacggaaacg tgccgtatgtt tacacctt	1496
SEQ ID NO: 105	moltype = DNA length = 1530
FEATURE	Location/Qualifiers
misc_feature	1..1530
note = Obtained from Intestinal Bacteria, F37	
source	1..1530
	mol_type = other DNA
	organism = unidentified
SEQUENCE: 105	
agagttttag catggctca attgaacgct ggcggccaggc ctaaacatcg caagtcgaaac	60
ggtaacagga aecagcttcg tgccgttgc acgagtggcg gacgggttgcg taatgttgc	120
gaaactgcctt gatgggggggataactact ggaaacgggtt gctaataacc cataacgtcg	180
caagaccaaa gaggggggacc ttccggccctc ttgcctatgg atgtggcccg atgggattag	240
ctagtaggtt gggtaacggc tcacccatggc gacgtatccctt agctgttgcg agaggatgtac	300
cggccacactt ggaatgttgcg cgggttccgg actccatcg acggcgttgc gggccgttgc	360
tgcacaatgg ggcggccgtt gatgcggca tcggccgtgt atgaaaggaa cttccgggtt	420
gtaaagtact ttccgggggg aggaaggggg taaagttat acctttgttgc attgacgtt	480
cccgccggaa aagcacccggc taactctgg ccggccgttgc cggtaatacg ggggttgc	540
cggttataatcg gaattactgg gctgttgcg acggccgttgc gttgttgcg tcaatgttgc	600
aatccccggg cttcaatggc gaaatgttgc tttatgttgcg aacttgcgtt aatccgtatgg	660
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aaggccggccc cctggaccaa gactgttgcg cttccgggggg gcaaaacaggaa	780
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cgttgcgttgc gggatgttgc gttgttgcg acccgttgggg ggttgcgttgc gcaaggatgg	900
aactcaatgtt aattgttgcggg gggccggcaca acgggttgcgat catgttgcgtt aatccgtatgc	960
aacgcgttgcg accttacccgtt gttttgcgtt ccacggaaat ttttgcgttgc gagaatgttgc	1020
cttcggggggcc cgttgcgttgc gttgttgcgtt gttttgcgttgc gttttgcgttgc	1080
ggttataatcg ccgttgcgttgc gcaacccatgtt ccctttgttgc gccacgggttgc gggccggaa	1140
tcaaaatggggat cttccggggat taaacttgcgtt ggggttgcgttgc gttttgcgttgc	1200
cccttacccgtt cttccggggat taaacttgcgtt ggggttgcgttgc gttttgcgttgc	1260
gaggttgcgttgc gggccgttgc gttttgcgttgc gttttgcgttgc gttttgcgttgc	1320
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ccttgcgttgc gttttgcgttgc gttttgcgttgc gttttgcgttgc gttttgcgttgc	1440
ccttcggggat gggccgttgc gttttgcgttgc gttttgcgttgc gttttgcgttgc	1500
accgttgcgttgc gttttgcgttgc gttttgcgttgc gttttgcgttgc gttttgcgttgc	1530
SEQ ID NO: 106	moltype = DNA length = 1339
FEATURE	Location/Qualifiers
misc_feature	1..1339
note = Obtained from Intestinal Bacteria, I01	
source	1..1339
	mol_type = other DNA
	organism = unidentified
SEQUENCE: 106	
ctgggttggat gtggcgaaacg ggttgcgttgc gctgttgcgttgc cctggcccat acaccggaaat	60
agcttccgttgc aacccgttgc gttttgcgttgc gttttgcgttgc gttttgcgttgc	120
agatttcatcg gtatgggggg ggttgcgttgc cttccggggat taaatggggat	180
ccatgttgcgttgc cttccggggat taaatggggat taaatggggat taaatggggat	240
ggcccgatctt cttccggggat taaatggggat taaatggggat taaatggggat	300

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gcagcganc	nnngtgcggg	atgacggcct	tcgggttcta	aaccgtttt	gactgggagc	360
aagcccttcg	gggtgagtgt	acccttcgaa	taagcacccg	ctaactacgt	gccacgaccc	420
gccccataac	gtaagggtcga	agcgttatcc	ggaattatttg	ggcgtaaagg	gtcgtaagc	480
gggtcgtn	gtcccggtgt	aaagtcatac	gcttaacggt	ggatccgcgc	cgggtacggg	540
cgggctttag	tgccgttaggg	gagactggaa	ttcccggtgt	aacggtgaa	tgttagata	600
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tggatgtggg	gaccattcca	cggttccgt	gtcgaggcaca	acgcgttaa	cateccgcct	780
ggggagtagc	gcccgaaggc	taaaactcaa	agaaattgac	gggggcccgc	acaacgcgc	840
gacgatcgcc	attaatccg	tgcaacgcga	aqaaccttac	ctgggttga	catgttcccg	900
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cagcctgt	cgtagatgt	tgggttaagt	cccccaacga	gwgcaacct	cgccctgtgt	1020
tgccagcac	tcgtgtggg	aactcacggg	ggaccgcggg	ggtcaactcg	gaggaagggt	1080
gggatgacgt	catagatcatc	tgcccttac	gtccagggtc	tcacgcatac	tacaatggcc	1140
ggtaacaacgg	gatgcganac	cgcgagggtt	ageggatccc	ttaaaacccg	tctcgtcg	1200
gatggagtc	tgcaacccgc	ctccataga	gwgagtcgc	tagtaatcgc	ggatcagcaa	1260
cgcgcgggt	aatgcgttcc	cggncttgt	acacaccgc	cgtcaagtca	tgaaagtggg	1320
tagcaccgc	agccgggtt					1339

SEQ ID NO: 107                    moltype = DNA length = 1346  
 FEATURE                          Location/Qualifiers  
 misc\_feature                    1..1346  
 note = Obtained from Intestinal Bacteria, I02  
 source                          1..1346  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 107

ttgcttgggt	gtgagagtgg	cgaacgggtt	agtaatgcgt	gaccgaccc	ccccataacac	60
cggaaatagct	cctggaaacg	ggtgttaatg	ccggatgtctc	cgactcttc	catggggtgt	120
cgggaaagat	ttcatacgta	ttggatgggg	tcgcgtctt	tcaggtagtc	ggcggggtaa	180
cggccacccg	agccatcgac	gggtagccgt	cctggagggg	cgacggccca	cattgggact	240
gagatacgcc	ccagacttct	acggggacca	gcagtggggg	atattgcaca	atgggcgc	300
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cacccgggt	aatacgtag	gtcgaacgg	tatccggaa	tattggggct	aaagggtctc	480
taggcgggtt	gtcgcgtcc	gtgtgaaat	ccatcgctt	acgggttgc	tgccgggg	540
acggccgggc	tggaatgtgg	tagggggaa	tggaaatccc	ggtgttaacgg	tggaaatgtgt	600
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cgcctgggg	gtacggccgc	aaggctaaaa	ctcaaaagaa	ttgacgggg	cccgacaa	840
cggcggagca	tgccgattaa	ttcgatc	cgcgaagaa	cttacctgg	tttgcacatgt	900
tcccgacgc	nnnagatata	tgncatccct	tcggggccgg	ttcacagggt	gtgcgttgt	960
gtcgctcaget	cggtgtcgta	gatgtgggt	taatgtccgc	aacggagcga	accctcgccc	1020
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tggccggatc	aacgggtatc	gacacggcc	cgtggaggg	atccctgaaa	accggcttca	1200
gttccggatgt	gagtcgtccaa	cccgacttca	tgaaggccgg	gtcgtagta	atcgcggatc	1260
agaacacgc	cggtgatgtc	gttccgggg	cttgcatacaca	ccggccgtca	agtcatgaaa	1320
gtgggtatc	cccgaaacgc	gtggcc				1346

SEQ ID NO: 108                    moltype = DNA length = 1353  
 FEATURE                          Location/Qualifiers  
 misc\_feature                    1..1353  
 note = Obtained from Intestinal Bacteria, I03  
 source                          1..1353  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 108

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gtaaacggc	accaaggcctt	cgacgggtag	ccggccttgc	aggggcgcac	gccacatgg	240
gactgagata	cgccggccac	tcctacgggg	ggcagcgttgc	gggaaatattg	cacaatgggc	300
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tgtttgggg	caagcttcg	gggtgtgt	ccttcgaat	aacgcggccgc	taactacgt	420
ccagcagcc	cggtataacg	tagggcgaa	gcgttatccg	gattttatgg	gcgtaaagg	480
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gggttacgggc	gggcgtgggt	ggcgtagggg	agactggaaat	tcccggttgc	acgggtggat	600
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caagcggccg	agcatgcgg	ttaattcgat	gcaacgcgaa	gaaccc	tgggttgac	900
atgttcccg	gacgcgcaga	gatggcg	ttccatgggg	ccgggttca	ggtgtgtc	960
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gccccgtt	gccagcacgt	tatggtggga	actcacgggg	gaccgcggg	gttaactcgg	1080
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acaatggccg	gtacagccgg	atgcacatg	gcgacatgga	goggatccct	gaaaaccgg	1200
cttagttcg	atcgagccct	gcaacccgg	tccgtgaagg	eggagtccgt	agtaatcg	1260
gatcagcaac	gcccgggtga	atgegttccc	gggccttgta	cacaccgccc	gtcaagtcat	1320
gaaagtgggc	agcacccgaa	gcccgtggcc	taa			1353

SEQ ID NO: 109	moltype = DNA length = 1338					
FEATURE	Location/Qualifiers					
misc_feature	1..1338					
	note = Obtained from Intestinal Bacteria, I04					
source	1..1338					
	mol_type = other DNA					
	organism = unidentified					
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cgctgggtt	gacgggttagc	cggtgtt	gagaatttgc	gggcgaccgg	ccacatttgg	240
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tgtggggggcc	gttccacggg	ttccgttgc	gagctaaccgc	gtttagatc	ccgcgtgggg	780
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atgcggat	attcgatgc	acgcgaagaa	ccttacccgtt	gcttgcacatg	ttccgcacgg	900
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tctgtgtcg	agatgttgg	ttaatgttcc	caacggggc	aaccttgc	ccgtgttgc	1020
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gcagtctgc	actcgacttc	gttgcgttgc	atgcgttgc	cagcaacgtc	1260	
gcccgttgaat	gtttcccccgg	ccttgcacac	accggccgtc	aagtcatgaa	agtggccac	1320
acccgaa	gggtggcc					1338

SEQ ID NO: 110	moltype = DNA length = 1326					
FEATURE	Location/Qualifiers					
misc_feature	1..1326					
	note = Obtained from Intestinal Bacteria, I05					
source	1..1326					
	mol_type = other DNA					
	organism = unidentified					
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aaagccccga	cgggagggga	tggctccgc	gcccatttgc	tagacgggg	gggtacggcc	180
caccgtggcc	acaacgggtt	gcccgttgc	gagacccgtt	ggccatgtt	ggacttgc	240
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acccagcgac	gcccgttgc	ggacggggcc	ccttgggttc	taaaccgttgc	tcacgggg	360
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ggaacacccgg	ttggcgttgc	ggcccttgc	ggcgagaccg	acgttgc	gccaaggct	660
gggggagccg	cagggttgc	tacccgttgc	gttccggccg	taaaccgttgc	acgttgcgttgc	720
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tgcgttgc	ccacgcgggg	ccgcgttgc	caaggccgg	ggggggccgg	acgcgttca	1080
gtcatcatgc	cccttatgc	ctgggttgc	cacgttgc	aatggccgtt	acaggaggat	1140
gcccgcacccg	gaggggggcc	ggatccggaa	aaggccggcc	cagttcggtt	tgggggttgc	1200
aaccggccgg	catgttgc	gatgttgc	taatcggttgc	tgcgttgc	gcccgttgaat	1260
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						1326

SEQ ID NO: 111	moltype = DNA length = 729				
FEATURE	Location/Qualifiers				
misc_feature	1..729				
	note = Obtained from Intestinal Bacteria, I06				
source	1..729				

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aaagccgggggtacacgt	1337
 SEQ ID NO: 114	moltype = DNA length = 1353
FEATURE	Location/Qualifiers
misc_feature	1..1353
	note = Obtained from Intestinal Bacteria, I09
source	1..1353
	mol_type = other DNA
	organism = unidentified
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ctagtaatcgccatcgatccgttgttgttgttgttgttgttgttgttgttgttgttgt	1320
cgtcaagccatggggatgttgttgttgttgttgttgttgttgttgttgttgttgttgt	1353
 SEQ ID NO: 115	moltype = DNA length = 1350
FEATURE	Location/Qualifiers
misc_feature	1..1350
	note = Obtained from Intestinal Bacteria, I10
source	1..1350
	mol_type = other DNA
	organism = unidentified
 SEQUENCE: 115	
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 SEQ ID NO: 116	moltype = DNA length = 1356
FEATURE	Location/Qualifiers
misc_feature	1..1356
	note = Obtained from Intestinal Bacteria, I11
source	1..1356
	mol_type = other DNA
	organism = unidentified

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**SEQUENCE: 116**

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gtaggcgggg taacggccca cctagtcaac gatggatagg ggttctgaga ggaaggccc 240
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**SEQ ID NO: 117** moltype = DNA length = 1353  
**FEATURE** Location/Qualifiers  
**misc\_feature** 1..1353  
**note** = Obtained from Intestinal Bacteria, I12  
**source** 1..1353  
**mol\_type** = other DNA  
**organism** = unidentified

**SEQUENCE: 117**

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atgggatataatgtttaaaga ttcatcgctt atagatggc atgcgttca tttagcgatgtt 180
ggcgccggtaa cggccacca aaccggacat ggtatgggggt tctgagggaa aggtccccca 240
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**SEQ ID NO: 118** moltype = DNA length = 824  
**FEATURE** Location/Qualifiers  
**misc\_feature** 1..824  
**note** = Obtained from Intestinal Bacteria, I13  
**source** 1..824  
**mol\_type** = other DNA  
**organism** = unidentified

**SEQUENCE: 118**

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attcgtatgttgc gatgtatggcgttgc catgttgcgttgc attaggatgttgc ttttgcgttgc 180
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 acctggggag tacgcggca acgggtgaaac tcaaaggaaat tgac 824

SEQ ID NO: 119 moltype = DNA length = 1348  
 FEATURE Location/Qualifiers  
 misc\_feature 1..1348  
 note = Obtained from Intestinal Bacteria, II14  
 source 1..1348  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 119  
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 cttttatgtt tgaaaaatcc gatgtttaga gatggcgtat cgtgttatta gctgttggt 180  
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 aactatatact gacgttgagg cacgaaacgc tggtggacaa acaggattaaatccctgtt 720  
 agtccacgc gtaaaacgtt ataaactcgat gtccggata cacagctgtt gactaaacgca 780  
 aacgcgttataa ttatccactt gggggatgttgc tgcgtcaagaa tgaaactcaa aggaaattgtac 840  
 gggggccccc acaaggcgag gaacatgtgg tttaaatcga tgatacgcga ggaaccttac 900  
 cccgggttgcg aagtttagcga cgattttgtt aagaggattt ccctttccggg cggaaacta 960  
 ggttgcgtcat ggttgcgtcc agctcggtcc tgaggggttc ggggtttaatgc ccataacgcg 1020  
 cggcaaccctt accgtttagt gccatcaggat gaaaggatgtt gacttgggtt gacttgggtt 1080  
 gtaagccgtt gggggatgttgc tgcgtcaagaa tgaaactcaa aggaaattgtac 1140  
 cacacgttgtt acaatggtagt gtcacagggg cagttaccca ggtttttttt gcaatctcg 1200  
 aaaggcttataa tcagttcggtt tggtggatgtt aaaccgcgtt ccataaactt ggattcgcta 1260  
 gtaatcgccg atcggccatc ggcgggttgcgaa tacgtttcccg ggccttgc tataccggcccg 1320  
 tcaaggccatg ggagccgggg gtcgtca 1348

SEQ ID NO: 120 moltype = DNA length = 1337  
 FEATURE Location/Qualifiers  
 misc\_feature 1..1337  
 note = Obtained from Intestinal Bacteria, II15  
 source 1..1337  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 120  
 ttctttgtctg gcgacccggcg cacgggtgag taacacgtat ccaacactgcg gatgacttgcg 60  
 ggtatgcctt tgcggaaagaa gattaatacc cgatggtata tctggaaaaggc atcttcacgc 120  
 tattaaagaaat tttcggtcat tgatgggttgc ggcgttccatt aggtttgttgc cgggttacgc 180  
 gcccaccaag ccacatcgatgg atagggttgc tgagggatgc gttcccccaca ttggaaactgat 240  
 gacacggcttcc aaactccatc gggaggccgcg agtgcgtatgg atttgcgtatcc ggcggacatgt 300  
 ctgaaaccgcg caagtaggtgtt gaaaggatgtt gtcgttccatgg ttgtttaactt tcttttatac 360  
 gggtaaaatgggatgttgc tgcgttccatgg tttttttttt gatgttgcgtt gatgttgcgtt 420  
 tcccggtccca gcacccggcgta taatacggat gatccggatccg tttatccggat ttatgggtt 480  
 taaaggggatgc gttagggatgttgc gtttaatgtca gttgttgcggat tttggggctt aaccgtaaaa 540  
 ttggcgttgcgat tactgggtgtt cttaggttgc gtagggatgttgc ggcggatccg tgggttgcgt 600  
 gtgaaatgttgc tagatatacc gaaacactgc gttgttgcgat gatccggatccg tgggttgcgt 660  
 tgacgtgtat gctgttgcgtt gttttttttt gatgttgcgtt gatccgttgc tttttttttt 720  
 agttaaacatgtt gtttttgcgtt atacagtttttgcgat gatccgttgc tttttttttt 780  
 gtatccatc tggggatgttgc gccggacacgc gttttttttt gatgttgcgtt gatccgttgc 840  
 cacaacggcg ggaacatgttgc gtttaatgttgc gatgttgcgtt gatccgttgc tttttttttt 900  
 aattgttcaatgttgc gttttttttt gatgttgcgtt gatccgttgc tttttttttt 960  
 ggttgcgttgc agctcggtcc gttttttttt gatgttgcgtt gatccgttgc tttttttttt 1020  
 atcgatgttgc accatcgatgttgc gttttttttt gatgttgcgtt gatccgttgc tttttttttt 1080  
 aggaagggttgc ggttgcgttgc aaatcggatccg gggcccttgcgat tttttttttt 1140  
 aataatggggatgttgc gttttttttt gatgttgcgtt gatccgttgc tttttttttt 1200  
 tcagttcggtt tggtggatgttgc caacccgttgc gttttttttt gatgttgcgtt gatccgttgc 1260  
 atcagccacgc ggcgggttgcgaa tacgtttcccg ggccttgc tttttttttt 1320  
 aacccggcccg tcaaggccatg ggagccgggg 1348

SEQ ID NO: 121 moltype = DNA length = 1343  
 FEATURE Location/Qualifiers  
 misc\_feature 1..1343  
 note = Obtained from Intestinal Bacteria, II16  
 source 1..1343  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 121  
 gatgcacgaa agcggtggga tcaaacagga ttagataccc tggttagtcca cgcgactaac 60  
 gatgatcact agctgtttgc gatacagtgt aaggccgaca gcgaaagcgta taagtgtacc 120  
 acctggggag tacgcggca acgggtgaaac tcaaaggaaat tgac 180

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cttgnanact	gaagatggcg	accggcgcac	gggtgagtaa	cacgtatcca	acctgcccgt	60
aactccggaa	tagccttcg	aaagaagat	taataccgga	tagcatacg	nnntcgcatg	120
atatttttat	taaagaattt	cggttatcg	tggggatgcg	ttccattatg	tttgtggcg	180
ggtaacggcc	caccaagact	acgtatggata	ggggttctga	gaggaaggtc	cccccaattt	240
gaactgagac	acggtccaaa	ctcctacggg	aggcagcagt	gaggaatattt	ggtcaatggg	300
cgagagccgt	aaccagccaa	gttagcgtaa	ggatganngc	tctatgggtc	gtaaaacttct	360
tttatatggg	aataaaagttt	tccacgtgt	gaatttttgta	tgtaccat	gaataaggat	420
cggctaactc	cgtgcagca	gccgcggtaa	tacggaggat	ccgagcgtta	tccggattta	480
ttgggtttaa	agggagcgt	ggtggattgt	taagtcaagt	gtgaaagttt	gcccgtcaac	540
cgtaaaattt	cgttgtaaac	tggcgttctt	gagtagcgtta	gaggtggggc	gaatttgcgtt	600
tgtacgggt	aatatgttag	atatacggaa	gaactccgat	tgcgaaggca	gtctactaga	660
ctgtcactga	cactgtatgc	cgaaaatgt	ggtatcaaac	aggattatgt	accctggtag	720
tccacacagt	aaacgtgaa	tactcgtgt	ttcgatata	cagtagcgg	ccaagcgaaa	780
gcattaaatgt	ttccacccgtt	ggatgtacgc	ggcaacccgtt	aaactcaaag	gaatttgcgg	840
ggggccgcac	aacgcggat	acatgtgtt	taatttgcgt	atacgcggat	aaccttaccc	900
gggcttaat	tgcaacagaa	tatattggaa	acagatatac	cgttaaggctt	ttgtqaagg	960
gtgtcatgtt	tgtcgtcagc	tcgtgcgtt	aggtgtcggt	ttaagtgc	taacgagcgc	1020
aacccttata	tttagtactt	aacatgtat	gtgtggatgt	ctagagagac	tgcgcgtcgta	1080
agatgtgagg	aggggtgggg	tgacgtcaaa	tcagcacggc	cttacgttcc	ggggctacac	1140
acgtgttaca	atgggggtt	cagaaggcan	ctacccgtgt	acaggatgt	aatccaaaaa	1200
acctctctca	gttcggatcg	aagtctgaa	cccgacttgc	tgaagcttgc	ttcgttagta	1260
atcgcgatc	agccatggcg	cggtaatac	gttccggggc	ttgtacacac	ccggccgtca	1320
agccatgaaa	gcggggggta	cct				1343

SEQ ID NO: 122	moltype = DNA	length = 1335				
FEATURE	Location/Qualifiers					
misc_feature	1..1335					
	note = Obtained from Intestinal Bacteria, I17					
source	1..1335					
	mol_type = other DNA					
	organism = unidentified					
SEQUENCE: 122						
gggtggcgac	cggcgcacgg	gtgegttaacg	cgtatgcac	ctacccataa	cagggggata	60
acactgagaa	atggtacta	ataccata	acatcagaac	cggtatcggt	tttgggtgaa	120
aactccgggt	gttatgtat	ggcgtatcggt	gtttagtgcgt	tttgggtgagg	taaccggtca	180
ccaaaggAAC	gatacatagg	gggactgaga	ggttaacccc	ccacattgtt	actgagacac	240
ggacccaaact	cctacgggg	gcacgtgt	ggaaatattgg	tcaatggac	cagtctgaa	300
ccagccatgc	cgcgtcgagg	aagacggctc	tatgagttgt	aaactgtttt	tgtacggagg	360
taaacgcgtt	tacgtgttag	agcgttgcgt	ataaggatcg	gtcaactccg	420	
tgccagcgc	cgcgttata	cgaggatcc	aagcgttattc	cggttattt	gggtttaaag	480
gggtgcgtagg	cggtttata	agtttaggtt	gaaataccgg	tgcttaaacac	cggaactgccc	540
tctaatactg	ttgaactaga	gagtagttgc	ggtagggcgaa	atgtatgttgc	tagcggtgaa	600
atgtcttagag	atcatcaga	acacccgttgc	cgttccaaact	atatctgac	660	
tttggggcgc	aaagcggtgg	gagcaacag	gattagatac	cgttccat	cacgcgttac	720
acgtatgtt	ctcgctgtcg	cgatcaca	gttccggcggt	aagcgttac	gataatgtt	780
ccaccttgggg	agtagtgcgt	caagaatggaa	actcaaaaggaa	atttgcgggg	ccccgcacaa	840
ggcgaggaaac	atgtgtttt	atccgtatgt	acggcgaggaa	ctttacccgg	gttggaaat	900
tactgtatgt	tctggaaaca	ggatgttcc	tcggggcgagg	aaactgttttgc	ctgtatgtt	960
gtgtgtatgt	cgtgcgtgt	gggtgtgggt	taagtccat	aacgttgcgt	acccttaccc	1020
tttagttccca	tcaggtcaag	ctggggactc	tggggggact	gcccgtttaa	gccggagat	1080
agggtggggat	gacgttcaat	cagcacggcc	cttacgttcc	gggttacaca	cggttacaa	1140
ttgttaggttac	agggggcgc	taccgtgt	tgggtatgcgt	atctcgaa	cctatctcgt	1200
ttccggatccg	aggctgaaac	ccgccttccgt	qaagttgtat	tcgtatgttac	tcgcgcgtat	1260
gccccatggcg	ggttaatac	gttccggggc	ttgtacacac	cgcccgtaa	gccatggaa	1320
ctgggggtgc	ctgaa					1335

SEQ ID NO: 123	moltype = DNA	length = 1309				
FEATURE	Location/Qualifiers					
misc_feature	1..1309					
	note = Obtained from Intestinal Bacteria, I18					
source	1..1309					
	mol_type = other DNA					
	organism = unidentified					
SEQUENCE: 123						
cgtatgcac	ctggccgata	ccggggata	gccccatggaa	acgtggat	acacccata	60
gtacttttat	cctgtatggg	atgttgcgtt	aatgttcaat	gtatcggttgc	ggcatcggtc	120
ctattatgtt	gttgggggg	taacagccca	ccaaagacgt	gataggttgcgt	gggttctgaga	180
ggaaagggtccc	ccacatttgg	actgtatgt	ggtccaaact	cctacgggg	gcagcgtgt	240
ggaaatattgg	tcaatggacgt	taatgttgcgt	ccagccaaatgt	cgcgttgcgt	aaagactgccc	300
tatgggttgcgt	aaacccctttt	tataaggggaa	gaaatgttgcgt	tacgtgttgcgt	atgtatgttgcgt	360
tacccatgtt	ataagcgtatgt	gtcaactccg	tgccagcgc	cgccgtataa	cggttgcgttgcgt	420
gagcgttata	cggtttata	gggtttaaag	gggtgttgcgt	cggtttat	atgtatgttgcgt	480
taaatatgtt	agctaaatgt	aattgttgcgt	ttaatactgg	taaaactgg	tacagacgt	540
gtaggcggaa	taagttatgt	agcgttgcgt	tgcata	taacttgcgt	ctccgtatgt	600
gaaggcgcgt	taccgtatgt	taactgtatgt	tgatgtatgt	gagcgttgcgt	agcgttgcgt	660
attagatacc	ctgggtatgt	acgcgttac	cgatgtatgt	cgatgtatgt	cgatgtatgt	720

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tacgggatta	agcgaaagta	ttaagtgago	cacctgggg	gtacgtcgcc	aacgatgaaa	780
ctcaaaggaa	ttgacggggg	ccgcacaaag	cgaggaaaca	tgtggttaa	ttcgatgata	840
cgcgaggAAC	cttacctggg	tttaaatggg	aaatgtcgta	tttggaaaca	gatattctct	900
tcggagcgTT	ttcaagggt	ctgcattgtt	gtcgtcgact	cgtgcgtga	ggtgtcggtt	960
taagtcccat	aacgagcgca	acccttaccg	ttagttgcta	gcatgtaatg	atgagactc	1020
taacgggact	gocacggtaa	ggtgagaggaa	aggcggggat	gacgtcaat	cagcacggcc	1080
cttacaccca	gggtcacaca	cgtgttaca	tggcggttac	agggggccgc	taccagggt	1140
cttgcgtcoca	atctcaaaag	ccggcgttag	ttcggatgtt	agtctgtaac	ccgactccat	1200
gaagtttggat	tcgcttagtaa	tcgcgcata	gcatggcgc	ggtaatacg	ttcccgggcc	1260
ttgtacacac	cgcccgctaa	gccatggaag	ccgggggtgc	ctgaagtcc		1309

SEQ ID NO: 124                    moltype = DNA length = 1339  
 FEATURE                          Location/Qualifiers  
 misc\_feature                    1..1339  
                                 note = Obtained from Intestinal Bacteria, I19  
 source                          1..1339  
                                 mol\_type = other DNA  
                                 organism = unidentified

SEQUENCE: 124  
 agagagactt ctttctcgag cgagtggcga acgggtgagt aacgcgtgag gaacctgcct 60  
 caaaagagggg gacaacagt tggaaacgact gctaataccg cataagccca cgggtcgca 120  
 tcgnncagag ggaaaaggag caatccgtt tgagatggcc tgcgtccga tttagctgtt 180  
 gggngaggtan nggcccacca aggccgacat cggttagccgg actgagaggt tgaacggcca 240  
 cattgggact gagacacggc ccacactct acggggggca gcaatggggaa atattgcaca 300  
 atgggggaaa ccctgtatgca ggcacggccg gtggaggaa aagggtctcg gattgttaac 360  
 tcttgttggt gggggagata atgcgttad ccaacaaggaa agtgacggct aactacgtc 420  
 cagcagccgc ggttacaaacgt aggttccaaag cggttgcggg aattactggg tgtaaaggaa 480  
 ggcggaggccc gagacaaagt tggatgttgg tcaaccatca aactgtttc 540  
 aaaaactgttt ttctttagtgcgtt gtcggatgtt agggcggaaat cccgggtgtt cgggtgaatg 600  
 cgttagatatac gggggagaa ccaatggcga aggccggctt ctggggcacca actgacgctg 660  
 aggctcgaaa gtgtgttggat caaacaggat tagatataccct ggtgtccac accgtaaacg 720  
 atgttactta cgtgttggat gatgttggcc ttcagtgccg cagttacac aataagtaat 780  
 ccacctgggg agtacgaccg caagggttggaa acttcaaaaggaa attgacgggg gcccccacaa 840  
 gcagtggagt atgtgttta attcgacgc acgcgaagaa ctttaccaag tcttgacatc 900  
 ccttgacaga natagaaata tggtttctt tccggagcaac gagacaggtt gtgcgtatgtt 960  
 gtcgtcgtatc gtcgtcgtga gatgttgggt ttaatgtcccg aacgacgcga acccttatgg 1020  
 tcagttacta ccgttcccg acttgcgttgc acatggcttgc acaaaaaggaa ggaagggtgg 1080  
 gatgacgtca aatcatcatg ccctttatga cttgggttac acacgtacta caatggctt 1140  
 aaacaaagag aagaacggcc gcgacgttggaa gcaaaactca gaaacaaacgtt cccagttccg 1200  
 actgcggatc gcaactcgcc tgcacgaaat cggaaattgtt gtaatcgtt gatcgtatc 1260  
 ccacgggttac ttcgttcccg ggccttgcac acaccggcccc ttcacaccatg agagccgggg 1320  
 ggacccgaag tcggtagtc 1339

SEQ ID NO: 125                    moltype = DNA length = 1339  
 FEATURE                          Location/Qualifiers  
 misc\_feature                    1..1339  
                                 note = Obtained from Intestinal Bacteria, I20  
 source                          1..1339  
                                 mol\_type = other DNA  
                                 organism = unidentified

SEQUENCE: 125  
 gagagagactt gctttctcgat gcgagtggcg aacgggtgag taacgcgtga ggaacctgccc 60  
 tcaaagaggg ggacaacagt tggaaacgac tgtaataccg qctataacccc acgggtcgcc 120  
 atcgaccaga gggaaaaggaa gtaatccgtt tttagatggcc tgcgtccgtt attagctgtt 180  
 tggtaggtt angggccacc aagggnacca tgggttagccg gactgagagg ttgaacggcc 240  
 acattgggac tggacacggc ccacactcc tacggggggc acaatggggg aatattgcac 300  
 aatggggaaa accctgtatc ggcacggccg cgtggggaa aagggttccgc ggattgtaaa 360  
 cttctgttgtt tggggagat aatgcgttgc cccacaaggaa aagtgcgttgc taactacgtc 420  
 ccacgcgcg cggtaaaacgt taggttccaaac gctgttgcgg gaattactgg tgtaaaggaa 480  
 agegcggccg gggaaaaggaa tggatgttgcgtt aatctatggcc tcaaccatca aactgtttc 540  
 caaaaactgttt ttctttagtgcgtt gtcggatgtt tccgggttgc ggggtggaaat 600  
 gctgtatcgtatc gggggagaa accatgttggc gaggccggcc actggggccacc aactgtatcgt 660  
 gaggctcgaa atgtgttggat gcaaaacaggaa ttagataccct tggtagtccca caccgttaac 720  
 gatgttactt atgtgttggat gatgttggcc cttcagtgcc gcaatggccca caataagtaa 780  
 tccacctggg gatgttggcc aacttcaaaaggaa aatttgcgttgg gggccgcaca 840  
 agcgttgcgtt atgtgttggcc aatcgacgc accttaccaat gtcgttgcacat 900  
 cccttgacac agatgttggcc aatcgacgc accttaccaat gtcgttgcacat 960  
 tggtaggttgcgtt gatgttggcc ttaatgtcccg aacgacgcgc acccttatgtt 1020  
 gtcgttgcgtt acgtgttggcc gatgttggcc gacaaaaacgg aggaaagggtgg 1080  
 gatgttggcc gatgttggcc gatgttggcc gacaaaaacgg aggaaagggtgg 1140  
 taaaacaaagaa gaagcaagac cggcgggtgg agcaaaaactca gaaacaaacgg tcccgatgtt 1200  
 gactgcggcc tgcaactcgcc tgcacgaaat tccggatgtt gtaatcgtt gatcgtatc 1260  
 ggcacgggttac atacgttccc gggcccttgcac acaccggcccc gtcacaccatg agagccgggg 1320  
 gggacccggaa tcggtagtgc 1339

SEQ ID NO: 126                    moltype = DNA length = 1354

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**FEATURE** Location/Qualifiers  
**misc\_feature** 1..1354  
**source** note = Obtained from Intestinal Bacteria, I21  
**mol\_type** = other DNA  
**organism** = unidentified

**SEQUENCE:** 126

cattgagact tcgggtggatt	tgtcttattt ctatggccg	acgggtgagt aacgcgtggg	60
taacctgcct tatacagggg	gataaacagtc agaaaatggct	gctaataccg cataaagcgca	120
cagagctgca tggctcagtg	tggaaaactc cggtggata	agatggaccg gcgttggatt	180
agcnmnnntgg tggggtaacg	gcccaccaag ggcgcgttcc	atagccggcc tgaggggtg	240
aacggccaca ttggggactga	gacacggccc agactctac	gggaggcage aatggggaaat	300
atttccaaat gggggaaacc	ctgtatcgacg	gacgcggccgaa gaaggaaata	360
atgttaactt ctatcagcag	ggaagatagt	gacggtaacct gactaagaag	420
ctacgtgcca gcagccgccc	taatacgtag	ggggcaagcg ttatccggat	480
taaaggggcgt gtagacggctg	tgccaaactc	ttactgggtt aacctgttga	540
ttatcttggaa aactgttata	cttggatggcc	gggnnggttgc ggcaatggcc	600
gtgaaatgcg tagatattag	gaggaacacc	tgatggcgaag ggcgcctact	660
tgacgtttag gctcgaaage	gtggggagca	aacaggatta gataccctgg	720
cgttaaaatcg gaataacta	tgctggggag	ttcnnnctt cgggtcgctc	780
taatgtttcc acctgtgggg	taatcgccg	gcaaaacggc tgcaatcgac	840
ccgcacaagg ggtggggat	gatgtttat	tcgaaggcaac ggcgaagaa	900
ttgacatccg cctgaccgt	ccttaacccg	ttaccaactc atctttcctt	960
gtgcgttggg tgcgtcagtg	ctgtatcgta	cgggacaggc gagacagggt	1020
acccttattcc tcaatcgca	gcatttaagg	ttggcactt ggggagactg	1080
cttggggatggaa ggccggatgt	acgtcaataat	ccaggatata atatcgcccc	1140
gtgctataat ggctaaaca	aaaggaaagcg	ttatgttttg tggatggat	1200
aacgtcccaag ttccgactgt	agtcgtcaac	ccgactacac gaagctggaa	1260
tcggggatcat gaatggccgc	gtgaatacgt	tcggggatct tgcgtatgaa	1320
ccatggggat cgtaaacgccc	cgaagtcaatg	ccgtacacacc gcccgtcaca	1384

**SEQ ID NO:** 127

**FEATURE** moltype = DNA length = 1264  
**Location/Qualifiers**

**misc\_feature** 1..1264  
**source** note = Obtained from Intestinal Bacteria, I22  
**mol\_type** = other DNA  
**organism** = unidentified

**SEQUENCE:** 127

ttacttggat ttcttcggaa	tgacggatat	tgtgtactgag cggccggacgg	60
cgtgggttaac ctgcctcata	cagggggata	gtgagtaacg acggatgtt	120
agacccacagg aacggatgtt	acggatgtt	atactgtctt ataccgcata	180
ctgatttagct ggttgggtgg	gcaatggctt	aaactccgtt gtatgtatgg	240
agggcggacc gccacattgg	accacggcc	ggacggcgat	300
ggggatatttg cacaatgggg	gactggacaa	tcctacggga ggcagcgtg	360
ttccgtttagt aaacttctat	cgtggggaa	gaaaatggacg	420
gtctaaatctcact	tcggggatgt	gtatctact gaaagcccc	480
gagaggttaag cggaaattcc	atgtgttccg	ttttttttttt tagtgcgt	540
gtggcgaagg cggcttacttg	gacgtatgt	ttttttttttt tagtgcgt	600
acaggatttg atacccttgg	atccacggc	ttttttttttt tagtgcgt	660
aaaggccattc ggtggcccg	gtttttttttt tagtgcgt	ttttttttttt tagtgcgt	720
aatgtttttttt tagtgcgt	aaatgtttttt tagtgcgt	ttttttttttt tagtgcgt	780
cgaaggcaacg cgaaggaaat	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	840
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	900
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	960
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	1020
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	1080
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	1140
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	1200
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	1260
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	1320
ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	ttttttttttt tagtgcgt	1384

**SEQ ID NO:** 128

**FEATURE** moltype = DNA length = 1340  
**Location/Qualifiers**

**misc\_feature** 1..1340  
**source** note = Obtained from Intestinal Bacteria, I23  
**mol\_type** = other DNA  
**organism** = unidentified

**SEQUENCE:** 128

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tgtttttttt atcaaaatgtt	tatcgctgaa	cataatataa ttgaaccgca	180
taaggtaacg gtttaccaat	agatgtatgt	ttcgctgttgc agtctatgtt	240
ttggggactga gacacggccc	agactctac	ttggggatcc aatggggccca	300
ggaggaaact ctgtatcgac	gtatggccgt	ttggggatcc aatggggccca	360

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ctgttccatg	ggacgaaaaa	tgacggtacc	tgaggaggaa	gctccggcta	actacgtgcc	420
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cgttaggcgg	atcgaagtgc	agatgtgaaa	actatgggct	taaccctaaa	actgcatttgc	540
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cagtggagta	tgtggattaa	ttcgaagcaa	cgcagaagac	cttaccaggt	tttgacatcg	900
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gattgtggc	tgcaacccgc	ctatcatgc	tcgaaattgc	tagaatcgc	agatcagcat	1260
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acacccggaa	gcctgtagtc					1340

SEQ ID NO: 129	moltype = DNA	length = 1337				
FEATURE	Location/Qualifiers					
misc_feature	1..1337					
source	note = Obtained from Intestinal Bacteria, I24					
	1..1337					
	mol_type = other DNA					
	organism = unidentified					
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cgttagatatc	ggggaggaa	ccatgtggcga	aggcggctt	ctggggacca	actgcacgt	660
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gatgacgtca	aatcatcatg	ccctttatga	ctggggctac	acacgtacta	caatgcgtt	1140
aaacaaaagag	aagcnngacc	gcgagggtgg	gcaaaactca	gaaacaacgt	cccagttcg	1200
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ggacccggaa	tcgggtng					1337

SEQ ID NO: 130	moltype = DNA	length = 1353				
FEATURE	Location/Qualifiers					
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source	note = Obtained from Intestinal Bacteria, I25					
	1..1353					
	mol_type = other DNA					
	organism = unidentified					
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tagttgtgg	ggtaacggcc	taccaagccg	acgatcgt	gcccacactga	gaggggtgacc	240
ggccacatcg	ggactgagac	acggcccaga	ctccatccgg	aggcagcgt	ggggatatt	300
gcacaatgg	ggaaactctg	atgcagcgc	gcccgtgtaa	ggatgaatgt	tttcggat	360
taaacttcta	tcagcagg	agaaaatgtac	ggtacactgt	taagaagccc	cggtacta	420
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catttggac	tgctgacgt	gagtgtcg	nnggcaatgt	gaattccat	tgtagcgt	600
aaatgcgt	atatttaggt	gaacaccat	ggcgaadggc	gcttgcgt	cgatgact	660
cgttgaggct	cgaaacgcgt	ggggacaaat	aggattat	accctgttgc	tccacgc	720
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catgggttgc	gtcagctgt	gtcgt	gatgtttaa	gtccgc	aaacgc	1020
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cgtctc当地gggatggtag tctgcaactc gactacatga agctggaatc gcttagtaatc 1260
gc当地atcaga atgctcggtt gaatacgtc ccgggtctt tacacaccgc cctgc当地acacc 1320
atgggaggtca gtaacgccc aagtcaatc ccc 1353
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SEQ ID NO: 131 moltype = DNA length = 1361
FEATURE Location/Qualifiers
misc_feature 1..1361
note = Obtained from Intestinal Bacteria, I26
source 1..1361
mol_type = other DNA
organism = unidentified
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agaccacatg actgcatggg acatgtt当地aa aaactccggg ggtatgagat ggaccggc当地gt 180
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agggtglocal gccacatggg gactgagaca cggcc当地gggac tectacggg ggc当地ggc当地gt 300
gggaaatattt cacaatggg gaaaggctt当地a tgccagc当地ggc cc当地ggctt当地gg 360
ttccggtatgtt aaacttctat cagcaggggaa gaaaatgagc gtacactt当地act aagaaggcccc 420
ggcttaactac gtgc当地ggc当地gg acgtt当地gggg caagc当地gtt当地ccggattt当地ac 480
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gtagc当地gggtt当地gg aatgctgtt当地gg tattaggagg aacaccatgtt gccaaggccg cttactggac 660
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ccacggc当地gtt当地gg aacatgtt当地gg gttt当地ggggatgg gggatggcaaa gctt当地atgggtt当地ggccgacta 780
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SEQ ID NO: 132 moltype = DNA length = 1345
FEATURE Location/Qualifiers
misc_feature 1..1345
note = Obtained from Intestinal Bacteria, I27
source 1..1345
mol_type = other DNA
organism = unidentified
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SEQ ID NO: 133 moltype = DNA length = 400
FEATURE Location/Qualifiers
misc_feature 1..400
note = Obtained from Intestinal Bacteria, I28
source 1..400
mol_type = other DNA
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<b>SEQ ID NO: 135</b> <b>FEATURE</b> <b>misc_feature</b> 1..1358 <b>source</b> note = Obtained from Intestinal Bacteria, I30 <b>mol_type</b> = other DNA <b>organism</b> = unidentified	<b>moltype</b> = DNA length = 1358 <b>Location/Qualifiers</b>
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<b>SEQ ID NO: 136</b> <b>FEATURE</b>	<b>moltype</b> = DNA length = 1342 <b>Location/Qualifiers</b>

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misc_feature          1..1342
                        note = Obtained from Intestinal Bacteria, I31
source                1..1342
                        mol_type = other DNA
                        organism = unidentified

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gactggtaga tgatggactt atggcgatt agctggtttg tagggtaacg gcctccaag 180
gecagcgttgc gtggccgacc tgagggttg accggccaca ctggactga gacacggcc 240
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gggatgacgtt ccaatcatca tggcccttat gacctgggtt acacacgtgc tacaatggac 1140
agagcagagg ggacggcaagc cggcgggtgg agcggaaaccctt ataaatgtt tctcgttgc 1200
gactgcgttgc tggcaacttgc ctgcacggat atgaaatcgc tagtaatcgc gaatcagcat 1260
gtcgcgggttatacgttgc gggcccttgc cacaccggcc gtcacacccat gagagtccgtt 1320
aacacccggaa gccgggtggcc ta 1342

SEQ ID NO: 137      moltype = DNA length = 1390
FEATURE
misc_feature          1..1390
                        note = Obtained from Intestinal Bacteria, I32
source                1..1390
                        mol_type = other DNA
                        organism = unidentified

SEQUENCE: 137
atgagaagct tgctttttat tgattcgagt ggcaaaacggg tgtagtaacgc gtaagcaacc 60
tgcccttcgat atggggacaa cagctggaaa cggctgtctaa taccgaatac gtttttttg 120
tcggcatggca gagggaaagaa agggaggctc ttccggatct tcgtcttggg agggttgc 180
gtctgatttag ctatgttgat gggtaacggc ccaccaaggc gacgtatcgtt acgcgttgc 240
agaggatgaa cggccacattt gggatgttgc caccggccacg actccatcg gaggcagcag 300
tggggatattt tccgcatacgcc acggaaatggc gacggagccaa cggccgttgc acgtacgg 360
ccttcgggtt gtaaaatgtt gttatacggtt acggatggcc tagcgttccaa taccgttac 420
gagtgcgttgc acggtaagat gaaaggccacgg ctaactacgtt gccagcggcc gcggttatac 480
gttaggttgc acgttgcgtt ggaattttt ggcgtttaagg ggcgcggcc ggcgttgc 540
gtcgggttca aaaaatggggc gtttaatccc gtcggggggc cggaaatgtt acgttagat 600
atccggatggg aaacggcgtt tccatgttgc gccgttgc gatgttgc gatgttgc 660
accagtggccgaa aacggcgctt tctggacgcg aactgtacgtt gaggcggccaa agccagggg 720
gcaaaacgggaa ttagataccctt cggatgttgc ggcgtttaacg gatgttgc gatgttgc 780
gtgtatcgacc cttctgttgc cggatgttgc gcaataatgtt tccgttgc ggcgttgc 840
cggcaaggctt aactcaaaatggggc gtttaatccc gtcggggggc cggaaatgtt acgttagat 900
taattcgacg caacgcgtt gtttttttttca gacccgttgc gtttttttttca tggatggaga 960
tatcccgatc cncttcggat ganaaaagaa nagggtggatc acggcgatgc tcagctcg 1020
tcgtcgatgtt tgggttgc tccgcatacgcc acggccaccc cttatgttgc ttaccacgg 1080
ttccggccggg gactcggatc agactggccg agacatgttgc gaggaaaggcg gggatgttgc 1140
caagtcatca tgcccccttgc ggttgggtt acacacgttgc tacaatggcc tttatagat 1200
ggaaaggccgg gacggatccg gggcccttgc caaaaacccaa gttcccgatc ggatgttgc 1260
ctgcacactcg cttgtatggaa gcaaggatcg ctgtatgttgc cggatgttgc tttatgttgc 1320
aatacgttcc cggcccttgc acacaccggcc gtcacacccat cggaaatgtt tcacacccgt 1380
agccgggttag 1390

SEQ ID NO: 138      moltype = DNA length = 1373
FEATURE
misc_feature          1..1373
                        note = Obtained from Intestinal Bacteria, I33
source                1..1373
                        mol_type = other DNA
                        organism = unidentified

SEQUENCE: 138
atctatgttgc aaacgggttgc gtaacacgtt aacaacctgc cttcaggatg gggacaacag 60
acggaaacgtt ctgtatgttgc cttgtatgttgc cttgtatgttgc ggttggatc 120
gtggcccttgc tttgtatgttgc atcgttgc gggcccttgc cttgtatgttgc ggttggatc 180
ggatgttgc gggcccttgc cttgtatgttgc cttgtatgttgc ggttggatc 240
ttccggccatc acacaccggcc gtcacacccat cggaaatgtt tcacacccgt 300

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ggcgtttaacc	cgtgtatggg	tggaaactga	gaggctggag	tatcgagag	gaaagtggaa	600
ttctctatgt	agccgttggaaa	tgccgttagaga	tttaggaagaa	caccgggtgc	gaaggcgact	660
ttctggacga	caactgtacgc	tgaggcgca	aagcgtgggg	agccaaacagg	attagatacc	720
cttgttagtc	acgcgttaaa	cgtatataac	taggtgttagg	aggtatcgac	cccttctgtg	780
ccggagctaa	cacaataagt	attecgcctg	ggaagtagcga	tcgcaaggatt	aaaactcaaa	840
ggaatttgcac	ggggccccca	caagcgttgg	agtatgtgtt	ttaattcgac	gcaacgcgaa	900
gaaccttacc	aggctttgtac	attgtatcg	atttggaaattt	atttggaaattt	ctccttcggg	960
agacgagaaa	acagggtgt	cacggctgtc	gtcagctcg	gtcgttagat	gttgggttaa	1020
gtcccgcaac	gagcgtcaacc	cctatctt	gttaccagca	cgttatgttg	gggactcatg	1080
agagacccgc	ggggcaacac	cggggaaagg	tggggatgac	gtcaagtcat	catccccctt	1140
atgacctggg	ctacacacgt	actacaatgg	gtgtcaacaa	agaaagcga	agccgcgagg	1200
caagcaaac	ctcaaaaaaca	cacccccc	tcagattcga	ggctcaaccc	cgccctcgat	1260
aagtaggaat	cgcttagtaat	cgcgggtcag	cataccgcgg	tgaatacgtt	cccgccctt	1320
gtacacacccg	cccgacacac	tatgagagtc	agaaacaccc	gaagccgggt	agg	1373

SEQ ID NO: 139	moltype = DNA	length = 1366				
FEATURE	Location/Qualifiers					
misc_feature	1..1366					
	note = Obtained from Intestinal Bacteria, I34					
source	1..1366					
	mol_type = other DNA					
	organism = unidentified					
SEQUENCE: 139						
ttcttagtgg	cgaacgggtg	agtaacgcgt	gggcaacctg	ccctccagg	tttggacaaca	60
ttccgaaagg	gatgtataa	ccgaatgtgc	tcctcttcc	gcatggagga	gggagaaag	120
atggcctctg	cttgcgttac	atcgttggaa	gatggggcc	cgtctgtt	gcttagttgt	180
gggggttacgg	ctcaccagg	cgtatgtac	tagccgttct	gagaggatga	acggccacat	240
tgggactgt	acacggccca	aacttctacg	ggaggcgtca	gtggggaaatc	ttccgcata	300
gacgaaatgc	tgacggagca	acgcggctgt	agtgatgaat	gttccctggat	tgtaaaactc	360
tgttgtttag	gacgaaagca	ccgtgttgc	acagggttac	gtgttgcgg	tacctaacga	420
ggaaaggccac	gtaatcgt	tgccgttgc	cgccgttata	cgtaggttgc	aagcgttgc	480
cggttattt	gggcgttac	agcatgttag	cgggttttta	agttctgtac	gaaaatgcgg	540
ggctttaacc	cgtatgtgc	tggatactgg	aagtcttgc	tgcaggagag	gaaaggggaa	600
ttccctgtgt	agccgttggaa	tgccgtatata	tttggggaggaa	caccagtggc	gaaggccct	660
ttctgtgt	tgtgtgcac	tgatgttgc	aagccatgg	agccaaacggg	attagatacc	720
ccggtagtcc	tggccgttac	cgatgtatac	taggtgttag	agttctgtac	cccttctgtg	780
ccggatgttac	cgcaataatgt	atccgcctg	gggactactga	tgcgaatagg	gaaactcaaa	840
ggaatttgcac	ggggccccca	caagcgttgg	agtatgtgtt	ttaattcgac	gcaacgcgaa	900
gaacccatacc	agggtgtac	atttggatgt	agacatgttac	atagggttcc	cccttcgggg	960
acacgaaaac	agggtgtca	tgtgtgttgc	cgatgtgttgc	cgtaggtatgt	tgggttaatg	1020
cccgcaacca	gogcaacccc	tatctatgt	taccaggccg	taatgggggg	gactcatagg	1080
agactgcac	ggataacttg	gaggaaggcg	gggatgtacgt	caagtcatca	tgcccttat	1140
gttttgggtt	acacacgtac	tacaatgttc	ggcaacaaac	ggcagcgaaa	ccgcgagggt	1200
gaccaaatcc	cccaatgttgc	ggatcgttgc	ggatcgttgc	cctacgttgc	tttgggtt	1260
gttggatgt	ctatgtatcg	cagggttgc	tactgcgttgc	aatactgttcc	ccggcccttgc	1320
acacaccgc	cgtcacacca	cgaaatgttgc	taacaccgcg	agccgg		1366

SEQ ID NO: 140	moltype = DNA	length = 1387				
FEATURE	Location/Qualifiers					
misc_feature	1..1387					
	note = Obtained from Intestinal Bacteria, I35					
source	1..1387					
	mol_type = other DNA					
	organism = unidentified					
SEQUENCE: 140						
cttgctctt	nttggattct	agttggcaac	gggtgagtaa	cacgttaaaca	acctgccttc	60
aggatgggg	caacagacgg	aaacgactgc	taataccgaa	taccttccaa	tttccgcata	120
gagataggaa	gaaagggtgg	cctctacttg	taagctatcg	cctgttgcgg	gggtttgcgtc	180
tgatttagctn	gttgggttgg	taacggccca	ccaaggcgtac	gatcgttgc	cgggttgcgt	240
ggatgttacgg	ccacacttgc	actgttgcac	gggttgcgttgc	cctacggggag	gcagcgttgc	300
ggaatcttcc	cgatgttgc	aaagtcttgc	ggatgttgc	cgccgttgcac	atgttgcgt	360
tcggatgttgc	aaagtcttgc	atccgggttgc	aaaggcatna	tttggaaatcat	tgatgttgcgt	420
tgacggtacc	ggaaaatgc	gccacggct	actacgttgc	agcagcgttgc	gttgcgttgc	480
gggtggcaac	gttggccgtt	attatgttgc	gttgcgttgc	cgccaggcgttgc	cgttgcgttgc	540
catcttaaaa	gggtgggttgc	taacccatgt	aggggttgcgttgc	aactgttgcgttgc	ctgggttgcgttgc	600
ggagggggaaa	gttggatattcc	taggtgttgc	gttggaaatgttgc	taggtgttgc	tttgggttgcgttgc	660
gggtggcaac	gogacttttgc	agacgttgcgttgc	tttggaaatcat	tttggaaatcat	tttgggttgcgttgc	720
aacaggattt	gataccctgg	tagtgcacgc	cgtaaaccat	ggatacttgc	tgttgggttgcgttgc	780
atcgaccctt	tctgttgcgttgc	agttaaacgc	ataagatgttgc	cccttgcgttgc	gttgcgttgc	840
aagattaaaa	ctcaaaaggaa	tttgcgttgcgttgc	cccgccacaac	cggttgcgttgc	tgttgggttgcgttgc	900
ttcgacgcac	cgcgaaaggaa	cttaccaacgc	tttgcgttgcgttgc	atcgatgttgc	gtcgttgcgttgc	960
ggatgttcc	ttcggaggac	gagaaaacac	gttgggttgcgttgc	cgatgttgcgttgc	gttgcgttgc	1020

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ttagatgttt ggtaagtcc cgcaacgagc gcaaccctt tctttgttg ccagcacgtt 1080  
aaggtgtggaa ctcaggagag accggcgccg acaacgcggg ggaaggccggg gatgacgtca 1140  
agtcatcatg ccccttatgg ctgggtac acacgtacta caatgggtgc aaacaagag 1200  
aagcgaatgc gcgagacgga gggaccta taaacgcact cccacttcg attcgaggct 1260  
gcaaccggcc tgcatgaagt aggaatcgct agtaatcgcg ggtcgcata ccggcggtgaa 1320  
tacgttccgg ggccttgcac acaccgcggc tcacactatg agagtcagag acacccaaag 1380  
cccgatgg 1387

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SEQ ID NO: 141      moltype = DNA    length = 1386
FEATURE          Location/Qualifiers
misc_feature     1..1386
                  note = Obtained from Intestinal Bacteria, I36
source           1..1386
                  mol_type = other DNA
                  organism = unidentified
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SEQUENCE: 141
gagaagcttgc ttctttatcn attcttagtgg caaaagggtg agtaacgcgt aagaacacctg 60
cccttcgat ggggacaaca gctggaaacg gctgetataa ccgaatacgt tnnnlnngcc 120
gcatgacan atgaagaaa ggaggccctc gggcttgcg tgaggagggg gcttgcgtt 180
gattagctng ttggaggggt aacggcccac caaggcgacg atcagttagcc ggtctgagag 240
gatgaacggc cacattggga ctgagacacg gcccagactc ctacgggagg cagcagtggg 300
gaatcttcgg caatggacga aagtctgacg gagaacgcg cgctgaaacgc tgacggccct 360
cgggttgtaa atggctgtta tatggacga acaggacate ggttaatacc cggtgtctt 420
gacgggtaccc taagagaaaag ccacggcttaa ctacgtgcgc caagccccggg taatactgt 480
gtggcaacgc ttgtccggaa ttattgggcg taaaggcgc gcaggccggca tcgcaagtgc 540
gtcttaaaag tgccggggctt aaccctgtg ggggacccga actgttgaaagc tcgactgtcg 600
gagagggaaaac cggaaattccct agtgttagcgg tgaatgcgt agatattagg aggaacacca 660
gtggccaaagg cggcttctc gacgacaacta gacgctgtgg cgccaaagcc agggggggca 720
acgggatttag ataccccggt agtcctgtcc gtaaaacgatg gataacttaggt gttaggaggta 780
ctgactcttctt ctgtggccga gttaaacgca taatgtatccc gcctggggggtag tacggccgc 840
aggcttggaaac tcaaaggaaat tgacggggc cgcacaaacg ggtggatgt gtggtttaat 900
tcgacgcacac gcaacggaaa ttaccaacggc ttgacatgtt tgctacggaa aagagatttc 960
cggttcttctt tcggaaagaca agaaaaacagg tggtgacccgg ctgtcgtcag ctgtgtcg 1020
gagatgttgg gttaaatgtcc gcaacggacg caacccctat ctcttgcgtcc cagacacccgt 1080
ggtagggggact cagaagagac tggccgcacac aatggggagg aaggccccggg tgacgtcaag 1140
tcatcatgcg cttttatgtt tggggctacac acgtactaca atggctttaa atagggggan 1200
ncgaaggaggc gatccggagc aaacccaaaaa aacagatgtcc cagttccggat tgccggctgc 1260
aactcgcttg catgaagcag gaatcgatgt taatcgccagg tcagatatact gccggtaata 1320
cggttccgggg ctttgcgttacac accggccgtc acaccacggaa agtcatttcac accggaaagcc 1380
gttgaaat 1386

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SEQ ID NO: 142          moltype = DNA    length = 1364
FEATURE                  Location/Qualifiers
misc_feature             1..1364
note = Obtained from Intestinal Bacteria, I37
source                   1..1364
mol_type = other DNA
organism = unidentified
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SEQUENCE:	142	Organism	- unidentified	
cgccagcgcg	gggagcttgc	tccctggcgg	cgagtggcgc acgggtgagt aatacatgg	60
aacgtgtttt	ctatgtgggg	ataactgcgc	gaaaggccg ctaataccgc atgagacctg	120
agggtggaaa	cgggggatcg	caagacccgt	cgctggaga gggccgcgat tccgattagc	180
tagtttgtga	ggtaaaaggct	caccaaggcg	acgtatcgta ctgttctga gaggacgacc	240
agccacactg	ggactgagac	acggccaga	ctctactcggtt aggcagcagt gggaaatttt	300
ggacaatggg	ggcaacccctg	atccagccat	gccgcgtgca ggatggaaaggctt cttccgtattg	360
atastactgtt	tttgtaggga	cgaaaaggga	tcgcataaca ccgttattccg ctgacggat	420
ctgaagaata	agcacccgtt	aactactgtc	cagcaggcgc ggttaatacgtt aggggttgcga	480
cgttaatcg	aattactggg	cgttaaaggct	gcgcaggcgg ttctgttataa tagatgtgaa	540
atccccggc	tcaacctggg	aattgttat	atgactgcgcgacttgcgtt tgtaggtt tgtaggtt	600
gggttggaaat	ccacgtgtat	cagtgttata	cgatgtatggatggaaaca ccgtatggcga	660
aggccgcctt	ctggggatcat	actgcgcgtt	atgcacggaa ggcgttgggg caaacaggat	720
tagataccct	ggtagtccac	gccttaaaacg	atgttactat gttgttgggg acgtatgttcc	780
tttgttaacgc	actctaaccgc	tgaagttagac	cgcctggggtt gtacggcgcg aagataaaa	840
ctcaaaggaa	tttagcgggaa	cccgacaaat	cggtgtatgc tgtaggttattt tcgcatgc	900
cgcggaaaaaa	cttacatgc	cttgcatgc	caggagggnn tgagatcatc ggcctgtccc	960
cgaaaggaaat	ctggacacac	gtgtgtatgc	gctctgttcg tgatgttgc	1020
ggtagtgc	cgcaacgcgc	gcaacccttg	tcatttagttt ctacggaaagg gcactctaat	1080
gagactgcgc	gtgacaaacc	ggaggaaagg	ggggatgcgc tcaagtccctt atggccctta	1140
tggcttaggg	ctcacacgtc	ataacaatgtt	cggaacatgg ggaacgcgaag ccgcggagggt	1200
aagccaaatcc	cagaaaaaccg	atcgtagtcc	ggattgcgtt ctgcacactcg actgcatgaa	1260
tgccgtatcc	ctagtaatcc	cggatcagca	tgccgcgtt aatacgttcc cgggttctgt	1320
acacacccgc	cgtcacacca	ttgggagtggg	gttacccaggaa	1364

SEQ ID NO: 143 moltype = DNA length = 1343  
FEATURE Location/Qualifiers  
misc feature 1..1343

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source          note = Obtained from Intestinal Bacteria, I38
                1..1343
                mol_type = other DNA
                organism = unidentified

SEQUENCE: 143
ggaaacggat tagccggcga cgggtgagta acacgtgggt aacctgcctc atagaggaga 60
atagecctccc gaaaggggaga ttaataccgc ataacattgc agtttgcgt gaaacagcaa 120
ttaaaggagc aatccgctat gagatggacc cgccgcgc cat tagctagt gtaaggtaat 180
ggcttaccaa ggcgacgatg cgttagccgc ctgagagggt gateggccac attggactg 240
agacacgcgc cagacttcata cgggaggcag caigtggggaa tattgcacaa tggggaaac 300
ctcgatgcg aacgcgcgc tgagtatgc cggcttcggg attgtaaacg tctgttttg 360
gggacgataa tgacgggtacc caaggagaa gccacggcta actacgtgcc agcagccgc 420
gtaatacgtg ggtggcgac gttgtccgga tttaactggg gtaaaaggag cgtaggccga 480
tttttaagtg gtatgtgaaa tacccgggtt caaacctgggt gtcgcattcc aaactggaa 540
tctagagtgc agggaggggag agtggaaatc ctatgttagc ggtggaaatgc gttagagatta 600
ggaagaacac cagtgccgaa ggacacttc tggactgtaa ctgacgctga ggctcgaaag 660
cgtggggagc gaacaggatt agataccctg gtatgtccacg cctgtaaacga tgaataactag 720
gtgttaggggt ttcaacaccc ctgtggccgc gctaacgcata taagtattcc gcctggggag 780
tacgggtcgca agattnaaac tcaaaaggatg tgacggggcc cccgacaatg aegggagcat 840
gtggtttaat tccaaggacac gccaaggaaatc ttacatcgatc ttgacatctt ctgcattacc 900
cttaatcggg gaagttccctt cgggaacaga gtgacagggt gtgcattgtt gtgcgtcgatc 960
cgtgtcgatgatgttgggt taatgtcccg aacgagccgc accccatttg ttatgtgtca 1020
ccattnaaatc tggacttcata gcgagatgc ctgggtttaac caggaggaaatg gtggggatga 1080
cgtcaatatac tcatggccct tatgtcttagc gtcacacacg tgcataatgc gcaagtacag 1140
agagatgcac taccggcgagg tggagctaaat cttcaaaact tgcgttcgtt cggattgttag 1200
gctgaaactc gcttacatgc agtggaggtt actagtaatc gcaatcgcg atgtcgccgt 1260
gaatacgttc cggggccctt tacacaccgc cccgtcacacc atgagatgt gcaataccca 1320
aagttcgtga gctaacgcgt aag 1343

SEQ ID NO: 144      moltype = DNA length = 1318
FEATURE           Location/Qualifiers
misc_feature      1..1318
source            note = Obtained from Intestinal Bacteria, I39
                1..1318
                mol_type = other DNA
                organism = unidentified

SEQUENCE: 144
cttagtggcg gacgggtgag taacgcgtga gtaacacctgc tttcagaggga gaataacatt 60
ctgaaaagaa tgctataacc gcatgagatc gtatgtatcg atggatcagc gaccaaaggaa 120
gcaatccgcgt gaaagatggc ctcgcgtccg attagatgtatggatgata aaggcccacc 180
aaggcgacga tcggtagccg gactgagagg ttgaaacggcc acattggac tgacacacgg 240
cccagactcc tacgggaggc agcagtgggg gatattgcac aatggggaa accctgtatgc 300
agcaacgcgc cgtggaggaa gaaggatctt cttctgtctt caggaaatg 360
aatgacggtt cctggaggagg aagtcctggg taactacgtt ccacgcgcg cggtaatacg 420
tagggagccaa gogttgtccg gattttactgg tggttggggatg tgcgttgcgc gatcttgc 480
tcagtagtgc aatcccgagg cttaaaccctg gaactgtatc tgaaactgtg ggttttgc 540
gaggtagagg caggcgatgt tccgggtgtt gtcgttgcgat gctgttgcgat cggggaggaa 600
accaggcgatgtt aaggccgcctt gctggggctt aactgcgtt gaggcagaa agcatgggtt 660
gcaaacaggaa ttagataccctt tggtagtccatcc tgcgttgcac gatgttactt aggtgtgggt 720
ggctctgaccctt catccgtgcc ggaggatcaaca caataatgtt tccacccggg gatgttgcgc 780
gcaagggttgc aactcaaaagg aatttgcggg ggccccgcaca agcgttgcgat tatgttgc 840
aatttgcgatc aacgcgcaaga accttaccatc gtcgttgcac aggttgcgat 900
acgtttaggtt cccttgcggg aacaggatgtt cagggttgcg atgttgcgc tcaatgtcgatc 960
tcgttgcgttgc ttgggtttaag tcccgcaacg agcgttgcgcctt ctgttatttttgc 1020
agagacttccctt aataggactt cccgttgcaccc aacggaggaaatg ggtggggaccc acgttgcgc 1080
atcatgttgcctt ttatgtatcc gtcgttgcaccc aggttgcgc 1140
aaaggccgcgaa ggttggaggaaatg aacgttcccgat ttcggatcgtt aggttgcgc 1200
ccgcctatgtt gaaatggggaaatg ttgttgcgtt tccgttgcgc gatgttgcgc 1260
tcccgccctt ttttgcgttgc gtcgttgcgc tcaatgtcgatc 1318

SEQ ID NO: 145      moltype = DNA length = 1360
FEATURE           Location/Qualifiers
misc_feature      1..1360
source            note = Obtained from Intestinal Bacteria, I40
                1..1360
                mol_type = other DNA
                organism = unidentified

SEQUENCE: 145
tcatgcacaga ggatttgcgtcc aatggatgtt gtttacttgcgat ggcggacggg tgatgttgc 60
gtgagtaacc tgccttggatc tggggatataa cagggtggaaa catctgttacccatgc 120
tgcgttgggg tccatgttgcgat ctgttgcgc aatgtttatc gtcgttgcgc gatgttgcgc 180
ctgttgcgttgc gtttggggatc gtaacggccca accaaggccgcgat cgttgcgc gatgttgcgc 240
aggttggccg cccatgttgcgat gactgagaca cggccgcacatc tccttgcgc ggcggacggc 300
ggaaatatttgc gcaatggggc gcaaggcttgc cccaggatgttcc gtcgttgcgc gatgttgcgc 360
ttcgggttgc ttttgcgttgc gtcgttgcgc tcaatgtcgatc 420
cacggcttgcgat ttcgttgcgc gtcgttgcgc tcaatgtcgatc 480

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tactgggtgt	aaaggcggtg	tagggggac	tgcaagtca	atgtaaaaac	catggccta	540
acctgtggcc	tcgcatttga	actgttagtt	ttgagactg	gagaggcaga	cggattccct	600
agtgttagcg	tgaaatcggt	agatattagg	aggaacacca	gtggcgaagg	cggctgtctg	660
gacagcaact	gacgctgagg	cgcgaagcg	tggggagca	acaggattag	atacccttgt	720
agtccacgct	gtaaacatgt	gatacttaggt	gtgggggttc	tgaccccttc	cgtgcccgag	780
ttAACACAAAT	aagtatcccc	cctggggagt	acgatcgca	gggttaact	caaaggatt	840
gacggggggcc	cgcacaagcg	gtggagatgt	tgggttatt	cgaagcaacg	cgaagaacct	900
taccaggcct	tgacatcccc	gtgacgggt	tagagataca	ccttcttctt	cggaaaggcc	960
ggtgacaggt	ggtgtatgg	tgctgtcago	tcgtgtcg	agatgttgg	ttaagtcccg	1020
caacgagcgc	aacccttatt	gttagttgt	acgcaagacg	actctagca	gactgcccgt	1080
gacaaaacgg	aggaagggtgg	ggacgacgt	aaatcatat	gccccttatg	tcctggggca	1140
cacacgtact	acaatgtgg	tcaacagagg	gaagcaagac	cgcgagggtgg	agcaaacccc	1200
tAAAAGCCAT	cccagttcg	attgcaggct	gcaactcgcc	tgtatgaat	tggaatcgct	1260
agtaatcg	gatcagcatg	ccgcggtaa	tacgttcccg	ggccttgcac	acaccgcccc	1320
tcacaccatg	agagtcggga	acacccgaag	tccgttagct			1360

SEQ ID NO: 146                    moltype = DNA length = 1370  
 FEATURE                            Location/Qualifiers  
 misc\_feature                    1..1370  
 note = Obtained from Intestinal Bacteria, I41  
 source                            1..1370  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 146

gtgctcatga	cgaggttttc	ggacaacgga	ttgggttact	tagtggcgga	cgggtgagta	60
acgcgtgagg	aacctgcctc	ggagtgggaa	ataaacacacc	gaaagggtgt	ctaataccgc	120
ataatgcagt	tgggttgc	gactgtact	gccaaagatt	tatcgctctg	agatggctc	180
gctgctgat	agcttagttg	cggggtaacg	gcccaccaag	gcgacgatca	gtagccggac	240
tgagagggtt	acccggccaca	ttgggactga	gacacggccc	agactcttac	gggaggcgac	300
agtggggat	atgggcaat	gggcgcaago	ctgacccagc	aacgcccgt	gaaggaagaa	360
ggttccggg	ttgttaactt	ctttgtcag	ggacggaaaca	aatcatggta	cctgacgaaat	420
aaggccacgg	ttactactgt	ccagcagccg	cggtataatc	tagtggccaa	gcgttatccg	480
gatttactgg	gtgttaagggg	cgtttaggg	ggactgcaag	tcaggtgtga	aaaccagggg	540
ctcaacccct	ggcctgcatt	tgaaaactgt	gttctttagt	gctggagagg	caatcggaaat	600
tcctgtgtt	ggcggtgaaat	gctgatagat	acggaggaaac	accagtggcc	aaggccgatt	660
gctggacagt	aactgacgt	ggggcgcaaa	gcgtggggaa	gcaaacagga	ttagataccc	720
tggtagtcca	cccgctaaac	gatggatact	aggtgtgggg	ggactgaccc	cctccgtgcc	780
gcagttaaaca	caataaagtat	cccacctggg	gagtagcgtc	gcaagggtga	aactcaaaagg	840
aatttgcggg	ggcccgccaca	agcggtggag	atgtgtttt	aattcgaacg	aacgcgaaga	900
accttaccc	ggcttgacat	cctactaaacg	aagcagagat	gcatttagtg	cccttcgggg	960
aaagtagaga	cagggtgtgc	atggtgtcg	tcagctcg	tcgtgagatg	ttgggttaag	1020
tcccgcacg	agcgcacacc	ctattgttag	ttgtacgc	agagcactct	agcggactg	1080
ccgttgcacaa	aacggggaggaa	gggtggggacg	acgtcaatcc	atcatgcccc	ttatgtctcg	1140
ggccacacac	gtactacaat	ggtgggttaac	agaggggacg	aataccgcga	ggtggagccaa	1200
atccctaaaa	gocatccac	ttcggtatgc	agggtgaaac	ccgcctgtat	gaagttggaa	1260
tcgttagtaa	tcgcggatca	gcatggcg	gtgaaatacg	tccgggcct	tgtacacacc	1320
ccccgtcaca	ccatgagagt	cggaacacc	cgaagtccgt	agcctaacc		1370

SEQ ID NO: 147                    moltype = DNA length = 1341  
 FEATURE                            Location/Qualifiers  
 misc\_feature                    1..1341  
 note = Obtained from Intestinal Bacteria, I42  
 source                            1..1341  
 mol\_type = other DNA  
 organism = unidentified

SEQUENCE: 147

ttgcaccc	aagtttagtg	cgagccgggt	agtaacgcgt	gagcaacctg	cctcaaagag	60
ggggataacg	tctggaaacg	gacgctaata	ccgcatgacg	tattcgatag	gcatctattn	120
nataaccaag	gacgaccc	cggccatccg	cggccatccg	ggctcgccgt	tgatttagctg	180
taaaggccct	ccaaggccac	gatcgatgc	cgactgtg	gggtgaacccg	ccacatttgg	240
actgagacac	ggcccgacact	cctacgggg	gcacgactgg	gggatattgc	acaatgggg	300
aaaccctgt	gcagcaacgc	cgcgtgaagg	aagacggttt	tccgattgt	aacttctgtt	360
cttagtgcac	ataatgacgg	tagtcaagga	gaaagctccg	gctactactg	tgccagcagc	420
cggcgtaata	cgtggggac	gaggctgttgc	cggttacttac	gggtgttaaag	ggagcgtagg	480
cggggatgtt	atgcagatgt	gaaaactatgt	ggctcaaccc	ataaccctgc	tttggaaactg	540
gttttcttgc	gtgttgcgt	ggcaggccga	atttcgatgt	tagcggtgaa	atgcgtatgt	600
attcggagga	acaccagggt	cgaaggccgc	ctgctgggt	tttactgtac	ctgaggctcg	660
aaagcatggg	gagcaacacag	gattagatac	cctggatgtc	catggcgtaa	acgatgatta	720
ctagggtgtt	gggtggctgac	ccatcccg	ccggaggtaa	cacaataatgt	aatccac	780
ggggatgtac	ccgcacagggtt	gaaactcaa	ggaatttgc	ggggcccgca	caagcgatgg	840
agtatgtgtt	ttaattcga	gcaacgcgc	gaaacccat	aggcttgc	atccgactaa	900
cgaagtagag	atacattagg	tgcccttcgg	ggaaggtcg	gacagggtgt	gcatgggtgt	960
cgtcagtcg	tgtcgatgt	tggttgcgtt	agtcccgca	cgagcgcaac	ccttgcatt	1020
agttgtacg	caagagcact	ctaatgagac	tgccgttgac	aaaacggagg	aagggtgggaa	1080
cgacgtcaaa	tcatcatgc	ccttgc	tgggtacac	acgtactaca	atggccgtt	1140
acagaggggaa	gcaataactgt	gaagttggac	aaacccctaa	aaacggccc	agttcagatt	1200

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gcaggctgca acccgctgc atgaagtcgg aattgctagt aatcgccgt cagcatgccg 1260
cggtaatac gttccgggc cttgtacaca ccgcccgtca caccatggga gccggtataa 1320
ccccaaatcg gtatctaac c 1341

SEQ ID NO: 148      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, 27Forward-mod
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 148
agrgrttttag ymtggctcag 20

SEQ ID NO: 149      moltype = DNA length = 19
FEATURE
misc_feature
1..19
note = Synthetic oligonucleotide sequence, 1492Reverse
source
1..19
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 149
ggytaccttg ttacgactt 19

SEQ ID NO: 150      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f01_42H6_Fw1
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 150
agtttcgcg gtatggatg 20

SEQ ID NO: 151      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f01_42H6_Rv1
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 151
gccgtatctc agtcccaatg 20

SEQ ID NO: 152      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f02_42I8_Fw1
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 152
caaactaaag atggcgacccg 20

SEQ ID NO: 153      moltype = DNA length = 21
FEATURE
misc_feature
1..21
note = Synthetic oligonucleotide sequence, f02_42I8_Rv3
source
1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 153
gcgggtttaa tatactatcg g 21

SEQ ID NO: 154      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f05_43D4_Fw4
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 154
cccgatggta taatcagacc 20

SEQ ID NO: 155      moltype = DNA length = 20
FEATURE
Location/Qualifiers

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misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f05_43D4_Rv2	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 155		
acctcaccaa ctgcctaata	20	
SEQ ID NO: 156	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f06_42F4_Fw1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 156		
taggcggacg cttaaatcg	20	
SEQ ID NO: 157	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f06_42F4_Rv1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 157		
ctgcctctac tgtactcaag	20	
SEQ ID NO: 158	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f07_42J6_Fw1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 158		
ttgc当地 actg gagatggcga	20	
SEQ ID NO: 159	moltype = DNA length = 21	
FEATURE	Location/Qualifiers	
misc_feature	1..21	
source	note = Synthetic oligonucleotide sequence, f07_42J6_Rv1	
	1..21	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 159		
ctcatgc当地 gaaaaataac c	21	
SEQ ID NO: 160	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f08_42B5_Fw1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 160		
atccaaacctg ccctttactc	20	
SEQ ID NO: 161	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f08_42B5_Rv1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 161		
cccatc当地 accggaatcc	20	
SEQ ID NO: 162	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f09_43F1_Fw1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 162		

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gaaaatcgga ctaataccgc          20
SEQ ID NO: 163      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f09_43F1_Rv1
source              1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 163
cctcaccaac tatctaattgg          20
SEQ ID NO: 164      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f10_43J3_Fw1
source              1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 164
ttgaaggcctt ggtgactgag          20
SEQ ID NO: 165      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f10_43J3_Rv1
source              1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 165
tttagcagccg tttccaactg          20
SEQ ID NO: 166      moltype = DNA length = 21
FEATURE
misc_feature        Location/Qualifiers
1..21
note = Synthetic oligonucleotide sequence, f12_42H4_Fw1
source              1..21
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 166
acacgtgtac gcatgtatcg          21
SEQ ID NO: 167      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f12_42H4_Rv1
source              1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 167
ccaaactagct aatcagacgc          20
SEQ ID NO: 168      moltype = DNA length = 19
FEATURE
misc_feature        Location/Qualifiers
1..19
note = Synthetic oligonucleotide sequence, f13_42H8_Fw1
source              1..19
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 168
acagcttcgc atggaggcag          19
SEQ ID NO: 169      moltype = DNA length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f13_42H8_Rv1
source              1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 169
ctgtatcgctcg ctttggttaag          20
SEQ ID NO: 170      moltype = DNA length = 21
FEATURE
misc_feature        Location/Qualifiers
1..21
note = Synthetic oligonucleotide sequence, f14_42L4_Fw1

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source          1..21
               mol_type = other DNA
               organism = synthetic construct
SEQUENCE: 170
acagtgtgc atggcacagt g                                21

SEQ ID NO: 171      moltype = DNA  length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f14_42L4_Rv1
1..20
source          mol_type = other DNA
               organism = synthetic construct
SEQUENCE: 171
tcgccttggc agggcgttac                                20

SEQ ID NO: 172      moltype = DNA  length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f16_43M1_Fw2
1..20
source          mol_type = other DNA
               organism = synthetic construct
SEQUENCE: 172
ctgaagattt ggtgatttag                                20

SEQ ID NO: 173      moltype = DNA  length = 22
FEATURE
misc_feature        Location/Qualifiers
1..22
note = Synthetic oligonucleotide sequence, f16_43M1_Rv2
1..22
source          mol_type = other DNA
               organism = synthetic construct
SEQUENCE: 173
accatgcggt gctgtggct ta                                22

SEQ ID NO: 174      moltype = DNA  length = 22
FEATURE
misc_feature        Location/Qualifiers
1..22
note = Synthetic oligonucleotide sequence, f17_42I7_Fw3
1..22
source          mol_type = other DNA
               organism = synthetic construct
SEQUENCE: 174
atgaaagttt cggtgaaat ag                                22

SEQ ID NO: 175      moltype = DNA  length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f17_42I7_Rv3
1..20
source          mol_type = other DNA
               organism = synthetic construct
SEQUENCE: 175
cacactgaat catgcagttcc                                20

SEQ ID NO: 176      moltype = DNA  length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f18_42I2_Fw5
1..20
source          mol_type = other DNA
               organism = synthetic construct
SEQUENCE: 176
gcgaagcaag tctgaagtga                                20

SEQ ID NO: 177      moltype = DNA  length = 20
FEATURE
misc_feature        Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f18_42I2_Rv5
1..20
source          mol_type = other DNA
               organism = synthetic construct
SEQUENCE: 177
ctccgacact ctagcaaaac                                20

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SEQ ID NO: 178      moltype = DNA length = 21
FEATURE
misc_feature
1..21
note = Synthetic oligonucleotide sequence, f19_43G2_Fw2
source
1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 178
cggttgaagt cgttataatc c                                21

SEQ ID NO: 179      moltype = DNA length = 21
FEATURE
misc_feature
1..21
note = Synthetic oligonucleotide sequence, f19_43G2_Rv2
source
1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 179
ccatgcagtc ccgtgcgcctt a                                21

SEQ ID NO: 180      moltype = DNA length = 21
FEATURE
misc_feature
1..21
note = Synthetic oligonucleotide sequence, f20_43G1_Fw2
source
1..21
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 180
cttgcttcca aagagactta g                                21

SEQ ID NO: 181      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f20_43G1_Rv2
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 181
gcagtttatcc cgacacatcg                                20

SEQ ID NO: 182      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f21_42A8_Fw2
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 182
aagtggatct ctccggattg                                20

SEQ ID NO: 183      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f21_42A8_Rv6
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 183
ttatgcggta ttagcagcca                                20

SEQ ID NO: 184      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f22_43C3_Fw2
source
1..20
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 184
gattctgaga tgactgagtg                                20

SEQ ID NO: 185      moltype = DNA length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, f22_43C3_Rv2
source
1..20
mol_type = other DNA

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SEQUENCE: 185          organism = synthetic construct
gcagtcattt ctaactgttg                                20

SEQ ID NO: 186        moltype = DNA  length = 20
FEATURE
misc_feature
source
note = Synthetic oligonucleotide sequence, f24_42I4_Fw1
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 186          organism = synthetic construct
tcggtataac ttagtgtggcgg                                20

SEQ ID NO: 187        moltype = DNA  length = 20
FEATURE
misc_feature
source
note = Synthetic oligonucleotide sequence, f24_42I4_Rv1
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 187          organism = synthetic construct
acaaccatgc ggttccgtgc                                20

SEQ ID NO: 188        moltype = DNA  length = 20
FEATURE
misc_feature
source
note = Synthetic oligonucleotide sequence, f25_42J1_Fw2
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 188          organism = synthetic construct
taccggattt cttcgggatg                                20

SEQ ID NO: 189        moltype = DNA  length = 20
FEATURE
misc_feature
source
note = Synthetic oligonucleotide sequence, f25_42J1_Rv2
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 189          organism = synthetic construct
gatcatgcaa tcctgtggtc                                20

SEQ ID NO: 190        moltype = DNA  length = 20
FEATURE
misc_feature
source
note = Synthetic oligonucleotide sequence, f26_42K2_Fw1
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 190          organism = synthetic construct
tttacgcgtc tgagatggcc                                20

SEQ ID NO: 191        moltype = DNA  length = 20
FEATURE
misc_feature
source
note = Synthetic oligonucleotide sequence, f26_42K2_Rv1
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 191          organism = synthetic construct
tcaaacctctc agtccggcta                                20

SEQ ID NO: 192        moltype = DNA  length = 20
FEATURE
misc_feature
source
note = Synthetic oligonucleotide sequence, f27_42J5_Fw2
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 192          organism = synthetic construct
ggaaatcaact tcatttggagac                                20

SEQ ID NO: 193        moltype = DNA  length = 20
FEATURE

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misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f27_42J5_Rv2	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 193		
gactgttatac cccctgtata		20
SEQ ID NO: 194	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f28_43A3_Fw1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 194		
gtacacacgg ataacatacc		20
SEQ ID NO: 195	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f28_43A3_Rv1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 195		
accaactagc taatcagacg		20
SEQ ID NO: 196	moltype = DNA length = 19	
FEATURE	Location/Qualifiers	
misc_feature	1..19	
source	note = Synthetic oligonucleotide sequence, f29_43J8_Fw2	
	1..19	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 196		
cttcggattg aagcaattg		19
SEQ ID NO: 197	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f29_43J8_Rv2	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 197		
ttagcagccg tttccaactg		20
SEQ ID NO: 198	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f30_43A5_Fw1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 198		
tatccccacgg gatagcacag		20
SEQ ID NO: 199	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f30_43A5_Rv1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 199		
tctcaggccg gctacgcatac		20
SEQ ID NO: 200	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, f31_43J5_Fw1	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 200		

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ttccttaatg actgagtggc	20
SEQ ID NO: 201	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide sequence, f31_43J5_Rv2
	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 201	
cacaccgaat catgcgattc	20
SEQ ID NO: 202	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide sequence, f32_42A7_Fw1
	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 202	
tgaagtcttt gtgactgagc	20
SEQ ID NO: 203	moltype = DNA length = 18
FEATURE	Location/Qualifiers
misc_feature	1..18
source	note = Synthetic oligonucleotide sequence, f32_42A7_Rv2
	1..18
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 203	
atgcggattt agcagtc	18
SEQ ID NO: 204	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide sequence, f33_43N2_Fw1
	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 204	
gtgcctcaaa gcactggtag	20
SEQ ID NO: 205	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide sequence, f33_43N2_Rv1
	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 205	
tctcaggatcg gtcacgcata	20
SEQ ID NO: 206	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide sequence, f34_43K4_Fw1
	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 206	
taagctatca ctgaaggagg	20
SEQ ID NO: 207	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
source	note = Synthetic oligonucleotide sequence, f34_43K4_Rv1
	1..20
	mol_type = other DNA
	organism = synthetic construct
SEQUENCE: 207	
cagaccggct actgatcatc	20
SEQ ID NO: 208	moltype = DNA length = 20
FEATURE	Location/Qualifiers
misc_feature	1..20
	note = Synthetic oligonucleotide sequence, f35_42L8_Fw2

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source          1..20
               mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 208
acttgatcct tcgggtgaag                                20

SEQ ID NO: 209      moltype = DNA  length = 20
FEATURE
misc_feature       Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f35_42L8_Rv2
1..20
source          mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 209
atgttgtccc agtctgttaag                                20

SEQ ID NO: 210      moltype = DNA  length = 20
FEATURE
misc_feature       Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f37_42G1_Fw3
1..20
source          mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 210
gctgcttgc tgacgagttgg                                20

SEQ ID NO: 211      moltype = DNA  length = 20
FEATURE
misc_feature       Location/Qualifiers
1..20
note = Synthetic oligonucleotide sequence, f37_42G1_Rv4
1..20
source          mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 211
tttgttgc gacgttatgc                                20

SEQ ID NO: 212      moltype = DNA  length = 19
FEATURE
misc_feature       Location/Qualifiers
1..19
note = Synthetic oligonucleotide sequence, KPC-F684
1..19
source          mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 212
ggcagtcgga gacaaaacc                                19

SEQ ID NO: 213      moltype = DNA  length = 18
FEATURE
misc_feature       Location/Qualifiers
1..18
note = Synthetic oligonucleotide sequence, KPC-R860
1..18
source          mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 213
ccctcgagcg cgagtctca                                18

SEQ ID NO: 214      moltype = DNA  length = 21
FEATURE
misc_feature       Location/Qualifiers
1..21
note = Synthetic oligonucleotide sequence, VanABF_JCM1998?
1..21
source          mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 214
gtaggctgcg atattcaaag c                                21

SEQ ID NO: 215      moltype = DNA  length = 21
FEATURE
misc_feature       Location/Qualifiers
1..21
note = Synthetic oligonucleotide sequence, VanAR_JCM1998?
1..21
source          mol_type = other DNA
               organism = synthetic construct

SEQUENCE: 215
cgattcaatt gcgttagtcca a                                21

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SEQ ID NO: 216      moltype = DNA length = 24
FEATURE           Location/Qualifiers
misc_feature      1..24
note = Synthetic oligonucleotide sequence, ESBL-F_AAC2001
source            1..24
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 216
gaaaagatcca ctatcgccag cagg                                24

SEQ ID NO: 217      moltype = DNA length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide sequence, ESBL-R_AAC2001
source            1..22
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 217
gttgcgcagtgc ctcgcgtcgc gc                                22

SEQ ID NO: 218      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide sequence, LF82-F
source            1..21
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 218
ccattcatgc agcagcttt t                                         21

SEQ ID NO: 219      moltype = DNA length = 21
FEATURE           Location/Qualifiers
misc_feature      1..21
note = Synthetic oligonucleotide sequence, LF82-R
source            1..21
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 219
atcggacaac attagcggtt t                                         21

SEQ ID NO: 220      moltype = DNA length = 25
FEATURE           Location/Qualifiers
misc_feature      1..25
note = Synthetic oligonucleotide sequence, C.jejuni_F
source            1..25
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 220
ctgaatttta taccttaagt gcagg                                25

SEQ ID NO: 221      moltype = DNA length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide sequence, C.jejuni_R
source            1..22
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 221
aggcacgcct aaacctatag ct                                         22

SEQ ID NO: 222      moltype = DNA length = 20
FEATURE           Location/Qualifiers
misc_feature      1..20
note = Synthetic oligonucleotide sequence, Universal_Fw_1387
source            1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 222
cttgtacaca ccgccccgtca                                         20

SEQ ID NO: 223      moltype = DNA length = 22
FEATURE           Location/Qualifiers
misc_feature      1..22
note = Synthetic oligonucleotide sequence, Universal_Rv_1492
source            1..22
mol_type = other DNA

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SEQUENCE: 223          organism = synthetic construct
tacggctacc ttgttacgac tt                                22

SEQ ID NO: 224          moltype = DNA  length = 23
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide sequence, tpi-F
source
1..23
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 224          organism = synthetic construct
aaagaagcta ctaagggtac aaa                                23

SEQ ID NO: 225          moltype = DNA  length = 23
FEATURE
misc_feature
1..23
note = Synthetic oligonucleotide sequence, tpi-R
source
1..23
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 225          organism = synthetic construct
cataatatgg ggtctattcc tac                                23

SEQ ID NO: 226          moltype = DNA  length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, Cupsaliensis_2F
source
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 226          organism = synthetic construct
aaatcagcca tgttgcgtg                                20

SEQ ID NO: 227          moltype = DNA  length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, Cupsaliensis_2R
source
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 227          organism = synthetic construct
tcaactccca tggtgtgacg                                20

SEQ ID NO: 228          moltype = DNA  length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, Cupsaliensis_3F
source
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 228          organism = synthetic construct
caaatcagcc atgttgcgtg                                20

SEQ ID NO: 229          moltype = DNA  length = 20
FEATURE
misc_feature
1..20
note = Synthetic oligonucleotide sequence, Cupsaliensis_3R
source
1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 229          organism = synthetic construct
ccagtcgctg attccactgt                                20

SEQ ID NO: 230          moltype = DNA  length = 16
FEATURE
misc_feature
1..16
note = Synthetic oligonucleotide sequence, khe-Fw
source
1..16
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 230          organism = synthetic construct
tggggatcca ccacga                                16

SEQ ID NO: 231          moltype = DNA  length = 22
FEATURE

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misc_feature	1..22	
source	note = Synthetic oligonucleotide sequence, khe-RV	
	1..22	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 231		
agagatagcc gtttatccac ac		22
SEQ ID NO: 232	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, Eg_2F	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 232		
tgcgtcactg atggatggac		20
SEQ ID NO: 233	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, Eg_2R	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 233		
tgcgcgaatg tccctactgc		20
SEQ ID NO: 234	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, P.mirabilis_NatMicro_F	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 234		
gttatttcgtg atggatgggg		20
SEQ ID NO: 235	moltype = DNA length = 20	
FEATURE	Location/Qualifiers	
misc_feature	1..20	
source	note = Synthetic oligonucleotide sequence, P.mirabilis_NatMicro_R	
	1..20	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 235		
ataaaagggtgg ttacgccaga		20

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1. An antibacterial composition against drug-resistant bacteria or pro-inflammatory bacteria, said composition comprising active ingredients, wherein the active ingredients are:

- (1) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 105 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 105,
- (2) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 69 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 69,
- (3) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 80 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 80,
- (4) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 85 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 85,

(5) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 86 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 86,

(6) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 87 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 87,

(7) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 88 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 88,

(8) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 89 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 89,

(9) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 90 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 90,

- (10) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 91 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 91,
  - (11) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 92 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 92,
  - (12) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 94 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 94,
  - (13) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 96 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 96,
  - (14) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 98 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 98,
  - (15) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 99 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 99,
  - (16) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 100 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 100,
  - (17) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 101 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 101, and
  - (18) a bacterium having a DNA composed of the nucleotide sequence of SEQ ID NO: 103 or a nucleotide sequence having at least 90% identity with the nucleotide sequence of SEQ ID NO: 103; and  
wherein said composition further comprises a medium and/or a buffer.
2. The antibacterial composition according to claim 1, which is a pharmaceutical composition.

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