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Schneider et al.

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(54) **TREATMENT OF CLOSTRIDIUM DIFFICILE INFECTION**

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Related U.S. Application Data

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(51) **Int. Cl.**

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A61K 9/00	(2006.01)
A61K 9/48	(2006.01)
A61K 35/742	(2015.01)
A61K 35/74	(2015.01)

(52) **U.S. Cl.**

CPC ***A61K 35/747*** (2013.01); ***A61K 9/0053*** (2013.01); ***A61K 9/48*** (2013.01); ***A61K 35/74*** (2013.01); ***A61K 35/742*** (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57) **ABSTRACT**

Provided herein are compositions and methods for the treatment or prevention of pathogenic infections.

8 Claims, 41 Drawing Sheets

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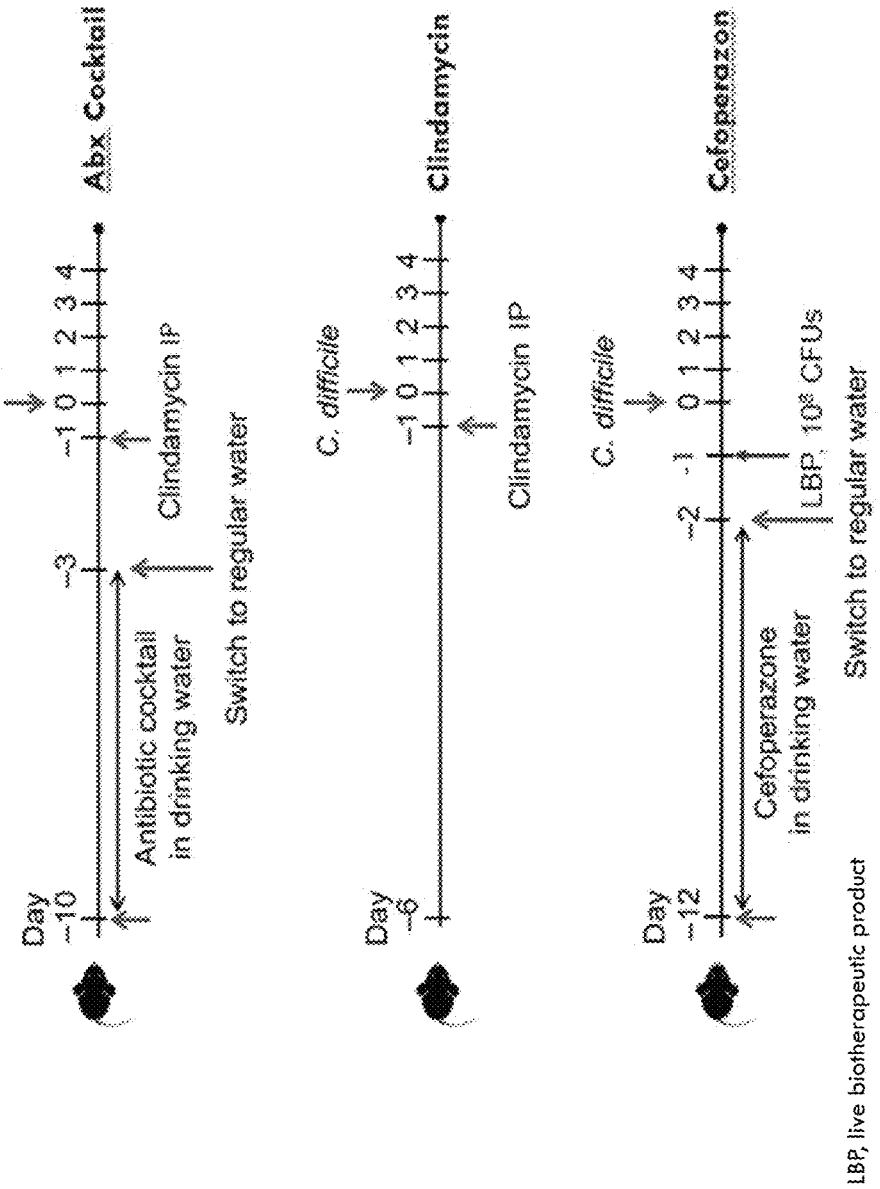
Figure 1

Composition A	Composition B	Composition C	Composition D
SEQ_03 - 5 - Clostridium_hathewayi (XIVa)*	**SEQ_10 - 211 - Flavonifractor_plautii (IV)**	SEQ_12 - VE202-26 - Clostridium_scindens (XIVa)*	SEQ_12 - VE202-26 - Clostridium_scindens (XIVa)*
SEQ_04 - 7 - Blautia_hansenii (XIVa)*	**SEQ_14 - VE202-13 - Anaerotruncus_colihominis (IV)**	SEQ_03 - 5 - Clostridium_hathewayi (XIVa)*	SEQ_03 - 5 - Clostridium_hathewayi (XIVa)*
SEQ_05 - 10 - Blautia_hansenii (XIVa)*	SEQ_15 - VE202-14 - Eubacterium_fissicatena (XIVa)	SEQ_05 - 10 - Blautia_hansenii (XIVa)*	SEQ_05 - 10 - Blautia_hansenii (XIVa)*
SEQ_07 - 59 - Blautia_producta / Blautia_coccoides (XIVa)	SEQ_16 - VE202-16 - Clostridium_symbiosum (XIVa)	SEQ_01 - 71 - Blautia_wexlerae (XIVa)*	SEQ_01 - 71 - Blautia_wexlerae (XIVa)*
SEQ_08 - 79 - Blautia_hansenii (XIVa)*	SEQ_17 - VE202-7 - Clostridium_bolteae (XIVa)	SEQ_07 - 59 - Blautia_producta/Blautia_coccoides (XIVa)*	**SEQ_14 - VE202-13 - Anaerotruncus_colihominis (IV)**
SEQ_09 - VE202-21 - Eubacterium_contortum / Eubacterium_fissicatena (XIVa)*	SEQ_20 – 170 – Dorea longicatena (XIVa)	SEQ_18 - 148 - Dorea_longicatena (XIVa)	SEQ_18 - 148 - Dorea_longicatena (XIVa)
SEQ_11 - VE202-9 - Anaerostipes_caccae (XIVa)*	SEQ_19 - 16 - Blautia_producta (XIVa)	**SEQ_21 - 189 - Clostridium_innocuum (XVII)**	**SEQ_21 - 189 - Clostridium_innocuum (XVII)**
SEQ_12 - VE202-26 - Clostridium_scindens (XIVa)*	**SEQ_21 - 189 - Clostridium_innocuum (XVII)**	**SEQ_10 - 211 - Flavonifractor_plautii (IV) /**	**SEQ_10 - 211 - Flavonifractor_plautii (IV) /**
SEQ_13 - 136 - Marvinbryantia_formatexigens (XIVa)*		**SEQ_14 - VE202-13 - Anaerotruncus_colihominis (IV)**	**SEQ_02 - 102 - Turicibacter_sanguinis (non-Clostridium)**
SEQ_23 - VE202-29 - Eisenbergiella_tayi (XIVa)*		SEQ_16 - VE202-16 - Clostridium_symbiosum (XIVa)	**SEQ_06 - 40 - Lactobacillus_mucosae (non-Clostridium)**

*= BaiCD+ ***bolding indicates strains other than Clostridium cluster XIVa***

Figure 2

Clostridium difficile Infection Mouse Models



LBP, live biotherapeutic product

Figure 3

Groups	# of animals	Abx	*C. difficile* Spores
(1) Control	5	-	10^1
(2) Control	5	-	10^4
(3) Abx cocktail	5	+	10^1
(4) Abx cocktail	5	+	10^4
(5) Clindamycin	5	+	10^1
(6) Clindamycin	5	+	10^4
(7) Cefoperazone	5	+	10^1
(8) Cefoperazone	5	+	10^4

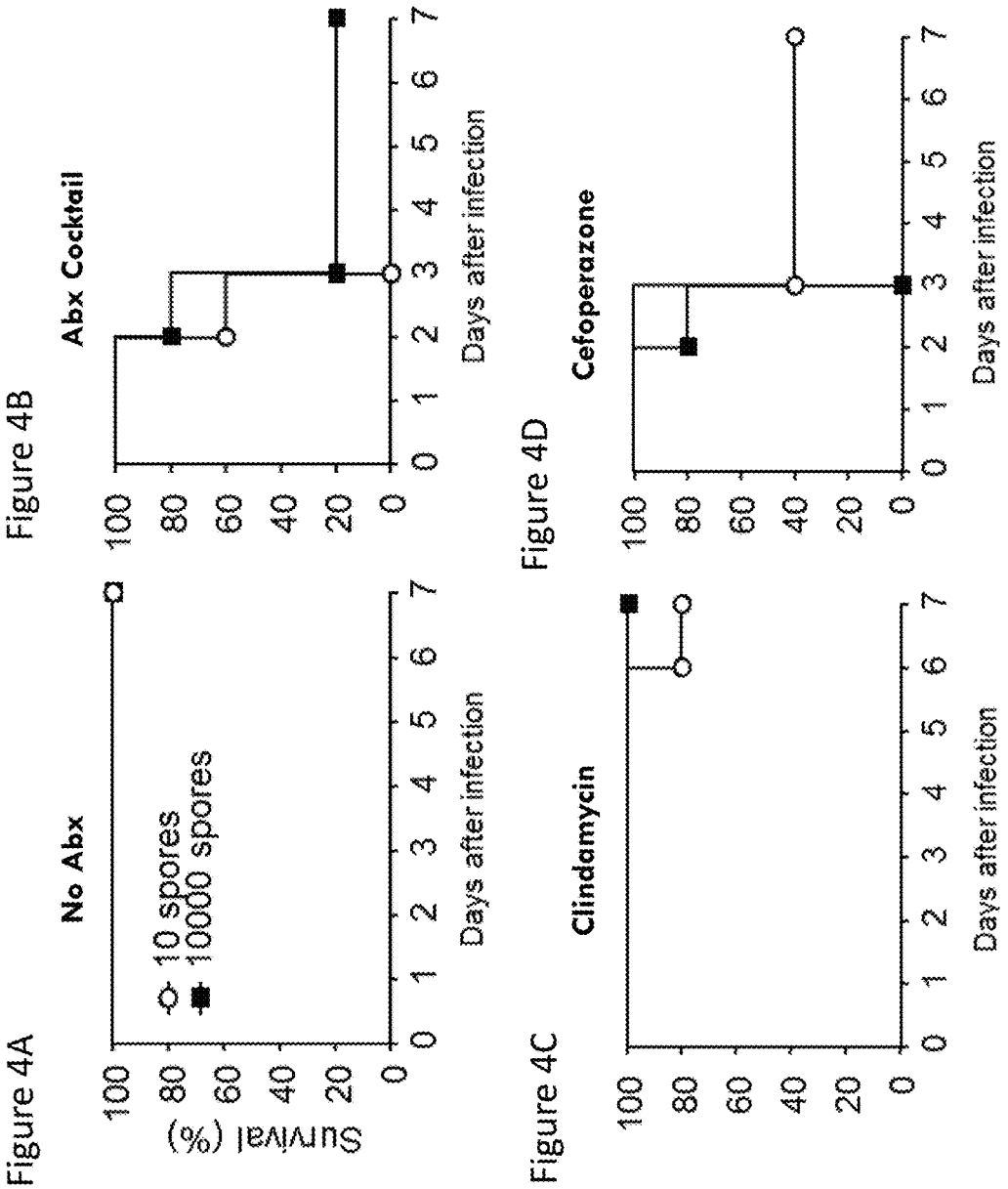


Figure 4A
No Abx
10 spores
10000 spores
Survival (%)
100
80
60
40
20
0
0 1 2 3 4 5 6 7
Days after infection
Figure 4B
Abx Cocktail
Figure 4C
Clindamycin
Figure 4D
Cefoperazone

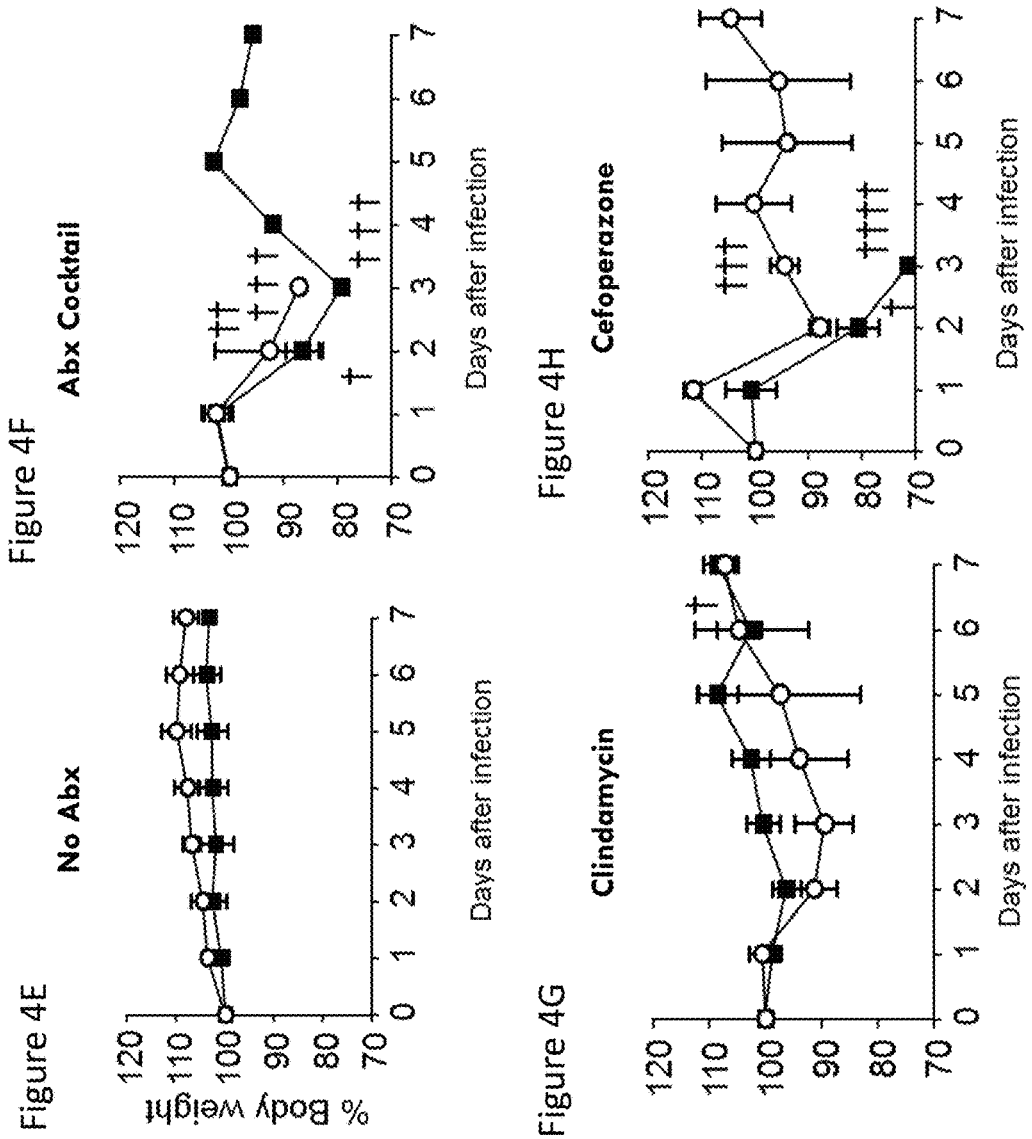


Figure 4E
No Abx
Figure 4F
Abx Cocktail
Figure 4G
Clindamycin
Figure 4H
Cefoperazone
% Body weight
Days after infection
120
110
100
90
80
70
0 1 2 3 4 5 6 7

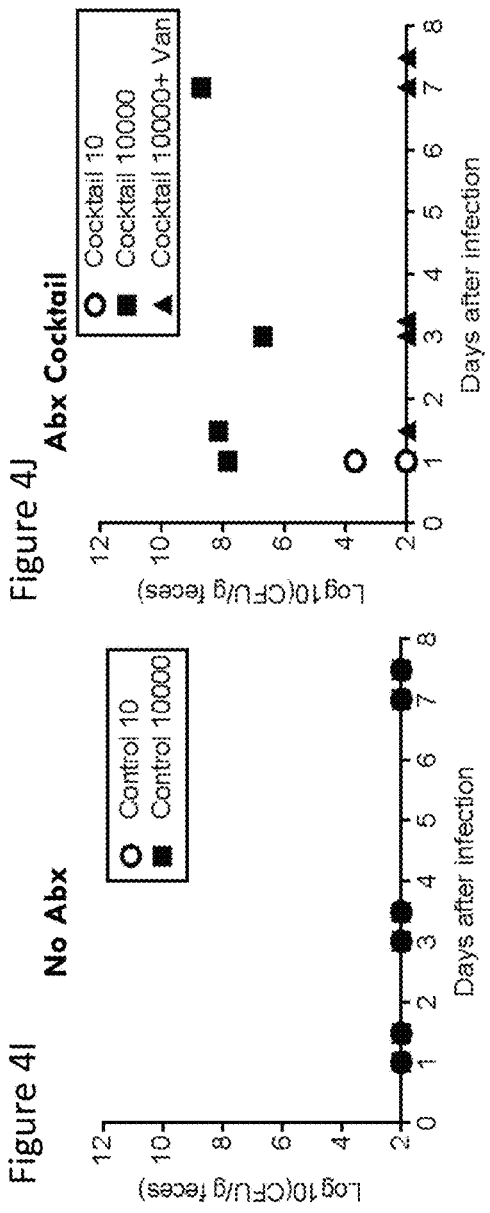


Figure 4I
No Abx
Control 10
Control 10000
Log10(CFU/g feces)
Days after infection
Figure 4J
Abx Cocktail
Cocktail 10
Cocktail 10000
Cocktail 10000+ Van
Log10(CFU/g feces)
Days after infection

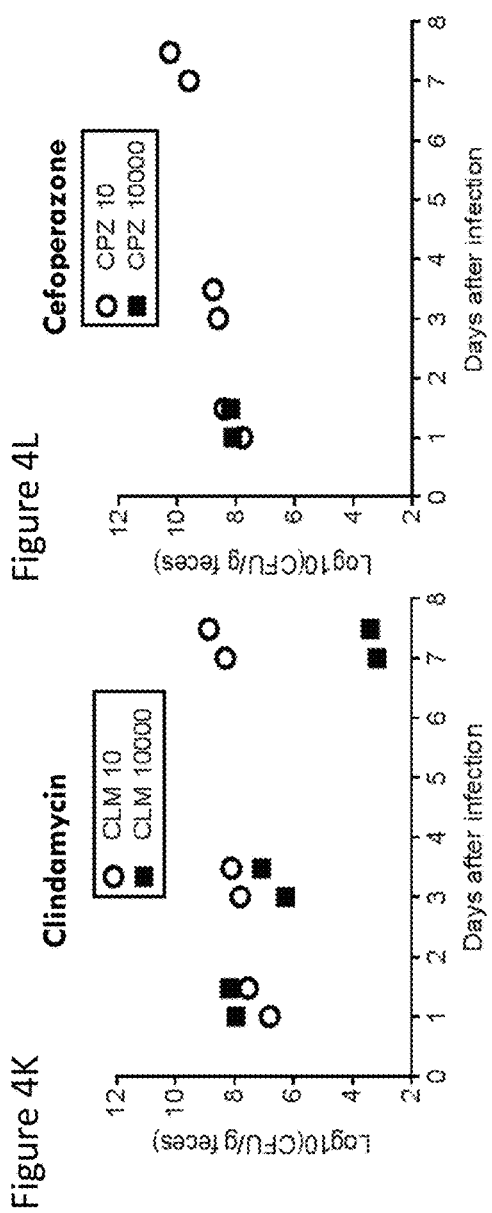


Figure 4L
Cefoperazone
CPZ 10
CPZ 10000
Log10(CFU/g feces)
Figure 4K
Clindamycin
CLM 10
CLM 10000
Log10(CFU/g feces)
Days after infection

Figure 5

Groups	# of animals	Abx	CFUs (Spores)
(1) Control-	5	-	10^4
(2) Control+	5	+	10^4
(3) Van	5	+	10^4
(4) Composition E	5	+	10^4
(5) Composition I	5	+	10^4
(6) Composition A	5	+	10^4
(7) Composition B	5	+	10^4
(8) Composition C	5	+	10^4
(9) Composition D	5	+	10^4

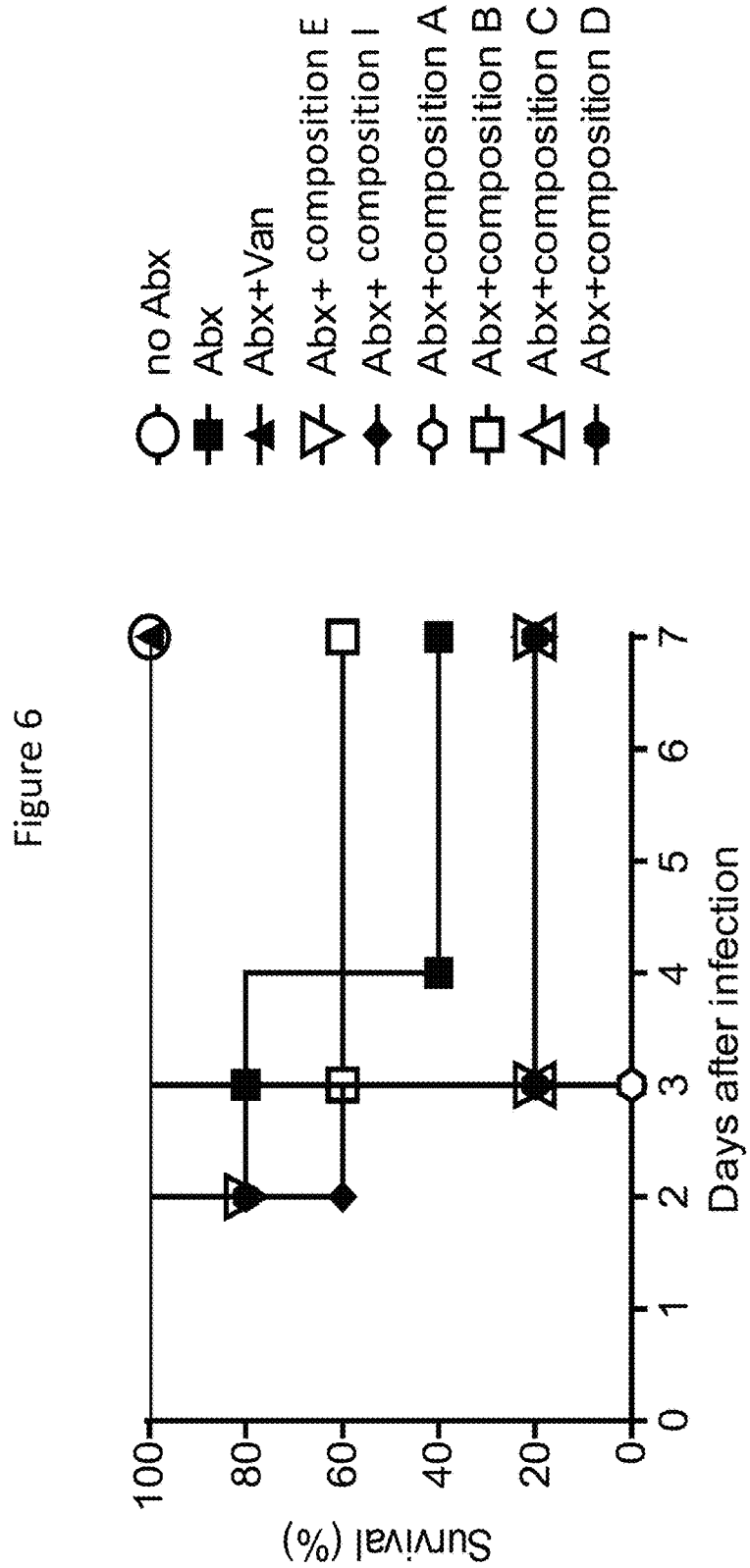

no Abx
Abx
Abx+Van
Abx+ composition E
Abx+ composition I
Abx+composition A
Abx+composition B
Abx+composition C
Abx+composition D
Survival (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
7
Days after infection

Figure 6

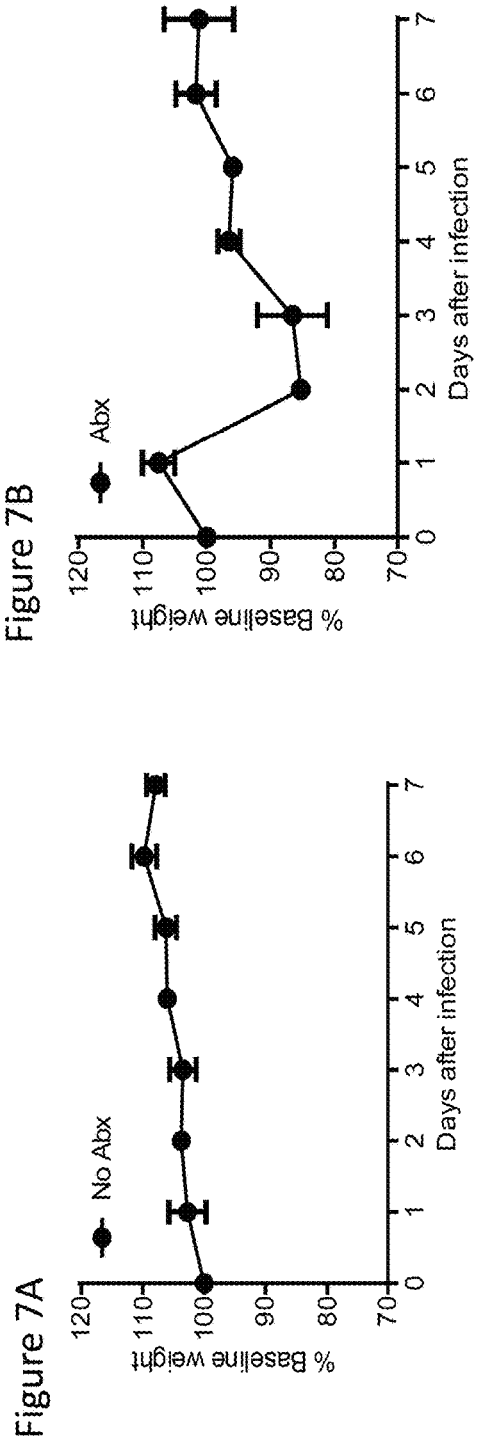


Figure 7A
No Abx
% Baseline weight
120
110
100
90
80
70
0 1 2 3 4 5 6 7
Days after infection

Figure 7B
Abx
% Baseline weight
120
110
100
90
80
70
0 1 2 3 4 5 6 7
Days after infection

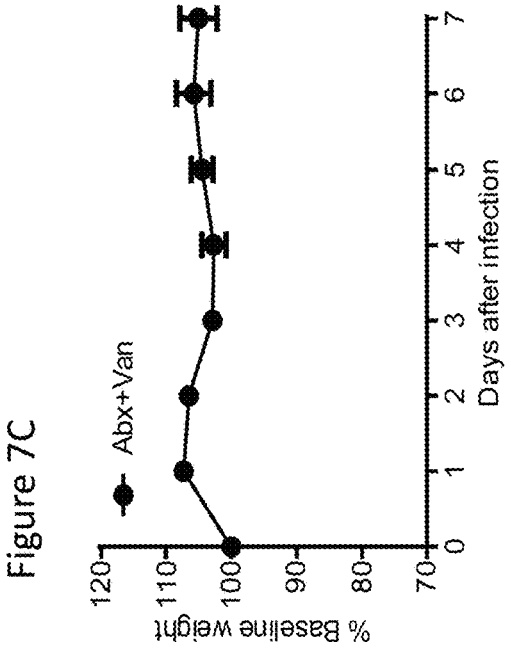


Figure 7C
Abx+Van
% Baseline weight
120
110
100
90
80
70
0 1 2 3 4 5 6 7
Days after infection

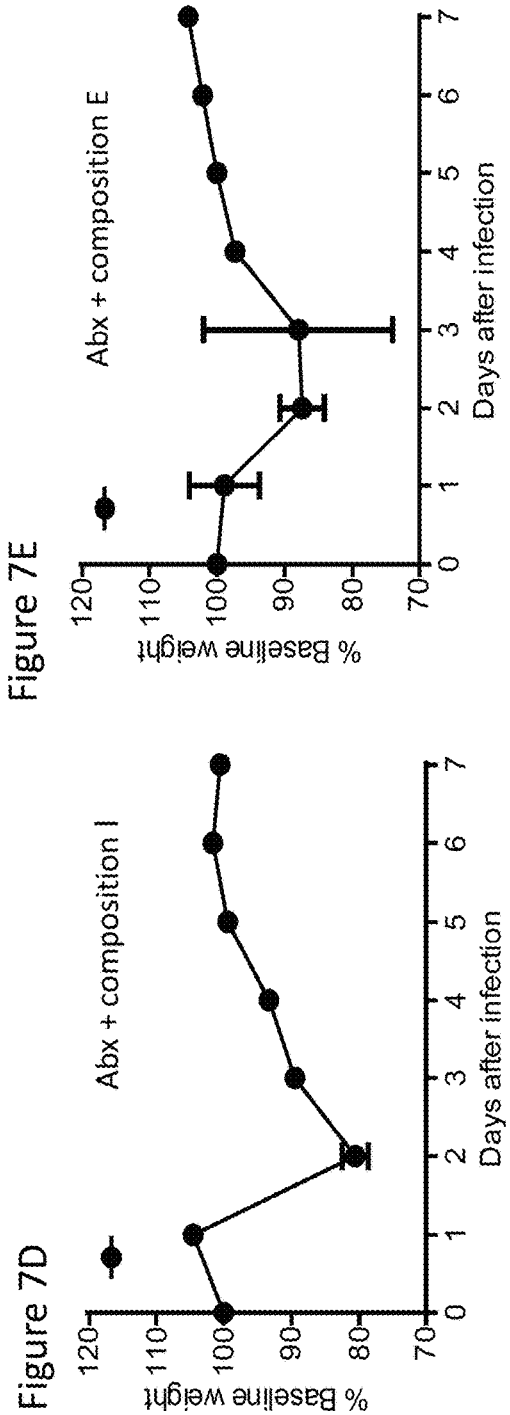


Figure 7D
Abx + composition I
% Baseline weight
120
110
100
90
80
70
0 1 2 3 4 5 6 7
Days after infection

Figure 7E
Abx + composition E
% Baseline weight
120
110
100
90
80
70
0 1 2 3 4 5 6 7
Days after infection

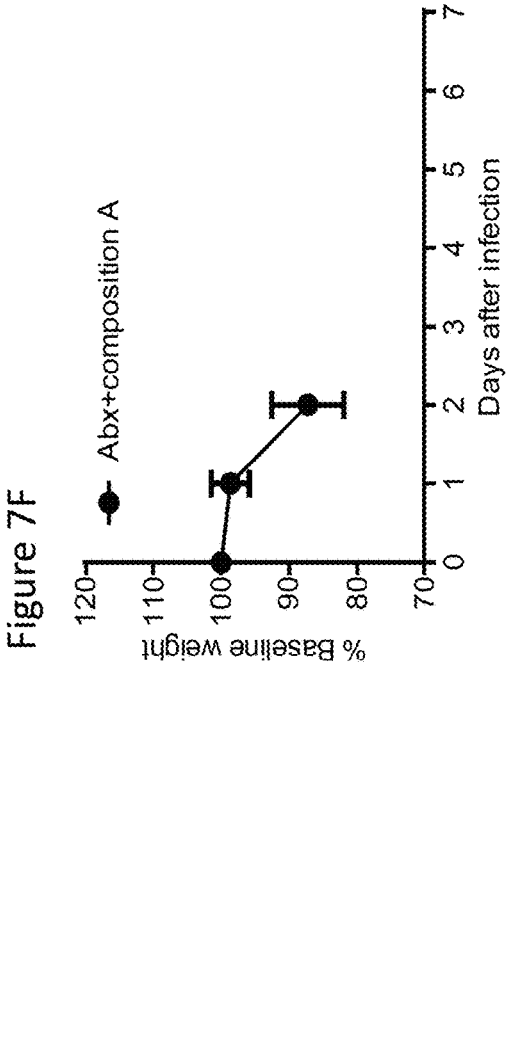


Figure 7F
Abx+composition A
% Baseline weight
120
110
100
90
80
70
0 1 2 3 4 5 6 7
Days after infection

Figure 7G

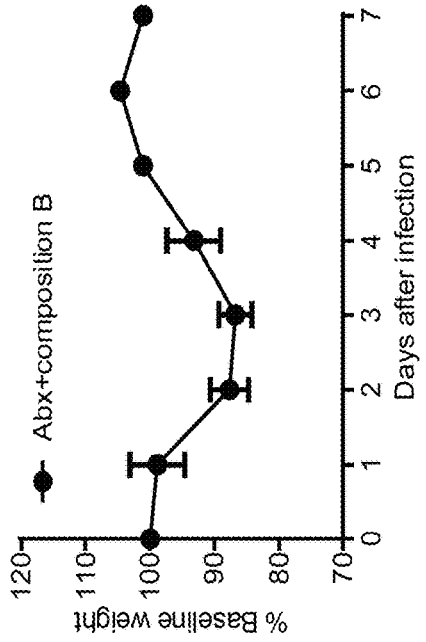


Figure 7H

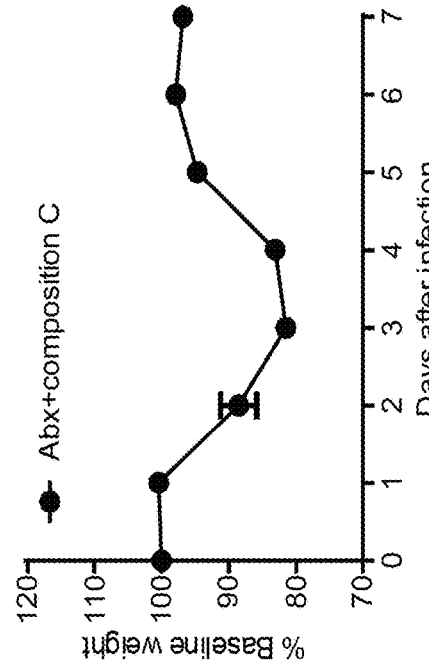
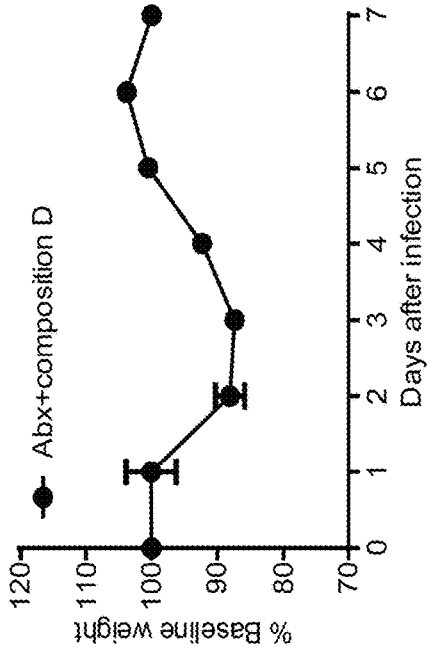


Figure 7I



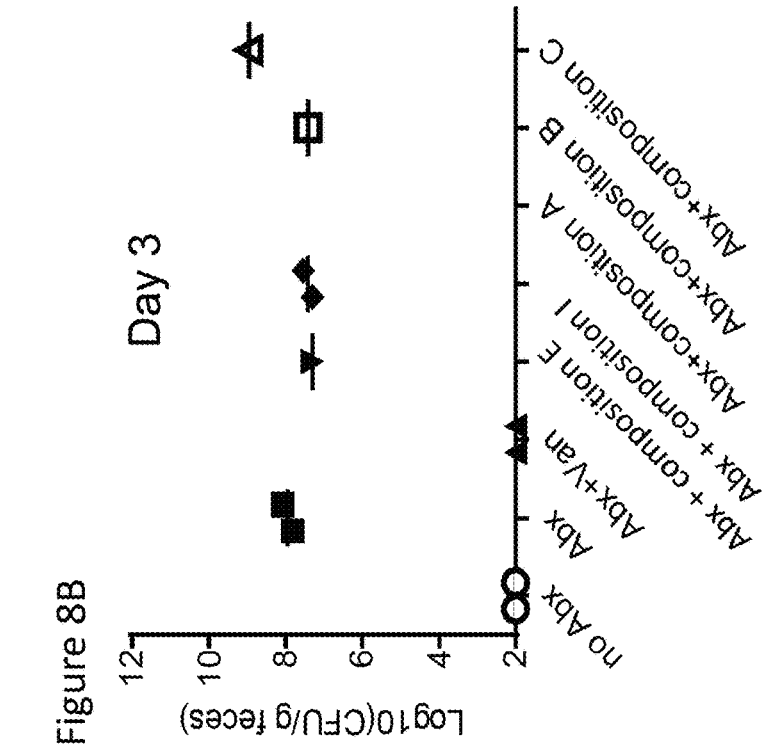


Figure 8B

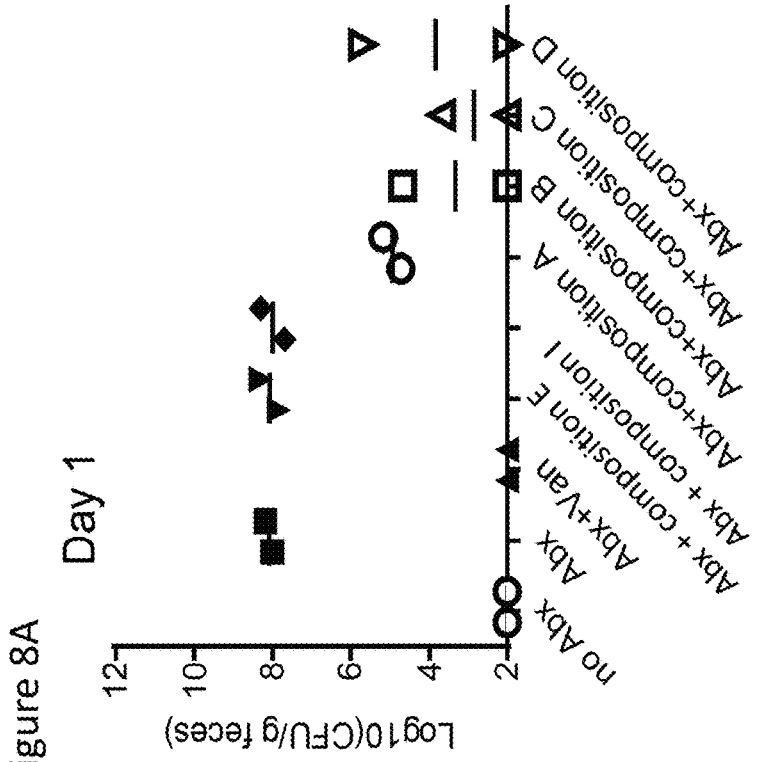


Figure 8A

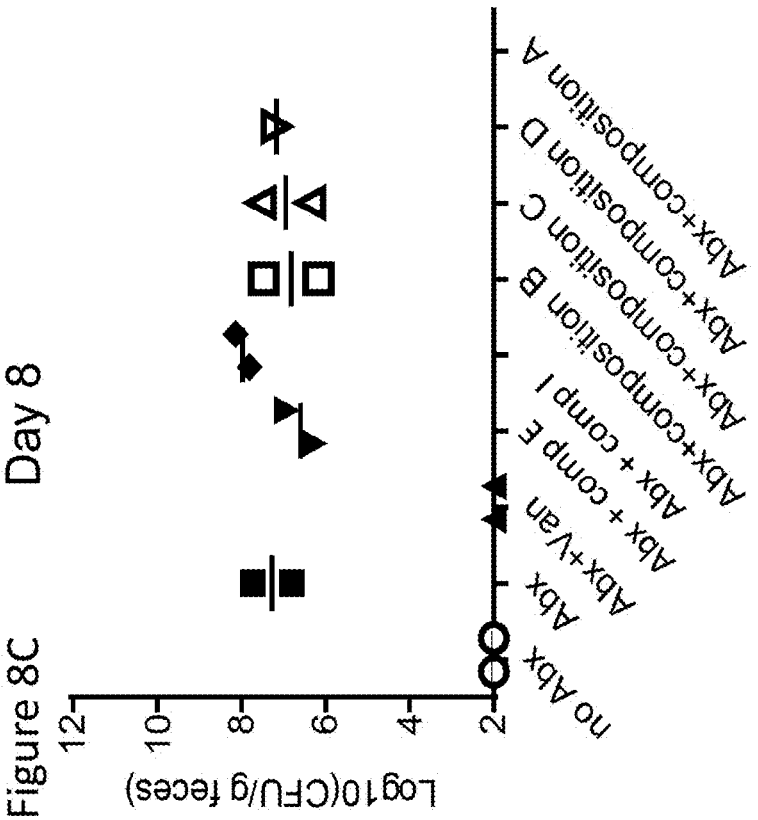
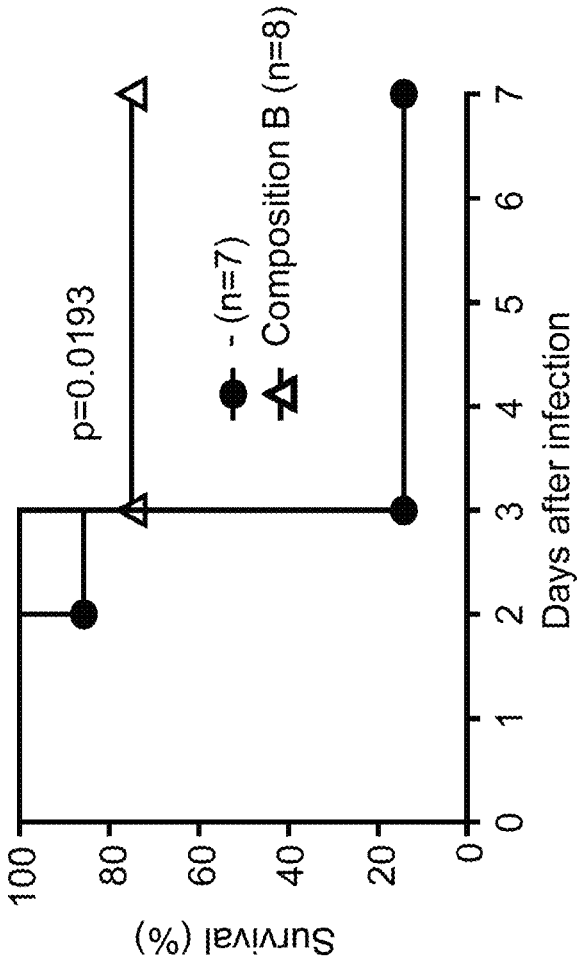

Day 8
Log10(CFU/g feces)
12
10
8
6
4
2
no Abx
Abx
Abx+Van
Abx + comp E
Abx + comp I
Abx+composition B
Abx+composition C
Abx+composition D
Abx+composition A

Figure 8C

Figure 9

Groups	# of animals	Abx	*C. difficile* spore	CFUs LBPs
(1) Control	7	+	10^4	-
(2) Composition B	8	+	10^4	10^8/mouse

Figure 10



(Natural death + >20% weight loss)

Figure 11

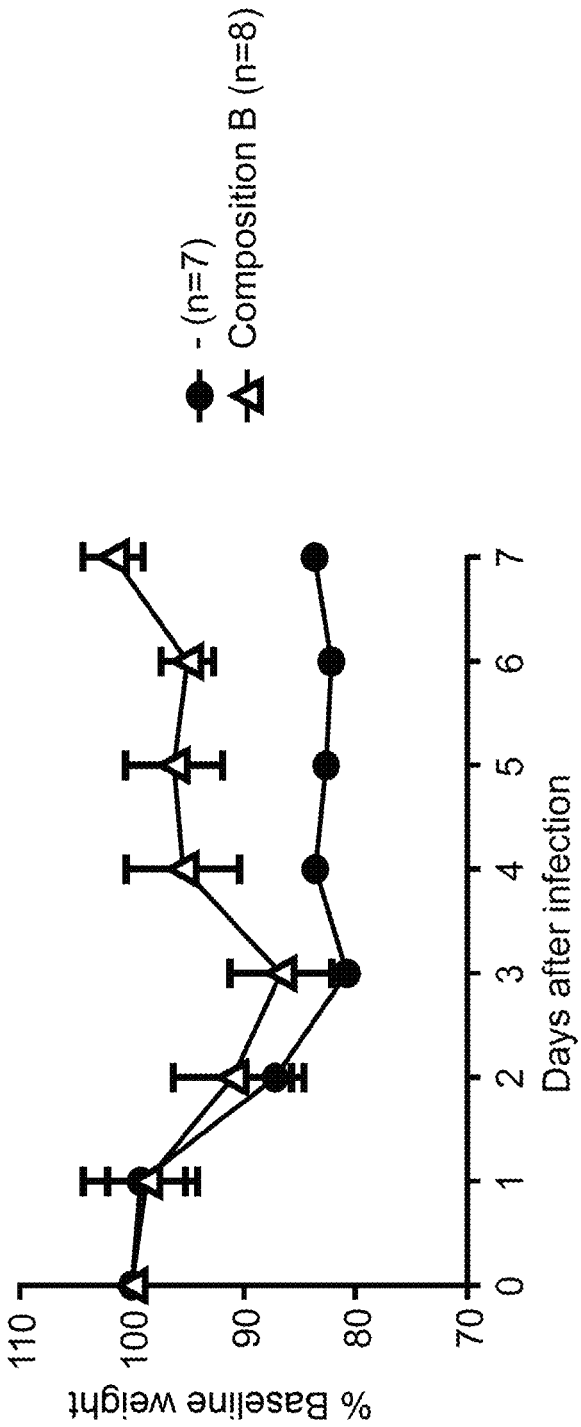

- (n=7)
Composition B (n=8)
% Baseline weight
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

Figure 12

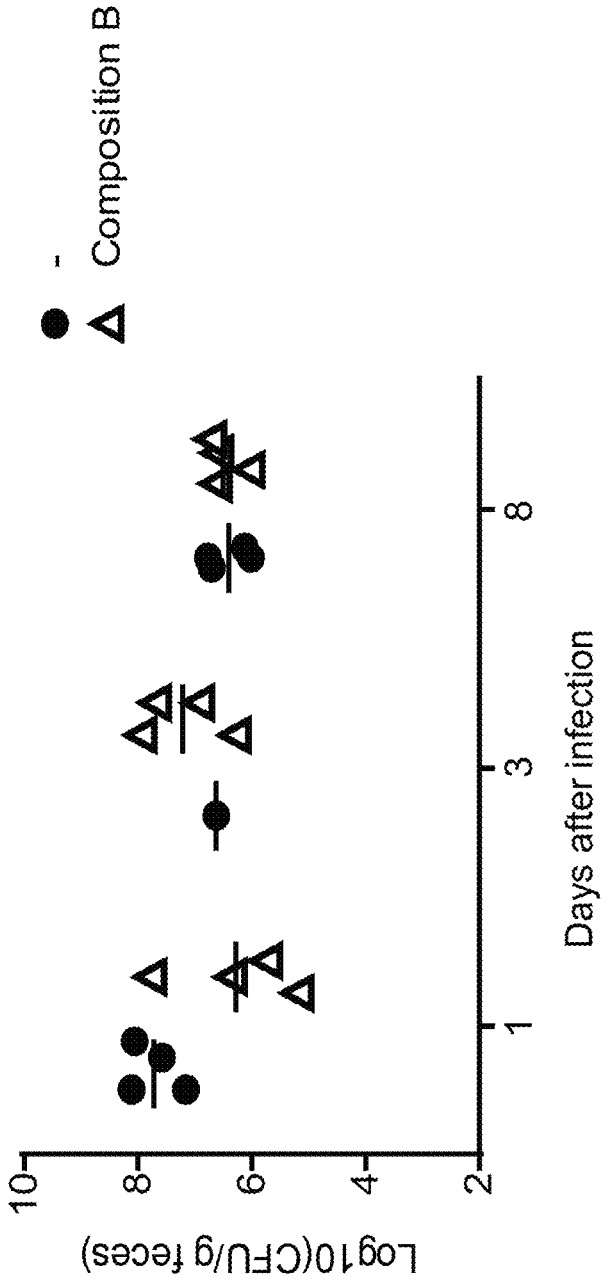

-
Composition B
Log10(CFU/g feces)
10
8
6
4
2
1
3
8
Days after infection

Figure 13

Composition F

SEQ_NO	StrainID	Genus_species	SEQ_NO	StrainID	Genus_species
SEQ_24	YK96	Dorea_longicatena	SEQ_52	YK51	Eubacterium_rectale
SEQ_25	YK101	Ruminococcus_obeum	SEQ_53	YK52	Eubacterium_rectale
SEQ_26	YK110	Megasphaera_elsdenii	SEQ_54	YK54	Anaerostipes_hadrus
SEQ_27	YK149	Acidaminococcus_fermentans / Acidaminococcus_intestini	SEQ_55	YK56	Ruminococcus_faecis
SEQ_28	YK154	Megasphaera_elsdenii	SEQ_56	YK57	Ruminococcus_faecis
SEQ_29	YK36	Ruminococcus_faecis	SEQ_57	YK58	Dorea_longicatena
SEQ_30	YK95	Bacteroides_cellulosilyticus	SEQ_58	YK65	Roseburia_faecis
SEQ_31	YK32	Anaerostipes_hadrus	SEQ_59	YK67	Blautia_luti
SEQ_32	YK64	Ruminococcus_obeum	SEQ_60	YK69	Fusicatenibacter_saccharivorans
SEQ_33	YK73	Flavonifractor_plautii	SEQ_61	YK70	Fusicatenibacter_saccharivorans
SEQ_34	YK87	Eubacterium_rectale	SEQ_62	YK71	Roseburia_faecis
SEQ_35	YK105	Flavonifractor_plautii	SEQ_63	YK74	Megasphaera_elsdenii
SEQ_36	YK153	Megasphaera_elsdenii	SEQ_64	YK88	Eubacterium_rectale
SEQ_37	YK163	Eubacterium_rectale	SEQ_65	YK89	Eubacterium_rectale
SEQ_38	YK191	Ruminococcus_champanellensis / Ruminococcus_albus	SEQ_66	YK97	Roseburia_faecis
SEQ_39	YK99	Ruminococcus_champanellensis	SEQ_67	YK98	Blautia_faecis
SEQ_40	YK55	Ruminococcus_faecis	SEQ_68	YK139	Fusicatenibacter_saccharivorans
SEQ_41	YK75	Bifidobacterium_bifidum	SEQ_69	YK141	Dorea_formicigenerans
SEQ_42	YK90	Anaerostipes_hadrus	SEQ_70	YK142	Ruminococcus_faecis
SEQ_43	YK30	Anaerostipes_hadrus	SEQ_71	YK152	Blautia_hansenii
SEQ_44	YK31	Anaerostipes_hadrus	SEQ_72	YK155	Blautia_hansenii
SEQ_45	YK12	Eubacterium_rectale	SEQ_73	YK157	Eubacterium_rectale
SEQ_46	YK27	Ruminococcus_faecis	SEQ_74	YK160	Roseburia_faecis
SEQ_47	YK28	Blautia_luti	SEQ_75	YK166	Eubacterium_rectale
SEQ_48	YK29	Ruminococcus_faecis	SEQ_76	YK168	Eubacterium_rectale
SEQ_49	YK33	Anaerostipes_hadrus	SEQ_77	YK169	Eubacterium_rectale
SEQ_50	YK34	Anaerostipes_hadrus	SEQ_78	YK171	Eubacterium_rectale
SEQ_51	YK35	Ruminococcus_faecis	SEQ_79	YK192	Roseburia_faecis

Figure 14

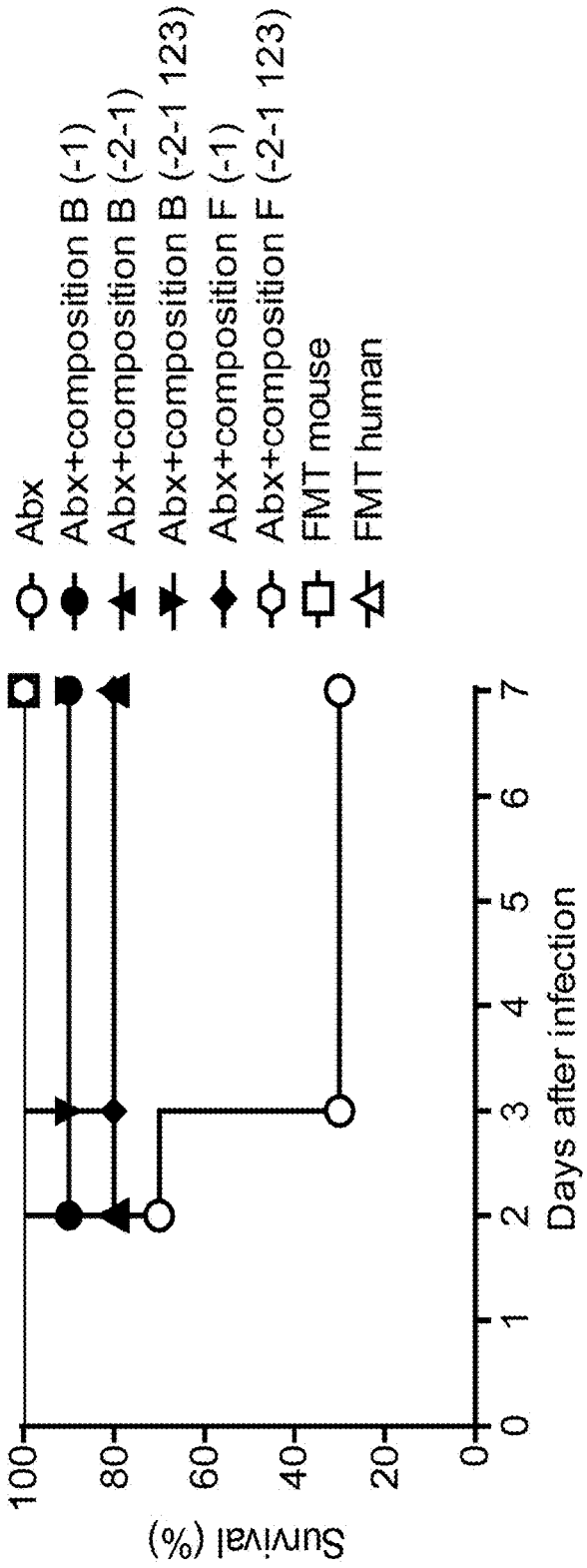
Cluster	Composition F	SCFAs
XIVa	*Eubacterium rectale* 12	A, B, L
	Ruminococcus faecis 8	A, L
	Ruminococcus obeum 2	A, L
	Blautia faecis 1	A, L
	Blautia hansenii 2	A, L
	Blautia luti 2	A, L
	Anaerostipes hadrus 7	B
	Roseburia faecis 5	A, B
	Fusicatenibacter saccharivorans 3	A, L
	Dorea formicigenerans 1	A
	Dorea longicatena 2	A
IV	*Flavonifractor_plautii* 2	A, B
	Ruminococcus champanellensis 2	A
IX	*Acidaminococcus fermentans* 1	A, B, P
	Megasphaera elsdeni 4	P
other	*Bacteroides cellulosilyticus* 1	A, S
	Bifiidobacterium Bifidum	L, A

A, acetate;
B, Butyrate;
L, lactate;
P, propionate;
S, succinate

Figure 15

Groups	# of animals	Abx	*C. difficile* spore	CFUs LBPs
(1) Control	10	+	10^4	-
(2) Composition B dosed at day -1	10	+	10^4	10^8/mouse
(3) Composition B dosed at day -2 and -1	10	+	10^4	10^8/mouse
(4) Composition B dosed at day -2, -1, 1, 2, and 3	10	+	10^4	10^8/mouse
(5) Composition F dosed at day -1	5	+	10^4	OD Normalized
(6) Composition F dosed at day -2, -1, 1, 2, and 3	5	+	10^4	OD Normalized
(7) FMT mouse	5	+	10^4	200ul of 10% fecal samples/mouse
(8) FMT human	5	+	10^4	200ul of 10% fecal samples/mouse

Figure 16


Abx
Abx+composition B (-1)
Abx+composition B (-2-1)
Abx+composition B (-2-1 123)
Abx+composition F (-1)
Abx+composition F (-2-1 123)
FMT mouse
FMT human
Survival (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
7
Days after infection

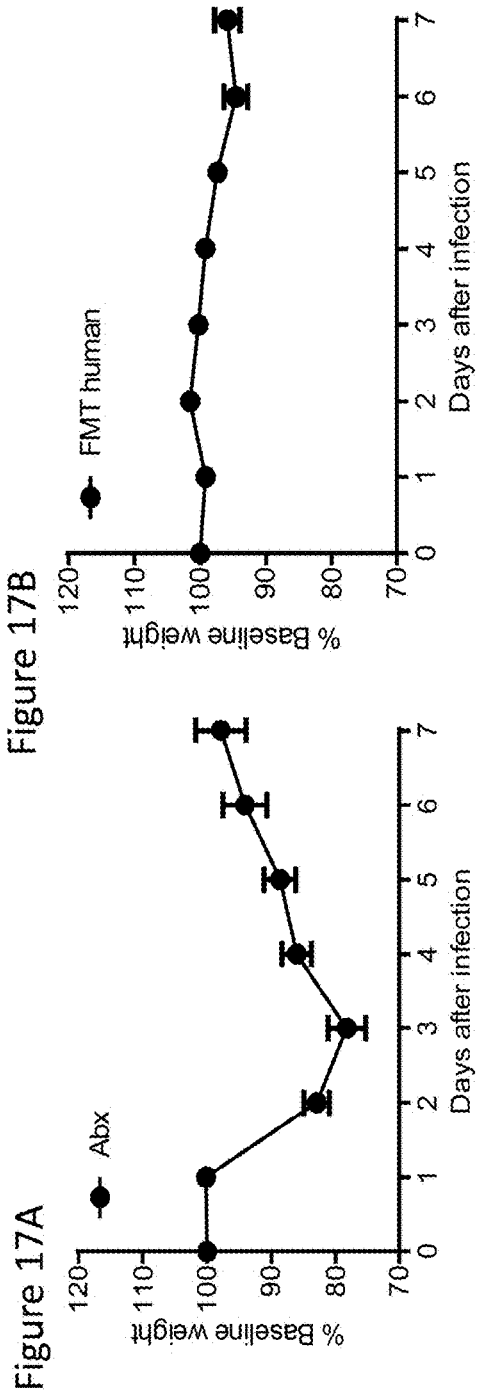


Figure 17A
Abx
% Baseline weight
120
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

Figure 17B
FMT human
% Baseline weight
120
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

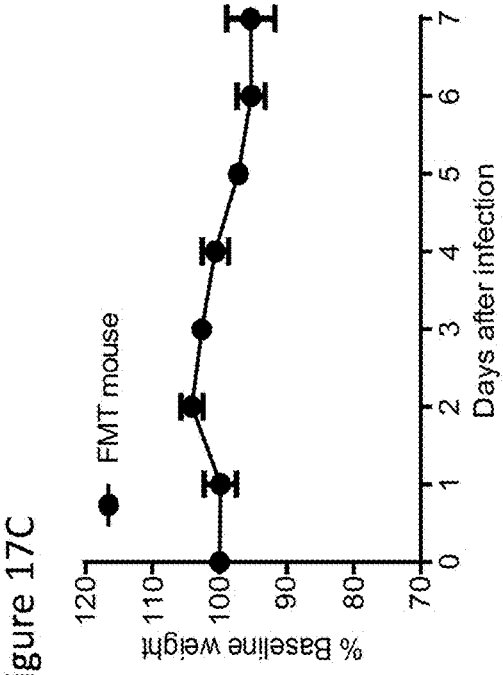


Figure 17C
FMT mouse
% Baseline weight
120
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

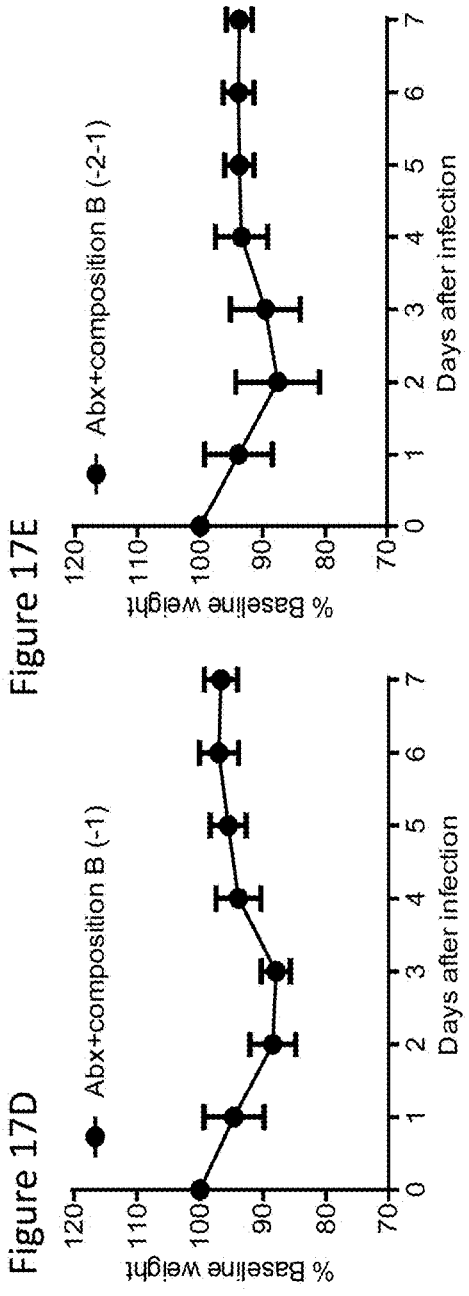


Figure 17D

Figure 17E

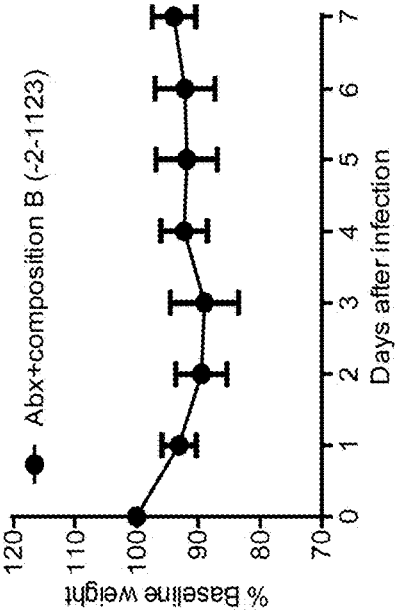


Figure 17F

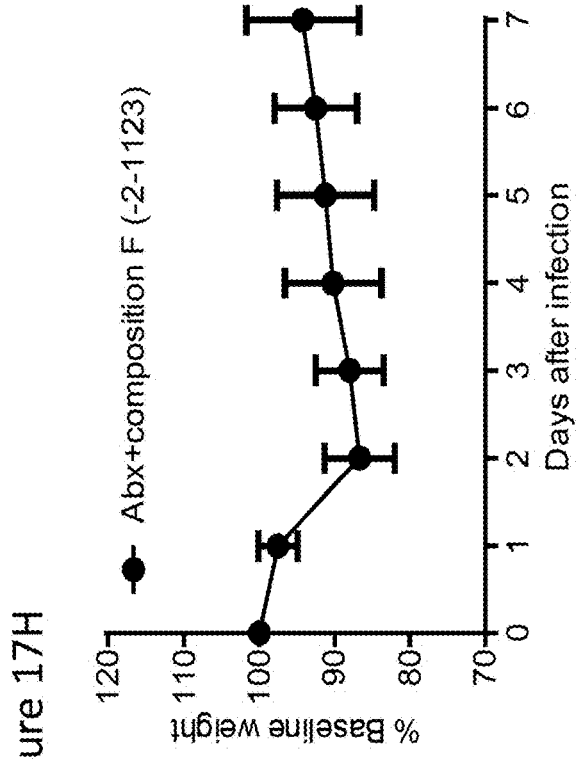


Figure 17H

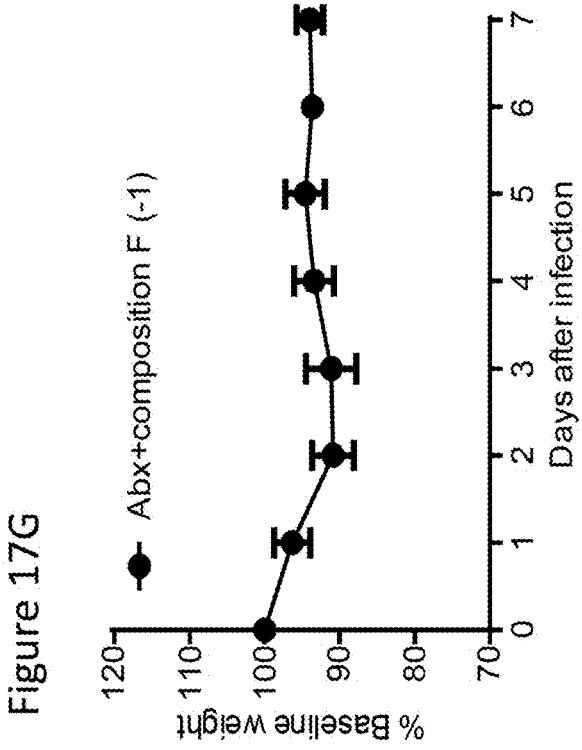


Figure 17G

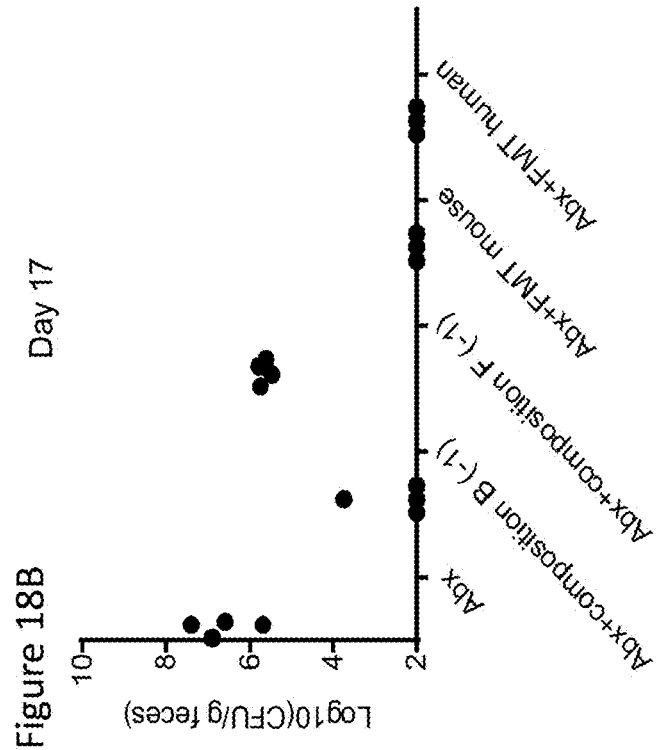


Figure 18B
Day 17
Log10(CFU/g feces)
10
8
6
4
2
Abx
Abx+composition B (-1)
Abx+composition F (-1)
Abx+FMT mouse
Abx+FMT human

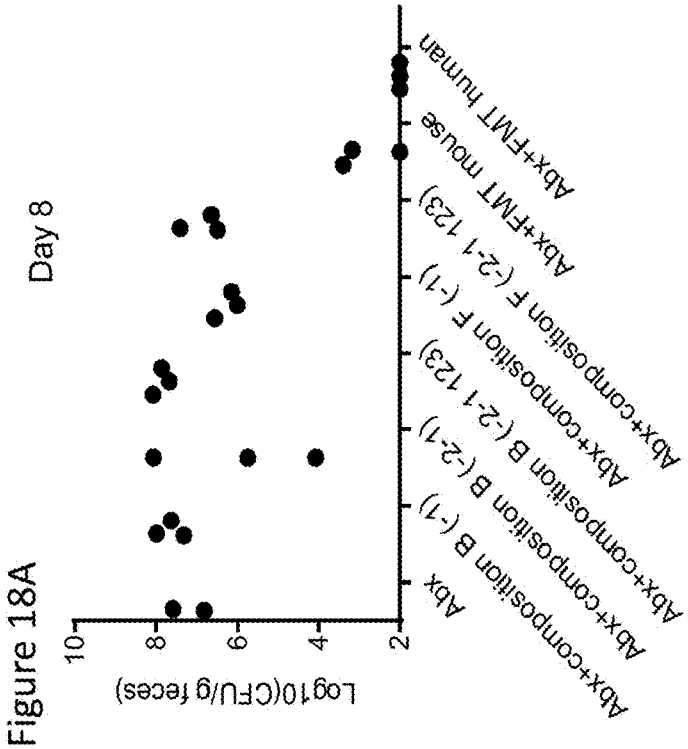


Figure 18A
Day 8
Log10(CFU/g feces)
10
8
6
4
2
Abx
Abx+composition B (-1)
Abx+composition B (-2-1)
Abx+composition B (-2-1 123)
Abx+composition F (-1)
Abx+composition F (-2-1 123)
Abx+FMT mouse
Abx+FMT human

Figure 19

Composition G

SEQ_27	YK149	Acidaminococcus_fermentans/Acidaminococcus_intesti
SEQ_43	YK90	Anaerostipes_hadrus
SEQ_44	YK30	Anaerostipes_hadrus
SEQ_51	YK34	Anaerostipes_hadrus
SEQ_55	YK54	Anaerostipes_hadrus
SEQ_68	YK98	Blautia_faecis
SEQ_72	YK152	Blautia_hansenii
SEQ_70	YK141	Dorea_formicigenerans
SEQ_24	YK96	Dorea_longicatena
SEQ_34	YK87	Eubacterium_rectale
SEQ_37	YK163	Eubacterium_rectale
SEQ_46	YK12	Eubacterium_rectale
SEQ_76	YK166	Eubacterium_rectale
SEQ_77	YK168	Eubacterium_rectale
SEQ_35	YK105	Flavonifractor_plautii
SEQ_62	YK70	Fusicatenibacter_saccharivorans
SEQ_26	YK110	Megasphaera_elsdenii
SEQ_63	YK71	Roseburia_faecis
SEQ_67	YK97	Roseburia_faecis
SEQ_40	YK99	Ruminococcus_champanellensis
SEQ_38	YK191	Ruminococcus_champanellensis/Ruminococcus_albus
SEQ_47	YK27	Ruminococcus_faecis
SEQ_56	YK56	Ruminococcus_faecis
SEQ_25	YK101	Ruminococcus_obeum
SEQ_32	YK64	Ruminococcus_obeum

Figure 20

Groups	N	Abx	CFUs *C. difficile*	CFUs LBPs
(1) Vehicle	7	+	10^4	200ul of PBS
(2) Composition B	8	+	10^4	10^8/mouse
(3) Composition B1	8	+	10^4	10^8/mouse
(4) Composition B2	8	+	10^4	10^8/mouse
(5) Composition F	7	+	10^4	OD Normalized
(6) Composition G	7	+	10^4	OD Normalized
(7) EtOH treated Human fecal samples	5	+	10^4	200ul of 10% fecal samples/mouse
(8) EtOH treated Composition B	5	+	10^4	10^8/mouse
(9) Frozen Composition B	5	+	10^4	10^8/mouse
(10) EtOH treated Composition J	5	+	10^4	colony scrapes

Figure 21

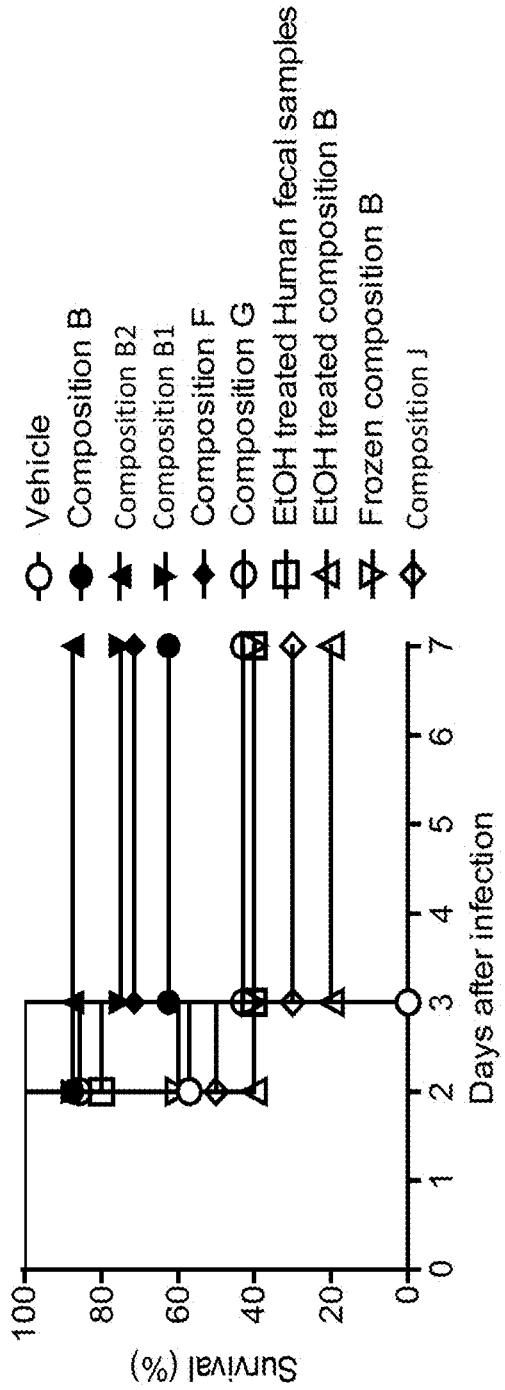

Vehicle
Composition B
Composition B2
Composition B1
Composition F
Composition G
EtOH treated Human fecal samples
EtOH treated composition B
Frozen composition B
Composition J
Survival (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
7
Days after infection

Figure 22A

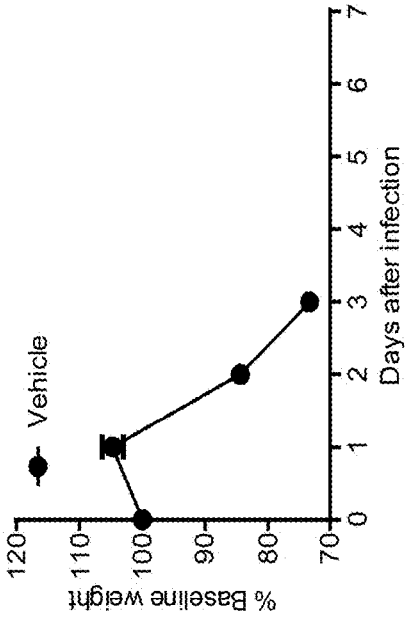


Figure 22B

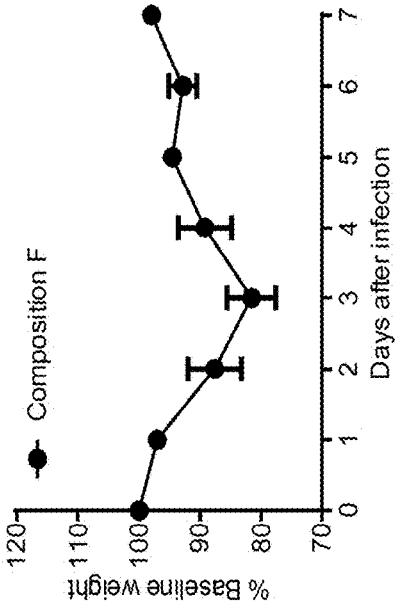
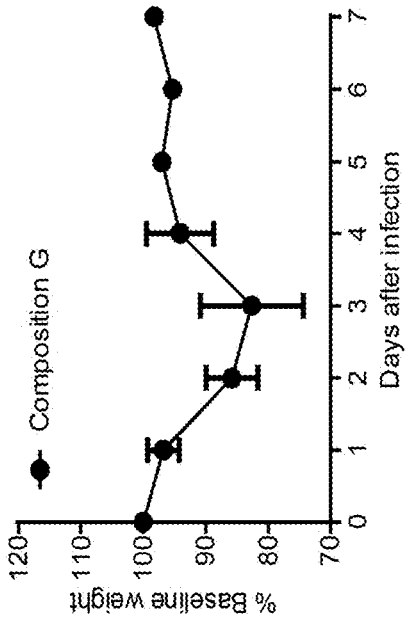


Figure 22C



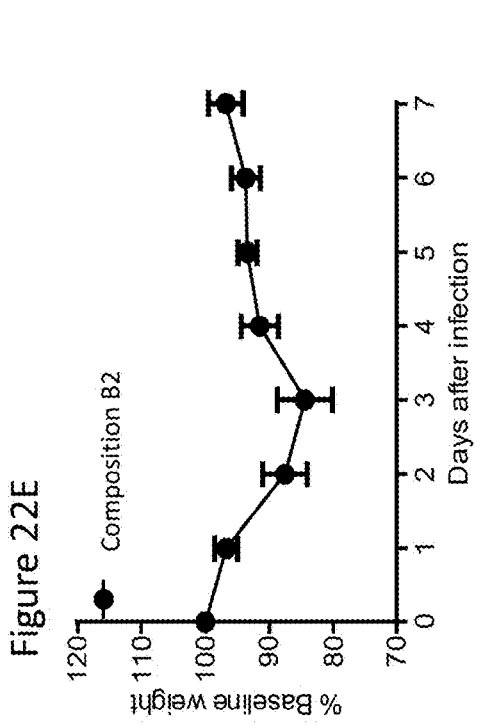


Figure 22E
Composition B2
% Baseline weight
Days after infection
120
110
100
90
80
70
0
1
2
3
4
5
6
7

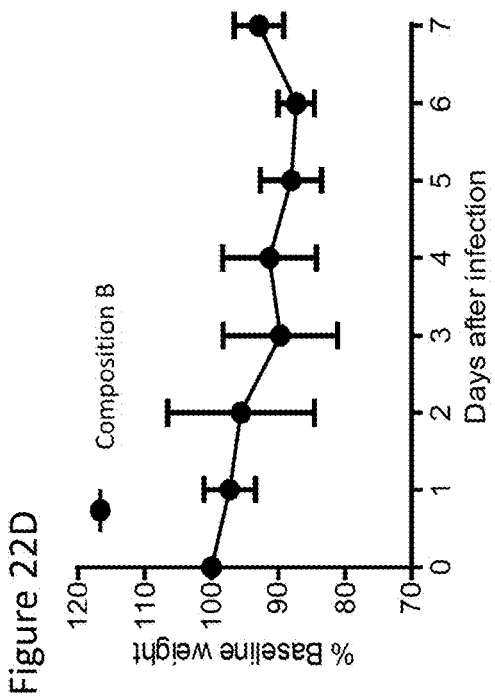


Figure 22D
Composition B
% Baseline weight
Days after infection
120
110
100
90
80
70
0
1
2
3
4
5
6
7

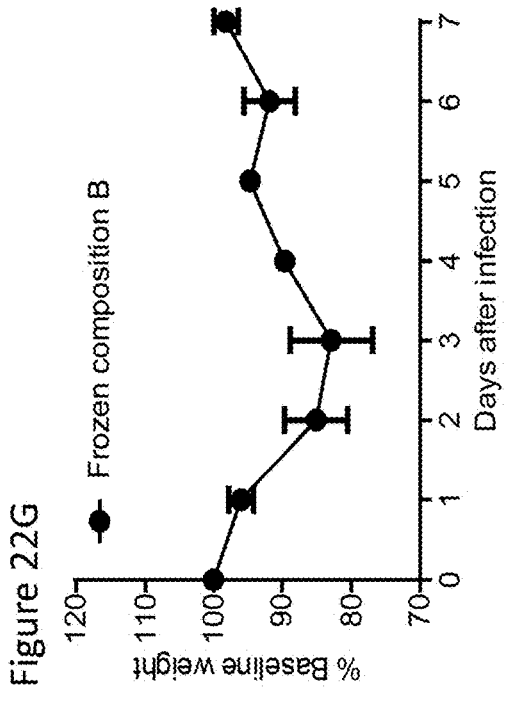


Figure 22G
Frozen composition B
% Baseline weight
Days after infection
120
110
100
90
80
70
0
1
2
3
4
5
6
7

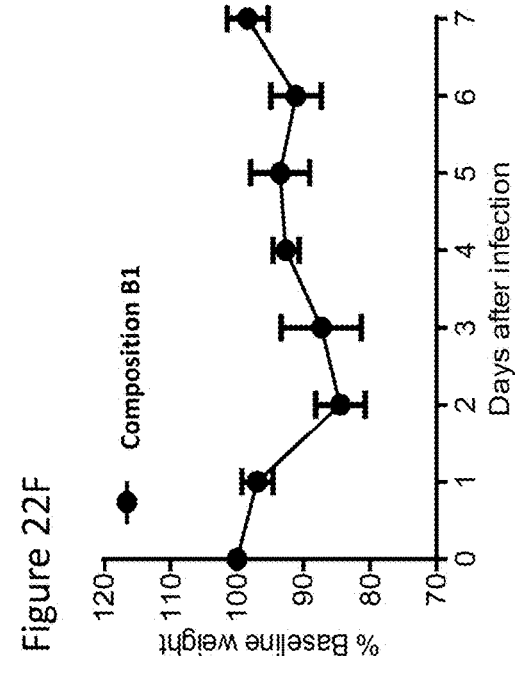


Figure 22F
Composition B1
% Baseline weight
Days after infection
120
110
100
90
80
70
0
1
2
3
4
5
6
7

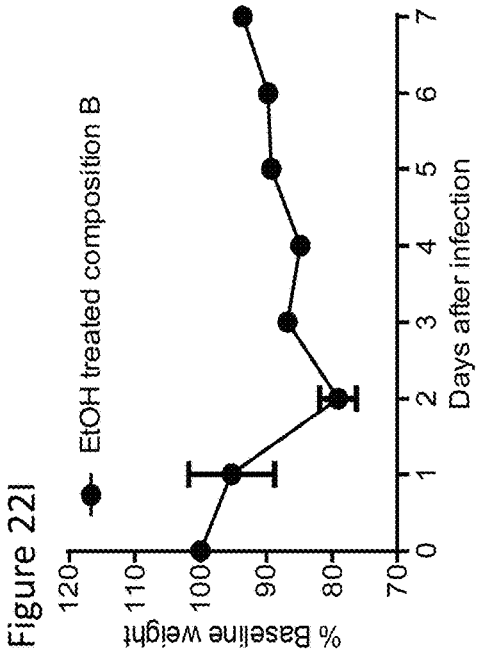


Figure 22I

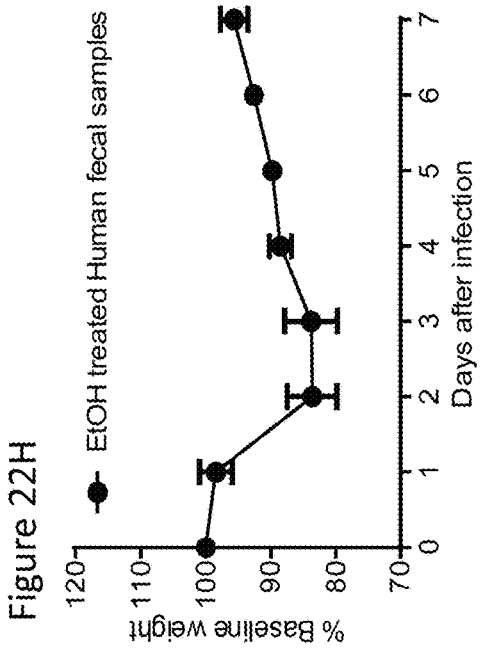


Figure 22H

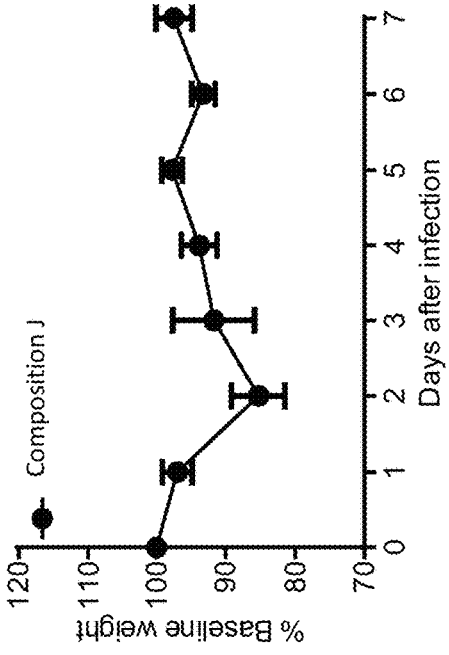


Figure 22J

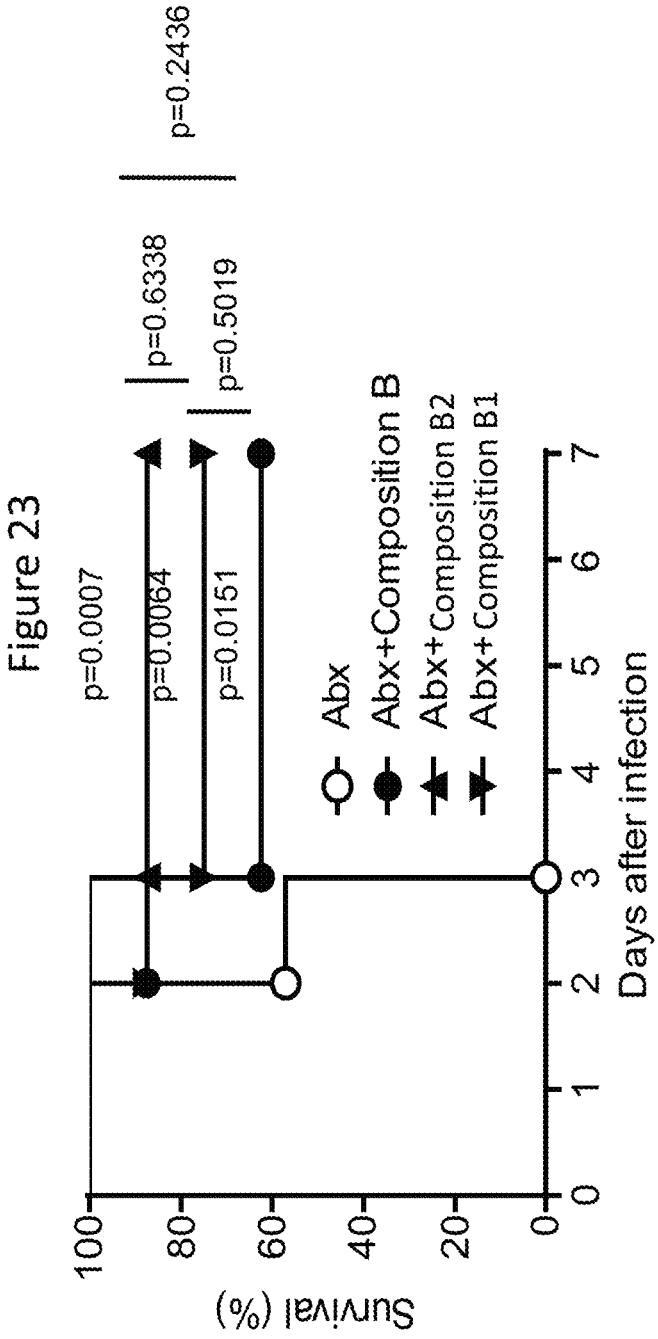


Figure 23
p=0.0007
p=0.0064
p=0.0151
p=0.6338
p=0.5019
p=0.2436
Abx
Abx+Composition B
Abx+Composition B2
Abx+Composition B1
Survival (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
7
Days after infection

Figure 24

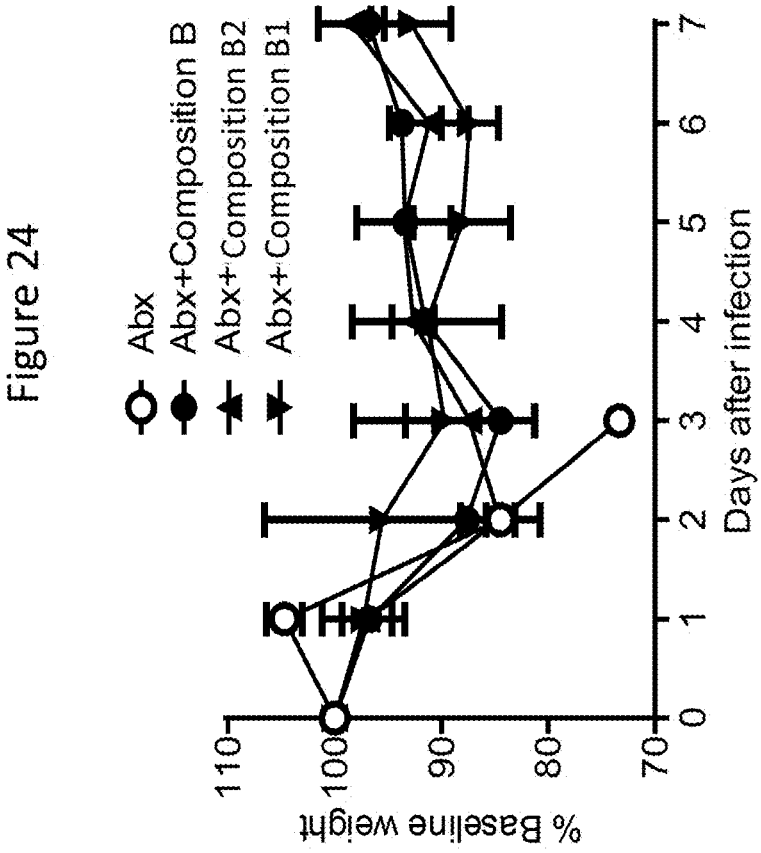

Abx
Abx+Composition B
Abx+Composition B2
Abx+Composition B1
% Baseline weight
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

Figure 25

Groups	N	Abx	CFUs *C. difficile*	CFUs LBPs
(1) Vehicle	10	+	10^4	200ul of PBS
(2) human FMT	10	+	10^4	200ul of 10% fecal samples/mouse
(3) Composition B	10	+	10^4	10^8/mouse
(4) Composition B + 4 spores*	10	+	10^4	10^8 live bacteria+spores/mouse
(5) Composition H**	10	+	10^4	10^8/mouse

*Composition B + 4 spores = The strains of Composition B plus the following four strains in spore form: *Clostrodium bolteae*, *Anaerotruncus colihominis*, *Clostridium symbiosum*, and *Clostridium innocuum*

**Composition H contains the following six strains in spore form: *Clostrodium bolteae*, *Anaerotruncus colihominis*, *Clostridium symbiosum*, *Clostridium innocuum*, *Clostridium disporicum*, and *Erysipelatoclostridium ramosum*

Figure 26

Composition H

**Composition H = The following six strains in spore form *Clostrodium bolteae, Anaerotruncus colihominis, Clostridium symbiosum, Clostridium innocuum, Clostridium disporicum and Erysipelatoclostridium ramosum*

Composition H sequence info:

SEQ ID NO: 14 - VE202-13 – *Anaerotruncus colihominis*	**Cluster IV**
SEQ ID NO: 16 - VE202-16 – *Clostridium symbiosum*	**Cluster XIVa**
SEQ ID NO: 21 - 189 – *Clostridium innocuum*	**Cluster XVII**
SEQ ID NO: 82 - PE9 – *Clostridium disporicum*	**Cluster I**
SEQ ID NO: 81 – PE5 – *Clostridium bolteae*	**Cluster XIVa**
SEQ ID NO: 80 – VE202-18 – *Erysipelatoclostridium ramosum*	**Cluster XVIII**

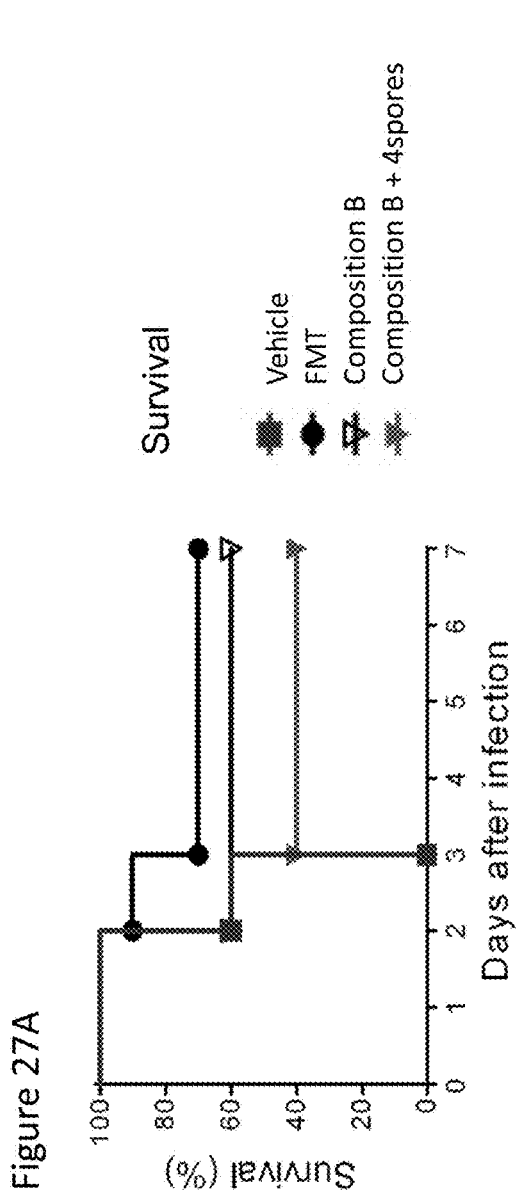


Figure 27A

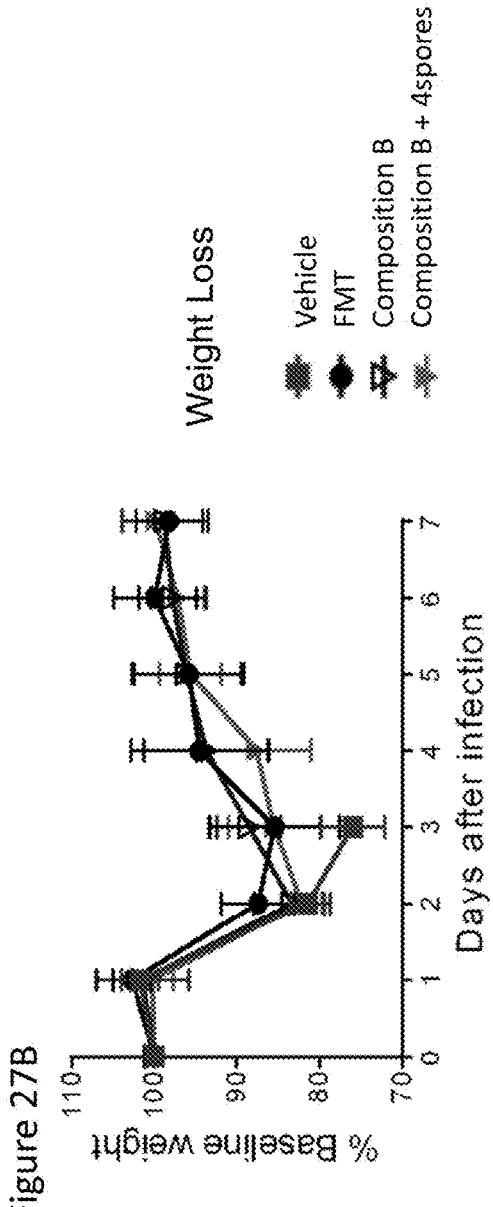


Figure 27B

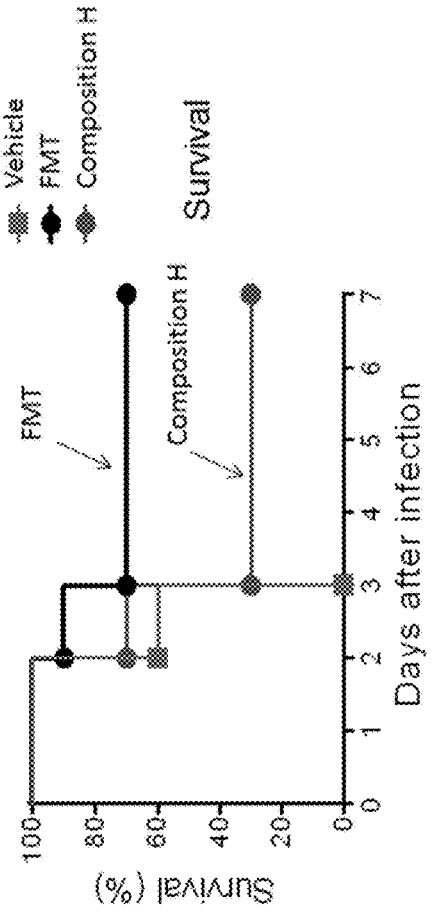


Figure 28A

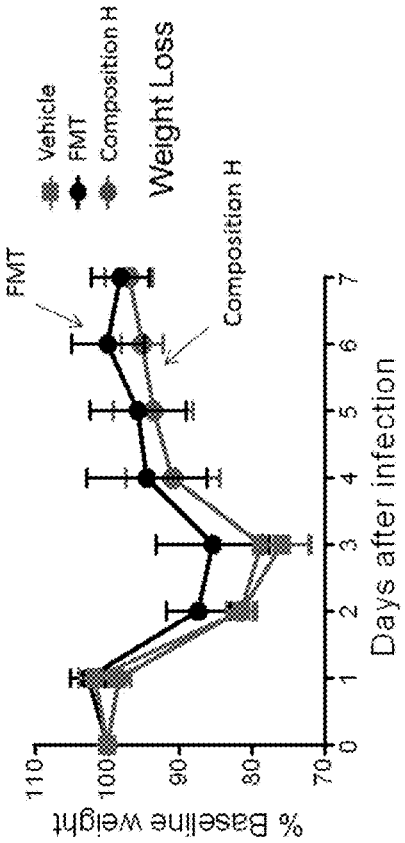


Figure 28B

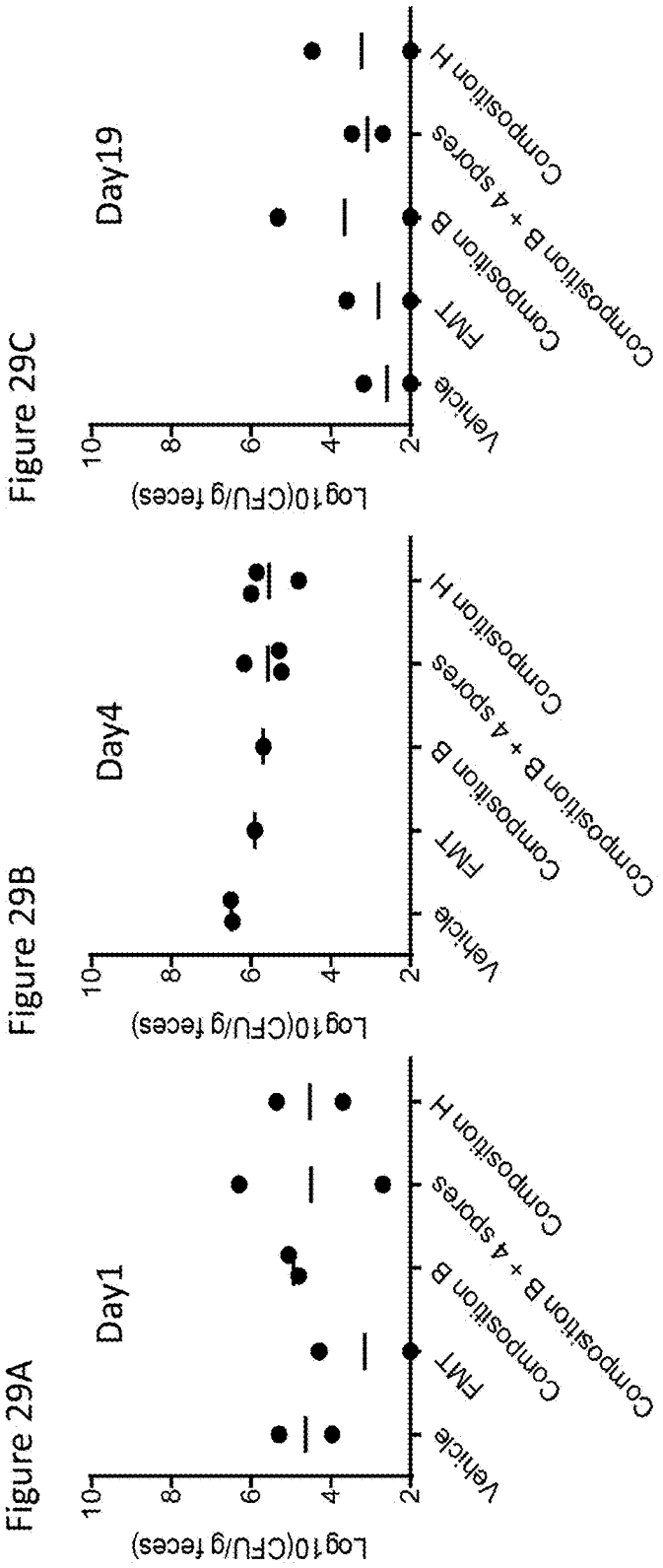


Figure 29A
Day1
Figure 29B
Day4
Figure 29C
Day19
Log10(CFU/g feces)
10
8
6
4
2
Vehicle
FMT
Composition B
Composition B + 4 spores
Composition H

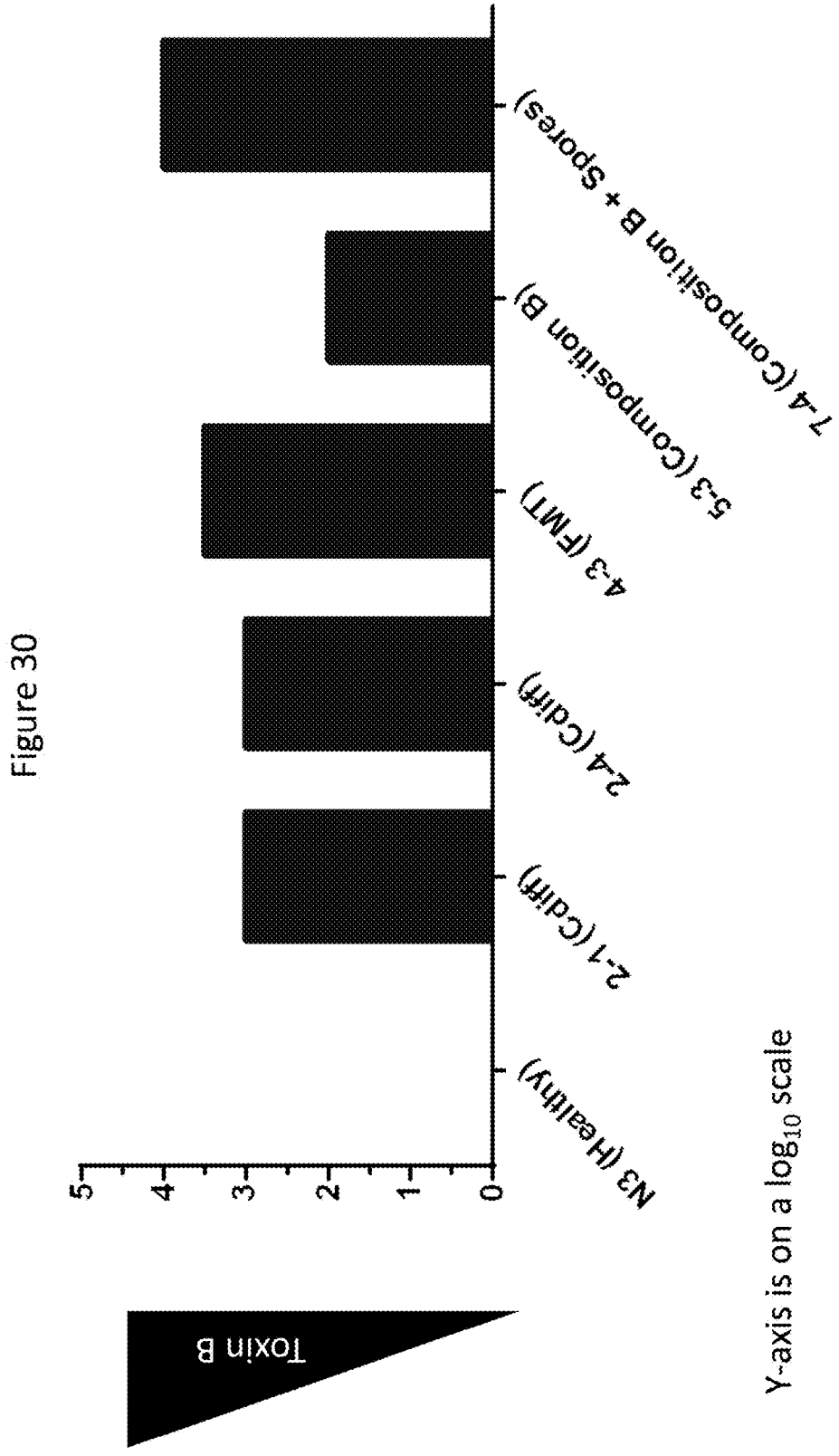


Figure 30
Toxin B
5
4
3
2
1
0
N3 (Healthy)
2-1 (Cdiff)
2-4 (Cdiff)
4-3 (FMT)
5-3 (Composition B)
7-4 (Composition B + Spores)
Y-axis is on a log10 scale

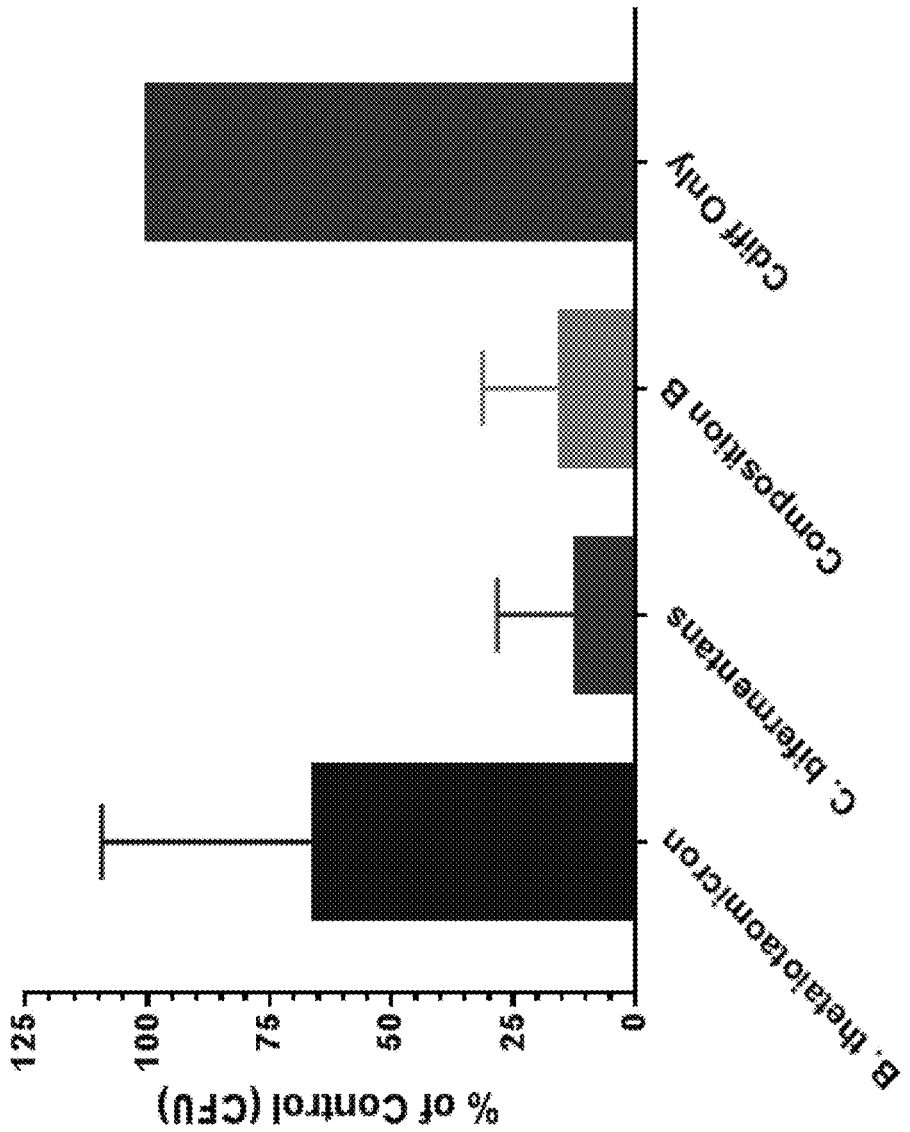

% of Control (CFU)
125
100
75
50
25
0
B. thetaiotaomicron
C. bifermentans
Composition B
Cdiff Only

Figure 31

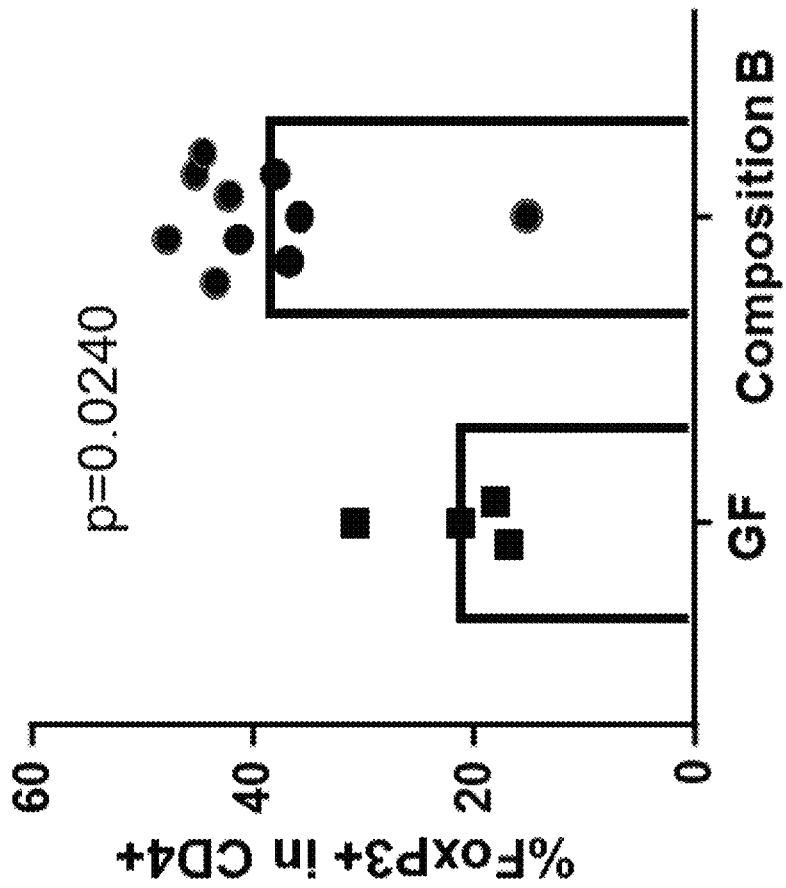


Figure 32

TREATMENT OF CLOSTRIDIUM DIFFICILE INFECTION

RELATED APPLICATIONS

This application is a continuation of international application number PCT/US2017/037498, filed Jun. 14, 2017, which claims the benefit under 35 U.S.C. § 119(e) of U.S. provisional application No. 62/349,914, filed Jun. 14, 2016, each of which is incorporated by reference herein in its entirety.

FIELD OF INVENTION

The disclosure relates to compositions of purified bacterial strains, and methods for treating pathogenic infections, such as *Clostridium difficile* infections, by administering the compositions to a subject having a pathogenic infection.

BACKGROUND OF THE INVENTION

The collection of bacterial, viral, and fungal commensal microorganisms that reside within and on the human body are collectively known as the human microbiome. The bacterial subset of the human microbiome plays an important role in host nutrient acquisition, development, immunological homeostasis, neurological health, and protection against pathogens (LeBlanc et al. *Curr. Opin. Biotechnol.* (2013) 24(2): 160-168; Hooper et al. *Science* (2012) 336 (6086): 1268-1273; Hughes et al. *Am. J. Gastroenterol.* (2013) 108(7): 1066-1074). As the largest reservoir of mammalian commensals, bacteria residing in the gastrointestinal (GI) tract influence nearly all of these aspects of human biology (Blaser *J. Clin. Invest.* (2014) 124(10): 4162-4165). Consequently, perturbation of the normal bacterial populations within the GI niche, a state known as dysbiosis, can predispose humans to a variety of diseases.

Clostridium difficile infection (CDI) arises after intestinal colonization by the anaerobic spore-forming Gram-positive pathogen *Clostridium difficile*. Upon colonization of the GI tract, *C. difficile* produces toxins which causes diarrhea and may ultimately lead to death. This illness is the most common identifiable cause of nosocomial diarrhea and is thought to arise as a direct result of dysbiosis (Calfee *Geriatrics* (2008) 63: 10-21; Shannon-Lowe et al *BMJ* (2010) 340: c1296). Not surprisingly, usage of nearly all classes of antibiotics has been associated with CDI, presumably by inducing dysbiosis in the GI tract and thereby enabling *C. difficile* outgrowth. The Center for Disease Control currently classifies CDI as a public health threat requiring immediate and aggressive action because of its natural resistance to many drugs and the emergence of a fluoroquinolone-resistant strain that is now prevalent throughout North America and Europe. *C. difficile* was responsible for almost half a million infections and was associated with approximately 29,000 deaths in 2011 (Lessa et al. *NEJM* 2015, 372: 825-834).

The antibiotics metronidazole, vancomycin, and fidaxomicin are the current therapeutic options for treatment of CDI. However, metronidazole is inadequate because of decreased response rates and neither metronidazole nor vancomycin prevent disease recurrence, with up to 30% of patients initially responding experiencing a clinical recurrence after antibiotic cessation (Miller *Expert Opin. Pharmacother.* (2010) 11: 1569-1578). Fidaxomicin has been shown to be superior to vancomycin in preventing recurrent CDI (Mullane *Ther. Adv. Chronic Dis.* (2014) 5(2): 69-84).

Because of its narrow spectrum of activity, fidaxomicin is thought to enable normal microbiome repopulation of the gut following dysbiosis and CDI, thereby lowering the likelihood of recurrent disease (Tannock et al. *Microbiology* (2010) 156 (Pt 11): 3354-3359; Louie et al. *Clin. Infect. Dis.* (2012) 55 Suppl. 2: S132-142). Nonetheless, 14% of fidaxomicin-treated patients experience CDI relapse and mutations conferring reduced sensitivity have already been reported (Eyre et al. *J. Infect. Dis.* (2014) 209(9): 1446-1451).

Because the risk of recurrent CDI is heightened by antibiotic use and *C. difficile* spores are inherently recalcitrant to the available chemotherapeutic arsenal, alternative therapeutic modalities are being pursued for the treatment of CDI. Fecal microbiota transplantation (FMT) is one such modality that has shown efficacy against CDI (Khoruts et al. *Immunol. Lett.* (2014) 162(2): 77-81; van Nood et al. *N. Engl. J. Med.* (2013) 368(5): 407-415). To date, results of FMT studies for the treatment of CDI, have reported cure rates up to 90% in three randomized controlled studies (Cammarota et al. *Alimen. Pharmacol. Therap.* (2015) 41(9): 835-843; Kassam et al. *Am. J. Gastroenterol.* (2013) 108(4): 500-508; van Nood et al. *N. Engl. J. Med.* (2013) 368(5): 407-415; Youngster et al. *Infec. Dis. Soc. Am.* (2014) 58(11): 1515-1522).

Despite the success of FMT, this therapeutic approach is not without risks and logistical concerns. Selection of FMT donors is critical and challenging. When FMT donor recruitment is performed with stringent screening and standardization protocols, most prospective donors fail this process. Only 6-10% of prospective FMT donors qualify, with the majority of failures arising from asymptomatic carriage of GI pathogens (Paramsothy et al. *Inflamm. Bowel Dis.* (2015) 21(7): 1600-1606; Borody et al. *Curr. Opin. Gastroenterol.* (2014) 30(10): 97-105; Burns et al. *Gastroenterology* (2015) 148: S96-S97; Surawicz *Ann. Intern. Med.* (2015) 162(9): 662-663). Furthermore, variation between donors may lead to variation in FMT efficacy. In addition, the risk of transmission of even non-infectious illnesses may be heightened by FMT. Indeed, significant weight gain has been reported in a patient who received an FMT from an overweight stool donor (Alang et al. *Open Forum Infect. Dis.* (Winter 2015) 2(1)).

SUMMARY OF THE INVENTION

Provided herein are compositions and methods for the treatment or prevention of pathogenic infections including *C. difficile*.

In one aspect, the disclosure provides compositions comprising two or more purified bacterial strains of species selected from the group consisting of: *Clostridium hathewayi, Blautia hansenii, Blautia producta, Blautia producta* ATCC 27340, *Clostridium bacterium* UC5.1-1D4, *Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Sellimonas intestinalis, Dracourtella massiliensis, Dracourtella massilinesis* GD1, *Ruminococcus torques, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens, Eisenbergiella tayi, Flavinofractor plautii, Clostridium orbiscindens* 1_3_50AFAA, *Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis, Anaerotruncus colihominis* DSM 17241, *Clostridium symbiosum, Clostridium symbiosum* WAL-14163, *Clostridium bolteae, Clostridium bolteae* 90A9, *Dorea longicatena, Dorea longicatena* CAG:42, *Clostridium innocuum, Erysipelotrichaceae_bacterium* 21-3, *Blautia wexlerae, Clostridium disporicum, Erysip-*

elatoclostridium ramosum, Pseudoflavinofractor capillosus, Turicibacter sanguinis, Lactobacillus mucosae, Ruminococcus obeum, Megasphaera elsdenii, Acidaminococcus fermentans, Acidaminococcus intestine, Ruminococcus faecis, Bacteroides cellulosilyticus, Anaerostipes hadrus, Eubacterium rectale, Ruminococcus champanellnsis, Ruminococcus albus, Bifidobacterium bifidum, Blautia luti, Roseburia faecis, Fusicatenibacter saccharivorans, Roseburia faecis, Blautia faecis, Dorea formicigenerans and *Bacteroides ovatus.*

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Clostridium hathewayi, Blautia hansenii, Blautia producta, Blautia producta* ATCC 27340, *Clostridium bacterium* UC5.1-1D4, *Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Sellimonas intestinalis, Dracourtella massiliensis, Dracourtella massilinesis* GD1, *Ruminococcus torques, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens, Eisenbergiella tayi, Flavinofractor plautii, Clostridium orbiscindens* 1_3_50AFAA, *Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis, Anaerotruncus colihominis* DSM 17241, *Clostridium symbiosum, Clostridium symbiosum* WAL-14163, *Clostridium bolteae, Clostridium bolteae* 90A9, *Dorea longicatena, Dorea longicatena* CAG:42, *Clostridium innocuum, Erysipelotrichaceae_bacterium*_21-3, *Blautia wexlerae, Turicibacter sanguinis, Lactobacillus mucosae*, and *Bacteroides ovatus.*

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Clostridium hathewayi, Blautia hansenii, Blautia producta, Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens*, and *Eisenbergiella tayi.*

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Flavinofractor plautii, Clostridium orbiscindens* 1_3_50AFAA, *Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis, Anaerotruncus colihominis* DSM 17241, *Eubacterium fissicatena, Sellimonas intestinalis, Dracourtella massiliensis, Dracourtella massilinesis* GD1, *Ruminococcus torques, Clostridium symbiosum, Clostridium symbiosum* WAL-14163, *Clostridium bolteae, Clostridium bolteae* 90A9, *Dorea longicatena, Dorea longicatena* CAG:42, *Blautia producta, Blautia producta* ATCC 27340, *Clostridium bacterium* UC5.1-1D4, *Clostridium innocuum*, and *Erysipelotrichaceae*_bacterium_21-3.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Clostridium orbiscindens* 1_3_50AFAA, *Anaerotruncus colihominis* DSM 17241, *Dracourtella massilinesis* GD1, *Clostridium symbiosum* WAL-14163, *Clostridium bolteae* 90A9, *Dorea longicatena* CAG:42, *Clostridium bacterium* UC5.1-1D4, and *Erysipelotrichaceae_bacterium*_21-3.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Clostridium orbiscindens* 1_3_50AFAA, *Anaerotruncus colihominis* DSM 17241, *Sellimonas intestinalis, Clostridium symbiosum* WAL-14163, *Clostridium bolteae* 90A9, *Dorea longicatena* CAG:42, *Clostridium bacterium* UC5.1-1D4, and *Erysipelotrichaceae_bacterium*_21_3.

In some embodiments of the compositions provided herein, the composition comprises purified bacterial strains *Clostridium orbiscindens* 1_3_50AFAA, *Anaerotruncus colihominis* DSM 17241, *Dracourtella massilinesis* GD1, *Clostridium symbiosum* WAL-14163, *Clostridium bolteae* 90A9, *Dorea longicatena* CAG:42, *Clostridium bacterium* UC5.1-1D4, and *Erysipelotrichaceae_bacterium*_21-3.

In some embodiments of the compositions provided herein, the composition comprises purified bacterial strains *Clostridium orbiscindens* 1_3_50AFAA, *Anaerotruncus colihominis* DSM 17241, *Sellimonas intestinalis* GD1, *Clostridium symbiosum* WAL-14163, *Clostridium bolteae* 90A9, *Dorea longicatena* CAG:42, *Clostridium bacterium* UC5.1-1D4, and *Erysipelotrichaceae_bacterium*_21_3.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Flavinofractor plautii, Anaerotruncus colihominis, Dracourtella massiliensis, Clostridium symbiosum, Clostridium bolteae, Dorea longicatena, Blautia producta*, and *Clostridium innocuum.*

In some embodiments of the compositions provided herein, the composition comprises purified bacterial strains *Flavinofractor plautii, Anaerotruncus colihominis, Dracourtella massiliensis, Clostridium symbiosum, Clostridium bolteae, Dorea longicatena, Blautia producta*, and *Clostridium innocuum.*

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Flavinofractor plautii, Anaerotruncus colihominis, Eubacterium fissicatena, Clostridium symbiosum, Clostridium bolteae, Dorea longicatena, Blautia producta*, and *Clostridium innocuum.*

In some embodiments of the compositions provided herein, the composition comprises purified bacterial strains *Flavinofractor plautii, Anaerotruncus colihominis, Eubacterium fissicatena, Clostridium symbiosum, Clostridium bolteae, Dorea longicatena, Blautia producta*, and *Clostridium innocuum.*

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Flavinofractor plautii, Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis, Eubacterium fissicatena, Ruminococcus torques, Clostridium symbiosum, Clostridium bolteae, Dorea longicatena, Blautia producta, Clostridium innocuum, Erysipelotrichaceae_bacterium*_21-3, and *Bacteroides ovatus.*

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Clostridium orbiscindens* 1_3_50 AFAA, *Anaerotruncus colihominis* DSM 17241, *Dracourtella massiliensis* GD1, *Clostridium symbiosum* WAL-14163, *Clostridium bolteae* 90A9, *Dorea longicatena* CAG:42, *Clostridium bacterium* UC5.1-1D4, *Erysipelotrichaceae_bacterium*_21-3, and *Bacteroides ovatus.*

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Clostridium orbiscindens* 1_3_50AFAA, *Anaerotruncus colihominis* DSM 17241, *Sellimonas intestinalis, Clostridium symbiosum* WAL-14163, *Clostridium*

bolteae 90A9, *Dorea longicatena* CAG:42, *Clostridium bacterium* UC5.1-1D4, *Erysipelotrichaceae_bacterium*_21-3, and *Bacteroides ovatus*.

In some embodiments of the compositions provided herein, the composition does not include a bacterial strain of the species *Flavinofractor plautii, Subdoligranulum*, or *Lachnospiraceae bacterium* 7_1_58FAA. In some embodiments of the compositions provided herein, the composition does not include a bacterial strain of the species *Bacteroides ovatus*. The composition of any one of claims **4-12**, wherein the composition does not include a bacterial strain of the species *Flavinofractor plautii, Subdoligranulum, Clostridium orbiscindens* 1_3_50AFAA, or *Lachnospiraceae bacterium* 7¬_1_58 FAA.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Clostridium scindens, Clostridium hathewayi, Blautia hansenii, Blautia wexlerae, Blautia producta, Blautia coccoides, Dorea longicatena, Clostridium innocuum, Erysipelotrichaceae_bacterium*_21-3, *Flavinofractor plautii, Lachnospiraceae bacterium* 7-_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis*, and *Clostridium symbiosum*. In some embodiments of the compositions provided herein, the composition does not include a bacterial strain of the species *Flavinofractor plautii, Subdoligranulum*, or *Lachnospiraceae bacterium* 7_1_58FAA.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Clostridium scindens, Clostridium hathewayi, Blautia hansenii, Blautia wexlerae, Anaerotruncus colihominis, Dorea longicatena, Clostridium innocuum, Erysipelotrichaceae*_bacterium_21-3, *Flavinofractor plautii, Lachnospiraceae bacterium* 7-_1_58FAA, *Subdoligranulum, Turicibacter sanguinis*, and *Lactobacillus mucosae*. In some embodiments of the compositions provided herein, the composition does not include a bacterial strain of the species *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58FAA.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Dorea longicatena, Ruminococcus obeum, Megasphaera elsdenii, Acidaminococcus fermentans, Acidaminococcus intestine, Ruminococcus faecis, Bacteroides cellulosilyticus, Anaerostipes hadrus, Flavinofractor plautii, Eubacterium rectale, Ruminococcus champanellensis, Ruminococcus albus, Bifidobacterium bifidum, Ruminococcus faecis, Blautia luti, Roseburia faecis, Fusicatenibacter saccharivorans, Blautia faecis, Dorea formicigenerans*, and *Blautia hansenii*.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains of species selected from the group consisting of: *Acidaminococcus fermentans, Acidaminococcus intestine, Anaerostipes hadrus, Blautia faecis, Blautia hansenii, Dorea formicigenerans, Dorea longicatena, Eubacterium rectale, Flavinofractor plautii, Fusicatenibacter saccharivorans, Megasphaera elsdenii, Roseburia faecis, Ruminococcus champanellensis, Ruminococcus albus, Ruminococcus faecis*, and *Ruminococcus obeum*.

In one aspect the disclosure provides compositions comprising two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:1-83 and 124-159.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:1-23, SEQ ID NO:83, SEQ ID NOs: 124-159.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21. In some embodiments of the compositions provided herein, the composition comprises purified bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO: 129, SEQ ID NO: 132, SEQ ID NO: 137, SEQ ID NO: 141, SEQ ID NO: 146, SEQ ID NO: 152, and SEQ ID NO: 157. In some embodiments of the compositions provided herein, the composition comprises purified bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO: 129, SEQ ID NO: 132, SEQ ID NO: 137, SEQ ID NO: 141, SEQ ID NO: 146, SEQ ID NO: 152, and SEQ ID NO: 157.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the

group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20 and SEQ ID NO:21, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:124-156, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:157-159.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 and SEQ ID NO:22. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequence selected from the group consisting of SEQ ID NO: 124-145, SEQ ID NO: 152-159, SEQ ID NO: 18, and SEQ ID NO: 22.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21 and SEQ ID NO:22, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124-145 and SEQ ID NO: 152-156, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:157-159.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10 and SEQ ID NOs:14-22. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequence selected from the group consisting of SEQ ID NOs: 124-159, SEQ ID NO: 18, and SEQ ID NO: 22.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:14-22 and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 129-156, SEQ ID NO: 18, SEQ ID NO: 22, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:157-159.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:83. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID Nos: 124-159 and SEQ ID NO: 83.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:83, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-156 and SEQ ID NO: 83, and wherein composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:157-159.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:83. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159, SEQ ID NO: 22, and SEQ ID NO: 83,

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:83, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-145, SEQ ID NOs: 152-156, SEQ ID NO: 22, and SEQ ID NO: 83, wherein composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:157-159.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NOs:14-22, and SEQ ID NO:83. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159, SEQ ID NO: 18, SEQ ID NO:22, and SEQ ID NO: 83.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:14-22 and SEQ ID NO:83, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124-15, SEQ ID NO: 18, SEQ ID NO:22, and SEQ ID NO: 83, wherein composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:157-159.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, and SEQ ID NO:21.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:6, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:18, and SEQ ID NO:21.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:24-79.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:24-27, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:76 and SEQ ID NO:77.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:21, and SEQ ID NOs:80-82.

In one aspect the disclosure provides compositions comprising two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:84-123.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:121, and SEQ ID NO:122.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:109, and SEQ ID NO:121.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:102, SEQ ID NO:106, SEQ ID NO:110, and SEQ ID NO:122.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial

strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:102, SEQ ID NO:106, SEQ ID NO:110, and SEQ ID NO:122, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:93.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:106, SEQ ID NO:110, and SEQ ID NO:122.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:106, SEQ ID NO:110, and SEQ ID NO:122, and wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:93.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:106, and SEQ ID NO:122.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, and SEQ ID NO:105.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, and SEQ ID NO:120.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:104, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, and SEQ ID NO:119.

In some embodiments of the compositions provided herein, the composition comprises two or more purified bacterial strains, wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:86, SEQ ID NO:95, SEQ ID NO:98, SEQ ID NO:110, SEQ ID NO:122, and SEQ ID NO:123.

In some embodiments of the compositions provided herein, the composition comprises at least one bacterial strain from *Clostridium* cluster XIVa and at least one bacterial strain from *Clostridium* cluster XVII. In some embodiments of the compositions provided herein, the composition comprises at least one bacterial strain from *Clostridium* cluster IV and at least one bacterial strain from *Clostridium* cluster XVII. In some embodiments of the compositions provided herein, the composition comprises at least one bacterial strain from *Clostridium* cluster XIVa, at least one strain from *Clostridium* cluster IV and at least one bacterial strain from *Clostridium* cluster XVII.

In some embodiments of the compositions provided herein, the composition comprises at least one *Bacteroides* strain. In some embodiments of the compositions provided herein, the composition does not include *Clostridium scindens*.

In some embodiments of the compositions provided herein, the composition comprises at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 purified bacterial strains.

In some embodiments of the compositions provided herein, one or more of the bacterial strains are spore formers. In some embodiments of the compositions provided herein, one or more of the bacterial strains are in spore form. In some embodiments of the compositions provided herein, each of the bacterial strains is in spore form.

In some embodiments of the compositions provided herein, one or more of the bacterial strains is in vegetative form. In some embodiments of the compositions provided herein, each of the bacterial strains is in vegetative form.

In some embodiments of the compositions provided herein, the composition comprises only obligate anaerobic bacterial strains. In some embodiments of the compositions provided herein, the composition comprises bacterial strains that originate from more than one human donor.

In some embodiments of the compositions provided herein, one or more of the bacterial strains are baiCD−. In some embodiments of the compositions provided herein, each of the bacterial strains is baiCD−. In some embodiments of the compositions provided herein, the composition does not mediate bile acid 7-alpha-dehydroxylation. In some embodiments of the compositions provided herein, the composition inhibits *C. difficile* toxin production. In some embodiments of the compositions provided herein, the composition inhibits *C. difficile* replication and/or survival.

In some embodiments of the compositions provided herein, the bacterial strains are lyophilized.

In some embodiments of the compositions provided herein, the composition induces the proliferation and/or accumulation of regulatory T cells (Tregs).

In one aspect, the disclosure provides compositions comprising two or more purified bacterial strains, wherein the composition comprises at least one bacterial strain from *Clostridium* cluster XIVa and at least one bacterial strain

from *Clostridium* cluster XVII. In one aspect, the disclosure provides compositions comprising two or more purified bacterial strains, wherein the composition comprises at least one bacterial strain from *Clostridium* cluster IV and at least one bacterial strain from *Clostridium* cluster XVII. In one aspect, the disclosure provides compositions comprising two or more purified bacterial strains, wherein the composition comprises at least one bacterial strain from *Clostridium* cluster IV, at least one bacterial strain from *Clostridium* cluster XIVa and at least one bacterial strain from *Clostridium* cluster XVII.

In some embodiments of the compositions provided herein, the composition comprises at least one *Bacteroides* strain. In some embodiments of the compositions provided herein, the composition does not include *Clostridium scindens*.

In some embodiments of the compositions provided herein, the composition comprises at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 purified bacterial strains.

In some embodiments of the compositions provided herein, one or more of the bacterial strains are spore formers. In some embodiments of the compositions provided herein, one or more of the bacterial strains are in spore form. In some embodiments of the compositions provided herein, each of the bacterial strains is in spore form.

In some embodiments of the compositions provided herein, one or more of the bacterial strains is in vegetative form. In some embodiments of the compositions provided herein, each of the bacterial strains is in vegetative form.

In some embodiments of the compositions provided herein, the composition comprises only obligate anaerobic bacterial strains.

In some embodiments of the compositions provided herein, the composition comprises bacterial strains that originate from more than one human donor.

In some embodiments of the compositions provided herein, one or more of the bacterial strains are baiCD−. In some embodiments of the compositions provided herein, each of the bacterial strains is baiCD−. In some embodiments of the compositions provided herein, the composition does not mediate bile acid 7-alpha-dehydroxylation. In some embodiments of the compositions provided herein, the composition inhibits *C. difficile* toxin production. In some embodiments of the compositions provided herein, the composition inhibits *C. difficile* replication and/or survival.

In some embodiments of the compositions provided herein, the bacterial strains are lyophilized.

In some embodiments of the compositions provided herein, the composition induces the proliferation and/or accumulation of regulatory T cells (Tregs).

In one aspect, the disclosure provides a pharmaceutical composition comprising any of the compositions provided herein further comprising a pharmaceutically acceptable excipient. In some embodiments of the pharmaceutical compositions provided herein, the pharmaceutical composition is formulated for oral delivery. In some embodiments of the pharmaceutical compositions provided herein, the pharmaceutical composition is formulated for rectal delivery. In some embodiments of the pharmaceutical compositions provided herein, the pharmaceutical composition is formulated for delivery to the intestine. In some embodiments of the pharmaceutical compositions provided herein, the pharmaceutical composition is formulated for delivery to the colon.

In one aspect, the disclosure provides a food product comprising any of the compositions provided herein further comprising a nutrient.

In one aspect, the disclosure provides a method of treating a pathogenic infection in a subject, comprising administering to the subject a therapeutically effective amount of any of the compositions or food products provided herein to treat the pathogenic infection.

In some embodiments of the methods provided herein, the pathogenic infection is *C. difficile*, Vancomycin Resistant Enterococci (VRE), Carbapenem Resistant Enterobacteriaceae (CRE), *Neisseria gonorrheae*, Multidrug Resistant *Acinetobacter, Campylobacter*, Extended spectrum beta-lactamese (ESBL) producing Enterobacteriaceae, Multidrug Resistant *Pseudomonas aeruginosa, Salmonella*, Drug resistant non-typhoid *Salmonella*, Drug resistant *Salmonella Typhi*, Drug resistant *Shigella*, Methicillin Resistant *Staphylococcus aureus*, Drug resistant *Streptococcus pneumoniae*, Drug resistant Tuberculosis, Vancomycin resistant *Staphylococcus aureus*, Erythromycin Resistant Group A *Streptococcus*, Clindamycin resistant Group B *Streptococcus*, and combinations thereof. In some embodiments of the methods provided herein, the pathogenic infection is *C. difficile*. In some embodiments of the methods provided herein, the pathogenic infection is Vancomycin-Resistant Enterococci.

In some embodiments of the methods provided herein, the subject is human. In some embodiments of the methods provided herein, the subject is an asymptotic carrier.

In some embodiments of the methods provided herein, the subject is administered a dose of an antibiotic prior to administration of the composition. In some embodiments of the methods provided herein, the subject is administered more than one dose of the antibiotic prior to administration of the composition. In some embodiments of the methods provided herein, the subject has not been administered an antibiotic prior to administration of the composition.

In some embodiments of the methods provided herein, the composition is administered to the subject by oral administration. In some embodiments of the methods provided herein, the composition is administered to the subject by rectal administration.

In some embodiments of the methods provided herein, the administering results in proliferation and/or accumulation of regulatory T cells (Tregs).

Each of the limitations of the invention can encompass various embodiments of the invention. It is, therefore, anticipated that each of the limitations of the invention involving any one element or combinations of elements can be included in each aspect of the invention. This invention is not limited in its application to the details of construction and the arrangement of components set forth in the following description or illustrated in the drawings. The invention is capable of other embodiments and of being practiced or of being carried out in various ways.

BRIEF DESCRIPTION OF THE DRAWINGS

The accompanying drawings are not intended to be drawn to scale. The figures are illustrative only and are not required for enablement of the disclosure. For purposes of clarity, not every component may be labeled in every drawing. In the drawings:

FIG. **1** shows the strains of Compositions A-D. Each entry includes the SEQ ID NO of the 16S rDNA sequence of the strain, a strain identifier, and the species with the closest known homology (can be more than one species). The bracketed roman numeral indicates the *Clostridium* cluster

classification of each strain based on the closest species homology. Strains that are not classified in Cluster XIVa are highlighted in bold. The two non-clostridial strains (SEQ ID NO:2, closest known species *Turicibacter sanguinis*, and SEQ ID NO:6, closest known species *Lactobacillus mucosae*) do not belong to the *Clostridium* genus.

FIG. **2** shows various *Clostridium difficile* infection models. Timelines indicate antibiotic type, duration of treatment, as well as exposure to *C. difficile* spores. The top panel shows an antibiotic cocktail treatment model in which the antibiotic cocktail is provided in the drinking water from day −10 to day −3 followed by intraperitoneal clindamycin on day −1. The middle panel shows a clindamycin IP injection model, in which clindamycin is administered by intraperitoneal injection on day −1. The bottom panel shows the cefoperazone treatment model, in which cefoperazone is provided in the drinking water from day −12 to day −2, followed by administration of a live biotherapeutic product (LBP) on day −1.

FIG. **3** shows the experimental conditions described in Example 1. The groups of mice were divided based on the antibiotic regimen received prior to administration of the indicated amount of *C. difficile* spores. "Abx" refers to treatment with any of the antibiotic regimens.

FIGS. **4**A-**4**L show data obtained in Example 1. FIGS. **4**A-**4**D show survival of mice that received no treatment (FIG. **4**A), antibiotic cocktail (FIG. **4**B), clindamycin (FIG. **4**C), or cefoperazone (FIG. **4**D) prior to *C. difficile* infection. FIGS. **4**E-**4**H show body weight of mice that received no treatment (FIG. **4**E), antibiotic cocktail (FIG. **4**F), clindamycin (FIG. **4**G), or cefoperazone (FIG. **4**H) prior to *C. difficile* infection. FIGS. **4**I-**4**L show *C. difficile* burden (CFU) per gram of feces from mice that received no treatment (FIG. **4**I), antibiotic cocktail (FIG. **4**J), clindamycin (FIG. **4**K), or cefoperazone (FIG. **4**L) prior to *C. difficile* infection. Open circles indicate infection with 10 *C. difficile* spores; closed squares indicate infection with 10,000 *C. difficile* spores. Black triangles in FIG. **4**J indicate an additional experimental arm in which mice were treated with vancomycin following *C. difficile* infection.

FIG. **5** shows experimental conditions evaluated in Example 2, the results for which are presented in FIGS. **7**-**9**. Composition E corresponds to a mixture of 17 bacterial strains (See e.g., Narushima et al., Gut Microbes 5: 3, 333-339). Composition I corresponds to a mixture of *Clostridium scindens, Pseudoflavonifractor capillosus*, and *Blautia hansenii*. "Abx" refers to treatment with any of the antibiotic regimens.

FIG. **6** shows survival of mice over time post infection with *C. difficile* spores, according to the experimental conditions shown in FIG. **5**. Mice losing >20% body weight of baseline were included in mortality numbers in survival curves.

FIGS. **7**A-**7**I show weight of the mice at various times post infection with *C. difficile* spores. Groups of mice received cefoperazone (Abx) treatment followed by the indicated composition, or no cefoperazone (no Abx), then were administered *C. difficile* spores. FIG. **7**A shows weight of the mice that received no antibiotic treatment. FIG. **7**B shows weight of the mice that received cefoperazone treatment. FIG. **7**C shows weight of the mice that received cefoperazone treatment followed by vancomycin. FIG. **7**D shows weight of the mice that received cefoperazone treatment followed by Composition I. FIG. **7**E shows weight of the mice that received cefoperazone treatment followed by Composition E. FIG. **7**F shows weight of the mice that received cefoperazone treatment followed by composition A. FIG. **7**G shows weight of the mice that received cefoperazone treatment followed by composition B. FIG. **7**H shows weight of the mice that received cefoperazone treatment followed by composition C. FIG. **7**I shows weight of the mice that received cefoperazone treatment followed by composition D.

FIGS. **8**A-**8**C show the load of *C. difficile* in colony forming units (CFUs) in fecal pellets at various times post infection with *C. difficile*. FIG. **8**A shows *C. difficile* CFU/g feces one-day post infection. FIG. **8**B shows *C. difficile* CFU/g feces 3 days post infection. FIG. **8**C shows *C. difficile* CFU/g feces 8 days post infection.

FIG. **9** shows experimental conditions evaluated in Example 3, the results for which are presented in FIGS. **10**-**12**.

FIG. **10** shows survival of the mice over time post infection with *C. difficile* spores, according to the experimental conditions shown in FIG. **9**. Mice losing >20% body weight of baseline were included in mortality numbers in survival curves.

FIG. **11** shows weight of the mice at various times post infection with *C. difficile* spores.

FIG. **12** shows the *C. difficile* burden in colony forming units (CFUs) in fecal pellets collected from mice 1, 3, and 8 days post infection with *C. difficile*.

FIG. **13** shows the strains of Composition F. The genus-species notation indicates the closest species based on the sequence of the isolated strain.

FIG. **14** shows the classification by *Clostridium* cluster of the strains in Composition F and their short-chain fatty acid producing abilities.

FIG. **15** shows experimental conditions evaluated in Example 4, the results for which are presented in FIGS. **16**-**18**. The dosing days are relative to *C. difficile* infection. FMT refers to Fecal Matter Transplant with fecal matter isolated from mice or from humans.

FIG. **16** shows survival of the mice over time post infection with *C. difficile* spores, according to the experimental conditions shown in FIG. **15**. Mice losing >20% body weight of baseline were included in mortality numbers in survival curves.

FIGS. **17**A-**17**H show weight of the mice at various times post infection with *C. difficile* spores. Groups of mice received cefoperazone (Abx) treatment followed by the indicated composition, then were administered *C. difficile* spores. FIG. **17**A shows weight of the mice that received cefoperazone treatment. FIG. **17**B shows weight of the mice that received cefoperazone treatment followed by FMT with fecal matter from a human. FIG. **17**C shows weight of the mice that received cefoperazone treatment followed by FMT with fecal matter from a mouse. FIG. **17**D shows weight of the mice that received cefoperazone treatment followed by Composition B on day −1. FIG. **17**E shows weight of the mice that received cefoperazone treatment followed by Composition B on days −2 and −1. FIG. **17**F shows weight of the mice that received cefoperazone treatment followed by Composition B on days −2, −1, 1, 2, and 3. FIG. **17**G shows weight of the mice that received cefoperazone treatment followed by Composition F on day −1. FIG. **17**H shows weight of the mice that received cefoperazone treatment followed by Composition F on days −2, −1, 1, 2, and 3.

FIGS. **18**A-**18**B show the load of *C. difficile* in colony forming units (CFUs) in fecal pellets at various times post infection with *C. difficile*. FIG. **18**A shows *C. difficile* CFU/g feces 8 days post infection. FIG. **18**B shows *C. difficile* CFU/g feces 17 days post infection.

FIG. **19** shows the strains of Composition G. The genus-species notation indicates the closest species based on the sequence of the isolated strain.

FIG. **20** shows experimental conditions evaluated in Example 5, the results for which are presented in FIGS. **21-23**. Composition B1=Composition B with *Bacteroides*; Composition B2=Composition B with *Bacteroides* but without *Flavonifractor plautii*.

FIG. **21** shows survival of the mice over time post infection with *C. difficile* spores, according to the experimental conditions shown in FIG. **20**. Mice losing >20% body weight of baseline were included in mortality numbers in survival curves.

FIGS. **22**A-**22**J show weight of the mice at various times post infection with *C. difficile* spores. FIG. **22**A shows weight of the mice that received vehicle control. FIG. **22**B shows weight of the mice that received Composition F. FIG. **22**C shows weight of the mice that received Composition G. FIG. **22**D shows weight of the mice that received cefoperazone treatment followed by Composition B. FIG. **22**E shows weight of the mice that received cefoperazone treatment followed by Composition B2 (=Composition B without *Flavonifractor plautii* and with added *Bacteroides*). FIG. **22**F shows weight of the mice that received cefoperazone treatment followed by Composition B1 (=Composition B with *Bacteroides* added). FIG. **22**G shows weight of the mice that received cefoperazone treatment followed by frozen Composition B. FIG. **22**H shows weight of the mice that received cefoperazone treatment followed by ethanol treated human fecal samples. FIG. **22**I shows weight of the mice that received cefoperazone treatment followed by ethanol treated Composition B. FIG. **22**J shows weight of the mice that received cefoperazone treatment followed by Composition J.

FIG. **23** shows the load of *C. difficile* in colony forming units (CFUs) in fecal pellets at various times post infection with *C. difficile*.

FIG. **24** shows weight of the indicated groups of mice at various times post infection with *C. difficile* spores.

FIG. **25** shows experimental conditions evaluated in Example 6, the results of which are presented in FIGS. **27-29**.

FIG. **26** shows the strains in Composition H (SEQ ID NO:14-VE202-13-*Anaerotruncus colihominis* (Cluster IV); SEQ ID NO:16-VE202-16-*Clostridium symbiosum* (Cluster XIVa); SEQ ID NO:21-189-*Clostridium innocuum* (Cluster XVII); SEQ ID NO:82-PE9-*Clostridium disporicum* (Cluster I); SEQ ID NO:81-PE5-*Clostridium bolteae* (Cluster XIVa); SEQ ID NO:80-VE202-18-*Erysipelatoclostridium ramosum* (Cluster XVIII).

FIGS. **27**A and **27**B shows survival and weight loss of the mice over time post infection with *C. difficile* spores, according to the experimental conditions shown in FIG. **25**. Mice losing >20% body weight of baseline were included in mortality numbers in survival curves. FIG. **29**A shows survival/mortality of mice that received the indicated treatment prior to *C. difficile* infection. FIG. **29**B shows the weight over time of mice that received the indicated treatment prior to *C. difficile* infection.

FIGS. **28**A and **28**B show results from the experimental conditions shown in FIG. **25**. FIG. **28**A shows survival/mortality of mice that received the indicated treatment prior to *C. difficile* infection. FIG. **28**B shows the weight over time of mice that received the indicated treatment prior to *C. difficile* infection.

FIGS. **29**A and **29**B show the *C. difficile* burden in CFU/gram feces collected from mice that received the indicated treatment prior to *C. difficile*. FIG. **29**A shows *C. difficile* burden at one-day post *C. difficile* infection. FIG. **29**B shows *C. difficile* burden at 4 days post *C. difficile* infection. FIG. **29**C shows *C. difficile* burden at 19 days post *C. difficile* infection.

FIG. **30** shows that Composition B reduced the amount of *C. difficile* Toxin B compared to no treatment controls: "2-1 (Cdiff)" and "2-4 (Cdiff)" and FMT. In addition, Composition B reduced the amount of *C. difficile* Toxin B compared to Composition B with additional spores.

FIG. **31** shows Composition B reduced *C. difficile* growth in in vitro competition experiments. Cultures of *C. difficile* were incubated in the presence of *B. thetaiotaomicron, C. bifermentans*, or Composition B, or in the absence of a competing strain(s) (*C. diff* only). The quantity of *C. difficile* is presented as the percentage of the control (*C. diff* only).

FIG. **32** shows that inoculation with Composition B induced the percentage of FoxP3+CD4+ cells (regulatory T cells) in the intestine of germ-free mice as compared to control mice ("GF").

DETAILED DESCRIPTION OF THE INVENTION

Disclosed herein are compositions comprising purified bacterial strains and pharmaceutical compositions and food products containing such compositions and bacterial strains. Also disclosed are methods of treating a pathogenic infection, such as *Clostridium difficile* (*C. difficile*) infection, in a subject by administering said compositions to the subject.

Various factors including antibiotic usage can induce dysbiosis of the gastrointestinal tract, which may allow for colonization by pathogenic microorganisms, such as *C. difficile*. Such colonization or pathogenic infection can lead to a variety of adverse effects in the subject including diarrhea, which is one of the primary symptoms characteristic of *C. difficile* infection (CDI). In the case of CDI, diarrhea is thought to be a result of *C. difficile* production of Toxin B (also referred to as cytotoxin TcdB), which results in opening of the tight junctions between intestinal epithelial cells, increasing vascular permeability, hemorrhage, and inflammation.

The compositions described herein are effective in the treatment of *C. difficile* infection. As shown herein, the disclosed compositions are effective in suppressing the pathogenic effects of *C. difficile* infection. The compositions provided herein reduce the amount of *C. difficile* after infection and thereby provide an effective method for eliminating *C. difficile* from the body (e.g., the gut). The compositions provided herein induce the proliferation and/or accumulation of regulatory T cells (Tregs), for example when administered to a subject. Remarkably, the compositions disclosed herein have been found to reduce or inhibit production or activity of *C. difficile* Toxin B and thereby represent effective compositions for the treatment or prevention of CDI. The compositions disclosed herein have also been found to inhibit the growth and/or survival of *C. difficile*.

The present disclosure provides compositions comprising purified bacterial strains that can be administered to subjects experiencing or having experienced a pathogenic infection to treat the infection. In some embodiments, the compositions may be administered to subjects who may be at risk for a pathogenic infection. Such subjects include subjects who previously had pathogenic infections, subjects who have been treated with antibiotics and subjects who will undergo a procedure that will put them at an increased risk for a

pathogenic infection (e.g., surgery and/or hospitalization). In some embodiments, the pathogenic infection, is infection by a pathogen that is present predominantly in the gut or the intestine. In some embodiments, the pathogen that is present predominantly in the gut or the intestine is *Clostridium difficile*.

In some embodiments, the one or more of the bacterial strains of the compositions provided herein colonize or recolonize the intestinal tract or parts of the intestinal tract (e.g., the colon or the cecum) of the subject. Such colonization or recolonization may also be referred to as grafting. In some embodiments, the one or more of the bacterial strains of the compositions recolonize the intestinal tract (e.g., the colon or the cecum) of the subject after the naturally present microbiome has been partially or completely removed, e.g., because of administration of antibiotics. In some embodiments, the one or more of the bacterial strains of the compositions colonize a dysbiotic gastrointestinal tract.

In some embodiments, the one or more of the bacterial strains of the compositions can "outgrow" a pathogen, such as *C. difficile*. Thus, in some embodiments, if a pathogen (e.g., *C. difficile*) and one or more bacteria of compositions provided herein are both present in the intestinal tract (e.g., the colon or the cecum), the one or more bacteria of compositions provided herein grow faster (e.g., have a shorter doubling time) than the pathogen, thereby preventing the pathogen from accumulating in the intestinal tract (e.g., the colon or the cecum). In some embodiments, the faster growth results because the one or more bacteria of the compositions provided herein are better at grafting in the intestinal tract (e.g., the colon or the cecum). In some embodiments, the faster growth results because the one or more bacteria of the compositions provided herein are better at metabolizing nutrients present in the intestinal tract (e.g., the colon or the cecum). In some embodiments, the compositions of bacterial strains provided herein prevent or inhibit production of bacterial toxins by the pathogenic infection, or prevent or inhibit the cytopathic or cytotoxic effects of such bacterial toxins. In some embodiments, the bacterial strains of the compositions provided herein can treat pathogenic infections, because of the synergy between the bacterial strains. Thus, without being limiting, in some embodiments, the combination of the bacterial strains of the compositions provided herein act synergistically because the combination of the strains is particularly well-suited to use nutrients in the intestinal tract (e.g., the colon or the cecum), or instance through metabolic interactions, and/or because the combination is superior in grafting (e.g., by providing a favorable microenvironment).

In some embodiments, a pathogenic infection such as *C. difficile* is treated because the combination of bacterial strains of the compositions provided herein is superior in the use of nutrients when compared to the pathogen such as *C. difficile*, thereby suppressing the growth of the pathogen such as *C. difficile*. In some embodiments, a pathogenic infection such as *C. difficile* is treated because the combination of bacterial strains of the compositions provided herein is superior in grafting when compared to the pathogen such as *C. difficile*, thereby suppressing the growth of the pathogen such as *C. difficile*. In some embodiments, a pathogenic infection such as *C. difficile* is treated because the combination of bacterial strains of the compositions provided herein is superior in the use of nutrients and in grafting when compared to the pathogen such as *C. difficile*, thereby suppressing the growth of the pathogen such as *C. difficile*. In some embodiments, a pathogenic infection such as *C. difficile* is treated because the combination of bacterial strains of the compositions provided herein inhibits the growth and/or survival of the pathogen such as *C. difficile*. In some embodiments, a pathogenic infection such as *C. difficile* is treated because the combination of bacterial strains of the compositions provided herein induces regulatory T cells (Tregs) in the subject that results in reduction or elimination of the pathogen such as *C. difficile*. In some embodiments, a pathogenic infection such as *C. difficile* is treated because the combination of bacterial strains of the compositions provided herein inhibits the growth and/or survival of the pathogen and induces regulatory T cells (Tregs) in the subject that results in reduction or elimination of the pathogen such as *C. difficile*.

In some embodiments, the synergistic effect is provided by the capacity of the combination to colonize specific niches in the intestinal tract (e.g., the colon or the cecum). In some embodiments, the synergistic effect is provided by the capacity of the combination to metabolize specific nutrients. In some embodiments, the synergistic effect is provided by the capacity of the combination to provide specific metabolites to the environment. Such specific metabolites may suppress growth of the pathogen and/or stimulate growth of non-pathogens. In some embodiments, the synergistic effect is provided by the capacity of the combination to provide short-chain fatty acids to the environment. In some embodiments, the synergistic effect is provided by the capacity of the combination to provide specific short-chain fatty acids to the environment. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce butyrate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce acetate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce lactate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce propionate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce succinate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce multiple metabolites. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce multiple short-chain fatty acids. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce both butyrate and acetate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce both butyrate and lactate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce both butyrate and propionate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce both butyrate and succinate. In some embodiments, the synergistic effect is provided by the capacity of the combination to produce butyrate, acetate and additional short-chain fatty acids.

The bacterial strains used in the compositions provided herein generally are isolated from the microbiome of healthy individuals. In some embodiments, the compositions include strains originating from a single individual. In some embodiments, the compositions include strains originating from multiple individuals. In some embodiments, the bacterial strains are obtained from multiple individuals, isolated and grown up individually. The bacterial compositions that are grown up individually may subsequently be combined to provide the compositions of the disclosure. It should be appreciated that the origin of the bacterial strains of the

compositions provided herein is not limited to the human microbiome from a healthy individual. In some embodiments, the bacterial strains originate from a human with a microbiome in dysbiosis. In some embodiments, the bacterial strains originate from non-human animals or the environment (e.g., soil or surface water). In some embodiments, the combinations of bacterial strains provided herein originate from multiple sources (e.g., human and non-human animals).

In some embodiments, the bacteria of the compositions provided herein are anaerobic bacteria. In some embodiments, the bacteria of the compositions provided herein are obligate anaerobic bacteria. In some embodiments, the bacteria of the compositions provided herein are *clostridia*. *Clostridia* may be classified into phylogenetic clusters with other closely related strains and species. (See e.g., Rajilic-Stojanovic, M., and de Vos, W. M. *FEMS Microbiol Rev* 38, (2014) 996-1047). In general, *clostridia* are classified as belonging to a specific cluster based on their 16S rRNA (or 16S rDNA) nucleic acid sequence. Methods for determining the identity of specific bacterial species based on their 16S rRNA (or 16S rDNA) nucleic acid sequence are well known in the art (See e.g., *Jumpstart Consortium Human Microbiome Project Data Generation Working, G. PLoS One* (2012) 7, e39315).

Provided herein are compositions comprising bacterial strains belonging to specific *Clostridium* clusters that have been found to be effective in treating and/or preventing pathogenic infection (e.g., *C. difficile* infection). In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IV. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XIVa. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XVII. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster I. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IX. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XIVa and at least one of the bacterial strains belongs to *Clostridium* cluster XVII. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IV and at least one of the bacterial strains belongs to *Clostridium* cluster XVII. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IV, at least one of the bacterial strains belongs to *Clostridium* cluster XIVa, and at least one of the bacterial strains belongs to *Clostridium* cluster XVII.

In some embodiments, the composition has at least twice as many bacterial strains that belong to *Clostridium* cluster XIVa when compared to the bacterial strains that belong to *Clostridium* cluster IV. In some embodiments, at least two of the bacterial strains of the composition belong to *Clostridium* cluster IV and at least five of the bacterial strains belong to *Clostridium* cluster XIVa. In some embodiments, the composition has at least twice as many bacterial strains that belong to *Clostridium* cluster XIVa when compared to the bacterial strains that belong to *Clostridium* cluster IV, and the composition has at least one strain that belongs to *Clostridium* cluster XVII. In some embodiments, at least two of the bacterial strains of the composition belong to *Clostridium* cluster IV, at least five of the bacterial strains belongs to *Clostridium* cluster XIVa, and at least one of the bacterial strains belongs to *Clostridium* cluster XVII.

In some embodiments, the compositions provided herein do not include bacterial strains belonging to *Clostridium* cluster XVIII. In some embodiments, the compositions provided herein do not include bacterial strains belonging to *Clostridium* cluster XVI. In some embodiments, the compositions provided herein do not include bacterial strains belonging to *Clostridium* cluster XI. In some embodiments, the compositions provided herein do not include bacterial strains belonging to *Clostridium* cluster I.

In one aspect, the disclosure provides bacterial strains comprising a 16S rDNA sequence with a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-83 and 124-159. It should be appreciated that SEQ ID NOs: 1-83 and 124-159 may include both full length and partial 16S rDNA sequences.

In one aspect, the disclosure provides compositions comprising a bacterial strain comprising a 16S rDNA sequence with a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-83 and 124-159. In one aspect, the disclosure provides compositions comprising as an active ingredient a bacterial strain comprising a 16S rDNA sequence with a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-83 and 124-159. It should be appreciated that for all compositions provided herein, in some embodiments, the bacterial strain or the bacterial strains are the active ingredient of the composition.

It should be appreciated that for all compositions provided herein, in some embodiments, the bacterial strains are purified. Thus, for example the disclosure provides purified bacterial strains comprising a 16S rDNA sequence with a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-83 and 124-159. In addition, for example, the disclosure provides compositions comprising purified bacterial strains comprising a 16S rDNA sequence with a nucleic acid sequence selected from the group consisting of SEQ ID NOs: 1-83 and 124-159. The bacterial strains disclosed herein originally may have been obtained and purified from the microbiota of one or more human individuals or obtained from sources other than the human microbiota, including soil and non-human microbiota. As provided herein, in some embodiments, bacteria isolated from the human microbiota, non-human microbiota, soil, or any alternative source are purified prior to use in the compositions and methods provided herein.

In one aspect, the disclosure provides compositions comprising one or more bacterial strains, wherein the one or more bacterial strains comprise a 16S rDNA sequence with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-83 and 124-159. In one aspect, the disclosure provides compositions comprising one or more bacterial strains wherein the one or more bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:1-83 and 124-159. As discussed previously, in some embodiments, the bacterial strains are purified. Thus, in one aspect, the disclosure provides compositions comprising one or more purified bacterial strains wherein the one or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:1-83 and 124-159.

In one aspect, the disclosure provides compositions comprising two or more purified bacterial strains wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:1-83 and 124-159. As discussed above, in some

embodiments, the bacterial strains are the active ingredient of the composition. Thus, in some embodiments, the disclosure provides compositions comprising as an active ingredient two or more purified bacterial strains wherein the two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:1-83 and 124-159.

In one aspect, the disclosure provides bacterial strains and combinations of bacterial strains that are homologous or have a high percent of homology with bacterial strains comprising 16S rDNA sequences selected from the group consisting of SEQ ID NOs:1-83 and 124-159. As discussed previously, in some embodiments, the bacterial strains are purified. The bacterial strains disclosed herein that have a 16S rDNA sequence with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-83 and 124-159 have a high percent of homology (e.g., greater than 90%) with 16S rDNA sequences of bacterial strains that have been described in various databases (See e.g., the National Center for Biotechnology Information). Table 1 and Table 3 provides the closest known species by homology when the 16S rDNA sequences comprising SEQ ID NOs:1-83 and 124-159 are compared to 16S rDNA sequences of bacterial species available in public databases. By way of example, the bacterial strain comprising a 16S rDNA sequence with SEQ ID NO:1 (also referred to herein as "Strain 71") disclosed herein has the highest homology with a bacterial strain of the species *Blautia wexlerae* as defined by Accession # NR_044054 (having 16S rDNA sequence SEQ ID NO:94). While the bacterial strain with SEQ ID NO:1 has homology with other published bacterial strains as well, the highest homology is with a bacterial strain of the species *Blautia wexlerae* as defined by Accession # NR_044054. In this particular example the homology of SEQ ID NO:1 is 96.6% with SEQ ID NO:94 (corresponding to *Blautia wexlerae*). It should be appreciated that multiple bacterial strains disclosed herein may have the highest homology with the same species. (e.g., both SEQ ID NO:4 and SEQ ID NO:5 have the highest homology with a 16S rDNA sequence of a strain of the species *Blautia hansenii*).

It should further be appreciated that the bacterial strains disclosed herein that have a 16S rDNA sequence with a nucleic acid sequence selected from the group consisting of SEQ ID NOs:1-83 and 124-159, are also homologous to other strains based on their whole genome sequence, or subset of their whole genome sequence. Homologies based on whole genome analysis are provided in Table 2 and Table 3.

In one aspect, the disclosure provides compositions comprising one or more bacterial strains wherein the one or more bacterial strains are of species selected from the group consisting of *Clostridium hathewayi, Blautia hansenii, Blautia producta, Blautia producta* ATCC 27340, *Clostridium bacterium* UC5.1-1D4, *Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Sellimona intestinalis, Dracourtella massiliensis, Dracourtella massiliensis* GD1, *Ruminococcus torques, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens, Eisenbergiella tayi, Flavinofractor plautii, Clostridium orbiscindens* 1_3_50AFAA, *Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis, Anaerotruncus colihominis* DSM 17241, *Clostridium symbiosum, Clostridium symbiosum* WAL-14163, *Clostridium bolteae, Clostrdium bolteae* 90A9, *Dorea longicatena, Dorea longicatena* CAG:42, *Clostridium innocuum, Erysipelotrichaceae_bacterium_21-3, Blautia wexlerae, Clostridium disporicum, Erysipelatoclostridium ramosum, Pseudoflavinofractor capillosus, Turicibacter sanguinis, Lactobacillus mucosae, Ruminococcus obeum, Megasphaera elsdenii, Acidaminococcus fermentans, Acidaminococcus intestine, Ruminococcus faecis, Bacteroides cellulosilyticus, Anaerostipes hadrus, Eubacterium rectale, Ruminococcus champanellensis, Ruminococcus albus, Bifidobacterium bifidum, Blautia luti, Roseburia faecis, Fusicatenibacter saccharivorans, Roseburia faecis, Blautia faecis, Dorea formicigenerans* and *Bacteroides ovatus.*

In some embodiments, the disclosure provides compositions comprising two or more bacterial strains, wherein the two or more bacterial strains are of species selected from the group consisting of *Clostridium hathewayi, Blautia hansenii, Blautia producta, Blautia producta* ATCC 27340, *Clostridium bacterium* UC5.1-1D4, *Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Sellimona intestinalis, Dracourtella massiliensis, Dracourtella massiliensis* GD1, *Ruminococcus torques, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens, Eisenbergiella tayi, Flavinofractor plautii, Clostridium orbiscindens* 1_3_50AFAA, *Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis, Anaerotruncus colihominis* DSM 17241, *Clostridium symbiosum, Clostridium symbiosum* WAL-14163, *Clostridium bolteae, Clostrdium bolteae* 90A9, *Dorea longicatena, Dorea longicatena* CAG:42, *Clostridium innocuum, Erysipelotrichaceae_bacterium_21-3, Blautia wexlerae, Clostridium disporicum, Erysipelatoclostridium ramosum, Pseudoflavinofractor capillosus, Turicibacter sanguinis, Lactobacillus mucosae, Ruminococcus obeum, Megasphaera elsdenii, Acidaminococcus fermentans, Acidaminococcus intestine, Ruminococcus faecis, Bacteroides cellulosilyticus, Anaerostipes hadrus, Eubacterium rectale, Ruminococcus champanellensis, Ruminococcus albus, Bifidobacterium bifidum, Blautia luti, Roseburia faecis, Fusicatenibacter saccharivorans, Roseburia faecis, Blautia faecis, Dorea formicigenerans* and *Bacteroides ovatus.*

It should be appreciated that the compositions may include multiple strains of a particular species. Thus, for illustration, a non-limiting example of the compositions disclosed herein, comprises one strain of *Clostridium hathewayi* and two strains of *Blautia hansenii.*

The invention also encompasses compositions comprising bacterial strains that are close in homology to and/or fall within the species *Clostridium hathewayi, Blautia hansenii, Blautia producta, Blautia producta* ATCC 27340, *Clostridia bacteria* UC5.1-1D4, *Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Sellimona intestinalis, Dracourtella massiliensis, Dracourtella massiliensis* GD1, *Ruminococcus torques, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens, Eisenbergiella tayi, Flavinofractor plautii, Clostridium orbiscindens* 1_3_50AFAA, *Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis, Anaerotruncus colihominis* DSM 17241, *Clostridium symbiosum, Clostridium symbiosum* WAL-14163, *Clostridium bolteae, Clostrdium bolteae* 90A9, *Dorea longicatena, Dorea longicatena* CAG:42, *Clostridium innocuum, Erysipelotrichaceae_bacterium_21-3, Blautia wexlerae, Clostridium disporicum, Erysipelatoclostridium ramosum, Pseudoflavinofractor capillosus, Turicibacter sanguinis, Lactobacillus mucosae, Ruminococcus obeum, Megasphaera elsdenii, Acidaminococcus fermentans, Acidaminococcus intestine, Ruminococcus faecis, Bacteroides cellulosilyticus, Anaerostipes hadrus, Eubacterium rectale, Ruminococcus champanellensis, Ruminococcus albus, Bifi-

dobacterium bifidum, Blautia luti, Roseburia faecis, Fusicatenibacter saccharivorans, Roseburia faecis, Blautia faecis, Dorea formicigenerans and *Bacteroides ovatus*. Thus, in one embodiment, the compositions of the disclosure include one or more bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 84-123. In some embodiments, the compositions of the disclosure include two or more bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:84-123.

In one aspect, the compositions of the disclosure include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:1-23 and 124-159. In some embodiments, the compositions of the disclosure include two or more bacterial strains of species selected from the group consisting of *Clostridium hathewayi, Blautia hansenii, Blautia producta, Blautia producta* ATCC 27340, *Clostridia bacteria* UC5.1-1D4, *Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Sellimona intestinalis, Dracourtella massiliensis, Dracourtella massiliensis* GD1, *Ruminococcus torques, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens, Eisenbergiella tayi, Flavinofractor plautii, Clostridium orbiscindens* 1_3_50AFAA, *Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis, Anaerotruncus colihominis* DSM 17241, *Clostridium symbiosum, Clostridium symbiosum* WAL-14163, *Clostridium bolteae, Clostrdium bolteae* 90A9, *Dorea longicatena, Dorea longicatena* CAG:42, *Clostridium innocuum, Erysipelotrichaceae_bacterium*_21-3, *Blautia wexlerae, Turicibacter sanguinis, Lactobacillus mucosae*, and *Bacteroides ovatus*. In some embodiments, the compositions of the disclosure include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:102, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:109, SEQ ID NO:110, SEQ ID NO:121, and SEQ ID NO:122.

In one aspect, the disclosure provides Composition A (See e.g., FIG. **1**, Table A). As shown in FIG. **1**, Composition A contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the disclosure provides compositions with two or more purified bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the disclosure provides compositions with five or more purified bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the disclosure provides compositions with at least ten purified bacterial strains, wherein the bacterial strains comprise 16S rDNA sequences with nucleic acid sequences SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23, respectively. In some embodiments, the disclosure provides a composition consisting of ten purified bacterial strains, wherein the bacterial strains comprise 16S rDNA sequences with nucleic acid sequences SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23, respectively. In some embodiments, the disclosure provides a composition essentially consisting of ten purified bacterial strains, wherein the bacterial strains comprise 16S rDNA sequences with nucleic acid sequences SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23, respectively. As used herein, essentially consisting of refers to a composition that includes no additional bacterial strains.

In some embodiments, the disclosure provides compositions with bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of: SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the disclosure provides compositions with two or more purified bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the disclosure provides compositions with five or more purified bacterial strains that comprise 16S rDNA having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the disclosure provides compositions with at least ten purified bacterial strains, wherein the bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23, respectively. In some embodiments, the disclosure provides a composition consisting of ten purified bacterial strains, wherein the bacterial strains comprise 16S rDNA sequences with nucleic acid sequences SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23, respectively. In some embodiments, the disclosure provides a composition essentially consisting of ten purified bacterial strains, wherein the bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23, respectively.

The bacterial strains in Composition A are related to the following bacterial species: *Clostridium hathewayi, Blautia* hansenii, *Blautia* producta, *Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens*, and *Eisenbergiella tayi* (See e.g., Table 1). It should be appreciated that multiple bacterial strains of the compositions disclosed herein can have the same related bacterial species.

For instance, the bacterial strains having 16S rDNA sequences with nucleic acid sequences SEQ ID NO:4, SEQ ID NO:5 and SEQ ID NO:7 all have *Blautia hansenii* as related species. In some embodiments, the disclosure provides compositions with two or more bacteria of species selected from the group consisting of *Clostridium hathewayi, Blautia* hansenii, *Blautia* producta, *Blautia coccoides, Eubacterium contortum, Eubacterium fissicatena, Anaerostipes caccae, Clostridium scindens, Marvinbryanta formatexigens*, and *Eisenbergiella tayi*. In some embodiments, the disclosure provides compositions with two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:88, SEQ ID NO:89, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:109, and SEQ ID NO:121.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5; SEQ ID NO:7, SEQ ID NO:8, and SEQ ID NO:13.

Each of the bacterial strains of Composition A are BaiCD+, meaning that the bacterial strains encode, or are predicted to encode, the bile inducible operon gene BaiCD and/or a protein with stereospecific NAD(H)-dependent 3-oxo-Δ^4-cholenoic acid oxidoreductase activity. The BaiCD status of a bacterial strain can be determined for instance by PCR (See e.g., Wells et al. *Clin Chim Acta* (2003) May; 331(1-2):127-34). Furthermore, each of the strains of Composition A are classified as belonging to *Clostridium* cluster XIVa. In some embodiments, the disclosure provides compositions comprising two or more bacterial strains, wherein the bacterial strains are BaiCD+ strains. In some embodiments, the disclosure provides compositions comprising two or more bacterial strains, wherein the bacterial strains are BaiCD+ and belong to *Clostridium* cluster XIVa. In some embodiments of the compositions comprising two or more bacterial strains that are BaiCD+ strains and that belong to *Clostridium* cluster XIVa, the compositions do not include bacterial strains that belong to *Clostridium* cluster IV.

In some embodiments, the disclosure provides compositions with two or more purified bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:3, SEQ ID NO:4, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:8, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:12, SEQ ID NO:13, and SEQ ID NO:23, wherein all the bacterial strains belong to *Clostridium* cluster XIVa.

TABLE A

Composition A
SEQ_03 - 5 - *Clostridium_hathewayi* (XIVa)*
SEQ_04 - 7 - *Blautia_hansenii* (XIVa)*
SEQ_05 - 10 - *Blautia_hansenii* (XIVa)*
SEQ_07 - 59 - *Blautia_producta/Blautia_coccoides* (XIVa)
SEQ_08 - 79 - *Blautia_hansenii* (XIVa)*
SEQ_09 - VE202-21 - *Eubacterium_contortum/Eubacterium_fissicatena* (XIVa)*
SEQ_11 - VE202-9 - *Anaerostipes_caccae* (XIVa)*
SEQ_12 - VE202-26 - *Clostridium_scindens* (XIVa)*
SEQ_13 - 136 - *Marvinbryantia_formatexigens* (XIVa)*
SEQ_23 - VE202-29 - *Eisenbergiella_tayi* (XIVa)*

*= BaiCD+

In one aspect, the disclosure provides Composition B (See e.g., FIG. **1**, Table B). As shown in FIG. **1**, Composition B contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159, respectively. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, respectively. In some embodiments, the composition consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NOs:124-159, respectively. In some embodiments, the compositions consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NOs:124-159, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the compositions include eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159, respectively. In some embodiments, the compositions include eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, respectively. In some embodiments, the compositions include eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159, respectively. In some embodiments, the compositions include eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159, respectively. In some embodiments, the composition consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, respectively. In some embodiments, the composition consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NOs:124-159, respectively. In some embodiments, the compositions consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition essentially consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19,

SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159, respectively. In some embodiments, the composition essentially consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, respectively. In some embodiments, the composition essentially consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NOs:124-159, respectively. In some embodiments, the composition essentially consists of eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157.

In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NOs: 124-159. In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22. In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NOs: 124-159. In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157.

In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159, respectively. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159, respectively. In some embodiments, the composition essentially consists of

at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO: 22, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In one aspect, the disclosure provides compositions that contain bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO: 124-159. In one aspect, the disclosure provides compositions that contain bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In one aspect, the disclosure provides compositions that contain bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of: SEQ ID NOs: 124-159. In one aspect, the disclosure provides compositions that contain bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO: 124-159, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NOs: 124-159, respectively. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, respectively. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs:124-159, respectively. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising

16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO: 124-159, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159. In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22. In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences: SEQ ID NO:22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159.

In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159.

In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 20, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159.

In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the compositions include at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159.

In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159, respectively. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the composition consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO: 22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159.

In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the composition essentially consists of at least eight purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO: 22, SEQ ID NO: 124-145, and SEQ ID NOs: 152-159.

In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO: 124-159. In one

aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22. In one aspect, the disclosure provides a composition that contains bacterial strains that comprise 16S rDNA sequences with nucleic acid sequences: SEQ ID NO:18, SEQ ID NO:22, and SEQ ID NO: 124-159.

In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO: 124-159. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:22, and SEQ ID NO: 124-159.

In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NOs: 124-159. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the compositions include five or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:22, and SEQ ID NOs: 124-159.

In some embodiments, the compositions include at least ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NOs: 124-159, respectively. In some embodiments, the compositions include at least ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the compositions include at least ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 18, SEQ ID NO: 22, and SEQ ID NOs: 124-159.

In some embodiments, the composition consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO: 124-159, respectively. In some embodiments, the composition consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the composition consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:22, SEQ ID NOs: 124-159, respectively.

In some embodiments, the composition essentially consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO: 124-159, respectively. In some embodiments, the composition essentially consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22, respectively. In some embodiments, the composition essentially consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:22, and SEQ ID NO: 124-159, respectively.

The bacterial strains in Composition B are related to the following bacterial species: *Flavinofractor plautii, Lachnospiraceae, bacterium* 7_1_58FAA, *Subdoligranulum Anaerotruncus colihominis, Eubacterium fissicatena, Ruminococcus torques Clostridium symbiosum, Clostridium bolteae, Dorea longicatena, Blautia producta, Clostridium innocuum*, and *Erysipelotrichaceae_bacterium*_21-3 (See e.g., Table 2).

Selected strains were subjected to whole genome sequencing using a PacBio Biosciences platform (Menlo Park, Calif.) and sequences were assembled into whole genomes (Table 3). The 16S rDNA sequences were identified using Prokka and Barrnap. It was found that several strains contained more than one 16S sequence. All identified 16S rRNA gene nucleotide sequences for each strain were then clustered at 97% identity using the usearch (v 5.2.236) algorithm and the cluster seed sequence was selected as the representative sequence for each Composition B strain (The Consensus 16S sequence: column labeled "*Consensus SEQ ID # of 16S region as determined by WGS" in Table 3). Table 3 provides identification of the indicated strains included in Composition B based on Sanger sequencing of the 16S region as well as on whole genome sequencing (WGS). The closest species of the bacterial strains were identified both by comparison to a 16S database (column labeled: "Closest species based on Consensus SEQ ID # of 16S region as compared with 16S database") and to whole genome databases (column labeled: "Closest species based on WGS compared versus WG databases).

Based on identification of 16S sequences through whole genome sequencing, and by comparing these sequences with 16S databases, the bacterial strains in Composition B are related to the following bacterial species: *Clostridium bolteae, Anaerotruncus colihominis, Dracourtella massiliensis, Clostridium symbiosum Blautia producta, Dorea longicatena Clostridium innocuum* and *Flavinofractor plautii* (see, e.g., Table 3).

Based on whole genome sequencing and comparing of the whole genome to whole genome databases, the bacterial strains in Composition B are most closely related to the following bacterial species: *Clostridium bolteae* 90A9, *Anaerotruncus colihominis* DSM 17241, *Dracourtella massiliensis* GD1, *Clostridium symbiosum* WAL-14163, *Clostridium bacterium* UC5.1-1D4, *Dorea longicatena* CAG:42, *Erysipelotrichaceae_bacterium_21_3*, and *Clostridium orbiscindens* 1_3_50AFAA (see, e.g., Table 3).

It should be appreciated that multiple strains of the compositions disclosed herein can have the same related bacterial species. For instance, the bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO 18, SEQ ID NO:20 and SEQ ID NO:22 all have *Dorea longicatena* as related bacterial species. In some embodiments, the disclosure provides compositions with two or more bacteria selected from the group consisting of *Flavinofractor plautii, Lachnospiraceae, bacterium* 7_1_58FAA, *Subdoligranulum Anaerotruncus colihominis, Eubacterium fissicatena, Ruminococcus torques Clostridium symbiosum, Clostridium bolteae, Dorea longicatena, Blautia producta, Clostridium innocuum* and *Erysipelotrichaceae_bacterium_21-3*. In some embodiments, the disclosure provides compositions with two or more bacteria selected from the group consisting of *Flavinofractor plautii, Anaerotruncus colihominis, Eubacterium fissicatena, Clostridium symbiosum, Clostridium bolteae, Dorea longicatena, Blautia producta*, and *Clostridium innocuum*. In some embodiments, the disclosure provides compositions that include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:102, SEQ ID NO:106, SEQ ID NO:110, and SEQ ID NO:122.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NOs: 124-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152 and SEQ ID NO:157.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO: 124-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:22, and SEQ ID NO: 124-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:22, SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO: 124-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO: 124-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18 and SEQ ID NO: 124-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO: 124-145, and SEQ ID NO: 151-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ

ID NO:22, SEQ ID NO: 124-145, and SEQ ID NO: 151-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:152, and SEQ ID NO:157

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO: 124-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, and SEQ ID NO:21. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO: 18, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-159.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NOs: 157-159, and SEQ ID NOs:141-156. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:22, SEQ ID NOs: 157-159, and SEQ ID NO:141-156.

Each of the bacteria of Composition B are BaiCD− strains, meaning that the strains do not encode and/or are not predicted to encode the bile inducible operon gene baiCD and/or a protein with stereospecific NAD(H)-dependent 3-oxo-Δ^4-cholenoic acid oxidoreductase activity. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the bacteria are BaiCD− strains. The strains of Composition B are classified as belonging to *Clostridium* clusters IV, XIVa, and XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and belong to *Clostridium* clusters IV, XIVa, or XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and belong to *Clostridium* clusters IV or XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and belong to *Clostridium* clusters XIVa or XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and belong to *Clostridium* clusters IV or XIVa. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and belong to *Clostridium* cluster IV. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and belong to *Clostridium* cluster XIVa. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and belong to *Clostridium* clusters XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and belong to *Clostridium* clusters IV, XIVa, and XVII and do not belong to *Clostridium* clusters XVI or XVIII.

In some embodiments, the disclosure provides two or more bacterial strains wherein the bacterial strains are spore forming bacterial strains. In some embodiments, the disclosure provides two or more bacterial strains wherein the bacteria are spore formers and wherein the bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NOs 124-140, and SEQ ID NO: 152-156. In some embodiments, the disclosure provides two or more bacterial strains wherein the bacteria are spore formers and wherein the bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:17, and SEQ ID NO:21. In some embodiments, the disclosure provides two or more bacterial strains wherein the bacteria are spore formers and wherein the bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-140, and SEQ ID NOs: 152-156.

In some embodiments, the disclosure provides two or more bacterial strains wherein the bacteria include both spore formers and non-spore formers. In some embodiments, the disclosure provides two or more bacterial strains wherein the bacteria include both spore formers and non-spore formers, and wherein the spore forming bacterial strains comprise two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:21, SEQ ID NOs: 124-140, and SEQ ID NOs: 152-156. In some embodiments, the disclosure provides two or more bacterial strains wherein the bacteria include both spore formers and non-spore formers, and wherein the spore forming bacterial strains comprise two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID

NO:14, SEQ ID NO:16, SEQ ID NO:17, and SEQ ID NO:21. In some embodiments, the disclosure provides two or more bacterial strains wherein the bacteria include both spore formers and non-spore formers, and wherein the spore forming bacterial strains comprise two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-140 and SEQ ID NO: 152-156.

TABLE B

Composition B
SEQ_10 - 211 - *Flavonifractor_plautii* (IV)
SEQ_14 - VE202-13 - *Anaerotruncus_colihominis* (IV)
SEQ_15 - VE202-14 - *Eubacterium_fissicatena* (XIVa)
SEQ_16 - VE202-16 - *Clostridium_symbiosum* (XIVa)
SEQ_17 - VE202-7 - *Clostridium_bolteae* (XIVa)
SEQ_19 - 16 - *Blautia_producta* (XIVa)
SEQ_20 - 170 - *Dorea_longicatena* (XIVa)
SEQ_21 - 189 - *Clostridium_innocuum* (XVII)

In some embodiments, the compositions include one or more bacterial species from the *Bacteroides* genus. In some embodiments, the compositions include one or more bacterial species selected from the group consisting of *B. acidifaciens, B. caccae, B. coprocola, B. coprosuis, B. eggerthii, B. finegoldii, B. fragilis, B. helcogenes, B. intestinalis, B. massiliensis, B. nordii, B. ovatus, B. thetaiotaomicron, B. vulgatus, B. plebeius, B. uniformis B. salyersai, B. pyogenes, B. goldsteinii, B. dorei*, and *B. johnsonii*. In some embodiments, the compositions include *Bacteroides ovatus*. In some embodiments, the *Bacteroides ovatus* has a 16S rDNA sequence comprising SEQ ID NO:83. In some embodiments, the *Bacteroides ovatus* has a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence comprising SEQ ID NO:83. In some embodiments, the *Bacteroides ovatus* has a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence comprising SEQ ID NO:101.

While not being limited to a specific mechanism it is thought that the inclusion of a *Bacteroides* species in the bacterial compositions disclosed herein increases the ability to sense and adapt to nutrient availability or influence the host immune system so that it becomes more effective in fighting pathogens (e.g., *C. difficile*). In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO: 124-159, and SEQ ID NO:83. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:83. (Composition B1, See e.g., Table B1). In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159, and SEQ ID NO: 83.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO: 124-145, SEQ ID NO: 152-159, and SEQ ID NO:83. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NO:83. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-145, SEQ ID NO: 152-159, and SEQ ID NO: 83.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO: 124-159, and SEQ ID NO:83. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:83. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-159, SEQ ID NO: 18, SEQ ID NO: 22, and SEQ ID NO: 83.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16s rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:106, SEQ ID NO:110, and SEQ ID NO:122. It should also be appreciated that in some embodiments, the compositions disclosed herein do not include bacterial species from the *Bacteroides* genus.

TABLE B1

Composition B1
SEQ_10 - 211 - *Flavonifractor_plautii* (IV)
SEQ_14 - VE202-13 - *Anaerotruncus_colihominis* (IV)
SEQ_15 - VE202-14 - *Eubacterium_fissicatena* (XIVa)
SEQ_16 - VE202-16 - *Clostridium_symbiosum* (XIVa)
SEQ_17 - VE202-7 - *Clostridium_bolteae* (XIVa)
SEQ_20 - 170 - *Dorea_longicatena* (XIVa)
SEQ_19 - 16 - *Blautia_producta* (XIVa)
SEQ_21 - 189 - *Clostridium_innocuum* (XVII)
SEQ_83 *Bacteroides ovatus*

In some embodiments, the compositions disclosed herein do not include *Clostridium orbiscindens* 1_3_50AFAA, *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58FAA. In some embodiments, the compositions disclosed herein do not include *Clostridium orbiscindens* 1_3_50AFAA. In some embodiments, the compositions disclosed herein do not include *Flavinofractor plautii*. In some embodiments, the composi-

tions disclosed herein do not include *Subdoligranulum*. In some embodiments, the compositions disclosed herein do not include *Lachnospiraceae bacterium* 7_1_58FAA.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO: 15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO: 124-156, wherein the composition does not include a bacterial strain comprising a 16s rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10 and SEQ ID NOs: 157-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO: 15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21, wherein the composition does not include a bacterial strain comprising a 16s rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NOs: 124-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NOs:157-159.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NOs: 124-146 and SEQ ID NO: 152-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10 and SEQ ID NOs: 157-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, and SEQ ID NO:22, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:22, SEQ ID NOs: 124-146, and SEQ ID NOs: 152-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NOs: 157-159.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, and SEQ ID NOs: 124-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10 and SEQ ID NOs: 157-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, and SEQ ID NO:22, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:22, and SEQ ID NOs: 124-159, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NOs: 157-159.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:102, SEQ ID NO:106, SEQ ID NO:110, and SEQ ID NO:122, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:93.

In some embodiments, the compositions include one or more bacterial species from the *Bacteroides* genus and do not include *Clostridium orbiscindens* 1_3_50AFAA, *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58FAA. (Composition B2, See e.g., Table B2). In some embodiments, the compositions include *Bacteroides ovatus* and do not include *Clostridium orbiscindens* 1_3_50AFAA, *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58FAA.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 SEQ ID NO:83, and SEQ ID NOs: 124-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10 and SEQ ID NOs: 157-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21 and SEQ ID NO:83, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:83 and SEQ ID NOs: 124-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NOs: 157-159.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID

NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:83, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10 and SEQ ID NOs: 157-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:83, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:22 SEQ ID NO:83, SEQ ID NOs: 124-145, and SEQ ID NOs: 152-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NOs: 157-159.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22, SEQ ID NO:83, and SEQ ID NO: 124-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10 and SEQ ID NOs: 157-159. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:18, SEQ ID NO:19, SEQ ID NO:20, SEQ ID NO:21, SEQ ID NO:22 and SEQ ID NO:83, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:22, SEQ ID NO:83, and SEQ ID NO: 124-156, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NOs: 157-159.

In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:101, SEQ ID NO:102, SEQ ID NO:106, SEQ ID NO:110, and SEQ ID NO:122, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:93.

TABLE B2

Composition B2
SEQ_14 - VE202-13 - *Anaerotruncus_colihominis* (IV)
SEQ_15 - VE202-14 - *Eubacterium_fissicatena* (XIVa)
SEQ_16 - VE202-16 - *Clostridium_symbiosum* (XIVa)
SEQ_17 - VE202-7 - *Clostridium_bolteae* (XIVa)
SEQ_20 - 170 - *Dorea_longicatena* (XIVa)
SEQ_19 - 16 - *Blautia_producta* (XIVa)
SEQ_21 - 189 - *Clostridium_innocuum* (XVII)
SEQ_83 *Bacteroides ovatus*

In one aspect, the disclosure provides Composition C (See e.g., FIG. **1**, Table C). As shown in FIG. **1**, Composition C contains bacteria that have the following 16S rDNA sequences: SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16. In some embodiments, the disclosure provides compositions with two or more purified bacterial strains that have 16S rDNA sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16. In some embodiments, the compositions include four or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16. In some embodiments, the compositions include at least ten purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16. In some embodiments, the composition consists of ten purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16, respectively. In some embodiments, the composition consists essentially of ten purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16, respectively.

In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16. In some embodiments, the compositions include four or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16. In some embodiments, the compositions include at least ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10,

SEQ ID NO:14, and SEQ ID NO:16. In some embodiments, the composition consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16, respectively. In some embodiments, the composition essentially consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16, respectively.

The bacterial strains in Composition C are related to the following species: *Clostridium scindens, Clostridium hathewayi, Blautia hansenii, Blautia wexlerae, Blautia producta, Blautia coccoides, Dorea longicatena, Clostridium innocuum, Flavonifractor plautii, Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis*, and *Clostridium symbiosum*. In some embodiments, the disclosure provides compositions with two or more bacterial strains of species selected from the group consisting of *Clostridium scindens, Clostridium hathewayi, Blautia hansenii, Blautia wexlerae, Blautia* product, *Blautia coccoides, Dorea longicatena, Clostridium innocuum, Flavonifractor plautii, Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Anaerotruncus colihominis*, and *Clostridium symbiosum*. In some embodiments, the disclosure provides compositions that include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:106, and SEQ ID NO:122.

In some embodiments, the compositions disclosed herein do not include *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58FAA. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:7, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:14, and SEQ ID NO:16, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:106, and SEQ ID NO:122, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:93.

The strains of Composition C include both BaiCD$^+$ strains and Bai CD− strains. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein one or more bacteria are BaiCD+ strains and one or more bacteria are BaiCD− strains. In some embodiments of the one or more bacteria that are BaiCD+ strains are selected from bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, and SEQ ID NO:7. In some embodiments the one or more bacteria that are BaiCD− strains are selected from bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:14, and SEQ ID NO:16. In some embodiments of the one or more bacteria that are BaiCD+ strains are selected from the bacterial species *Clostridium scindens, Clostridium hathewayi, Blautia hansenii, Blautia wexlerae, Blautia* product, and *Blautia coccoides*. In some embodiments of the one or more bacteria that are BaiCD− strains are selected from the bacterial species *Dorea longicatena, Clostridium innocuum, Flavonifractor plautii*, or *Lachnospiraceae bacterium* 7_1_58FAA, *Anaerotruncus colihominis*, and *Clostridium symbiosum*. The clostridial strains of Composition C are classified as belonging to *Clostridium* clusters IV, XIVa, and XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and BaiCD+ strains and belong to *Clostridium* clusters IV, XIVa, or XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and BaiCD+ strains and belong to *Clostridium* clusters XIVa or XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and BaiCD+ strains and belong to *Clostridium* clusters IV or XIVa.

TABLE C

Composition C
SEQ_12 - VE202-26 - *Clostridium_scindens* (XIVa)*
SEQ_03 - 5 - *Clostridium_hathewayi* (XIVa)*
SEQ_05 - 10 - *Blautia_hansenii* (XIVa)*
SEQ_01 - 71 - *Blautia_wexlerae* (XIVa)*
SEQ_07 - 59 - *Blautia_producta/Blautia_coccoides* (XIVa)*
SEQ_18 - 148 - *Dorea_longicatena* (XIVa)
SEQ_21 - 189 - *Clostridium_innocuum* (XVII)
SEQ_10 - 211 - *Flavonifractor_plautii* (IV)
SEQ_14 - VE202-13 - *Anaerotruncus_colihominis* (IV)
SEQ_16 - VE202-16 - *Clostridium_symbiosum*) (XIVa)

*= BaiCD+

In one aspect, the disclosure provides Composition D (See e.g., FIG. **1**, Table D). As shown in FIG. **1**, Composition D contains bacteria that have the following 16S rDNA sequences: SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6. In some embodiments, the disclosure provides compositions with two or more purified bacterial strains that have 16S rDNA sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6. In some embodiments, the disclosure provides compositions that include three or more purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6. In some embodiments, the disclosure provides compositions that include at least ten purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6. In some embodiments,

the disclosure provides a composition that consists of ten purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6, respectively. In some embodiments, the disclosure provides a composition that consists essentially of ten purified bacterial strains comprising 16S rDNA sequences with nucleic acid sequences SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6, respectively In some embodiments, the disclosure provides compositions that include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6. In some embodiments, the disclosure provides compositions that include three or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6. In some embodiments, the disclosure provides compositions that include at least ten more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6. In some embodiments, the disclosure provides a composition that consists of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6, respectively. In some embodiments, the disclosure provides a composition that consists essentially of ten purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, SEQ ID NO:2, and SEQ ID NO:6, respectively.

The bacterial strains in Composition D are related to the following bacteria: *Clostridium scindens, Clostridium hathewayi, Blautia hansenii, Blautia wexlerae, Anaerotruncus colihominis, Dorea longicatena, Clostridium innocuum, Flavonifractor plautii, Lachnospiraceae bacterium* 7_1_58FAA, *Subdoligranulum, Turicibacter sanguinis*, and *Lactobacillus* mucosae. In some embodiments, the disclosure provides compositions with two or more bacterial strains of species selected from the group consisting of *Clostridium scindens, Clostridium hathewayi, Blautia hansenii, Blautia wexlerae, Anaerotruncus colihominis, Dorea longicatena, Clostridium innocuum, Erysipelotrichaceae_bacterium*_21-3, *Flavonifractor plautii, Lachnospiraceae bacterium* 7_1_58FAA, *Turicibacter sanguinis*, and *Lactobacillus* mucosae. In some embodiments, the disclosure provides compositions that include two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, and SEQ ID NO:105.

In some embodiments, the compositions disclosed herein do not include *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58FAA. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:1, SEQ ID NO:14, SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:2, and SEQ ID NO:6, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:10. In some embodiments, the composition comprises two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:87, SEQ ID NO:90, SEQ ID NO:91, SEQ ID NO:94, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:98, SEQ ID NO:99, and SEQ ID NO:105, wherein the composition does not include a bacterial strain comprising a 16S rDNA sequence having at least 97% homology with a nucleic acid sequence of SEQ ID NO:93.

The strains of Composition D include both BaiCD$_+$ strains and Bai CD− strains. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein one or more bacteria are BaiCD+ strains and one or more bacteria are BaiCD− strains. In some embodiments of the one or more bacteria that are BaiCD+ strains are selected from bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:12, SEQ ID NO:3, SEQ ID NO:5, and SEQ ID NO:1. In some embodiments the one or more bacteria that are BaiCD− strains are selected from bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:18, SEQ ID NO:21, SEQ ID NO:10, and SEQ ID NO:14. In some embodiments of the one or more bacteria that are BaiCD+ strains are selected from the bacterial species *Clostridium scindens, Clostridium hathewayi, Blautia hansenii*, and *Blautia wexlerae*. In some embodiments of the one or more bacteria that are BaiCD− strains are selected from the bacterial species *Dorea longicatena, Clostridium innocuum, Flavonifractor plautii*, and *Anaerotruncus colihominis*. The Clostridial strains of Composition D are classified as belonging to *Clostridium* clusters IV, XIVa, and XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and BaiCD+ strains and belong to *Clostridium* clusters IV, XIVa, or XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and BaiCD+ strains and belong to *Clostridium* clusters XIVa or XVII. In some embodiments, the disclosure provides two or more bacterial strains, wherein the bacteria are BaiCD− strains and BaiCD+ strains and belong to *Clostridium* clusters IV or XIVa.

Composition D includes the non-*Clostridium* strains *Turicibacter sanguinis* and *Lactobacillus* mucosae. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition includes both *Clostridium* strains and non-*Clostridium* strains. In some embodiments, the non-*clostridium* strains are the members of the genus *Lactobacillus*. Members of the genus *Lactobacillus* include, without limitation *L. acetotolerans, L. acidifarinae, L. acidipiscis, L. acidophilus, L.*

agilis, L. algidus, L. alimentarius, L. amylolyticus, L. amylophilus, L. amylotrophicus, L. amylovorus, L. animalis, L. antri, L. apodemi, L. aviarius, L. bifermentans, L. brevis, L. buchneri, L. camelliae, L. casei, L. catenaformis, L. ceti, L. coleohominis, L. collinoides, L. composti, L. concavus, L. coryniformis, L. crispatus, L. crustorum, L. curvatus, L. delbrueckii subsp. *bulgaricus, L. delbrueckii* subsp. *delbrueckii, L. delbrueckii* subsp. *lactis, L. dextrinicus, L. diolivorans, L. equi, L. equigenerosi, L. farraginis, L. farciminis, L. fermentum, L. fornicalis, L. fructivorans, L. frumenti, L. fuchuensis, L. gallinarum, L. gasseri, L. gastricus, L. ghanensis, L. graminis, L. hammesii, L. hamsteri, L. harbinensis, L. hayakitensis, L. helveticus, L. hilgardii, L. homohiochii, L. iners, L. ingluviei, L. intestinalis, L. jensenii, L. johnsonii, L. kalixensis, L. kefiranofaciens, L. kefiri, L. kimchii, L. kitasatonis, L. kunkeei, L. leichmannii, L. lindneri, L. malefermentans, L. mali, L. manihotivorans, L. mindensis, L. mucosae, L. murinus, L. nagelii, L. namurensis, L. nantensis, L. oligofermentans, L. oris, L. panis, L. pantheris, L. parabrevis, L. parabuchneri, L. paracasei, L. paracollinoides, L. parafarraginis, L. parakefiri, L. paralimentarius, L. paraplantarum, L. pentosus, L. perolens, L. plantarum, L. pontis, L. protectus, L. psittaci, L. rennini, L. reuteri, L. rhamnosus, L. rimae, L. rogosae, L. rossiae, L. ruminis, L. saerimneri, L. sakei, L. salivarius, L. sanfranciscensis, L. satsumensis, L. secaliphilus, L. sharpeae, L. siliginis, L. spicheri, L. suebicus, L. thailandensis, L. ultunensis, L. vaccinostercus, L. vaginalis, L. versmoldensis, L. vini, L. vitulinus, L. zeae*, and *L. zymae*. In some embodiments, the non-*clostridium* strain is *Lactobacillus mucosae*. In some embodiments, the non-*clostridium* strain is *Lactobacillus* mucosae. In some embodiments, the *Lactobacillus mucosae* has a 16S rDNA sequence comprising SEQ ID NO:2. In some embodiments, the *Lactobacillus mucosae* has a 16S rDNA sequence having at least 97% homology with a nucleic acid comprising SEQ ID NO:2. In some embodiments, the *Lactobacillus mucosae* has a 16S rDNA sequence having at least 97% homology with a nucleic acid comprising SEQ ID NO:91.

In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition includes both *Clostridium* strains and non-*Clostridium* strains. In some embodiments, the non-*clostridium* strains are members of the genus *Turicibacter*. In some embodiments, the non-*clostridium* strain is *Turicibacter sanguinis*. In some embodiments, the *Turicibacter sanguinis* has a 16S rDNA sequence comprising SEQ ID NO:6. In some embodiments, the *Turicibacter sanguinis* has a 16S rDNA sequence having at least 97% homology with a nucleic acid comprising SEQ ID NO:6. In some embodiments, the *Turicibacter sanguinis* has a 16S rDNA sequence having at least 97% homology with a nucleic acid comprising SEQ ID NO:90.

In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition includes both *Clostridium* strains and non-*Clostridium* strains. In some embodiments, the non-*Clostridium* strains are *Lactobacillus mucosae* and *Turicibacter sanguinis*.

In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Lactobacillus*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Turicibacter*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Lactobacillus* or *Turicibacter*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition only includes *clostridia* strains. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition only includes *clostridia* strains belonging to *Clostridium* cluster IV, XIVa or XVII strains. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Clostridium* cluster XI strains.

In some embodiments, the disclosure provides compositions comprising two or more purified bacterial strains selected from the group consisting of: *Clostridium scindens, Pseudoflavonifractor capillosus*, and *Blautia hansenii*. In some embodiments, the compositions disclosed herein do not include *Clostridium scindens, Pseudoflavonifractor capillosus*, or *Blautia hansenii*.

TABLE D

Composition D
SEQ_12 - VE202-26 - *Clostridium_scindens* (XIVa)*
SEQ_03 - 5 - *Clostridium_hathewayi* (XIVa)*
SEQ_05 - 10 - *Blautia_hansenii* (XIVa)*
SEQ_01 - 71 - *Blautia_wexlerae* (XIVa)*
SEQ_14 - VE202-13 - *Anaerotruncus_colihominis* (IV)
SEQ_18 - 148 - *Dorea_longicatena* (XIVa)
SEQ_21 - 189 - *Clostridium_innocuum* (XVII)
SEQ_10 - 211 - *Flavonifractor_plautii* (IV
SEQ_02 - 102 - *Turicibacter_sanguinis* (non-*Clostridium*)
SEQ_06 - 40 - *Lactobacillus_mucosae* (non-*Clostridium*)

*= BaiCD+

In one aspect, the disclosure provides Composition F (See e.g., FIGS. **13** and **14**, and Tables F1 and F2). As shown in FIG. **13**, Composition F contains bacteria that have the following 16S rDNA sequences: SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, and SEQ ID NO:79.

In some embodiments, the disclosure provides compositions with two or more purified bacterial strains that have 16S rDNA sequences selected from the group consisting of SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72,

SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, and SEQ ID NO:79.

In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:24, SEQ ID NO:25, SEQ ID NO:26, SEQ ID NO:27, SEQ ID NO:28, SEQ ID NO:29, SEQ ID NO:30, SEQ ID NO:31, SEQ ID NO:32, SEQ ID NO:33, SEQ ID NO:34, SEQ ID NO:35, SEQ ID NO:36, SEQ ID NO:37, SEQ ID NO:38, SEQ ID NO:39, SEQ ID NO:40, SEQ ID NO:41, SEQ ID NO:42, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:45, SEQ ID NO:46, SEQ ID NO:47, SEQ ID NO:48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53, SEQ ID NO:54, SEQ ID NO:55, SEQ ID NO:56, SEQ ID NO:57, SEQ ID NO:58, SEQ ID NO:59, SEQ ID NO:60, SEQ ID NO:61, SEQ ID NO:62, SEQ ID NO:63, SEQ ID NO:64, SEQ ID NO:65, SEQ ID NO:66, SEQ ID NO:67, SEQ ID NO:68, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:72, SEQ ID NO:73, SEQ ID NO:74, SEQ ID NO:75, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:78, and SEQ ID NO:79.

The bacterial strains in Composition F are related to the following bacteria: *Dorea longicatena, Ruminococcus obeum, Megasphaera elsdenii, Acidaminococcus fermentans, Acidaminococcus intestine, Megasphaera elsdenii, Ruminococcus faecis, Bacteroides cellulosilyticus, Anaerostipes hadrus, Ruminococcus obeum, Flavonifractor plautii, Eubacterium rectale, Flavonifractor plautii, Megasphaera elsdenii, Eubacterium rectale, Ruminococcus champanellensis, Ruminococcus albus, Ruminococcus champanellensis, Ruminococcus faecis, Bifidobacterium bifidum, Anaerostipes hadrus, Anaerostipes hadrus, Anaerostipes hadrus, Eubacterium rectale, Ruminococcus faecis, Blautia luti, Ruminococcus faecis, Anaerostipes hadrus, Anaerostipes hadrus, Ruminococcus faecis, Eubacterium rectale, Eubacterium rectale, Anaerostipes hadrus, Ruminococcus faecis, Ruminococcus faecis, Dorea longicatena, Roseburia faecis, Blautia luti, Fusicatenibacter saccharivorans, Fusicatenibacter saccharivorans, Roseburia faecis, Megasphaera elsdenii, Eubacterium rectale, Eubacterium rectale, Roseburia faecis, Blautia faecis, Fusicatenibacter saccharivorans*, and *Dorea formicigenerans.*

In some embodiments, the disclosure provides compositions with two or more bacterial strains of species selected from the group consisting of *Dorea longicatena, Ruminococcus obeum, Megasphaera elsdenii, Acidaminococcus fermentans, Acidaminococcus intestine, Megasphaera elsdenii, Ruminococcus faecis, Bacteroides cellulosilyticus, Anaerostipes hadrus, Ruminococcus obeum, Flavonifractor plautii, Eubacterium rectale, Flavonifractor plautii, Megasphaera elsdenii, Eubacterium rectale, Ruminococcus champanellensis, Ruminococcus albus, Ruminococcus champanellensis, Ruminococcus faecis, Bifidobacterium bifidum, Anaerostipes hadrus, Anaerostipes hadrus, Anaerostipes hadrus, Eubacterium rectale, Ruminococcus faecis, Blautia luti, Ruminococcus faecis, Anaerostipes hadrus, Anaerostipes hadrus, Ruminococcus faecis, Eubacterium rectale, Eubacterium rectale, Anaerostipes hadrus, Ruminococcus faecis, Ruminococcus faecis, Dorea longicatena, Roseburia faecis, Blautia luti, Fusicatenibacter saccharivorans, Fusicatenibacter saccharivorans, Roseburia faecis, Megasphaera elsdenii, Eubacterium rectale, Eubacterium rectale, Roseburia faecis, Blautia faecis, Fusicatenibacter saccharivorans*, and *Dorea formicigenerans.*

In some embodiments, the disclosure provides compositions that include two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:100, SEQ ID NO:104, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, SEQ ID NO:118, SEQ ID NO:119, and SEQ ID NO:120. It should be appreciated that multiple strains of the compositions disclosed herein can have the same related bacterial species. For instance, Composition F includes 12 strains that have *Eubacterium rectale* as the closest related species.

In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IV. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XIVa. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IX. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IV. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XIVa and at least one of the bacterial strains belongs to *Clostridium* cluster IX. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IV and at least one of the bacterial strains belongs to *Clostridium* cluster IX. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IV, at least one of the bacterial strains belongs to *Clostridium* cluster XIVa, and at least one of the bacterial strains belongs to *Clostridium* cluster IX. In some embodiments, the compositions provided herein do not include bacterial strains belonging to *Clostridium* cluster XVIII. In some embodiments, the compositions provided herein do not include bacterial strains belonging to *Clostridium* cluster XVI or XVIII.

Composition F includes non-*clostridium* bacterial strains. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition includes both *Clostridium* strains and non-*clostridium* strains. In some embodiments, the non-*clostridium* strains are the members of the genus *Bacteroides*. In some embodiments, the non-*clostridium* strain is *Bacteroides* cellulosilyticus. In some embodiments, the non-*clostridium* strains are the members of the genus *Bifidobacterium*. In some embodiments, the non-*clostridium* strain is *Bifidobacterium bifidum*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition includes both *Clostridium* strains and non-*Clostridium* strains, and wherein the non-*Clostridium* strains are *Bacteroides* cellulosilyticus and *Bifidobacterium bifidum.*

In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Bacteroides*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Bifidobacterium*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Bacteroides* and does not include *Bifidobacterium*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include non-*Clostridium* strains. In some embodiments, the disclosure

provides compositions comprising two or more bacteria, wherein the composition only includes *clostridia* strains belonging to *Clostridium* cluster IV, XIVa or XVII strains. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Clostridium* cluster XI strains.

TABLE F1

Composition F

SEQ_NO	StrainID	Genus_species
SEQ_24	YK96	*Dorea_longicatena*
SEQ_25	YK101	*Ruminococcus_obeum*
SEQ_26	YK110	*Megasphaera_elsdenii*
SEQ_27	YK149	*Acidaminococcus_fermentans/ Acidaminococcus_intestini*
SEQ_28	YK154	*Megasphaera_elsdenii*
SEQ_29	YK36	*Ruminococcus_faecis*
SEQ_30	YK95	*Bacteroides_cellulosilyticus*
SEQ_31	YK32	*Anaerostipes_hadrus*
SEQ_32	YK64	*Ruminococcus_obeum*
SEQ_33	YK73	*Flavonifractor_plautii*
SEQ_34	YK87	*Eubacterium_rectale*
SEQ_35	YK105	*Flavonifractor_plautii*
SEQ_36	YK153	*Megasphaera_elsdenii*
SEQ_37	YK163	*Eubacterium_rectale*
SEQ_38	YK191	*Ruminococcus_champanellensis/ Ruminococcus_albus*
SEQ_39	YK99	*Ruminococcus_champanellensis*
SEQ_40	YK55	*Ruminococcus_faecis*
SEQ_41	YK75	*Bifidobacterium_bifidum*
SEQ_42	YK90	*Anaerostipes_hadrus*
SEQ_43	YK30	*Anaerostipes_hadrus*
SEQ_44	YK31	*Anaerostipes_hadrus*
SEQ_45	YK12	*Eubacterium_rectale*
SEQ_46	YK27	*Ruminococcus_faecis*
SEQ_47	YK28	*Blautia_luti*
SEQ_48	YK29	*Ruminococcus_faecis*
SEQ_49	YK33	*Anaerostipes_hadrus*
SEQ_50	YK34	*Anaerostipes_hadrus*
SEQ_51	YK35	*Ruminococcus_faecis*
SEQ_52	YK51	*Eubacterium_rectale*
SEQ_53	YK52	*Eubacterium_rectale*
SEQ_54	YK54	*Anaerostipes_hadrus*
SEQ_55	YK56	*Ruminococcus_faecis*
SEQ_56	YK57	*Ruminococcus_faecis*
SEQ_57	YK58	*Dorea_longicatena*
SEQ_58	YK65	*Roseburia_faecis*
SEQ_59	YK67	*Blautia_luti*
SEQ_60	YK69	*Fusicatenibacter_saccharivorans*
SEQ_61	YK70	*Fusicatenibacter_saccharivorans*
SEQ_62	YK71	*Roseburia_faecis*
SEQ_63	YK74	*Megasphaera_elsdenii*
SEQ_64	YK88	*Eubacterium_rectale*
SEQ_65	YK89	*Eubacterium_rectale*
SEQ_66	YK97	*Roseburia_faecis*
SEQ_67	YK98	*Blautia_faecis*
SEQ_68	YK139	*Fusicatenibacter_saccharivorans*
SEQ_69	YK141	*Dorea_formicigenerans*
SEQ_70	YK142	*Ruminococcus_faecis*
SEQ_71	YK152	*Blautia_hansenii*
SEQ_72	YK155	*Blautia_hansenii*
SEQ_73	YK157	*Eubacterium_rectale*
SEQ_74	YK160	*Roseburia_faecis*
SEQ_75	YK166	*Eubacterium_rectale*
SEQ_76	YK168	*Eubacterium_rectale*
SEQ_77	YK169	*Eubacterium_rectale*
SEQ_78	YK171	*Eubacterium_rectale*
SEQ_79	YK192	*Roseburia_faecis*

TABLE F2

Composition F, strain groupings

Cluster	Composition F	*SCFAs
XIVa	*Eubacterium rectale* 12	A, B, L
	Ruminococcus faecis 8	A, L
	Ruminococcus obeum 2	A, L
	Blautia faecis 1	A, L
	Blautia hansenii 2	A, L
	Blautia luti 2	A, L
	Anaerostipes hadrus 7	B
	Roseburia faecis 5	A, B
	Fusicatenibacter saccharivorans 3	A, L
	Dorea formicigenerans 1	A
	Dorea longicatena 2	A
IV	*Flavonifractor_plautii* 2	A, B
	Ruminococcus champanellensis 2	A
IX	*Acidaminococcus fermentans* 1	A, B, P
	Megasphaera elsdeni 4	P
other	*Bacteroides cellulosilyticus* 1	A, S
	Bifiidobacterium Bifidum	L, A

*Short chain fatty acid legend: A, acetate; B, Butyrate; L, lactate; P, propionate; S, succinate

In one aspect, the disclosure provides Composition G (See e.g., FIG. **19**; Table G). As shown in FIG. **19**, Composition G contains bacteria that have the following 16S rDNA sequences: SEQ ID NO:27, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:70, SEQ ID NO:24, SEQ ID NO:34, SEQ ID NO:37, SEQ ID NO:46, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:35, SEQ ID NO:62, SEQ ID NO:26, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:40, SEQ ID NO:38, SEQ ID NO:47, SEQ ID NO:56, SEQ ID NO:25, and SEQ ID NO: 32.

In some embodiments, the disclosure provides compositions with two or more purified bacterial strains that have 16S rDNA sequences selected from the group consisting of SEQ ID NO:27, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:70, SEQ ID NO:24, SEQ ID NO:34, SEQ ID NO:37, SEQ ID NO:46, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:35, SEQ ID NO:62, SEQ ID NO:26, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:40, SEQ ID NO:38, SEQ ID NO:47, SEQ ID NO:56, SEQ ID NO:25, and SEQ ID NO: 32.

In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:27, SEQ ID NO:43, SEQ ID NO:44, SEQ ID NO:51, SEQ ID NO:55, SEQ ID NO:68, SEQ ID NO:72, SEQ ID NO:70, SEQ ID NO:24, SEQ ID NO:34, SEQ ID NO:37, SEQ ID NO:46, SEQ ID NO:76, SEQ ID NO:77, SEQ ID NO:35, SEQ ID NO:62, SEQ ID NO:26, SEQ ID NO:63, SEQ ID NO:67, SEQ ID NO:40, SEQ ID NO:38, SEQ ID NO:47, SEQ ID NO:56, SEQ ID NO:25, and SEQ ID NO: 32.

The bacterial strains in Composition G are related to the following bacteria: *Acidaminococcus fermentans, Acidaminococcus intestine, Anaerostipes hadrus, Blautia faecis, Blautia hansenii, Dorea formicigenerans, Dorea longicatena, Eubacterium rectale, Flavonifractor plautii, Fusicatenibacter saccharivorans, Megasphaera elsdenii, Roseburia faecis, Ruminococcus champanellensis, Ruminococcus albus, Ruminococcus faecis*, and *Ruminococcus obeum.*

In some embodiments, the disclosure provides compositions with two or more bacterial strains of species selected from the group consisting of *Acidaminococcus fermentans, Acidaminococcus intestine, Anaerostipes hadrus, Blautia faecis, Blautia hansenii, Dorea formicigenerans, Dorea longicatena, Eubacterium rectale, Flavonifractor plautii, Fusicatenibacter saccharivorans, Megasphaera elsdenii, Roseburia faecis, Ruminococcus champanellensis, Ruminococcus albus, Ruminococcus faecis*, and *Ruminococcus obeum.*

In some embodiments, the disclosure provides compositions that include two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:84, SEQ ID NO:85, SEQ ID NO:92, SEQ ID NO:93, SEQ ID NO:96, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:104, SEQ ID NO:107, SEQ ID NO:111, SEQ ID NO:112, SEQ ID NO:113, SEQ ID NO:114, SEQ ID NO:115, SEQ ID NO:116, SEQ ID NO:117, and SEQ ID NO:119.

TABLE G

Composition G

SEQ_27	YK149	*Acidaminococcus_fermentans/ Acidaminococcus_intesti*
SEQ_43	YK90	*Anaerostipes_hadrus*
SEQ_44	YK30	*Anaerostipes_hadrus*
SEQ_51	YK34	*Anaerostipes_hadrus*
SEQ_55	YK54	*Anaerostipes_hadrus*
SEQ_68	YK98	*Blautia_faecis*
SEQ_72	YK152	*Blautia_hansenii*
SEQ_70	YK141	*Dorea_formicigenerans*
SEQ_24	YK96	*Dorea_longicatena*
SEQ_34	YK87	*Eubacterium_rectale*
SEQ_37	YK163	*Eubacterium_rectale*
SEQ_46	YK12	*Eubacterium_rectale*
SEQ_76	YK166	*Eubacterium_rectale*
SEQ_77	YK168	*Eubacterium_rectale*
SEQ_35	YK105	*Flavonifractor_plautii*
SEQ_62	YK70	*Fusicatenibacter_saccharivorans*
SEQ_26	YK110	*Megasphaera_elsdenii*
SEQ_63	YK71	*Roseburia_faecis*
SEQ_67	YK97	*Roseburia_faecis*
SEQ_40	YK99	*Ruminococcus_champanellensis*
SEQ_38	YK191	*Ruminococcus_champanellensis/ Ruminococcus_albus*
SEQ_47	YK27	*Ruminococcus_faecis*
SEQ_56	YK56	*Ruminococcus_faecis*
SEQ_25	YK101	*Ruminococcus_obeum*
SEQ_32	YK64	*Ruminococcus_obeum*

In one aspect, the disclosure provides Composition H (See e.g., FIG. **26**, Table H). As shown in FIG. **26**, Composition H contains bacteria that have the following 16S rDNA sequences: SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:21, SEQ ID NO:82, SEQ ID NO:81, and SEQ ID NO:80. In some embodiments, the disclosure provides compositions with two or more purified bacterial strains that have 16S rDNA sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:21, SEQ ID NO:82, SEQ ID NO:81, and SEQ ID NO:80.

In some embodiments, the compositions include two or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:21, SEQ ID NO:82, SEQ ID NO:81, and SEQ ID NO:80. In some embodiments, the compositions include four or more purified bacterial strains comprising 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:21, SEQ ID NO:82, SEQ ID NO:81, and SEQ ID NO:80.

The bacterial strains in Composition H are related to the following bacteria: *Anaerotruncus colihominis, Clostridium symbiosum, Clostridium innocuum, Erysipelotrichaceae*_bacterium_21-3, *Clostridium disporicum, Clostridium bolteae*, and *Erysipelatoclostridium ramosum.* In some embodiments, the disclosure provides compositions with two or more bacterial strains selected from the group consisting of *Anaerotruncus colihominis, Clostridium symbiosum, Clostridium innocuum, Erysipelotrichaceae_bacterium_21-3, Clostridium disporicum, Clostridium bolteae*, and *Erysipelatoclostridium ramosum.*

In some embodiments, the disclosure provides compositions that include two or more purified bacterial strains comprise 16S rDNA sequences having at least 97% homology with nucleic acid sequences selected from the group consisting of SEQ ID NO:86, SEQ ID NO:95, SEQ ID NO:98, SEQ ID NO:110, SEQ ID NO:122, and SEQ ID NO:123.

Composition H includes bacteria from *Clostridium* cluster I, IV, XIVa, XVII and XVIII. In some embodiments, the disclosure provides compositions that include two or more purified bacterial strains from *Clostridium* cluster I, IV, XIVa, XVII and XVIII. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster IV. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XIVa. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XVII. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster I. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XVIII. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XIVa and at least one of the bacterial strains belongs to *Clostridium* cluster IV. In some embodiments, at least one of the bacterial strains of the composition belongs to *Clostridium* cluster XIVa and at least one of the bacterial strains belongs to *Clostridium* cluster XVII.

TABLE H

Composition H

SEQ ID NO	Strain	Closest species	Cluster
SEQ ID NO: 14	VE202-13	*Anaerotruncus colihominis*	Cluster IV
SEQ ID NO: 16	VE202-16	*Clostridium symbiosum* WAL-14163	Cluster XIVa
SEQ ID NO: 21	189	*Clostridium innocuum*	Cluster XVII
SEQ ID NO: 82	PE9	*Clostridium disporicum*	Cluster I
SEQ ID NO: 81	PE5	*Clostridium bolteae*	Cluster XIVa
SEQ ID NO: 80	VE202-18	*Erysipelatoclostridium ramosum*	Cluster XVIII

In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include bacteria from *Clostridium* cluster I. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include bacteria from *Clostridium* cluster XVIII. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include bacteria from *Clostridium* cluster I and does not include bacteria from *Clostridium* cluster XVIII.

In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein all the bacteria are anaerobic bacteria. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein all the bacteria are obligate anaerobic bacteria.

In some embodiments, the disclosure provides compositions comprising two or more bacteria (e.g., purified bacterial strains), wherein the composition does not include *Clostridium scindens*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Flavonifractor plautii*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include Parabacteroides. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Lactobacillus*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Colinsella*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Dialister*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Raoultella*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Streptococcus*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Staphylococcus*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Microbacterium*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Proteobacteria*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Peptostreptococcaceae*. In some embodiments, the disclosure provides compositions comprising two or more bacteria, wherein the composition does not include *Oscillospiraceae*.

In one aspect, the disclosure provides bacterial strains with 16S rDNA sequences that have homology to a nucleic acid sequence of any one of the sequences of the bacterial strains or species described herein. In some embodiments, the bacterial strain has at least 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% homology relative to any of the strains or bacterial species described herein over a specified region or over the entire sequence. It would be appreciated by one of skill in the art that the term "homology" or "percent homology," in the context of two or more nucleic acid sequences or amino acid sequences, refers to a measure of similarity between two or more sequences or portion(s) thereof. The homology may exist over a region of a sequence that is at least about 50 nucleotides in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides in length. In some embodiments, the homology exists over the length the 16S rRNA or 16S rDNA sequence, or a portion thereof.

Additionally, or alternatively, two or more sequences may be assessed for the identity between the sequences. The terms "identical" or percent "identity" in the context of two or more nucleic acids or amino acid sequences, refer to two or more sequences or subsequences that are the same. Two sequences are "substantially identical" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (e.g., at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% identical) over a specified region or over the entire sequence, when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the identity exists over a region that is at least about 50 nucleotides in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides in length. In some embodiments, the identity exists over the length the 16S rRNA or 16S rDNA sequence.

Additionally, or alternatively, two or more sequences may be assessed for the alignment between the sequences. The terms "alignment" or percent "alignment" in the context of two or more nucleic acids or amino acid sequences, refer to two or more sequences or subsequences that are the same. Two sequences are "substantially aligned" if two sequences have a specified percentage of amino acid residues or nucleotides that are the same (e.g., at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8% or 99.9% identical) over a specified region or over the entire sequence, when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. Optionally, the alignment exists over a region that is at least about 50 nucleotides in length, or more preferably over a region that is 100 to 500 or 1000 or more nucleotides in length. In some embodiments, the identity exists over the length the 16S rRNA or 16S rDNA sequence.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. Methods of alignment of sequences for comparison are well known in the art. See, e.g., by the local homology algorithm of Smith and Waterman (1970) *Adv. Appl. Math.* 2:482c, by the homology alignment algorithm of Needleman and Wunsch, *J. Mol. Biol.* (1970) 48:443, by the search for similarity method of Pearson and Lipman. *Proc. Natl. Acad. Sci. USA* (1998) 85:2444, by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group. Madison. Wis.), or by manual alignment and visual inspection (see. e.g., Brent et al., Current Protocols in Molecular Biology, John Wiley & Sons, Inc. (Ringbou ed., 2003)). Two examples of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., *Nuc. Acids Res.* (1977) 25:3389-3402, and Altschul et al., *J. Mol. Biol.* (1990) 215:403-410, respectively.

In one aspect, the disclosure provides compositions comprising multiple purified bacterial strains (e.g., Compositions A-J). For instance, FIGS. **1**, **13**, **19**, and **26** present several example compositions comprising multiple bacterial strains. In one aspect, the 16S rDNA sequences of purified bacterial strains of the compositions were compared to 16S rDNA sequences of known bacterial species/strains in a bacterial genome database to identify the closest known related bacterial species to the bacterial strains disclosed herein (See e.g., Table 1). It should be appreciated that multiple bacterial strains of the compositions disclosed herein may have the same closest related bacterial species. In one aspect, the disclosure provides compositions comprising one or more bacterial strains or species with 16S rDNA sequences that have homology to a nucleic acid

sequence of any one of the sequences provided by SEQ ID NOs:1-83 and 124-159. In some embodiments, the species with 16S rDNA sequences with homology to a nucleic acid sequence of any one of the closest related species to any of the strains described herein, correspond to bacterial strains with 16S rDNA sequences provided by SEQ ID NOs:84-123.

In some embodiments, the compositions disclosed herein provide at least one of the bacterial strains (e.g., purified bacterial strains) described herein. In some embodiments, the compositions that comprise at least one bacterial strain, comprise at least one bacterial strain with a 16S rDNA sequence selected from any one of SEQ ID NOs:1-122 and 124-159. In some embodiments, the compositions that comprise at least one bacterial strain, comprise at least one bacterial strain with a 97% homology to 16S rDNA sequence selected from any one of SEQ ID NOs:1-122 and 124-159.

In some embodiments, the compositions disclosed herein comprise two or more bacterial strains. In some embodiments, the compositions described herein comprise at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, or at least 20 or more bacterial strains (e.g., purified bacterial strains).

It should be appreciated the compositions and methods provided herein can be distinguished from compositions and methods associated with the treatment of *C. difficile* infection that are available. For instance, it has been proposed that non-toxigenic *C. difficile* strains, i.e., strains that do not produce *C. difficile* toxins, may be used to treat *C. difficile* infection (See, e.g., U.S. Pat. No. 6,635,260). The compositions disclosed herein can be distinguished at least because the compositions described herein do not comprise non-toxigenic strains of *C. difficile*. Thus, in some embodiments, the compositions herein do not include comprise non-toxigenic strains of *C. difficile*. *C. difficile* belongs to *Clostridium* cluster XI. In some embodiments, the compositions herein do not include bacterial strains belonging to *Clostridium* cluster XI.

It is also considered in the art that bacterial strains expressing a bile inducible 7α/β-dehydroxylation operon can be used in the treatment of *C. difficile* (see, e.g., Buffie et al. *Nature* (2015) 517:205-208). The catalysis of bile acid 7a dihydroxylation is mediated by a stereo-specific NAD (H)-dependent 3-oxo-Δ^4-cholenoic acid oxidoreductase encoded by the gene baiCD. In some embodiments, the compositions provided herein do not mediate bile acid 7-alpha-dehydroxylation.

In contrast to the findings in the art, in some embodiments, as shown herein, combinations of bacterial strains that do not encode baiCD (or a homolog thereof), or encode a baiCD that comprises one or more mutations that result in a non-functional BaiCD protein ("baiCD−"), are more effective at treating *C. difficile* infection and/or reducing or inhibiting production of Toxin B by *C. difficile* than combinations of bacterial strains that have a functional BaiCD protein ("baiCD+"). Thus, in some embodiments, the compositions of bacterial strains provided herein are baiCD− (i.e., the combination of the bacteria has no effective baiCD+ function). In some embodiments, all of bacterial strains in the compositions provided herein are baiCD−. In some embodiments, the majority (i.e., 50% or greater) of the bacterial strains in the compositions are baiCD−. In some embodiments, the majority (i.e., 50% or greater) of the bacterial strains in the compositions are baiCD− and the composition has no effective BaiCD function. In some embodiments, the minority (i.e., 50% or less) of the bacterial strains in the compositions are baiCD- and the composition has no effective BaiCD function. In some embodiments, bacterial strains for the compositions are selected based on the absence (or presence) of a baiCD gene or a predicted baiCD gene. In some embodiments, bacterial strains may be modified (e.g., genetically engineered) to prevent or reduce expression of a baiCD gene and/or to reduce or eliminate NAD(H)-dependent 3-oxo-Δ^4-cholenoic acid oxidoreductase activity of BaiCD protein. The NAD(H)-dependent 3-oxo-Δ^4-cholenoic acid oxidoreductase activity of a bacterial strain may be assessed by methods such as measuring the amount of 7α-dehydroxylated bile acid. In some embodiments, the compositions described herein comprise bacterial strains without the baiCD operon (baiCD$^-$) or baiCD function.

In some embodiments, the compositions described herein do not include *Clostridium scindens*. In some embodiments, the compositions described herein do not include *Barnesiella intestihominis*. In some embodiments, the compositions described herein do not include *Blautia hansenii*. In some embodiments, the compositions described herein do not include *Pseudoflavinofractor capillosus*. In some embodiments, the compositions described herein do not include *Clostridium scindens. Barnesiella intestihominis, Blautia hansenii* or *Pseudoflavinofractor capillosus*.

In some embodiments, the compositions provided herein do not include *Colinsella aerofaciens*. In some embodiments, the compositions provided herein do not include *Acetovibrio ethanolgignens*. In some embodiments, the compositions provided herein do not bacterial strains belonging to *Clostridum* cluster I. In some embodiments, the compositions provided herein do not include *Clostridium butyricum*. In some embodiments, the compositions provided herein do not include *Clostridium disporicum*. In some embodiments, the compositions provided herein do not include strains belonging to *Clostridum* cluster XI. In some embodiments, the compositions provided herein do not include *Clostridium glycolicum*. In some embodiments, the compositions provided herein do not include *Faecalibacterium prausnitzii*. In some embodiments, the compositions provided herein do not include *Turicibacter sanguinis*. In some embodiments, the compositions provided herein do not include *Eubacterium rectale*. In some embodiments, the compositions provided herein do not include *Eubacterium ventriosum*. In some embodiments, the compositions provided herein do not include *Ruminococcus obeum*. In some embodiments, the compositions provided herein do not include *Pseudobutyrivibrio*. In some embodiments, the compositions provided herein do not include *Christensenellaceae*. In some embodiments, the compositions do not comprise gram-negative bacteria. In some embodiments, the compositions do not comprise *E. coli*. In some embodiments, the compositions do not comprise fungi, such as *Monilla* species.

In some embodiments of the compositions provided herein, the compositions do not include bacterial strains that are resistant to one or more antibiotics. It should be appreciated that it may be desirable to have a mechanism to remove the bacterial compositions provided herein from the body of the subject after administration. One such mechanism is to remove the bacterial compositions by antibiotic treatment. Thus, in some embodiments, the compositions do not include bacterial strains that are resistant to one or more antibiotics. In some embodiments, the compositions do not include bacterial strains that are resistant to one or more

antibiotics selected from the group consisting of penicillin, benzylpenicillin, ampicillin, sulbactam, amoxicillin, clavulanate, tazobactam, piperacillin, cefmetazole, vancomycin, imipenem, meropenem, metronidazole and clindamycin. In some embodiments, the compositions do not include bacterial strains that are resistant to vancomycin.

In some embodiments, the compositions include bacterial strains that are susceptible to at least four antibiotics that are efficacious in humans. In some embodiments, the compositions include bacterial strains that are susceptible to at least three antibiotics that are efficacious in humans. In some embodiments, the compositions include bacterial strains that are susceptible to at least two antibiotics that are efficacious in humans. In some embodiments, the compositions include bacterial strains that are susceptible to at least one antibiotic that is efficacious in humans. In some embodiments, the compositions include only bacterial strains that are susceptible to at least four antibiotics that are efficacious in humans. In some embodiments, the compositions include only bacterial strains that are susceptible to at least three antibiotics that are efficacious in humans. In some embodiments, the compositions include only bacterial strains that are susceptible to at least two antibiotics that are efficacious in humans. In some embodiments, the compositions include bacterial strains that are susceptible to at least one antibiotic that is efficacious in humans. As used herein, an "antibiotic that is efficacious in a human" refers to an antibiotic that has been used to successfully treat bacterial infections in a human.

In some embodiments, the compositions described herein comprise spore forming and non-spore forming bacterial strains. In some embodiments, the compositions described herein comprise spore forming bacterial strains. In some embodiments, the compositions described herein comprise only spore forming bacterial strains. In some embodiments, the compositions described herein comprise only non-spore forming bacterial strains. The spore-forming bacteria can be in spore form (i.e., as spores) or in vegetative form (i.e., as vegetative cells). In spore form, bacteria are generally more resistant to environmental conditions, such as heat, acid, radiation, oxygen, chemicals, and antibiotics. In contrast, in the vegetative state or actively growing state, bacteria are more susceptible to such environmental conditions, compared to in the spore form. In general, bacterial spores are able to germinate from the spore form into a vegetative/actively growing state, under appropriate conditions. For instance, bacteria in spore format may germinate when they are introduced in the intestine.

In some embodiments, at least one (e.g., 1, 2, 3, 4, 5, or more) of the bacterial strains in the composition is a spore former. In some embodiments, at least one (e.g., 1, 2, 3, 4, 5, or more) of the bacterial strains in the composition is in spore form. In some embodiments, at least one (e.g., 1, 2, 3, 4, 5, or more) of the bacterial strains in the composition is a non-spore former. In some embodiments, at least one (e.g., 1, 2, 3, 4, 5, or more) of the bacterial strains in the composition is in vegetative form (As discussed above, spore forming bacteria can also be in vegetative form). In some embodiments, at least one (e.g., 1, 2, 3, 4, 5, or more) of the bacterial strains in the composition is in spore form and at least one (e.g., 1, 2, 3, 4, 5, or more) of the bacterial strains in the composition is in vegetative form. In some embodiments, at least one bacterial strain that is considered able to form spores (i.e., a spore-former) but is present in the composition in vegetative form. In some embodiments, at least one bacterial strain that is considered able to form spores is present in the composition both in spore form and in vegetative form.

In some embodiments, the disclosure provides compositions wherein the compositions comprise bacterial strains that are spore forming bacterial strains. In some embodiments, the disclosure provides compositions wherein the compositions comprise bacterial strains that are non-spore forming bacterial strains. In some embodiments, the disclosure provides compositions wherein the compositions comprise bacterial strains that are spore forming bacterial strains and bacterial strains that are non-spore forming bacterial strains. In some embodiments, the disclosure provides compositions, wherein the compositions comprise a mixture of bacterial strains wherein at least 10% of the bacterial strains are spore forming bacterial strains, at least 20% of the bacterial strains are spore forming bacterial strains, at least 30% of the bacterial strains are spore forming bacterial strains, at least 40% of the bacterial strains are spore forming bacterial strains, at least 50% of the bacterial strains are spore forming bacterial strains, at least 60% of the bacterial strains are spore forming bacterial strains, at least 70% of the bacterial strains are spore forming bacterial strains, at least 80% of the bacterial strains are spore forming bacterial strains, at least 90% of the bacterial strains are spore forming bacterial strains bacteria up to 100% spore forming bacterial strains. Whether a bacterial strain is a spore forming strain can be determined for instance by evaluating the genome of the bacterial strain for the presence of sporulation genes. However, it should be appreciated that not all bacteria that are predicted to encode spore forming genes can be made to sporulate. In addition, whether a bacterial strain is a spore forming strain can be determined by exposing the bacterial strain to stress conditions, e.g., heat or exposure to chemicals (e.g., ethanol or chloroform), that are known to induce sporulation.

It should be appreciated that spore forming bacteria can be in spore form or in vegetative form. In some embodiments of the compositions provided herein, the spore forming bacteria are in spore form. In some embodiments of the compositions provided herein, the spore forming bacteria are in vegetative form. In some embodiments of the compositions provided herein, the spore forming bacteria are both present in spore form and in vegetative form. In some embodiments, the disclosure provides compositions, wherein the compositions comprise spore forming bacteria at least 10% of the spore forming bacteria are in spore format, at least 20% of the spore forming bacteria are in spore format, at least 30% of the spore forming bacteria are in spore format, at least 40% of the spore forming bacteria are in spore format, at least 50% of the spore forming bacteria are in spore format, at least 60% of the spore forming bacteria are in spore format, at least 70% of the spore forming bacteria are in spore format, at least 80% of the spore forming bacteria are in spore format, at least 90% of the spore forming bacteria are in spore format, up to 100% in spore format.

It is envisioned that the bacterial strains of the compositions provided herein are alive and will be alive when they reach the target area (e.g., the intestines). Bacterial spores are considered to be alive in this regards. In some embodiments, bacteria that are administered as spores may germinate in the target area (e.g., the intestines). It should further be appreciated that not all of the bacteria are alive and the compositions can include a percentage (e.g., by weight) that is not alive. In addition, in some embodiments, the compositions include bacterial strains that are not alive when

administered or at the time when the composition reaches the target area (e.g., the intestines). It is envisioned that non-living bacteria may still be useful by providing some nutrients and metabolites for the other bacterial strains in the composition.

Methods of inducing sporulation of spore-forming bacterial strains are well known in the art (See e.g., Paredes-Sabja et al., *Trends Microbial.* (2011) 19(2):85-94). Generally, bacterial strains that are spore-formers can be made to go into spore form by stressing the bacterial strains. Non-limiting examples of stresses that can induce sporulation are an increase in temperature, change in the nutrients available and/or exposure to chemicals (e.g., ethanol or chloroform). It should be noted that bacteria that are non-spore formers, for instance because they are missing sporulation genes, cannot be made to sporulate by stress. To prepare compositions in which all the bacterial strains are in the spore form, the composition or bacterial cultures used to prepare the composition may be subjected to treatment to kill any bacteria not in spore form (e.g., in vegetative form), for example by exposing the composition to heat and are chemically breaking down the non-spore bacteria. The bacteria in spore format can subsequently be separated from the non-spore bacteria for instance by filtration.

The amount of spores can be quantified using techniques know in the art. These techniques include phase contrast microscopy for enumerating spores using a hemocytometer. In addition, the viability of spores can be determined by plating the spores and growing the spores. For instance, spores can be plated in appropriate media and incubated in the anaerobic chamber for a period of time (e.g., 48-96 hrs.). Viability can subsequently be determined by quantifying the colony forming units which correspond to spores that germinated. For instance, spores can be plated on TCCFA plates (Taurocholate, cycloserine, cefoxintin, fructose agar plates), in which taurocholate helps the spores to germinate. In addition, spores can be quantified using the dipicolinic assay (DPA assay). DPA is an agent that allows for spore selection and is a clear indicator of endospores. When complexed with terbium, bright green luminescence is observed.

In any of the compositions provided herein, in some embodiments, the bacterial strains are purified. In any of the compositions provided herein, in some embodiments, the bacterial strains are isolated. Any of the bacterial strains described herein may be isolated and/or purified, for example, from a source such as a culture or a microbiota sample (e.g., fecal matter). The bacterial strains used in the compositions provided herein generally are isolated from the microbiome of healthy individuals. However, bacterial strains can also be isolated from individuals that are considered not to be healthy. In some embodiments, the compositions include strains originating from multiple individuals.

As used herein, the term "isolated" bacteria that have been separated from one or more undesired component, such as another bacterium or bacterial strain, one or more component of a growth medium, and/or one or more component of a sample, such as a fecal sample. In some embodiments, the bacteria are substantially isolated from a source such that other components of the source are not detected.

As also used herein, the term "purified" refers to a bacterial strain or composition comprising such that has been separated from one or more components, such as contaminants. In some embodiments, the bacterial strain is substantially free of contaminants. In some embodiments, one or more bacterial strains of a composition may be independently purified from one or more other bacteria produced and/or present in a culture or a sample containing the bacterial strain. In some embodiments, a bacterial strain is isolated or purified from a sample and then cultured under the appropriate conditions for bacterial replication, e.g., under anaerobic culture conditions. The bacteria that is grown under appropriate conditions for bacterial replication can subsequently be isolated/purified from the culture in which it is grown.

In some embodiments, the bacterial strains of the compositions provided herein are obligate anaerobes. In some embodiments, the bacterial strains of the compositions provided herein are facultative anaerobes.

Aspects of the present disclosure are related to methods for treating a pathogenic infection in a subject by administering a therapeutically effective amount of any of the compositions described herein. In some embodiments, the subject is a mammalian subject, such as a human, non-human primate, rodent, rabbit, sheep, pig, dog, cat, horse, or cow. In some embodiments, the subject is a human subject. In some embodiments, the subject is a pig.

In some embodiments, the subject is a carrier of a pathogenic organism and is suffering from the effects of the infection (e.g., diarrhea caused by *C. difficile* toxins). In some embodiments the subject is an asymptomatic carrier of a pathogen. In some embodiments, the subject is a carrier of *C. difficile*. In some embodiments the subject is an asymptomatic *C. difficile* carrier. In some embodiments, the subject has experienced recurrent or chronic pathogenic infections. In some embodiments, the subject is suffering from a first occurrence of a particular pathogenic infection. In some embodiments, the subject has been treated with antibiotics which resulted in the recurrence of the pathogenic infection. In some embodiments, the subject has been treated with antibiotics which resulted in a first occurrence of a pathogenic infection. In some embodiments, the subject is to undergo a procedure that puts the subject at a higher risk of infection. In some embodiments, the compositions provided herein are administered to a subject to lower the risk of becoming infected by a pathogen.

In some embodiments, the compositions provided herein are administered to a subject if the subject has a dysbiosis (e.g., has as microbiome associated with a disease state). In some embodiments, treatment with the compositions provided herein results in the change in the microbiome of the subject. In some embodiments, treatment with the compositions provided herein removes the dysbiosis in the subject resulting in a healthy microbiome. In some embodiments, treatment with the compositions provided herein removes the dysbiosis in the subject resulting in microbiome refractory or less susceptible to infection by a pathogen.

As used herein, the term "pathogen" in regard to a pathogenic infection refers to a microorganism (e.g., a bacterium) that causes a disease or a disease state in a subject. In some embodiments, the disease or disease state of the subject may include symptoms such as colitis, diarrhea, watery diarrhea, abdominal cramping, fever, blood or pus in the stool, nausea, dehydration, loss of appetite, chills, weight loss, and/or kidney failure. In some embodiments, the pathogenic infection may be diagnosed, for example, by detecting a pathogen (or protein or nucleic acid associated with a pathogen) in a fecal sample collected from the subject. In some embodiments, the pathogenic infection may be diagnosed, for example, by comparing the microbiota of a fecal sample of the subject with the microbiota in a fecal sample of a healthy subject.

In some embodiments, the pathogenic infection is *C. difficile; Clostridium perfringens; Clostridium botulinum;*

Clostridium tributrycum; Clostridium sporogenes; Escherichia coli; Pseudomonas aeruginosa, such as Multidrug Resistant *Pseudomonas aeruginosa*; Vancomycin Resistant Enterococci (VRE); Carbapenem Resistant Enterobacteriaceae (CRE); *Neisseria gonorrheae; Acinetobacter*; Multidrug Resistant *Acinetobacter; Campylobacter*; Multi-drug resistant *Campylobacter; Candida*; Fluconazole-resistant *Candida*; Extended spectrum beta-lactamese (ESBL) producing Enterobacteriaceae; *Salmonella, Salmonella Typhimurium*, Drug resistant non-typhoid *Salmonella* spp.; Drug resistant *Salmonella Typhi*; Drug resistant *Shigella; Staphylococcus aureus*, such as Methicillin Resistant *S. aureus* or vancomycin resistant *S. aureus*; Drug resistant *Streptococcus pneumoniae*; Drug resistant Tuberculosis; Erythromycin Resistant Group A *Streptococcus*; Clindamycin resistant Group B *Streptococcus*, and any combinations thereof. In some embodiments, the pathogenic infection is *C. difficile*. In some embodiments, the *C. difficile* is an antibiotic-resistant *C. difficile*, e.g., fluoroquinolone resistant *C. difficile*. In some embodiments, the pathogenic infection is vancomycin-resistant Enterococci.

Additional non-limiting examples of pathogens responsible for pathogenic infection that can be treated according to the methods provided herein are *Leishmania, Staphylococcus epidermis, Staphylococcus saprophyticus, Streptococcus pyogenes, Streptococcus pneumoniae, Streptococcus agalactiae, Enterococcus faecalis, Corynebacterium diptheriae, Bacillus anthracis, Listeria monocytogenes, Clostridium perfringens, Clostridium tetanus, Clostridium botulinum, Clostridium difficile, Neisseria meningitidis, Neisseria gonorrhoeae, Escherichia coli, Salmonella typhimurium, Salmonella cholerasuis, Salmonella enterica, Salmonella enteriditis, Yersinia pestis, Yersinia pseudotuberculosis, Yersinia enterocolitica, Vibrio cholerae, Campylobacter jejuni, Campylobacter fetus, Helicobacter pylori, Pseudomonas aeruginosa, Pseudomonas mallei, Haemophilus influenzae, Bordetella pertussis, Mycoplasma pneumoniae, Ureaplasma urealyticum, Legionella pneumophila, Treponema pallidum, Leptospira interrogans, Borrelia burgdorferi, Mycobacterium tuberculosis, Mycobacterium leprae, Chlamydia psittaci, Chlamydia trachomatis, Chlamydia pneumoniae, Rickettsia ricketsii, Rickettsia akari, Rickettsia prowazekii, Brucella abortus, Brucella melitens, Brucella suis*, and *Francisella tularensis*. In general, any bacterium that is capable of inducing a disease in a subject and/or that is not present in healthy individual is considered a pathogen herein. It should be appreciated that a subject may carry multiple pathogens and/or have multiple pathogenic infections.

Any of the compositions described herein may be administered to a subject in a therapeutically effective amount or a dose of a therapeutically effective amount to treat or prevent a pathogenic infection (e.g., one or more pathogenic infections). The terms "treat" or "treatment" refer to reducing or alleviating one or more of the symptoms associated with a pathogenic infection, reducing the amount of bacterial toxin produced by the pathogenic infection, and/or reducing the bacterial load of the pathogenic infection. The terms "prevent" or "prevention" encompass prophylactic administration and may reduce the incidence or likelihood of pathogenic infection or a recurrent or chronic pathogenic infection. For instance, in some embodiments, administration of the compositions provided herein result in a healthy microbiome that is refractory to pathogenic infection, thereby preventing the pathogenic infection.

As used herein, a "therapeutically effective amount" of composition, such as a pharmaceutical composition, is any amount that results in a desired response or outcome in a subject, such as those described herein, including but not limited to prevention of infection, an immune response or an enhanced immune response to the pathogenic infection, prevention or reduction of symptoms associated with pathogenic infection, and/or a reduction or inhibition of toxin production by the pathogenic infection. It should be appreciated that the term effective amount may be expressed in number of bacteria or bacterial spores to be administered. It should further be appreciated that the bacteria can multiply once administered. Thus, administration of even a relatively small amount of bacteria may have therapeutic effects.

In some embodiments, the therapeutically effective amount of any of the compositions described herein is an amount sufficient to enhance survival of the subject, reduce the bacterial burden of the pathogenic infection in the subject, and/or reduce or inhibit toxin production by the pathogenic infection. In some embodiments, the therapeutically effective amount is an amount sufficient to reduce the bacterial burden of the pathogenic infection in a fecal sample from the subject by at least 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold, 100-fold, 1000-fold, 10^4-fold, 10^5-fold or more, as compared to the bacterial burden in a subject with a pathogenic infection that has not received any of the compositions described herein, or as compared to a fecal sample from the same subject that was collected prior to administration of any of the compositions.

In some embodiments, the compositions provided herein inhibit the production of a bacterial toxin, e.g., *C. difficile* Toxin B. In some embodiments, the therapeutically effective amount is an amount sufficient to reduce or inhibit the amount of bacterial toxin (e.g., *C. difficile* Toxin B) produced by pathogenic infection in a fecal sample from the subject by at least 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold, 100-fold, 150-fold, 200-fold, 500-fold or more, as compared to the amount of the bacterial toxin in a subject with a pathogenic infection that has not received any of the compositions described herein or as compared to a fecal sample from the same subject that was collected prior to administration of any of the compositions.

In some embodiments, the compositions provided herein induce the proliferation and/or accumulation of regulatory T cells in the subject. As will be evident to one of ordinary skill in the art, regulatory T cells, also referred to as "Tregs," are a subset of T lymphocytes that are generally thought to suppress an abnormal or excessive immune response and play a role in immune tolerance. Regulatory T cells may be identified based expression of the markers Foxp3 and CD4 (Foxp3+CD4+). The term regulatory T cells may also include Foxp3-negative regulatory T cells that are IL-10-producing CD4-positive T cells.

In some embodiments, the therapeutically effective amount is an amount sufficient to induce the proliferation and/or accumulation of Tregs in the subject (or in a sample obtained from a subject) by at least 1.5-fold, 2-fold, 3-fold, 4-fold, 5-fold, 6-fold, 7-fold, 8-fold, 9-fold, 10-fold, 20-fold, 30-fold, 40-fold, 50-fold, 100-fold, 150-fold, 200-fold, 500-fold or more, as compared to the amount of Tregs in a subject (e.g., a subject with a pathogenic infection) that has not received any of the compositions described herein or as compared to a fecal sample from the same subject that was collected prior to administration of any of the compositions.

As used herein, the phrase "induces proliferation and/or accumulation of regulatory T cells" refers to an effect of inducing the differentiation of immature T cells into regu-

latory T cells, which differentiation leads to the proliferation and/or the accumulation of regulatory T cells. Further, the meaning of "induces proliferation and/or accumulation of regulatory T cells" includes in vivo effects, in vitro effects, and ex vivo effects. In some embodiments, the proliferation and/or accumulation of regulatory T cells may be assessed by detecting and/or quantifying the number of cells that express markers of regulatory T cells (e.g., Foxp3 and CD4), for example by flow cytometry. In some embodiments, the proliferation and/or accumulation of regulatory T cells may be assessed by determining the activity of the regulatory T cells, such as the production of cytokines (e.g., IL-10).

In some embodiments, the therapeutically effective amount is an amount sufficient to recolonize or repopulate the gastrointestinal tract of the subject with non-pathogenic bacteria. In some embodiments, the therapeutically effective amount is an amount sufficient to graft one or more of the bacterial strains of the composition in the gastrointestinal tract of the subject. In some embodiments, a fecal sample is obtained from the subject to assess the bacterial burden of the pathogenic infection and/or evaluate the efficacy of administration of the bacterial compositions described herein. In some embodiments, the microbiota of the subject (e.g., the identity and abundance of strains and/or species of the microbiota) may be assessed to determine a disease state of the subject and/or assess progress of the treatment. In some embodiments, the microbiota of the subject having a pathogenic infection is compared to the microbiota of a healthy subject, such as a subject that is not experiencing or has not experienced the pathogenic infection. In some embodiments, the microbiota of the subject having a pathogenic infection is compared to the microbiota of the same subject from a fecal sample obtained from the subject prior to the pathogenic infection.

Any of the compositions described herein, including the pharmaceutical compositions and food products comprising the compositions, may contain bacterial strains in any form, for example in an aqueous form, such as a solution or a suspension, embedded in a semi-solid form, in a powdered form or freeze dried form. In some embodiments, the composition or the bacterial strains of the composition are lyophilized. In some embodiments, a subset of the bacterial strains in a composition is lyophilized. Methods of lyophilizing compositions, specifically compositions comprising bacteria, are well known in the art. See, e.g., U.S. Pat. No. 3,261,761; U.S. Pat. No. 4,205,132; PCT Publications WO 2014/029578 and WO 2012/098358, herein incorporated by reference in their entirety. The bacteria may be lyophilized as a combination and/or the bacteria may be lyophilized separately and combined prior to administration. A bacterial strain may be combined with a pharmaceutical excipient prior to combining it with the other bacterial strain or multiple lyophilized bacteria may be combined while in lyophilized form and the mixture of bacteria, once combined may be subsequently be combined with a pharmaceutical excipient. In some embodiments, the bacterial strain is a lyophilized cake. In some embodiments, the compositions comprising the one or more bacterial strains are a lyophilized cake.

The bacterial strains of the composition can be manufactured using fermentation techniques well known in the art. In some embodiments, the active ingredients are manufactured using anaerobic fermenters, which can support the rapid growth of anaerobic bacterial species. The anaerobic fermenters may be, for example, stirred tank reactors or disposable wave bioreactors. Culture media such as BL media and EG media, or similar versions of these media devoid of animal components, can be used to support the growth of the bacterial species. The bacterial product can be purified and concentrated from the fermentation broth by traditional techniques, such as centrifugation and filtration, and can optionally be dried and lyophilized by techniques well known in the art.

In some embodiments, the composition of bacterial strains may be formulated for administration as a pharmaceutical composition. The term "pharmaceutical composition" as used herein means a product that results from the mixing or combining of at least one active ingredient, such as any two or more purified bacterial strains described herein, and one or more inactive ingredients, which may include one or more pharmaceutically acceptable excipient.

An "acceptable" excipient refers to an excipient that must be compatible with the active ingredient and not deleterious to the subject to which it is administered. In some embodiments, the pharmaceutically acceptable excipient is selected based on the intended route of administration of the composition, for example a composition for oral or nasal administration may comprise a different pharmaceutically acceptable excipient than a composition for rectal administration. Examples of excipients include sterile water, physiological saline, solvent, a base material, an emulsifier, a suspending agent, a surfactant, a stabilizer, a flavoring agent, an aromatic, an excipient, a vehicle, a preservative, a binder, a diluent, a tonicity adjusting agent, a soothing agent, a bulking agent, a disintegrating agent, a buffer agent, a coating agent, a lubricant, a colorant, a sweetener, a thickening agent, and a solubilizer.

Pharmaceutical compositions of the invention can be prepared in accordance with methods well known and routinely practiced in the art (see e.g., Remington: The Science and Practice of Pharmacy, Mack Publishing Co. 20th ed. 2000). The pharmaceutical compositions described herein may further comprise any carriers or stabilizers in the form of a lyophilized formulation or an aqueous solution. Acceptable excipients, carriers, or stabilizers may include, for example, buffers, antioxidants, preservatives, polymers, chelating reagents, and/or surfactants. Pharmaceutical compositions are preferably manufactured under GMP conditions. The pharmaceutical compositions can be used orally, nasally or parenterally, for instance, in the form of capsules, tablets, pills, sachets, liquids, powders, granules, fine granules, film-coated preparations, pellets, troches, sublingual preparations, chewables, buccal preparations, pastes, syrups, suspensions, elixirs, emulsions, liniments, ointments, plasters, cataplasms, transdermal absorption systems, lotions, inhalations, aerosols, injections, suppositories, and the like.

In some embodiments, the bacteria are formulated for delivery to the intestines (e.g., the small intestine and/or the colon). In some embodiments, the bacteria are formulated with an enteric coating that increases the survival of the bacteria through the harsh environment in the stomach. The enteric coating is one which resists the action of gastric juices in the stomach so that the bacteria which are incorporated therein will pass through the stomach and into the intestines. The enteric coating may readily dissolve when in contact with intestinal fluids, so that the bacteria enclosed in the coating will be released in the intestinal tract. Enteric coatings may consist of polymer and copolymers well known in the art, such as commercially available EUDRAGIT (Evonik Industries). (See e.g., Zhang, *AAPS PharmSciTech*, (2016) 17 (1), 56-67).

The bacteria may also be formulated for rectal delivery to the intestine (e.g., the colon). Thus, in some embodiments, the bacterial compositions may be formulated for delivery

by suppository, colonoscopy, endoscopy, sigmoidoscopy or enema. A pharmaceutical preparation or formulation and particularly a pharmaceutical preparation for oral administration, may include an additional component that enables efficient delivery of the compositions of the disclosure to the intestine (e.g., the colon). A variety of pharmaceutical preparations that allow for the delivery of the compositions to the intestine (e.g., the colon) can be used. Examples thereof include pH sensitive compositions, more specifically, buffered sachet formulations or enteric polymers that release their contents when the pH becomes alkaline after the enteric polymers pass through the stomach. When a pH sensitive composition is used for formulating the pharmaceutical preparation, the pH sensitive composition is preferably a polymer whose pH threshold of the decomposition of the composition is between about 6.8 and about 7.5. Such a numeric value range is a range in which the pH shifts toward the alkaline side at a distal portion of the stomach, and hence is a suitable range for use in the delivery to the colon. It should further be appreciated that each part of the intestine (e.g., the duodenum, jejunum, ileum, cecum, colon and rectum), has different biochemical and chemical environment. For instance, parts of the intestines have different pHs, allowing for targeted delivery by compositions that have a specific pH sensitivity. Thus, the compositions provided herein may be formulated for delivery to the intestine or specific parts of the intestine (e.g., the duodenum, jejunum, ileum, cecum, colon and rectum) by providing formulations with the appropriate pH sensitivity. (See e.g., Villena et al., *Int J Pharm* 2015, 487 (1-2): 314-9).

Another embodiment of a pharmaceutical preparation useful for delivery of the compositions to the intestine (e.g., the colon) is one that ensures the delivery to the colon by delaying the release of the contents (e.g., the bacterial strains) by approximately 3 to 5 hours, which corresponds to the small intestinal transit time. In one embodiment of a pharmaceutical preparation for delayed release, a hydrogel is used as a shell. The hydrogel is hydrated and swells upon contact with gastrointestinal fluid, with the result that the contents are effectively released (released predominantly in the colon). Delayed release dosage units include drug-containing compositions having a material which coats or selectively coats a drug or active ingredient to be administered. Examples of such a selective coating material include in vivo degradable polymers, gradually hydrolyzable polymers, gradually water-soluble polymers, and/or enzyme degradable polymers. A wide variety of coating materials for efficiently delaying the release is available and includes, for example, cellulose-based polymers such as hydroxypropyl cellulose, acrylic acid polymers and copolymers such as methacrylic acid polymers and copolymers, and vinyl polymers and copolymers such as polyvinylpyrrolidone.

Additional examples of pharmaceutical compositions that allow for the delivery to the intestine (e.g., the colon) include bioadhesive compositions which specifically adhere to the colonic mucosal membrane (for example, a polymer described in the specification of U.S. Pat. No. 6,368,586) and compositions into which a protease inhibitor is incorporated for protecting particularly a biopharmaceutical preparation in the gastrointestinal tracts from decomposition due to an activity of a protease.

Another example of a system enabling the delivery to the intestine (e.g., the colon) is a system of delivering a composition to the colon by pressure change in such a way that the contents are released by utilizing pressure change caused by generation of gas in bacterial fermentation at a distal portion of the stomach. Such a system is not particularly limited, and a more specific example thereof is a capsule which has contents dispersed in a suppository base and which is coated with a hydrophobic polymer (for example, ethyl cellulose).

A further example of a system enabling the delivery of a composition to the intestine (e.g., the colon), is a composition that includes a coating that can be removed by an enzyme present in the gut (e.g., the colon), such as, for example, a carbohydrate hydrolase or a carbohydrate reductase. Such a system is not particularly limited, and more specific examples thereof include systems which use food components such as non-starch polysaccharides, amylose, xanthan gum, and azopolymers.

The compositions provided herein can also be delivered to specific target areas, such as the intestine, by delivery through an orifice (e.g., a nasal tube) or through surgery. In addition, the compositions provided herein that are formulated for delivery to a specific area (e.g., the cecum or the colon), may be administered by a tube (e.g., directly into the small intestine). Combining mechanical delivery methods such as tubes with chemical delivery methods such as pH specific coatings, allow for the delivery of the compositions provided herein to a desired target area (e.g., the cecum or the colon).

The compositions comprising bacterial strains are formulated into pharmaceutically acceptable dosage forms by conventional methods known to those of skill in the art. Dosage regimens are adjusted to provide the optimum desired response (e.g., the prophylactic or therapeutic effect). In some embodiments, the dosage form of the composition is a tablet, pill, capsule, powder, granules, solution, or suppository. In some embodiments, the pharmaceutical composition is formulated for oral administration. In some embodiments, the pharmaceutical composition is formulated such that the bacteria of the composition, or a portion thereof, remain viable after passage through the stomach of the subject. In some embodiments, the pharmaceutical composition is formulated for rectal administration, e.g. as a suppository. In some embodiments, the pharmaceutical composition is formulated for delivery to the intestine or a specific area of the intestine (e.g., the colon) by providing an appropriate coating (e.g., a pH specific coating, a coating that can be degraded by target area specific enzymes, or a coating that can bind to receptors that are present in a target area).

Dosages of the active ingredients in the pharmaceutical compositions of the present invention can be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired pharmaceutical response for a particular subject, composition, and mode of administration, without being toxic or having an adverse effect on the subject. The selected dosage level depends upon a variety of factors including the activity of the particular compositions of the present invention employed, the route of administration, the time of administration, the duration of the treatment, other drugs, compounds and/or materials used in combination with the particular compositions employed, the age, sex, weight, condition, general health and prior medical history of the subject being treated, and like factors.

A physician, veterinarian or other trained practitioner, can start doses of the pharmaceutical composition at levels lower than that required to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect (e.g., treatment of a pathogenic infection, reduction of bacterial burden of pathogenic infection, reduction or inhibition of toxin production) is achieved. In general, effective doses of the compositions of the present invention, for the

prophylactic treatment of groups of people as described herein vary depending upon many different factors, including routes of administration, physiological state of the subject, whether the subject is human or an animal, other medications administered, and the therapeutic effect desired. Dosages need to be titrated to optimize safety and efficacy. In some embodiments, the dosing regimen entails oral administration of a dose of any of the compositions described herein. In some embodiments, the dosing regimen entails oral administration of multiple doses of any of the compositions described herein. In some embodiments, the composition is administered orally the subject once, twice, 3 times, 4 times, 5 times, 6 times, 7 times, 8 times, 9 times, or at least 10 times.

The compositions, including the pharmaceutical compositions disclosed herein, include compositions with a range of active ingredients (e.g., live bacteria, bacteria in spore format). The amount of bacteria in the compositions may be expressed in weight, number of bacteria and/or CFUs (colony forming units). In some embodiments, the pharmaceutical compositions disclosed herein contain about 10, about 10^2, about 10^3, about 10^4, about 10^5, about 10^6, about 10^7, about 10^8, about 10^9, about 10^{10}, about 10^{11}, about 10^{12}, about 10^{13} or more of each of the bacteria of the composition per dosage amount. In some embodiments, the pharmaceutical compositions disclosed herein contain about 10, about 10^2, about 10^3, about 10^4, about 10^5, about 10^6, about 10^7, about 10^8, about 10^9, about 10^{10}, about 10^{11}, about 10^{12}, about 10^{13} or more total bacteria per dosage amount. It should further be appreciated that the bacteria of the compositions may be present in different amounts. Thus, for instance, as a non-limiting example, a composition may include 10^3 of bacteria A, 10^4 of bacteria B and 10^6 of bacteria C. In some embodiments, the pharmaceutical compositions disclosed herein contain about 10, about 10^2, about 10^3, about 10^4, about 10^5, about 10^6, about 10^7, about 10^8, about 10^9, about 10^{10}, about 10^{11}, about 10^{12}, about 10^{13} or more CFUs of each of the bacteria in the composition per dosage amount. In some embodiments, the pharmaceutical compositions disclosed herein contain about 10^1, about 10^2, about 10^3, about 10^4, about 10^5, about 10^6, about 10^7, about 10^8, about 10^9, about 10^{10}, about 10^{11}, about 10^{12}, about 10^{13} or more CFUs in total for all of the bacteria combined per dosage amount. As discussed above, bacteria of the compositions may be present in different amounts. In some embodiments, the pharmaceutical compositions disclosed herein contain about 10^{-7}, about 10^{-6}, about 10^{-5}, about 10^{-4}, about 10^{-3}, about 10^{-2}, about 10^{-1} or more grams of each of the bacteria in the composition per dosage amount. In some embodiments, the pharmaceutical compositions disclosed herein contain about 10^{-7}, about 10^{-6}, about 10^{-5}, about 10^{-4}, about 10^{-3}, about 10^{-2}, about 10^{-1} or more grams in total for all of the bacteria combined per dosage amount. In some embodiment, the dosage amount is one administration device (e.g., one table, pill or capsule). In some embodiment, the dosage amount is the amount that is administered in a particular period (e.g., one day or one week).

In some embodiments, the pharmaceutical compositions disclosed herein contain between 10 and 10^{13}, between 10^2 and 10^{13}, between 10^3 and 10^{13}, between 10^4 and 10^{13}, between 10^5 and 10^{13}, between 10^6 and 10^{13}, between 10^7 and 10^{13}, between 10^8 and 10^{13}, between 10^9 and 10^{13}, between 10^{10} and 10^{13}, between 10^{11} and 10^{13}, between 10^{12} and 10^{13}, between 10 and 10^{12}, between 10^2 and 10^{12}, between 10^3 and 10^{12}, between 10^4 and 10^{12}, between 10^5 and 10^{12}, between 10^6 and 10^{12}, between 10^7 and 10^{12}, between 10^8 and 10^{12}, between 10^9 and 10^{12}, between 10^{10} and 10^{12}, between 10^{11} and 10^{12}, between 10 and 10^{11}, between 10^2 and 10^{11}, between 10^3 and 10^{13}, between 10^4 and 10^{13}, between 10^5 and 10^{13}, between 10^6 and 10^{13}, between 10^7 and 10^{11}, between 10^8 and 10^{11}, between 10^9 and 10^{11}, between 10^{10} and 10^{11}, between 10 and 10^{10}, between 10^2 and 10^{10}, between 10^3 and 10^{10}, between 10^4 and 10^{10}, between 10^5 and 10^{10}, between 10^6 and 10^{10}, between 10^7 and 10^{10}, between 10^8 and 10^{10}, between 10^9 and 10^{10}, between 10 and 10^9, between 10^2 and 10^9, between 10^3 and 10^9, between 10^4 and 10^9, between 10^5 and 10^9, between 10^6 and 10^9, between 10^7 and 10^9, between 10^8 and 10^9, between 10 and 10^8, between 10^2 and 10^8, between 10^3 and 10^8, between 10^4 and 10^8, between 10^5 and 10^8, between 10^6 and 10^8, between 10^7 and 10^8, between 10 and 10^7, between 10^2 and 10^7, between 10^3 and 10^7, between 10^4 and 10^7, between 10^5 and 10^7, between 10^6 and 10^7, between 10 and 10^6, between 10^2 and 10^6, between 10^3 and 10^6, between 10^4 and 10^6, between 10^5 and 10^6, between 10 and 10^5, between 10^2 and 10^5, between 10^3 and 10^5, between 10^4 and 10^5, between 10 and 10^4, between 10^2 and 10^4, between 10^3 and 10^4, between 10 and 10^3, between 10^2 and 10^3, or between 10 and 10^2 of each of the bacteria of the composition per dosage amount. In some embodiments, the pharmaceutical compositions disclosed herein contain between 10 and 10^{13}, between 10^2 and 10^{13}, between 10^3 and 10^{13}, between 10^4 and 10^{13}, between 10^5 and 10^{13}, between 10^6 and 10^{13}, between 10^7 and 10^{13}, between 10^8 and 10^{13}, between 10^9 and 10^{13}, between 10^{10} and 10^{13}, between 10^{11} and 10^{13}, between 10^{12} and 10^{13}, between 10 and 10^{12}, between 10^2 and 10^{12}, between 10^3 and 10^{12}, between 10^4 and 10^{12}, between 10^5 and 10^{12}, between 10^6 and 10^{12}, between 10^7 and 10^{12}, between 10^8 and 10^{12}, between 10^9 and 10^{12}, between 10^{10} and 10^{12}, between 10^{11} and 10^{12}, between 10 and 10^{11}, between 10^2 and 10^{11}, between 10^3 and 10^{13}, between 10^4 and 10^{13}, between 10^5 and 10^{13}, between 10^6 and 10^{13}, between 10^7 and 10^{11}, between 10^8 and 10^{11}, between 10^9 and 10^{11}, between 10^{10} and 10^{11}, between 10 and 10^{10}, between 10^2 and 10^{10}, between 10^3 and 10^{10}, between 10^4 and 10^{10}, between 10^5 and 10^{10}, between 10^6 and 10^{10}, between 10^7 and 10^{10}, between 10^8 and 10^{10}, between 10^9 and 10^{10}, between 10 and 10^9, between 10^2 and 10^9, between 10^3 and 10^9, between 10^4 and 10^9, between 10^5 and 10^9, between 10^6 and 10^9, between 10^7 and 10^9, between 10^8 and 10^9, between 10 and 10^8, between 10^2 and 10^8, between 10^3 and 10^8, between 10^4 and 10^8, between 10^5 and 10^8, between 10^6 and 10^8, between 10^7 and 10^8, between 10 and 10^7, between 10^2 and 10^7, between 10^3 and 10^7, between 10^4 and 10^7, between 10^5 and 10^7, between 10^6 and 10^7, between 10 and 10^6, between 10^2 and 10^6, between 10^3 and 10^6, between 10^4 and 10^6, between 10^5 and 10^6, between 10 and 10^5, between 10^2 and 10^5, between 10^3 and 10^5, between 10^4 and 10^5, between 10 and 10^4, between 10^2 and 10^4, between 10^3 and 10^4, between 10 and 10^3, between 10^2 and 10^3, or between 10 and 10^2 total bacteria per dosage amount.

In some embodiments, the pharmaceutical compositions disclosed herein contain between 10 and 10^{13}, between 10^2 and 10^{13}, between 10^3 and 10^{13}, between 10^4 and 10^{13}, between 10^5 and 10^{13}, between 10^6 and 10^{13}, between 10^7 and 10^{13}, between 10^8 and 10^{13}, between 10^9 and 10^{13}, between 10^{10} and 10^{13}, between 10^{11} and 10^{13}, between 10^{12} and 10^{13}, between 10 and 10^{12}, between 10^2 and 10^{12}, between 10^3 and 10^{12}, between 10^4 and 10^{12}, between 10^5 and 10^{12}, between 10^6 and 10^{12}, between 10^7 and 10^{12}, between 10^8 and 10^{12}, between 10^9 and 10^{12}, between 10^{10} and 10^{12}, between 10^{11} and 10^{12}, between 10 and 10^{11},

between 10^2 and 10^{11}, between 10^3 and 10^{13}, between 10^4 and 10^{13}, between 10^5 and 10^{13}, between 10^6 and 10^{13}, between 10^7 and 10^{11}, between 10^8 and 10^{11}, between 10^9 and 10^{11}, between 10^{10} and 10^{11}, between 10 and 10^{10}, between 10^2 and 10^{10}, between 10^3 and 10^{10}, between 10^4 and 10^{10}, between 10^5 and 10^{10}, between 10^6 and 10^{10}, between 10^7 and 10^{10}, between 10^8 and 10^{10}, between 10^9 and 10^{10}, between 10 and 10^9, between 10^2 and 10^9, between 10^3 and 10^9, between 10^4 and 10^9, between 10^5 and 10^9, between 10^6 and 10^9, between 10^7 and 10^9, between 10^8 and 10^9, between 10 and 10^8, between 10^2 and 10^8, between 10^3 and 10^8, between 10^4 and 10^8, between 10^5 and 10^8, between 10^6 and 10^8, between 10^7 and 10^8, between 10 and 10^7, between 10^2 and 10^7, between 10^3 and 10^7, between 10^4 and 10^7, between 10^5 and 10^7, between 10^6 and 10^7, between 10 and 10^6, between 10^2 and 10^6, between 10^3 and 10^6, between 10^4 and 10^6, between 10^5 and 10^6, between 10 and 10^5, between 10^2 and 10^5, between 10^3 and 10^5, between 10^4 and 10^5, between 10 and 10^4, between 10^2 and 10^4, between 10^3 and 10^4, between 10 and 10^3, between 10^2 and 10^3, or between 10 and 10^2 CFUs of each of the bacteria of the composition per dosage amount. In some embodiments, the pharmaceutical compositions disclosed herein contain between 10 and 10^{13}, between 10^2 and 10^{13}, between 10^3 and 10^{13}, between 10^4 and 10^{13}, between 10^5 and 10^{13}, between 10^6 and 10^{13}, between 10^7 and 10^{13}, between 10^8 and 10^{13}, between 10^9 and 10^{13}, between 10^{10} and 10^{13}, between 10^{11} and 10^{13}, between 10^{12} and 10^{13}, between 10 and 10^{12}, between 10^2 and 10^{12}, between 10^3 and 10^{12}, between 10^4 and 10^{12}, between 10^5 and 10^{12}, between 10^6 and 10^{12}, between 10^7 and 10^{12}, between 10^8 and 10^{12}, between 10^9 and 10^{12}, between 10^{10} and 10^{12}, between 10^{11} and 10^{12}, between 10 and 10^{11}, between 10^2 and 10^{11}, between 10^3 and 10^{13}, between 10^4 and 10^{13}, between 10^5 and 10^{13}, between 10^6 and 10^{13}, between 10^7 and 10^{11}, between 10^8 and 10^{11}, between 10^9 and 10^{11}, between 10^{10} and 10^{11}, between 10 and 10^{10}, between 10^2 and 10^{10}, between 10^3 and 10^{10}, between 10^4 and 10^{10}, between 10^5 and 10^{10}, between 10^6 and 10^{10}, between 10^7 and 10^{10}, between 10^8 and 10^{10}, between 10^9 and 10^{10}, between 10 and 10^9, between 10^2 and 10^9, between 10^3 and 10^9, between 10^4 and 10^9, between 10^5 and 10^9, between 10^6 and 10^9, between 10^7 and 10^9, between 10^8 and 10^9, between 10 and 10^8, between 10^2 and 10^8, between 10^3 and 10^8, between 10^4 and 10^8, between 10^5 and 10^8, between 10^6 and 10^8, between 10^7 and 10^8, between 10 and 10^7, between 10^2 and 10^7, between 10^3 and 10^7, between 10^4 and 10^7, between 10^5 and 10^7, between 10^6 and 10^7, between 10 and 10^6, between 10^2 and 10^6, between 10^3 and 10^6, between 10^4 and 10^6, between 10^5 and 10^6, between 10 and 10^5, between 10^2 and 10^5, between 10^3 and 10^5, between 10^4 and 10^5, between 10 and 10^4, between 10^2 and 10^4, between 10^3 and 10^4, between 10 and 10^3, between 10^2 and 10^3, or between 10 and 10^2 total CFUs per dosage amount.

In some embodiments, the pharmaceutical compositions disclosed herein contain between 10^{-7} and 10^{-1}, between 10^{-6} and 10^{-1}, between 10^{-5} and 10^{-1}, between 10^4 and 10^{-1}, between 10^{-3} and 10^{-1}, between 10^{-2} and 10^{-1}, between 10^{-7} and 10^{-2}, between 10^{-6} and 10^{-2}, between 10^{-5} and 10^{-2}, between 10^4 and 10^{-2}, between 10^{-3} and 10^{-2}, between 10^{-7} and 10^{-3}, between 10^{-6} and 10^{-3}, between 10^{-5} and 10^{-3}, between 10^4 and 10^{-3}, between 10^{-7} and 10^4, between 10^{-6} and 10^4, between 10^{-5} and 10^4, between 10^{-7} and 10^{-5}, between 10^{-6} and 10^{-5}, or between 10^{-7} and 10^{-6} grams of each of the bacteria in the composition per dosage amount. In some embodiments, the pharmaceutical compositions disclosed herein contain between 10^{-7} and 10^{-1}, between 10^{-6} and 10^{-1}, between 10^{-5} and 10^{-1}, between 10^4 and 10^{-1}, between 10^{-3} and 10^{-1}, between 10^{-2} and 10^{-1}, between 10^{-7} and 10^{-2}, between 10^{-6} and 10^{-2}, between 10^{-5} and 10^{-2}, between 10^4 and 10^{-2}, between 10^{-3} and 10^{-2}, between 10^{-7} and 10^{-3}, between 10^{-6} and 10^{-3}, between 10^{-5} and 10^{-3}, between 10^4 and 10^{-3}, between 10^{-7} and 10^4, between 10^{-6} and 10^4, between 10^{-5} and 10^4, between 10^{-7} and 10^{-5}, between 10^{-6} and 10^{-5}, or between 10^{-7} and 10^{-6} grams of all of the bacteria combined per dosage amount.

Also with the scope of the present disclosure are food products comprising any of the bacterial strains described herein and a nutrient. Food products are, in general, intended for the consumption of a human or an animal. Any of the bacterial strains described herein may be formulated as a food product. In some embodiments, the bacterial strains are formulated as a food product in spore form. In some embodiments, the bacterial strains are formulated as a food product in vegetative form. In some embodiments, the food product comprises both vegetative bacteria and bacteria in spore form. The compositions disclosed herein can be used in a food or beverage, such as a health food or beverage, a food or beverage for infants, a food or beverage for pregnant women, athletes, senior citizens or other specified group, a functional food, a beverage, a food or beverage for specified health use, a dietary supplement, a food or beverage for patients, or an animal feed. Non-limiting examples of the foods and beverages include various beverages such as juices, refreshing beverages, tea beverages, drink preparations, jelly beverages, and functional beverages; alcoholic beverages such as beers; carbohydrate-containing foods such as rice food products, noodles, breads, and pastas; paste products such as fish hams, sausages, paste products of seafood; retort pouch products such as curries, food dressed with a thick starchy sauces, soups; dairy products such as milk, dairy beverages, ice creams, cheeses, and yogurts; fermented products such as fermented soybean pastes, yogurts, fermented beverages, and pickles; bean products; various confectionery products such as Western confectionery products including biscuits, cookies, and the like, Japanese confectionery products including steamed bean-jam buns, soft adzuki-bean jellies, and the like, candies, chewing gums, gummies, cold desserts including jellies, cream caramels, and frozen desserts; instant foods such as instant soups and instant soybean soups; microwavable foods; and the like. Further, the examples also include health foods and beverages prepared in the forms of powders, granules, tablets, capsules, liquids, pastes, and jellies.

Food products containing bacterial strains described herein may be produced using methods known in the art and may contain the same amount of bacteria (e.g., by weight, amount or CFU) as the pharmaceutical compositions provided herein. Selection of an appropriate amount of bacteria in the food product may depend on various factors, including for example, the serving size of the food product, the frequency of consumption of the food product, the specific bacterial strains contained in the food product, the amount of water in the food product, and/or additional conditions for survival of the bacteria in the food product.

Examples of food products which may be formulated to contain any of the bacterial strains described herein include, without limitation, a beverage, a drink, a bar, a snack, a dairy product, a confectionery product, a cereal product, a ready-to-eat product, a nutritional formula, such as a nutritional supplementary formulation, a food or beverage additive.

In some embodiments, the subject has not received a dose of an antibiotic prior to administration of the bacterial

composition. In some embodiments, the subject has not been administered an antibiotic at least 1, at least 2, at least 3, at least 5, at least 10, at least 15, at least 20, at least 25, at least 30, at least 60, at least 90, at least 120, at least 180 or at least 360 days prior to administration of the compositions provided herein. In some embodiments, the person has not been administered and antibiotic to treat the pathogenic infection. In some embodiments, the compositions provided herein comprise the first treatment of the pathogenic infection.

In some embodiments, the subject may be administered one or more doses of an antibiotic prior to or concurrently with a bacterial composition. Generally, the first line of defense in the treatment of a pathogenic infection is the administration of an antibiotic. In some embodiments, the subject is administered a single dose of an antibiotic prior to the bacterial composition. In some embodiments, the subject is administered multiple doses of an antibiotic prior to the bacterial composition. In some embodiments, the subject is administered at least 2, 3, 4, 5 or more doses of an antibiotic prior to the bacterial composition. In some embodiments, the subject is administered a dose of an antibiotic at substantially the same time as the bacterial composition. Examples of antibiotics that can be administered include, without limitation, kanamycin, gentamicin, colistin, metronidazole, vancomycin, clindamycin, fidaxomicin, and cefoperazone.

Table 1 below provides sequence identifier numbers (SEQ ID NOs) used in the compositions of the experiments disclosed herein, along with the accompanying strain identification number (Strain ID). The closest bacterial species to the indicated strain is presented by genus-species. The 16S rDNA sequence associated with each genus species identified as the closest related genus species is also provided. The percent alignment presents the percent identity between the sequence of the indicated strain with the sequence from the closest genus species and the length of the alignment. The GenBank Accession Number of the closest related species is provided in the last column.

TABLE 1

Closest bacterial species to the strains described herein

SEQ ID	Strain ID	Closest Genus_species	SEQ ID NO. of closest species	Percent alignment	Alignment length	Accession # of closest species
SEQ ID NO: 01	71	*Blautia wexlerae*	SEQ_94	96.62	207	NR_044054
SEQ ID NO: 02	102	*Turicibacter_sanguinis*	SEQ_91	97.81	183	NR_028816
SEQ ID NO: 03	5	*Clostridium_hathewayi*	SEQ_105	92.42	198	NR_036928
SEQ ID NO: 04	7	*Blautia_hansenii*	SEQ_99	96.62	207	NR_104687
SEQ ID NO: 05	10	*Blautia_hansenii*	SEQ_99	98.06	206	NR_104687
SEQ ID NO: 06	40	*Lactobacillus_mucosae*	SEQ_90	87.57	185	NR_024994
SEQ ID NO: 07	59	*Blautia_producta*	SEQ_106	98.54	206	NR_113270
SEQ ID NO: 07	59	*Blautia_coccoides*	SEQ_103	98.54	206	NR_104700
SEQ ID NO: 08	79	*Blautia_hansenii*	SEQ_99	100	194	NR_104687
SEQ ID NO: 09	VE202-21	*Eubacterium_contortum*	SEQ_109	94.59	296	NR_117147
SEQ ID NO: 09	VE202-21	*Eubacterium_fissicatena*	SEQ_108	94.59	296	NR_117142
SEQ ID NO: 10	211	*Flavonifractor_plautii*	SEQ_93	98.49	199	NR_043142
SEQ ID NO: 11	VE202-9	*Anaerostipes_caccae*	SEQ_88	99.5	399	NR_028915
SEQ ID NO: 12	VE202-26	*Clostridium_scindens*	SEQ_87	95.76	354	NR_028785
SEQ ID NO: 13	136	*Marvinbryantia_formatexigens*	SEQ_89	94.66	131	NR_042152
SEQ ID NO: 14	VE202-13	*Anaerotruncus_colihominis*	SEQ_95	99.34	1365	NR_027558
SEQ ID NO: 15	VE202-14	*Eubacterium_fissicatena*	SEQ_102	93.33	1530	NR_117563
SEQ ID NO: 16	VE202-16	*Clostridium_symbiosum*	SEQ_122	98.43	1469	NR_118730
SEQ ID NO: 17	VE202-7	*Clostridium_bolteae*	SEQ_110	99.86	1390	NR_113410
SEQ ID NO: 18	148	*Dorea_longicatena*	SEQ_97	99.7	1318	NR_028883
SEQ ID NO: 19	16	*Blautia_producta*	SEQ_106	98.33	1493	NR_113270
SEQ ID NO: 20	170	*Dorea_longicatena*	SEQ_97	99.7	1318	NR_028883
SEQ ID NO: 21	189	*Clostridium_innocuum*	SEQ_98	98.64	1476	NR_029164
SEQ ID NO: 22	169	*Dorea_longicatena*	SEQ_97	99.58	475	NR_028883
SEQ ID NO: 23	VE202-29	*Eisenbergiella_tayi*	SEQ_121	100	354	NR_118643

TABLE 1-continued

Closest bacterial species to the strains described herein

SEQ ID	Strain ID	Closest Genus_species	SEQ ID NO. of closest species	Percent alignment	Alignment length	Accession # of closest species
SEQ ID NO: 24	YK96	*Dorea_longicatena*	SEQ_97	99.48	191	NR_028883
SEQ ID NO: 25	YK101	*Ruminococcus_obeum*	SEQ_85	96.81	188	NR_118692
SEQ ID NO: 26	YK110	*Megasphaera_elsdenii*	SEQ_119	96.62	207	NR_102980
SEQ ID NO: 27	YK149	*Acidaminococcus_fermentans*	SEQ_115	99.48	192	NR_074928
SEQ ID NO: 27	YK149	*Acidaminococcus_intestini*	SEQ_112	99.48	192	NR_074306
SEQ ID NO: 28	YK154	*Megasphaera_elsdenii*	SEQ_119	96.12	206	NR_102980
SEQ ID NO: 29	YK36	*Ruminococcus_faecis*	SEQ_96	99.29	425	NR_116747
SEQ ID NO: 30	YK95	*Bacteroides_cellulosilyticus*	SEQ_100	99.54	437	NR_112933
SEQ ID NO: 31	YK32	*Anaerostipes_hadrus*	SEQ_107	98.8	415	NR_104799
SEQ ID NO: 32	YK64	*Ruminococcus_obeum*	SEQ_84	99.04	415	NR_119185
SEQ ID NO: 33	YK73	*Flavonifractor_plautii*	SEQ_93	98.56	418	NR_043142
SEQ ID NO: 34	YK87	*Eubacterium_rectale*	SEQ_114	99.52	416	NR_074634
SEQ ID NO: 35	YK105	*Flavonifractor_plautii*	SEQ_93	99.26	407	NR_043142
SEQ ID NO: 36	YK153	*Megasphaera_elsdenii*	SEQ_119	96.04	429	NR_102980
SEQ ID NO: 37	YK163	*Eubacterium_rectale*	SEQ_114	99.76	415	NR_074634
SEQ ID NO: 38	YK191	*Ruminococcus_champanellensis*	SEQ_117	94.47	416	NR_102884
SEQ ID NO: 38	YK191	*Ruminococcus_albus*	SEQ_113	94.47	416	NR_074399
SEQ ID NO: 39	YK99	*Ruminococcus_champanellensis*	SEQ_117	97.28	184	NR_102884
SEQ ID NO: 40	YK55	*Ruminococcus_faecis*	SEQ_96	99.02	408	NR_116747
SEQ ID NO: 41	YK75	*Bifidobacterium_bifidum*	SEQ_118	99.45	183	NR_102971
SEQ ID NO: 42	YK90	*Anaerostipes_hadrus*	SEQ_107	98.97	194	NR_104799
SEQ ID NO: 43	YK30	*Anaerostipes_hadrus*	SEQ_107	99.48	191	NR_104799
SEQ ID NO: 44	YK31	*Anaerostipes_hadrus*	SEQ_107	98.97	194	NR_104799
SEQ ID NO: 45	YK12	*Eubacterium_rectale*	SEQ_114	99.27	412	NR_074634
SEQ ID NO: 46	YK27	*Ruminococcus_faecis*	SEQ_96	99.51	412	NR_116747
SEQ ID NO: 47	YK28	*Blautia_luti*	SEQ_111	99.5	400	NR_041960
SEQ ID NO: 48	YK29	*Ruminococcus_faecis*	SEQ_96	99.03	413	NR_116747
SEQ ID NO: 49	YK33	*Anaerostipes_hadrus*	SEQ_107	99.27	413	NR_104799
SEQ ID NO: 50	YK34	*Anaerostipes_hadrus*	SEQ_107	99.51	410	NR_104799
SEQ ID NO: 51	YK35	*Ruminococcus_faecis*	SEQ_96	99.51	409	NR_116747
SEQ ID NO: 52	YK51	*Eubacterium_rectale*	SEQ_114	99.27	413	NR_074634
SEQ ID NO: 53	YK52	*Eubacterium_rectale*	SEQ_114	99.03	413	NR_074634
SEQ ID NO: 54	YK54	*Anaerostipes_hadrus*	SEQ_107	85.82	409	NR_104799
SEQ ID NO: 55	YK56	*Ruminococcus_faecis*	SEQ_96	99.03	413	NR_116747
SEQ ID NO: 56	YK57	*Ruminococcus_faecis*	SEQ_96	98.79	413	NR_116747

TABLE 1-continued

Closest bacterial species to the strains described herein

SEQ ID	Strain ID	Closest Genus_species	SEQ ID NO. of closest species	Percent alignment	Alignment length	Accession # of closest species
SEQ ID NO: 57	YK58	*Dorea_longicatena*	SEQ_97	98.8	417	NR_028883
SEQ ID NO: 58	YK65	*Roseburia_faecis*	SEQ_92	99.27	413	NR_042832
SEQ ID NO: 59	YK67	*Blautia_luti*	SEQ_111	98.57	419	NR_041960
SEQ ID NO: 60	YK69	*Fusicatenibacter_saccharivorans*	SEQ_116	99.27	413	NR_114326
SEQ ID NO: 61	YK70	*Fusicatenibacter_saccharivorans*	SEQ_116	98.79	414	NR_114326
SEQ ID NO: 62	YK71	*Roseburia_faecis*	SEQ_92	99.28	414	NR_042832
SEQ ID NO: 63	YK74	*Megasphaera_elsdenii*	SEQ_119	96.06	431	NR_102980
SEQ ID NO: 64	YK88	*Eubacterium_rectale*	SEQ_114	99.28	415	NR_074634
SEQ ID NO: 65	YK89	*Eubacterium_rectale*	SEQ_114	99.27	413	NR_074634
SEQ ID NO: 66	YK97	*Roseburia_faecis*	SEQ_92	99.28	414	NR_042832
SEQ ID NO: 67	YK98	*Blautia_faecis*	SEQ_104	98.02	405	NR_109014
SEQ ID NO: 68	YK139	*Fusicatenibacter_saccharivorans*	SEQ_116	99.03	412	NR_114326
SEQ ID NO: 69	YK141	*Dorea_formicigenerans*	SEQ_120	98.51	402	NR_044645
SEQ ID NO: 70	YK142	*Ruminococcus_faecis*	SEQ_96	98.79	413	NR_116747
SEQ ID NO: 71	YK152	*Blautia_hansenii*	SEQ_99	99.5	401	NR_104687
SEQ ID NO: 72	YK155	*Blautia_hansenii*	SEQ_99	98.79	413	NR_104687
SEQ ID NO: 73	YK157	*Eubacterium_rectale*	SEQ_114	99.27	413	NR_074634
SEQ ID NO: 74	YK160	*Roseburia_faecis*	SEQ_92	99.03	414	NR_042832
SEQ ID NO: 75	YK166	*Eubacterium_rectale*	SEQ_114	99.27	409	NR_074634
SEQ ID NO: 76	YK168	*Eubacterium_rectale*	SEQ_114	99.27	413	NR_074634
SEQ ID NO: 77	YK169	*Eubacterium_rectale*	SEQ_114	99.28	416	NR_074634
SEQ ID NO: 78	YK171	*Eubacterium_rectale*	SEQ_114	97.87	188	NR_074634
SEQ ID NO: 79	YK192	*Roseburia_faecis*	SEQ_92	99.03	414	NR_042832
SEQ ID NO: 80	VE202-18	*Erysipelatoclostridium_ramosum*	SEQ_123	100	1485	NR_113243
SEQ ID NO: 81	PE5	*Clostridium_bolteae*	SEQ_110	100	1385	NR_113410
SEQ ID NO: 82	PE9	*Clostridium_disporicum*	SEQ_86	99.21	382	NR_026491
SEQ ID NO: 83	211-B	*Bacteroides_ovatus*	SEQ_101	95.64	436	NR_112940

TABLE 2

Bacterial species with a high degree of homology based on whole genome analysis:

Strain	Whole genome homology
SEQ_10 - 211	*Lachnospiraceae bacterium* 7_1_58FAA
	Subdoligranulum
	Flavinofractor plautii
SEQ_14 - VE202-13	*Anaerotruncus_colihominis*
SEQ_15 - VE202-14	*Eubacterium_fissicatena*
	Ruminococcus torques
SEQ_16 - VE202-16	*Clostridium_symbiosum*
SEQ_17 - VE202-7	*Clostridium_bolteae*

TABLE 2-continued

Bacterial species with a high degree of homology based on whole genome analysis:

Strain	Whole genome homology
SEQ_22 - 169/SEQ_20-170	*Dorea_longicatena*
SEQ_19 - 16	*Blautia_producta*
SEQ_21 - 189	*Clostridium_innocuum*
	*Erysipelotrichaceae_bacterium*_21_3

TABLE 3

Bacterial species with highest degree of homology based on whole genome analysis

Composition B strain number	Strain identifier	SEQ ID # of 16S region as determined by Sanger sequencing	Closest species based on Sanger sequencing of 16S region	SEQ ID # of 16S regions as determined by WGS^	*Consensus SEQ ID # of 16S region as determined by WGS	Closest species based on Concensus SEQ ID # of 16S region as compared with 16S database	Closest species based on WGS compared versus WG databases	Additional closely related sequences	*Clostridium* cluster
1	VE202-7	17	*Clostridium bolteae*	124, 125, 126, 127, 128	124	*Clostridium bolteae*	*Clostridium bolteae* 90A9		XIVa
2	VE202-13	14	*Anaerotruncus colihominis*	129, 130, 131	129	*Anaerotruncus colihominis*	*Anaerotruncus colihominis* DSM 17241		IV
3	VE202-14	15	*Eubacterium fissicatena*	132, 133, 134, 135, 136	132	*Dracourtella massiliensis*	*Dracourtella massiliensis* GD1	*Ruminococcus torques*; *Sellimonas intestinalis*	XIVa
4	VE202-16	16	*Clostridium symbiosum*	137, 138, 139, 140	137	*Clostridium symbiosum*	*Clostridium symbiosum* WAL-14163		XIVa
5	strain #16	19	*Blautia producta*	141, 142, 143, 144, 145	141	*Blautia producta*	*Clostridium bacterium* UC5.1-1D4	*Blautia* product ATCC 27340	XIVa
6	strain #170	20	*Dorea longicatena*	146, 147, 148, 149, 150, 151	146	*Dorea longicatena*	*Dorea longicatena* CAG:42		XIVa
7	strain #189	21	*Clostridium innocuum*	152, 153, 154, 155, 156	152	*Clostridium innocuum*	*Erysipelotrichaceae bacterium* 21_3		XVII
8	strain #211	10	*Flavinofractor plautii*	157, 158, 159	157	*Flavinofractor plautii*	*Clostridium orbiscindens* 1_3_50AFAA	Subdolinogranulum	IV

^WGS refers to Whole Genome Sequencing performed on a PacBio Biosciences platform (Menlo Park, CA).
*Consensus sequence is defined as the 16S sequence that has the most overlap with all other identified 16S sequences.

In some embodiments, in any of the compositions described herein, *Clostridum bolteae* can be replaced with *Clostridium bolteae* 90A9. In some embodiments, in any of the compositions described herein, *Anaerotruncus colihominis* can be replaced with *Anaerotruncus colihominis* DSM 17241. In some embodiments, in any of the compositions described herein, *Eubacterium fissicatena* can be replaced with *Sellimonas instestinalis, Drancourtella massiliensis* or *Drancourtella massiliensis* GP1. In some embodiments, in any of the compositions described herein, *Clostridium symbiosum* can be replaced with *Clostridium symbiosum* WAL-14163. In some embodiments, in any of the compositions described herein, *Blautia producta* can be replaced with *Clostridium bacterium* CD5.1-1D4 or *Blautia* product ATCC27340. In some embodiments, in any of the compositions described herein, *Dorea longicatena* can be replaced with *Dorea longicatena* CAG:42. In some embodiments, in any of the compositions described herein, *Clostridium innocuum* can be replaced with *Erysipelotrichaceae_bacterium_21_3*. In some embodiments, in any of the compositions described herein, *Flavonifractor plautii* can be replaced with *Clostridium orbiscindens* 1_3_50AFAA.

Aspects described herein provide pharmaceutical composition comprising a purified bacterial mixture consisting of bacterial strains comprising 16S rDNA sequences of at least 95% homology to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some aspects, the bacterial strains have at least 97% homology to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some aspects, the bacterial strains have at least 98% homology to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some aspects, the bacterial strains have at least 99% homology to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21.

In some aspects, at least a portion of the bacteria of the pharmaceutical composition are in spore-form. In some aspects, the pharmaceutical composition further comprises a pharmaceutically acceptable excipient.

In some aspects, the pharmaceutical composition is formulated for oral administration. In some aspects, the pharmaceutical composition is in the form of a capsule. In some aspects, the pharmaceutical composition is formulated for delivery to the colon. In some aspects, the pharmaceutical composition further comprises a pH sensitive composition comprising one or more enteric polymers.

Aspects described herein provide pharmaceutical compositions comprising a purified bacterial mixture consisting of bacterial strains comprising 16S rDNA sequences of at least 95% homology to SEQ ID NO:124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157. In some aspects, the bacterial strains have at least 97% homology to SEQ ID NO:124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157. In some aspects, the bacterial strains have at least 98% homology to SEQ ID NO:124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ

ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157. In some aspects, the bacterial strains have at least 99% homology to SEQ ID NO:124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157.

In some aspects, at least a portion of the bacterial strains are in spore-form. In some aspects, the pharmaceutical composition further comprises a pharmaceutically acceptable excipient.

In some aspects, the pharmaceutical composition is formulated for oral administration. In some aspects, the pharmaceutical composition is in the form of a capsule. In some aspects, the pharmaceutical composition is formulated for delivery to the colon. In some aspects, the pharmaceutical composition further comprises a pH sensitive composition comprising one or more enteric polymers.

Aspects described herein provide pharmaceutical compositions comprising a purified bacterial mixture comprising bacterial strains comprising 16S rDNA sequences of at least 95% homology to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some aspects, the bacterial strains have at least 97% homology to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some aspects, the bacterial strains have at least 98% homology to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21. In some aspects, the bacterial strains have at least 99% homology to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21.

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Aspects described herein provide pharmaceutical compositions comprising a purified bacterial mixture comprising bacterial strains comprising 16S rDNA sequences of at least 95% homology to SEQ ID NO:124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157. In some aspects, the bacterial strains have at least 97% homology to SEQ ID NO:124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157. In some aspects, the bacterial strains have at least 98% homology to SEQ ID NO:124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157. In some aspects, the bacterial strains have at least 99% homology to SEQ ID NO:124, SEQ ID NO:129, SEQ ID NO:132, SEQ ID NO:137, SEQ ID NO:141, SEQ ID NO:146, SEQ ID NO:152, and SEQ ID NO:157. In some aspects, at least a portion of the bacterial strains are in spore-form. In some aspects, the pharmaceutical composition further comprises a pharmaceutically acceptable excipient.

In some aspects, the pharmaceutical composition is formulated for oral administration. In some aspects, the pharmaceutical composition is in the form of a capsule. In some aspects, the pharmaceutical composition is formulated for delivery to the colon. In some aspects, the pharmaceutical composition further comprises a pH sensitive composition comprising one or more enteric polymers.

Aspects described herein provide pharmaceutical compositions comprising a purified bacterial mixture consisting of the following bacterial strains: *Clostridium bolteae, Anaerostruncus colihominis, Sellimonas intestinalis, Clostridium symbiosum, Blautia producta, Dorea Longicatena, Erysipelotrichaceae bacterium*, and *Clostridium orbiscindens*.

In some aspects, at least a portion of the bacterial strains are in spore-form. In some aspects, the pharmaceutical composition further comprises a pharmaceutically acceptable excipient.

In some aspects, the pharmaceutical composition is formulated for oral administration. In some aspects, the pharmaceutical composition is in the form of a capsule. In some aspects, the pharmaceutical composition is formulated for delivery to the colon. In some aspects, the pharmaceutical composition further comprises a pH sensitive composition comprising one or more enteric polymers.

Aspects described herein provide pharmaceutical compositions comprising a purified bacterial mixture comprising the following bacterial strains: *Clostridium bolteae, Anaerostruncus colihominis, Sellimonas intestinalis, Clostridium symbiosum, Blautia producta, Dorea Longicatena, Erysipelotrichaceae bacterium*, and *Clostridium orbiscindens*.

In some aspects, at least a portion of the bacterial strains are in spore-form. In some aspects, the pharmaceutical composition further comprises a pharmaceutically acceptable excipient.

In some aspects, the pharmaceutical composition is formulated for oral administration. In some aspects, the pharmaceutical composition is in the form of a capsule. In some aspects, the pharmaceutical composition is formulated for delivery to the colon. In some aspects, the pharmaceutical composition further comprises a pH sensitive composition comprising one or more enteric polymers.

Aspects described herein provide methods of treating an infectious disease in a subject, the method comprising administering the pharmaceutical composition of any of the aspects described herein to the subject in an amount sufficient to treat the infectious disease. In some aspects, the infectious disease is *Clostridium difficile* infection.

The nucleic acid sequences of the 16S rDNA, or portion thereof, for the bacterial strains described herein are provided below:

> SEQ ID NO: 01|71|
GCCCGGAGCAGTTGATGTGAAGGATGGGTCACCTGTGGACTGCATTGGAACTGTCATACTTGAGTGCCGGAGGGTAA

GCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGT

AACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAA

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> SEQ ID NO: 02|102|
CTAACCGTGGAGGTCATTGGAAACTGGTCAACTTGAGTGCAGAAGAGGGAAGTGGAATTCCATGTGTAGCGGTGAAA

TGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCCTGGTCTGTAACTGACACTGAGGCGCGAAAGCGTG

GGGGGCAAACAGGATTAGATCCCCCGGTAA

> SEQ ID NO: 03|5|
ATGAAAGCCGGGGCTCAACCCCGGTACTGCTTTGGAAACTGTTTGACTTGAGTGCTTGAGAGGTAAGTGGAATTCCT

AGTGTAGCGGGAAATGTTTAGATATTAGGAGGACACCAGTGGCGAAGGCGGCTTACTGGACTGTAACTGACGTTGTG

GCTCGATTTGTGGGGAGCAAACAGGATTATATCCCCTGGTAA

> SEQ ID NO: 04|7|
CGGAAGGTCTGATGTGAAGGTTGGGGCTTACCCCGGACTGCATTGGAAACTGTTTTTCTAGAGTGCCCGAGAGGTAA

GCGGAATTCCTAGTGTAGCGGTGAAATGCTTTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGG

TAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAA

> SEQ ID NO: 05|10|
CGATGTCTGAGTGAAGGCTGGGGCTTACCCCAGGACTGCATTGGAACTGTTTTTCTAGAGTGCCGGAGAGGTAAGCG

GAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAAC

TGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAA

> SEQ ID NO: 06|40|
TTAACCAAGAAGTGCATTGGAACTGTCAGACTTGGGGGAAAAAAAGACAGTGCAACTCCATGTGTAGCGGTGGAATG

CTCCATATATATGGAAGAACACCAGTGGCGAAGGCGGCTGTCTGGTCTGCAACTGACGCTGAGGCTCGAATTCATGG

GTAAGAAAGTATTAGTCCCTTGTAA

> SEQ ID NO: 07|59|
ACCCGCTTGGTCTGAGGTGAGGCTGGGGCTTAACCCCAGGACTGCATTGGAAACTGTTGTTCTAGAGTGCCGGAGAG

GTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGA

CGGTAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAA

> SEQ ID NO: 08|79|
TAGGCTGGGGCTTAACCCCAGGACTGCATTGGAAACTGTTTTTCTAGAGTGCCGGAGAGGTAAGCGGAATTCCTAGT

GTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGTTGAGG

CTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAA

> SEQ ID NO: 09|VE202-21|
TTGCATTGGACACTATGTCAGCTGAGTGTCGGAGAGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATAT

TAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGCACGTTTTCTGACGTTGAGGCTCGAAATCGTGGGGAGCAAACA

AAAATAGATACCCTGGTAGTCCACGCCGTAAACGATGCATACTAGGTGTCGGGTGGCAAAGCCATTCGGTGCCGCAG

CAAACGCAATAAGTATGCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAATAAATTGACGGA

> SEQ ID NO: 10|211|
CCCGTCGTAGATGTGAACTGGGGGCTCACCTCCAGCCTGCATTTGAAACTGTAGTTCTTGAGTGCTGGAGAGGCAAT

CGGAATTCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCGGATTGCTGGACAGTA

ACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTCATAA

> SEQ ID NO: 11|VE202-9|
ACCTGATGCAGCGACGCCGCGTGAGTGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGAAGAAAAAAGACG

GTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCGGAAT

TACTGGGTGTAAAGGGTGCGTAGGTGGCATGGTAAGTCAGAAGTGAAAGCCCGGGGCTTAACCCCGGGACTGCTTTT

GAAACTGTCATGCTGGAGTGCAGGAGAGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGA

ACACCAGTGGCGAAGGCGGCTTACTGGACTGTCACTGACACTGATGCACGAAAGCGTGGGGAGCAAACAGGATTAGA

TACCCTGGAAGTCCAT

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> SEQ ID NO: 12|VE202-26|
ATGGGAGCGTAGATGGCGACTGGGCCATATGTGACAGCCCTGGTCTCAACCCCTTAACTGCATTTGGAACTGAGTGG

CTGGAGTGTCGGAGAGGCAGGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCG

AAGGCGGCCTGCTGGACGATGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGT

CCACGCCGTAAACGATGACTACTAGGTGTCGGGTGGCAAGGACATTCGGTGCCGCAGCAAACGCAATAAGTAGTCCA

CCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAAATTGACGGA

> SEQ ID NO: 13|136|
CGCAGCGGAGTGTATCCTAGGCTCACCTGGCTGCTTTCGAACTGGTTTTCTAGATCGTGTAGAGGGGGAGATTCCTG

GTGTAGCGTGAAATGCGTAGATATCTGGAGGAACACCAGTGGCGAAGGCGGCCTCCTGGACGGCAACTGACGTTGAG

GCTCGAAAGTGTGGGGAGCAAACAGGATTAGATACCCTGGTAA

> SEQ ID NO: 14|VE202-13|
TCAAAGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGCGCCTAACACATGCAAGTCGAACGGAGCTTACGTTT

TGAAGTTTTCGGATGGACGAATGTAAGCTTAGTGGCGGACGGGTGAGTAACACGTGAGCAACCTGCCTTTCAGAGGG

GGATAACAGCCGGAAACGGCTGCTAATACCGCATGATGTTGCGGGGGCACATGCCCCTGCAACCAAAGGAGCAATCC

GCTGAAAGATGGGCTCGCGTCCGATTAGCCAGTTGGCGGGGTAACGGCCCACCAAAGCGACGATCGGTAGCCGGACT

GAGAGGTTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGGATATTGCACA

ATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGGAAGACGGTCTTCGGATTGTAAACCTCTGTCTTTGGGGAAG

AAAATGACGGTACCCAAAGAGGAAGCTCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGAGCAAGCGTT

GTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGATGGCAAGTAGAATGTTAAATCCATCGGCTCAACCGGTGG

CTGCGTTCTAAACTGCCGTTCTTGAGTGAAGTAGAGGCAGGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATAT

TAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACA

GGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGATTACTAGGTGTGGGGGGACTGACCCCTTCCGTGCCGCAG

TTAACACAATAAGTAATCCACCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAA

GCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCGGATGCATAGCCTAGAG

ATAGGTGAAGCCCTTCGGGGCATCCAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA

GTCCCGCAACGAGCGCAACCCTTATTATTAGTTGCTACGCAAGAGCACTCTAATGAGACTGCCGTTGACAAAACGGA

GGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTACTACAATGGCACTAAAACAG

AGGGCGGCGACACCGCGAGGTGAAGCGAATCCCGAAAAAGTGTCTCAGTTCAGATTGCAGGCTGCAACCCGCCTGCA

TGAAGTCGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGT

CACACCATGGGAGTCGGTAACACCCGAAGCCAGTAGCCTAACCGCAAGGGGGGCGCTGTCGAAGGTGGGATTGATGA

CTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTT

> SEQ ID NO: 15|VE202-14|
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CAGAATCTTCGGAGGAAGAGGACAGTGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGCAACCTGCCTCATACAGG

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CTTGCACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTC

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> SEQ ID NO: 38|YK191|
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GGGTTAAGCCCATAGTTTTCACATCTGACTTGCGATCCCGCCTACGCTCCCTTTACACCCAGTAATTCCGGACAACG

CTCGCTCCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGAGCTTCCTCCTCAGGTACCGTCTTTTTTCGT

CCCTGAAGACAGAGGTTTACAATCCTAAAACCTTCTTCCCTCACGCGGCATCGCTGCATCAGAGTTTCCTCCATTGT

GCAATATTCCCCACTGCTGCCTCCCGTAGGAGTTTGGAA

> SEQ ID NO: 39|YK99|
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TGAAATGCGTAGATATTAGGAGGAACATCAGTGGCGAAGGCGGCTTACTGGGCTTTAACTGACGCTGAGGCTCGAAA

GCGTGGGGAGCAAACAGGATTAGATACCCAAGTAA

> SEQ ID NO: 40|YK55|
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CCCCGGGTTTTCACATCAGACTTGCCACTCCGTCTACGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTGCACC

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CCCACTGCTGCCTCCCGAGGGAGTTTGGA

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> SEQ ID NO: 41|YK75|
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GGTGGAATGTGTAGATATCGGGAAGAACACCGATGGCGAAGGCAGGTCTCTGGGCCGTCACTGACGCTGAGGAGCGA

AAGCGTGGGGAGCGAACAGGATTAGATACAACGGTAA

> SEQ ID NO: 42|YK90|
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GTAGCGGTGAAATGCGTAGATATTAGGAGGAACATCAGTGGCGAAGGCGGCTTACTGGACTGAAACTGACACTGAGG

CACGAAAGCGTGGGGAGCAAACAGGATTAGATACCATGGTAA

> SEQ ID NO: 43|YK30|
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CGGTGAAATGCGTAGATATTAGGAGGAACATCAGTGGCGAAGGCGGCTTACTGGACTGAAACTGACACTGAGGCACG

AAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAA

> SEQ ID NO: 44|YK31|
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TAGCGGTGAAATGCGTAGATATTAGGAGGAACATCAGTGGCGAAGGCGGCTTACTGGACTGAAACTGACACTGAGGC

ACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCCGGTAA

> SEQ ID NO: 45|YK12|
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CATTTCACCGCTACACTAGGAATTCCGCTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGGGT

TGAGCCCCGGGCTTTCACATCAGACTTGCCGCACCGCCTGCGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTG

CACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTG

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> SEQ ID NO: 46|YK27|
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TCCCCACTGCTGCCTCCCGTAGGAGTTTGGA

> SEQ ID NO: 47|YK28|
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> SEQ ID NO: 48|YK29|
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CATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTTTCTTCCCTGCTG

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CCCCACTGCTGCCTCCCGTGGGGAGTTTGGA

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> SEQ ID NO: 49|YK33|
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TGCCCCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTTCTTAGTCAGGTACCGTCATTTTCTTCCC

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ATATTCCCCACTGCTGCCTCCCGAAGGAAGTTTGGA

> SEQ ID NO: 50|YK34|70A_009_YK34_A1_A02
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ATTTCACCGCTACACTAGGAATTCCGCTTACCTCTCCTGCACTCCAGTCTGACAGTTTCAAAAGCAGTCCCAGAGTT

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CCCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTTCTTAGTCAGGTACCGTCATTTTCTTCCCTGC

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TTCCCCACTGCTGCCTCCCGTAGGGAGTTTGGA

> SEQ ID NO: 51|YK35|
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> SEQ ID NO: 52|YK51|
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GAGCCCCGGGCTTTCACATCAGACTTGCCGCACCGCCTGCGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTGC

ACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTGC

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> SEQ ID NO: 53|YK52|
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CCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTGCT

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TCCCCACTGCTGCCTCCCGAGGGGAGTTTGG

> SEQ ID NO: 54|YK54|
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ACTCCCCGAGAGAAACCCTGGGTTTTTTCTTCTGACATGCGATATCCCACCCCCACCCTTTATACACCCAAAAATCG

GATAAAAGGTGCGACCTACGTATTATACCGGCTGCTGGGGCGTAGATAGCCGGGGGTTCTTATACAGGGACCGTCAT

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> SEQ ID NO: 55|YK56|
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GAGCCCCGGGTTTTCACATCAGACTTGCCACTCCGTCTACGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTGC

ACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTTTCTTCCCTGC

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> SEQ ID NO: 56|YK57|
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CATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTTTCTTCCCTGCTG

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> SEQ ID NO: 57|YK58|
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> SEQ ID NO: 58|YK65|
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TTTCACCGCTACACTAGGAATTCCACTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGGGTTG

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> SEQ ID NO: 59|YK67|
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CCCCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTTCTTAGTCAGGTACCGTCATTTTCTTCCCTG

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> SEQ ID NO: 60|YK69|
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CCCCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTG

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ATTCCCCACTGCTGCCTCCCGAAGGGAGTTTGGA

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> SEQ ID NO: 61|YK70|
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GCATTTCACCGCTACACTAGGAATTCCGCTTACCTCTCCGGCACTCGAGCCAGACAGTTTCCAATGCAGTCCCAGGG

TTAAGCCCTGGGTTTTCACATCAGACTTGCCTTGCCGTCTACGCTCCCTTTACACCCAGTAAATCCGGATAACGCTT

GCCCCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTTCTTAGTCAGGTACCGTCATTATCTTCCCT

GCTGATAGAGCTTTACATACCGAAATACTTCTTCGCTCACGCGGCGTCGCTGCATCAGGGTTTCCCCCATTGTGCAA

TATTCCCCACTGCTGCCTCCCGAAGGAAAGTTTGGA

> SEQ ID NO: 62|YK71|
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CATTTCACCGCTACACTAGGAATTCCACTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGGGT

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TATTCCCCACTGCTGCCTCCCGAAGGGAGTTTGGA

> SEQ ID NO: 63|YK74|
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CGCATTTCACCGCTACACTAGGAATTCCGCTTTCCTCTCCGACACTCGAGCTTCACAGTTTCGGTCCCCTCACGGGG

TTAAGCCCCGCACTTTTAAGACCGACTTGCGATGCCGCCTGCGCGCCCTTTACGCCCAATAATTCCGGACAACGCTT

GCCACCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGTGGCTTTCTCTTACGGTACCGTCAGGGATAACGGG

TATTGACCGCTATCCTGTTCGTCCCATATAACAGAACTTTACAACCCGAAGGCCGTCATCGTTCACGCGGCGTTGCT

CCGTCAGACTTTCGTCCATTGCGGAAGATTCCCCACTGCTGCCTCCCGGGGGGAGTTTGGA

> SEQ ID NO: 64|YK88|
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CATTTCACCGCTACACTAGGAATTCCGCTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGGGT

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CACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTG

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> SEQ ID NO: 65|YK89|
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GAGCCCCGGGCTTTCACATCAGACTTGCCGCACCGCCTGCGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTGC

ACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTGC

TGATAGAGCTTTACATACCGAAATACTTCTTCGCTCACGCGGCGTCGCTGCATCAGGCTTTCGCCCATTGTGCAATA

TTCCCCACTGCTGCCTCCCGAAGGGAGTTTGGA

> SEQ ID NO: 66|YK97|
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TGAGCCCCGGGCTTTCACATCAGACTTGCCGCACCGCCTGCGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTG

CACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTCTTCTTCCCT

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TATTCCCCACTGCTGCCTCCCGAAGGGAGTTTGGA

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> SEQ ID NO: 67|YK98|
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TTTCACCGCTACACTAGGAATTCCGCTTACCCCTCCGGCACTCAAGCATACCAGTTTCCAATGCAGTCCAGGGGTTA

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CCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTGCT

GATAGAAGTTTACATACCGAGATACTTCTTCCTTCACGCGGCGTCGCTGCATCAGGGTTTCCCCCATTGTGCAATAT

TCCCCACTGCTGCCTCCCGAGGGAAGTTTGGA

> SEQ ID NO: 68|YK139|
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ATTTCACCGCTACACTAGGAATTCCGCTTACCTCTCCGGCACTCGAGCCAGACAGTTTCCAATGCAGTCCCAGGGTT

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> SEQ ID NO: 69|YK141|
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> SEQ ID NO: 70|YK142|
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GAGCCCCGGGTTTTCACATCAGACTTGCCACTCCGTCTACGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTGC

ACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTTTCTTCCCTGC

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> SEQ ID NO: 71|YK152|
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GCCCCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTTCTTAGTCAGGTACCGTCATTTTCTTCCCT

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TATTCCCCACTGCTGCCTCCCGGGGGAAGTTTGGA

> SEQ ID NO: 72|YK155|
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CCCCCTACGTATTACCGCGGCTGCTGGCACGTAGTTAGCCGGGGCTTCTTAGTCAGGTACCGTCATTTTCTTCCCTG

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ATTCCCCACTGCTGCCTCCCGAAGGGAGTTTGG

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> SEQ ID NO: 73|YK157|
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CGCATTTCACCGCTACACTAGGAATTCCGCTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGG

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TGCACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCC

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ATATTCCCCACTGCTGCCTCCCGAAGGGAGTTTGGA

> SEQ ID NO: 74|YK160|
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ATTTCACCGCTACACTAGGAATTCCACTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGGGTT

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> SEQ ID NO: 75|YK166|
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ATTTCACCGCTACACTAGGAATTCCGCTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGGGTT

GAGCCCCGGGCTTTCACATCAGACTTGCCGCACCGCCTGCGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTGC

ACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTGC

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TTCCCCACTGCTAGCTCCCGAAGGAGTTTGGA

> SEQ ID NO: 76|YK168|
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CATTTCACCGCTACACTAGGAATTCCGCTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGGGT

TGAGCCCCGGGCTTTCACATCAGACTTGCCGCACCGCCTGCGCTCCCTTTACACCCAGTAAATCCGGATAACGCTTG

CACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTG

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ATTCCCCACTGCTGCCTCCCGAAGGGAGTTTGGA

> SEQ ID NO: 77|YK169|
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CATTTCACCGCTACACTAGGAATTCCGCTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCGGGGT

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CACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTATCTTCCCTG

CTGATAGAGCTTTACATACCGAAATACTTCTTCGCTCACGCGGCGTCGCTGCATCAGGCTTTCGCCCATTGTGCAAT

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> SEQ ID NO: 78|YK171|
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GCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGATAACTGACGCTGAGGCTC

GAAAGCGTGGGGAGCAAACAGGATTAGATACACCGGTAA

> SEQ ID NO: 79|YK192|
CACGATGTCAGCTTTCGAGCTCAGCGTCAGTTATCGTCCAGTAAGCCGCCTTCGCCACTGGTGTTCCTCCTAATATC

TACGCATTTCACCGCTACACTAGGAATTCCACTTACCCCTCCGACACTCTAGTACGACAGTTTCCAATGCAGTACCG

GGGTTGAGCCCCGGGCTTTCACATCAGACTTGCCGCACCGCCTGCGCTCCCTTTACACCCAGTAAATCCGGATAACG

CTTGCACCATACGTATTACCGCGGCTGCTGGCACGTATTTAGCCGGTGCTTCTTAGTCAGGTACCGTCATTCTTCTT

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GCAATATTCCCCACTGCTGCCTCCCGAGGGGAGTTTGGA

> SEQ ID NO: 80|VE202-18|

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CGCATTAGCTGGTTGGCGGGGTAACGGCCCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACAC

TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATTTTCGGCAATGGGGGAAACCCTGACCGA

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> SEQ ID NO: 81|PE5|

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> SEQ ID NO: 82|PE9|
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GGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTAGGGGTTGTCATGACCT

CTGTGCCGCCGCTAACGCATTAAGTATTCCGCCTGGGGAGTACGGTCGCAAGATTAAAACTCAAAGAAATTGACGGA

> SEQ ID NO: 83|211-B|
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GTAAAATTGCAGTTGAAACTGGCAGTCTTGAGTACAGTAGAGGTGGGCGGAATTCGTGGTGTAGCGGTGAAATGCTT

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CAAACAGGATTAGATACCCTGGTAGTCCACACAGTAAACGATGAATACTCGCTGTTTGCGATATACAGTAAGCGGCC

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CAGGGGGGAAAAACATGGGGTTTAGTTGGATGATACGGGGAGGAACCTC

> SEQ ID NO: 84|NR_119185.1|*Ruminococcus obeum* 16S ribosomal RNA gene, complete sequence
GGCGGCGTGCTTAACACATGCAAGTCGAACGGGAAACCTTTCATTGAAGCTTCGGCAGATTTGGNNTGTTTCTAGTG

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GTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCCCAGTAG

CCAGCAGTCCGGCTGGGCACTCTGAGGAGACTGCCAGGGATAACCTGGAGGAAGGCGGGGATGACGTCAAATCATCA

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CCCAAAAATAACGTCCCAGTTCGGACTGCAGTCTGCAACTCGACTGCACGAAGCTGGAATCGCTAGTAATCGCGGAT

CAGAATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTCAGTAACGCCCGAAG

TCAGTGACCTAACTGCAAAGAAGGAGCTGCCGAAGGCGGGACCGATGACTGGGGTGAAGTCGTAACAAGGT

> SEQ ID NO: 85|NR_118692.1|*Ruminococcus obeum* strain ATCC 29174 16S ribosomal RNA gene, complete sequence
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GACGGGTGAGTAACGCGTGGGTAACCTGCCTTATACAGGGGGATAACAACCAGAAATGGTTGCTAATACCGCATAAG

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AGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGG

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CAGTNCGGCTGGGCACTCTGAGGAGACTGCCAGGGATAACCTGGAGGAAGGCGGGGATGACGTCAAATCATCATGCC

CCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAACAAAGGGAAGCNAGCCTKCGRAGGTAAGCAAATCCCA

NAAATAACGTCCCAGTTCGGACTGCAGTCTGCAACTCGACTGCACGAAGCTGGAATCGCTAGTAATCGCGGATCAGA

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TGACCTAACTGC

> SEQ ID NO: 86|NR_026491.1|*Clostridium disporicum* strain DS1 16S ribosomal RNA gene, partial sequence

GCTCAGGACGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAGCGAGTTGATTCTCTTCGGAGATGAAGCTAGCG

GCGGACGGGTGAGTAACACGTGGGCAACCTGCCTCATAGAGGGGAATAGCCTCCCGAAAGGGAGATTAATACCGCAT

AAGATTGTAGCTTCGCATGAAGTAGCAATTAAAGGAGCAATCCGCTATGAGATGGGCCCGCGGCGCATTAGCTAGTT

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GTGATGACGGCCTTCGGGTTGTAAAGCTCTGTCTTCAGGGACGATAATGACGGTACCTGAGGAGGAAGCCACGGCTA

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CAGCATGTCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGAGAGTTGGCAATACCCAACG

TACGTGATCTAACCCGCAAGGGAGGAAGCGTCCTAAGGTAGGGTCAGCGATTGGGGTGAAGTCGTAACAAGGTAGCC

GTAGGAGAA

> SEQ ID NO: 87|NR_028785.1|*Clostridium scindens* strain ATCC 35704 16S ribosomal RNA gene, complete sequence

GAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGAAGCGCCTGGCCCCG

ACTTCTTCGGAACGAGGAGCCTTGCGACTGAGTGGCGGACGGGTGAGTAACGCGTGGGCAACCTGCCTTGCACTGGG

GGATAACAGCCAGAAATGGCTGCTAATACCGCATAAGACCGAAGCGCCGCATGGCGCGGCGGCCAAAGCCCCGGCGG

TGCAAGATGGGCCCGCGTCTGATTAGGTAGTTGGCGGGGTAACGGCCCACCAAGCCGACGATCAGTAGCCGACCTGA

GAGGGTGACCGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAAT

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CCTGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCAGGGCTACACACGTGCTACAATGGCGTAA

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CCGATAACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTC

> SEQ ID NO: 88|NR_028915.1|*Anaerostipes caccae* strain L1-92 16S ribosomal RNA gene, partial sequence

GCGCTTAATACATGTCAAGTCGAACGAAGCATTTAGGATTGAAGTTTTCGGATGGATTTCCTATATGACTGAGTGGC

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GCGCACAGAATCGCATGATTCAGTGTGAAAAGCCCTGGCAGTATAGGATGGTCCCGCGTCTGATTAGCTGGTTGGTG

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CATGGTAAGTCAGAAGTGAAAGCCCGGGGCTTAACCCCGGGACTGCTTTTGAAACTGTCATGCTGGAGTGCAGGAGA

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GTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCTTTAGTAG

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CAGAATGTCACGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTCAGTAACGCCCGAAG

TCAGTGACCCAACCGCAAGGAGGGAGCTGCCGAAGGTGGGACCGATAACTGGGGTGAAGTCGTAACAAGG

> SEQ ID NO: 89|NR_042152.1|*Marvinbryantia formatexigens* strain I-52 16S ribosomal RNA gene, partial sequence >gi|636558750|ref|NR_114807.1|*Marvinbryantia formatexigens* strain I-52 16S ribosomal RNA gene, complete sequence

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GGCGGGGTAAAGGCCCACCAAACCGACGATCCATAGCCGGCCTGAGAGGGTGGACGGCCACATTGGGACTGAGACAC

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ATCCCAGAAATAACGTCCCAGTTCGGATTGTAGTCTGCAACCCGGCTACATGAAGCTGGAATCGCTAGTAATCGCGG

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AGTCAGTGACCCAACCGGAAGGAGGGAGCTGCCGAAGGCGGGGCCGGTAACTGGGGTGAAGTCGTAACAA

> SEQ ID NO: 90|NR_024994.1|*Lactobacillus mucosae* strain S32 16S ribosomal RNA gene, complete sequence

AGAGTTTGATCCTGGCTCAGGATGAACGCCGGCGGTGTGCCTAATACATGCAAGTCGAACGCGTTGGCCCAACTGAT

TGAACGTGCTTGCACGGACTTGACGTTGGTTTACCAGCGAGTGGCGGACGGGTGAGTAACACGTAGGTAACCTGCCC

CAAAGCGGGGGATAACATTTGGAAACAGATGCTAATACCGCATAACAATTTGAATCGCATGATTCAAATTTAAAAGA

TGGCTTCGGCTATCACTTTGGGATGGACCTGCGGCGCATTAGCTTGTTGGTAGGGTAACGGCCTACCAAGGCTGTGA

TGCGTAGCCGAGTTGAGAGACTGATCGGCCACAATGGAACTGAGACACGGTCCATACTCCTACGGGAGGCAGCAGTA

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> SEQ ID NO: 91|NR_028816.1|*Turicibacter sanguinis* strain MOL361 16S ribosomal RNA gene, complete sequence

AGAGTTTGATCATGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAGCGAACCACTTCGGTGGTG

AGCGGCGAACGGGTGAGTAACACGTAGGTTATCTGCCCATCAGACGGGGACAACGATTGGAAACGATCGCTAATACC

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TCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGCGAAAGCCTGACCGAGCAACGCCGCGTGAATGATGAAG

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CAACTTGAGTGCAGAAGAGGGAAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGAGATATGGAGGAACACCAGTG

GCGAAGGCGGCTTCCTGGTCTGTAACTGACACTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGT

AGTCCACGCCGTAAACGATGAGTGCTAAGTGTTGGGGGTCGAACCTCAGTGCTGAAGTTAACGCATTAAGCACTCCG

CCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTA

ATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATACCAGTGACCGTCCTAGAGATAGGATTTTCCCTTCGGG

GACAATGGATACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA

ACCCCTGTCGTTAGTTGCCAGCATTCAGTTGGGGACTCTAACGAGACTGCCAGTGACAAACTGGAGGAAGGTGGGGA

TGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGCTACAATGGTTGGTACAAAGAGAAGCGAAGCG

GTGACGTGGAGCAAACCTCATAAAGCCAATCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGTTGGAATC

GCTAGTAATCGCGAATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCACGAGAG

TTTACAACACCCGAAGTCAGTGGCCTAACCGCAAGGAGGGAGCTGCCTAAGGTGGGGTAGATGATTGGGGTGAAGTC

GTAACAAGGTATCCCTACCGGAAGGTGGGGTTGGATCACCTCCTT

> SEQ ID NO: 92|NR_042832.1|*Roseburia faecis* strain M72/1 16S ribosomal RNA gene, partial sequence

GATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAAGCACTCTATTTGATTTTCTTCGGAAATGAAGATT

TTGTGACTGAGTGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTCATACAGGGGGATAACAGTTGGAAACGACT

GCTAATACCGCATAAGCGCACAGGATCGCATGATCCGGTGTGAAAAACTCCGGTGGTATGAGATGGACCCGCGTCTG

ATTAGCCAGTTGGCAGGGTAACGGCCTACCAAAGCGACGATCAGTAGCCGACCTGAGAGGGTGACCGGCCACATTGG

GACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCG

ACGCCGCGTGAGCGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGAAGAAGAATGACGGTACCTGACTAAG

AAGCACCGGCTAAATACGTGCCAGCAGCCGCGGTAATACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAA

GGGAGCGCAGGCGGTGCGGCAAGTCTGATGTGAAAGCCCGGGGCTCAACCCCGGTACTGCATTGGAAACTGTCGTAC

TAGAGTGTCGGAGGGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGA

AGGCGGCTTACTGGACGATAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTC

CACGCCGTAAACGATGAATACTAGGTGTCGGGGAGCATTGCTCTTCGGTGCCGCAGCAAACGCAATAAGTATTCCAC

CTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAA

TTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCCGATGACAGAGTATGTAATGTACYTTCTCTTCGGAGC

ATCGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC

CCTGTCCTTAGTAGCCAGCGGTTCGGCCGGGCACTCTAGGGAGACTGCCAGGGATAACCTGGAGGAAGGCGGGGATG

ACGTCAAATCATCATGCCCCTTATGACTTGGGCTACACACGTGCTACAATGGCGTAAACAAAGGGAAGCGGAGCCGT

GAGGCCGAGCAAATCTCAAAAATAACGTCTCAGTTCGGACTGTAGTCTGCAACCCGACTACACGAAGCTGGAATCGC

TAGTAATCGCAGATCAGAATGCTGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTT

GGAAATGCCCGAAGTCAGTGACCCAACCGCAAGGAGGGAGCTGCCGAAGGCAGGTTCGATAACTGGGGTG

> SEQ ID NO: 93|NR_043142.1|*Flavonifractor plautii* strain Prevot S1 16S ribosomal RNA gene, partial sequence

CGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGGGTGCTCATGACGGAGGATTCGTCCAATGGATTGAGTTACC

TAGTGGCGGACGGGTGAGTAACGCGTGAGGAACCTGCCTTGGAGAGGGGAATAACACTCCGAAAGGAGTGCTAATAC

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CGCATGAAGCAGTTGGGTCGCATGGCTCTGACTGCCAAAGATTTATCGCTCTGAGATGGCCTCGCGTCTGATTAGCT

AGTAGGCGGGGTAACGGCCCACCTAGGCGACGATCAGTAGCCGGACTGAGAGGTTGACCGGCCACATTGGGACTGAG

ACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGGGCAATGGGCGCAAGCCTGACCCAGCAACGCCGC

GTGAAGGAAGAAGGCTTTCGGGTTGTAAACTTCTTTTGTCGGGGACGAAACAAATGACGGTACCCGACGAATAAGCC

ACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGCG

TGTAGGCGGGATTGCAAGTCAGATGTGAAAACTGGGGGCTCAACCTCCAGCCTGCATTTGAAACTGTAGTTCTTGAG

TGCTGGAGAGGCAATCGGAATTCCGTGTGTAGCGGTGAAATGCGTAGATATACGGAGGAACACCAGTGGCGAAGGCG

GATTGCTGGACAGTAACTGACGCTGAGGCGCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGC

CGTAAACGATGGATACTAGGTGTGGGGGGTCTGACCCCCTCCGTGCCGCAGTTAACACAATAAGTATCCCACCTGGG

GAGTACGATCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGA

AGCAACGCGAAGAACCTTACCAGGGCTTGACATCCCACTAACGAGGCAGAGATGCGTTAGGTGCCCTTCGGGGAAAG

TGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT

TATTGTTAGTTGCTACGCAAGAGCACTCTAGCGAGACTGCCGTTGACAAAACGGAGGAAGGTGGGGACGACGTCAAA

TCATCATGCCCCTTATGTCCTGGGCCACACACGTACTACAATGGTGGTTAACAGAGGGAGGCAATACCGCGAGGTGG

AGCAAATCCCTAAAAGCCATCCCAGTTCGGATTGCAGGCTGAAACCCGCCTGTATGAAGTTGGAATCGCTAGTAATC

GCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGAGAGTCGGGAACAC

CCGAAGTCCGTAGCCTAACCGCAAGGAGGGCGCGGCCGAAGGTGGGTTCGATAATTGGGGTGAAGTCGTAACAAGGT

AG

> SEQ ID NO: 94|NR_044054.1|*Blautia wexlerae* strain DSM 19850 16S ribosomal RNA gene, partial sequence

CAAGTCGAACGGGAATTANTTTATTGAAACTTCGGTCGATTTAATTTAATTCTAGTGGCGGACGGGTGAGTAACGCG

TGGGTAACCTGCCTTATACAGGGGGATAACAGTCAGAAATGGCTGCTAATACCGCATAAGCGCACAGAGCTGCATGG

CTCAGTGTGAAAAACTCCGGTGGTATAAGATGGACCCGCGTTGGATTAGCTTGTTGGTGGGGTAACGGCCCACCAAG

GCGACGATCCATAGCCGGCCTGAGAGGGTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC

AGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCGACGCCGCGTGAAGGAAGAAGTATCTCGGTATGT

AAACTTCTATCAGCAGGGAAGATAGTGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGT

AATACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTGTGGCAAGTCTGATGTGAA

AGGCATGGGCTCAACCTGTGGACTGCATTGGAAACTGTCATACTTGAGTGCCGGAGGGGTAAGCGGAATTCCTAGTG

TAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGTTGAGGC

TCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATAACTAGGTGTCGGGT

GGCAAAGCCATTCGGTGCCGTCGCAAACGCAGTAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAA

GGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTT

GACATCCGCCTGACCGATCCTTAACCGGATCTTTCCTTCGGGACAGGCGAGACAGGTGGTGCATGGTTGTCGTCAGC

TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCTCAGTAGCCAGCATTTAAGGTGGGCA

CTCTGGGGAGACTGCCAGGGATAACCTGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGC

TACACACGTGCTACAATGGCGTAAACAAAGGGAAGCGAGATTGTGAGATGGAGCAAATCCCAAAAATAACGTCCCAG

TTCGGACTGTAGTCTGCAACCCGACTACACGAAGCTGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGGTGAATA

CGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCTAACTGCAAA

GAAGGAGCTGCCGAAGGCGGGACCGATGACTGGGGTGAAGTCGTAACAAGGT

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> SEQ ID NO: 95|NR_027558.1|*Anaerotruncus colihominis* strain WAL 14565 16S ribosomal RNA gene, partial sequence

AACGGAGCTTACGTTTTGAAGTTTTCGGATGGATGAATGTAAGCTTAGTGGCGGACGGGTGAGTAACACGTGAGCAA

CCTGCCTTTCAGAGGGGGATAACAGCCGGAAACGGCTGCTAATACCGCATGATGTTGCGGGGGCACATGCCCCTGCA

ACCAAAGGAGCAATCCGCTGAAAGATGGGCTCGCGTCCGATTAGCCAGTTGGCGGGGTAACGGCCCACCAAAGCGAC

GATCGGTAGCCGGACTGAGAGGTTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG

TGGGGGATATTGCACAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGGGAAGACGGTCTTCGGATTGTAAACC

TCTGTCTTTGGGGAAGAAAATGACGGTACCCAAAGAGGAAGCTCCGGCTAACTACGTGCCAGCAGCCGCGGTAATAC

GTAGGGAGCAAGCGTTGTCCGGAATTACTGGGTGTAAAGGGAGCGTAGGCGGGATGGCAAGTAGAATGTTAAATCCA

TCGGCTCAACCGGTGGCTGCGTTCTAAACTGCCGTTCTTGAGTGAAGTAGAGGCAGGCGGAATTCCTAGTGTAGCGG

TGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCCTGCTGGGCTTTAACTGACGCTGAGGCTCGAAA

GCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGATTACTAGGTGTGGGGGGACTGAC

CCCTTCCGTGCCGCAGTTAACACAATAAGTAATCCACCTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGAATTG

ACGGGGGCCCGCACAAGCAGTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCG

GCGTAATAGCCTAGAGAGTAGGTGAAGCCCTTCGGGGCATCCAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTC

GTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATTATTAGTTGCTACGCAAGAGCACTCTAATGAGACT

GCCGTTGACAAAACGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTACTA

CAATGGCACTAAAACAGAGGGCGGCGACACCGCGAGGTGAAGCGAATCCCAGAAAAAGTGTCTCAGTTCAGATTGCA

GGCTGCAACCCGCCTGCATGAAGTCGGAATTGCTAGTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGC

CTTGTACACACCGCCCGTCACACCATGGGAGTCCGGGTAACACCCGAAGCCAGTAG

> SEQ ID NO: 96|NR_116747.1|*Ruminococcus faecis* strain Eg2 16S ribosomal RNA gene, partial sequence

ATGCAAGTCGAACGAAGCACCTTGATTTGATTCTTCGGATGAAGATCTTGGTGACTGAGTGGCGGACGGGTGAGTAA

CGCGTGGGTAACCTGCCTCATACAGGGGGATAACAGTTAGAAATGACTGCTAATACCGCATAAGACCACAGCACCGC

ATGGTGCAGGGGTAAAAACTCCGGTGGTATGAGATGGACCCGCGTCTGATTAGGTAGTTGGTGGGGTAACGGCCTAC

CAAGCCGACGATCAGTAGCCGACCTGAGAGGGTGACCGGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGG

AGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCGACGCCGCGTGAGCGATGAAGTATTTCGGT

ATGTAAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGACTAAGAAGCACCGGCTAAATACGTGCCAGCAGCCG

CGGTAATACGTATGGTGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGAGTGGCAAGTCTGATG

TGAAAACCCGGGGCTCAACCCCGGGACTGCATTGGAAACTGTCAATCTAGAGTACCGGAGAGGTAAGCGGAATTCCT

AGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGTTG

AGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGACTACTAGGTGTCG

GGCAGCAAAGCTGTTCGGTGCCGCAGCAAACGCAATAAGTAGTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTC

AAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGCT

CTTGACATCTCCCTGACCGGCAAGTAATGTTGCCTTTCCTTCGGGACAGGGATGACAGGTGGTGCATGGTTGTCGTC

AGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCTTTAGTAGCCAGCGGTTTGGCCGG

GCACTCTAGAGAGACTGCCAGGGATAACCTGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGAGCAG

GGCTACACACGTGCTACAATGGCGTAAACAAAGGGAGGCAGAACCGCGAGGTCGAGCAAATCCCAAAAATAACGTCT

CAGTTCGGATTGTAGTCTGCAACTCGACTACATGAAGCTGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGA

ATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCCAACCGT

AAGGAGGAGCTGCCGAAG

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> SEQ ID NO: 97|NR_028883.1|*Dorea longicatena* strain 111-35 16S ribosomal RNA gene, partial sequence

TAACGCGTGGGTAACCTGCCTCATACAGGGGGATAACAGTTAGAAATGACTGCTAATACCGCATAAGACCACGTACC

GCATGGTACAGTGGTAAAAACTCCGGTGGTATGAGATGGACCCGCGTCTGATTAGGTAGTTGGTGGGGTAACGGCCT

ACCAAGCCGACGATCAGTAGCCGACCTGAGAGGGTGACCGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACG

GGAGGCAGCAGTGGGGAATATTGCACAATGGAGGAAACTCTGATGCAGCGACGCCGCGTGAAGGATGAAGTATTTCG

GTATGTAAACTTCTATCAGCAGGGAAGAAAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGC

CGCGGTAATACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCACGGCAAGCCAGA

TGTGAAAAGCCCGGGGCTCAACCCCGGGACTGCATTTGGAACTGCTGAGCTAGAGTGTCGGAGAGGCAAGTGGAATT

CCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTGCTGGACGATGACTGACG

TTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGACTGCTAGGTG

TCGGGTGGCAAAGCCATTCGGTGCCGCAGCTAACGCAATAAGCAGTCCACCTGGGGAGTACGTTCGCAAGAATGAAA

CTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCT

GATCTTGACATCCCGATGACCGCTTCGTAATGGAAGTTTTTCTTCGGAACATCGGTGACAGGTGGTGCATGGTTGTC

GTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCTTCAGTAGCCAGCAGGTTAAG

CTGGGCACTCTGGAGAGACTGCCAGGGATAACCTGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGA

CCAGGGCTACACACGTGCTACAATGGCGTAAACAAAGAGAAGCGAACTCGCGAGGGTAAGCAAATCTCAAAAATAAC

GTCTCAGTTCGGATTGTAGTCTGCAACTCGACTACATGAAGCTGGAATCGCTAGTAATCGCAGATCAGAATGCTGCG

GTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTCATAACGCCCGAAGTCAGTGACCCAAC

CGTAAGG

> SEQ ID NO: 98|NR_029164.1|*Clostridium innocuum* strain B-3 16S ribosomal RNA gene, partial sequence

ATGGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCATGCCTAATACATGCAAGTCGAACGAAGTCTTCAGGA

AGCTTGCTTCCAAAAAGACTTAGTGGCGAACGGGTGAGTAACACGTAGGTAACCTGCCCATGTGTCCGGGATAACTG

CTGGAAACGGTAGCTAAAACCGGATAGGTATACGGAGCGCATGCTCTGTATATTAAAGCGCCCTTCAAGGCGTGAAC

ATGGATGGACCTGCGACGCATTAGCTAGTTGGTGAGGTAACGGCCCACCAAGGCGATGATGCGTAGCCGGCCTGAGA

GGGTAAACGGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTAGGGAATTTTCGTCAATGG

GGGAAACCCTGAACGAGCAATGCCGCGTGAGTGAAGAAGGTCTTCGGATCGTAAAGCTCTGTTGTAAGTGAAGAACG

GCTCATAGAGGAAATGCTATGGGAGTGACGGTAGCTTACCAGAAAGCCACGGCTAACTACGTGCCAGYAGCCGCGGT

AATACGTAGGTGGCAAGCGTTATCCGGAATCATTGGGCGTAAAGGGTGCGTAGGTGGCGTACTAAGTCTGTAGTAAA

AGGCAATGGCTCAACCATTGTAAGCTATGGAAACTGGTATGCTGGAGTGCAGAAGAGGGCGATGGAATTCCATGTGT

AGCGGTAAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGTCGCCTGGTCTGTAACTGACACTGAGGCA

CGAAAGCGTGGGGAGCAAATAGGATTAGATACCCTAGTAGTCCACGCCGTAAACGATGAGAACTAAGTGTTGGAGAA

ATTCAGTGCTGCAGTTAACGCAATAAGTTCTCCGCCTGGGGAGTATGCACGCAAGTTNGAAACTCAAAGGAATTGAC

GGGGGCCCGCACAAGCGNTGGAGTATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGCCTTGACATGGAA

ACAAATACCCTAGAGATAGGGGGATAATTATGGATCACACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGA

TGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCGCATGTTACCAGCATCAAGTTGGGGACTCATGCGAGACTG

CCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGGCCTGGGCTACACACGTACTAC

AATGGCGACCACAAAGAGCAGCGACTTGGTGACAAGAAGCGAATCTCATAAAGATCGTCTCAGTTCGGATTGAAGTC

TGCAACTCGACTTCATGAAGTCGGAATCGCTAGTAATCGCAGATCAGCATGCTGCGGTGAATACGTTCTCGGGCCTT

GTACACACCGCCCGTCAAACCATGGGAGTCAGTAATACCCGAAGCCGGTGGCATAACCGTAAGGAGTGAGCCGTCGA

AGGTAGGACCGA

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> SEQ ID NO: 99|NR_104687.1|*Blautia hansenii* strain JCM 14655 16S ribosomal RNA gene, partial sequence

AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGAAGCACTTATCATTGA

CTCTTCGGAAGATTTGATATTTGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTCATACAGGGGAA

TAACAGTTAGAAATGGCTGCTAATGCCGCATAAGCGCACAGGACCGCATGGTCTGGTGTGAAAAACTGAGGTGGTAT

GAGATGGACCCGCGTCTGATTAGGTAGTTGGTGGGGTAACGGCCTACCAAGCCGACGATCAGTAGCCGGCCTGAGAG

GGTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGG

GGAAACCCTGATGCAGCGACGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAACTTCTATCAGCAGGGAAGAAAAT

GACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCG

GATTTACTGGGTGTAAAGGGAGCGTAGACGGAAGAGCAAGTCTGATGTGAAAGGCTGGGGCTTAACCCCAGGACTGC

ATTGGAAACTGTTTTTCTAGAGTGCCGGAGAGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGG

AGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGAT

TAGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTCGGGGTGCAAAGCAGTTCGGTGCCGCAGCAAA

CGCAATAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGG

TGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCTGCCTGACCGTTCCTTAACCG

GAGCTTTCCTTCGGGACAGGCAAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTC

CCGCAACGAGCGCAACCCCTATCCTTAGTAGCCAGCAGTCCGGCTGGGCACTCTAGGGAGACTGCCGGGGATAACCC

GGAGGAAGGCGGGGACGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAACA

AAGGGAAGCGAAGCGGTGACGCTTAGCAAATCTCAAAAATAACGTCCCAGTTCGGACTGCAGTCTGCAACTCGACTG

CACGAAGCTGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCC

GTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCCAACCTTATGGAGGGAGCTGCCGAAGGCGGGACCGAT

AACTGGGGTGAAGTCGTAACAAGGTAACC

> SEQ ID NO: 100|NR_ 112933.1|*Bacteroides cellulosilyticus* strain JCM 15632 16S ribosomal RNA gene, partial sequence

AGAGTTTGATCCTGGCTCAGGATGAACGCTAGCTACAGGCTTAACACATGCAAGTCGAGGGGCAGCATGACCTAGCA

ATAGGTTGATGGCGACCGGCGCACGGGTGAGTAACACGTATCCAACCTACCGGTTATTCCGGGATAGCCTTTCGAAA

GAAAGATTAATACCGGATAGTATAACGAGAAGGCATCTTTTTGTTATTAAAGAATTTCGATAACCGATGGGGATGCG

TTCCATTAGTTTGTTGGCGGGGTAACGGCCCACCAAGACATCGATGGATAGGGGTTCTGAGAGGAAGGTCCCCCACA

TTGGAACTGAGACACGGTCCAAACTCCTACGGGAGGCAGCAGTGAGGAATATTGGTCAATGGACGAGAGTCTGAACC

AGCCAAGTAGCGTGAAGGATGACTGCCCTATGGGTTGTAAACTTCTTTTATATGGGAATAAAGTGAGCCACGTGTGG

CTTTTTGTATGTACCATACGAATAAGGATCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGATCCGAGCGT

TATCCGGATTTATTGGGTTTAAAGGGAGCGTAGGCGGACTATTAAGTCAGCTGTGAAAGTTTGCGGCTCAACCGTAA

AATTGCAGTTGATACTGGTCGTCTTGAGTGCAGTAGAGGTAGGCGGAATTCGTGGTGTAGCGGTGAAATGCTTAGAT

ATCACGAAGAACTCCGATTGCGAAGGCAGCTTACTGGACTGTAACTGACGCTGATGCTCGAAAGTGTGGGTATCAAA

CAGGATTAGATACCCTGGTAGTCCACACAGTAAACGATGAATACTCGCTGTTTGCGATATACAGCAAGCGGCCAAGC

GAAAGCATTAAGTATTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAG

CGGAGGAACATGTGGTTTAATTCGATGATACGCGAGGAACCTTACCCGGGCTTAAATTGCATCTGAATAATTTGGAA

ACAGATTAGCCGCAAGGCAGATGTGAAGGTGCTGCATGGTTGTCGTCAGCTCGTGCCGTGAGGTGTCGGCTTAAGTG

CCATAACGAGCGCAACCCTTATCTTTAGTTACTAACAGGTCATGCTGAGGACTCTAGAGAGACTGCCGTCGTAAGAT

GTGAGGAAGGTGGGGATGACGTCAAATCAGCACGGCCCTTACGTCCGGGGCTACACACGTGTTACAATGGGGGGTAC

AGAAGGCAGCTACACAGCGATGTGATGCTAATCCCAAAAGCCTCTCTCAGTTCGGATTGGAGTCTGCAACCCGACTC

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CATGAAGCTGGATTCGCTAGTAATCGCGCATCAGCCACGGCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCC

CGTCAAGCCATGAAAGCCGGGGGGTACCTGAAGTCCGTAACCGCAAGGAGCGGCCTAGGGTAAAACTGGTAATTGGGG

CTAAGTCGTA

> SEQ ID NO: 101|NR_112940.1|*Bacteroides ovatus* strain JCM 5824 16S ribosomal RNA gene, partial sequence

GGCTCAGGATGAACGCTAGCTACAGGCTTAACACATGCAAGTCGAGGGGCAGCATTTTAGTTTGCTTGCAAACTGAA

GATGGCGACCGGCGCACGGGTGAGTAACACGTATCCAACCTGCCGATAACTCCGGAATAGCCTTTCGAAAGAAAGAT

TAATACCGGATAGCATACGAATATCGCATGATATTTTTATTAAAGAATTTCGGTTATCGATGGGGATGCGTTCCATT

AGTTTGTTGGCGGGGTAACGGCCCACCAAGACTACGATGGATAGGGGTTCTGAGAGGAAGGTCCCCCACATTGGAAC

TGAGACACGGTCCAAACTCCTACGGGAGGCAGCAGTGAGGAATATTGGTCAATGGGCGAGAGCCTGAACCAGCCAAG

TAGCGTGAAGGATGAAGGCTCTATGGGTCGTAAACTTCTTTTATATGGGAATAAAGTTTTCCACGTGTGGAATTTTG

TATGTACCATATGAATAAGGATCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGATCCGAGCGTTATCCGG

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GTTGAAACTGGCAGTCTTGAGTACAGTAGAGGTGGGCGGAATTCGTGGTGTAGCGGTGAAATGCTTAGATATCACGA

AGAACTCCGATTGCGAAGGCAGCTCACTAGACTGTTACTGACACTGATGCTCGAAAGTGTGGGTATCAAACAGGATT

AGATACCCTGGTAGTCCACACAGTAAACGATGAATACTCGCTGTTTGCGATATACAGTAAGCGGCCAAGCGAAAGCA

TTAAGTATTCCACCTGGGGAGTACGCCGGCAACGGTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGAGGA

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AGCCGTAAGGCTGTTGTGAAGGTGCTGCATGGTTGTCGTCAGCTCGTGCCGTGAGGTGTCGGCTTAAGTGCCATAAC

GAGCGCAACCCTTATCTTTAGTTACTAACAGGTTATGCTGAGGACTCTAGAGAGACTGCCGTCGTAAGATGTGAGGA

AGGTGGGGATGACGTCAAATCAGCACGGCCCTTACGTCCGGGGCTACACACGTGTTACAATGGGGGGTACAGAAGGC

AGCTACCTGGCGACAGGATGCTAATCCCAAAAACCTCTCTCAGTTCGGATCGAAGTCTGCAACCCGACTTCGTGAAG

CTGGATTCGCTAGTAATCGCGCATCAGCCATGGCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCAAG

CCATGAAAGCCGGGGGTACCTGAAGTACGTAACCGCAAGGAGCGTCCTAGGGTAAAACTGGTAATTGGGGCTA

> SEQ ID NO: 102|NR_117563.1|*Eubacterium fissicatena* 16S ribosomal RNA gene, partial sequence

TAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGAAGCGCTTTACTTAG

ATTTCTTCGGATTGAAGAGTTTTGCGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTCATACAGGG

GGATAACAGTTAGAAATGACTGCTAATACCGCATAAGACCACAGTACCGCATGGTACAGTGGGAAAAACTCCGGTGG

TATGAGATGGACCCGCGTCTGATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCGACGATCAGTAGCCGACCTGA

GAGGGTGACCGGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAAT

GGGGGAAACCCTGATGCAGCGACGCCGCGTGAAGGATGAAGTATTTCGGTATGTAAACTTCTATCAGCAGGGAAGAA

AATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTAT

CCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTTATGTAAGTCTGATGTGAAAACCCGGGGCTCAACCCCGGGAC

TGCATTGGAAACTATGTAACTAGAGTGTCGGAGAGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATT

AGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGATCACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAG

GATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTCGGGTGGCAAAGCCATTCGGTGCCGCAGC

AAACGCAATAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAG

CGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGCTCTTGACATCCCACTGACCGGCGTGTAA

TGGCGCCTTCCCTTCGGGGCAGTGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA

GTCCCGCAACGAGCGCAACCCTTATCTTTAGTAGCCAGCGGTTTGGCCGGGCACTCTAGAGAGACTGCCAGGGATAA

CCTGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGAGCAGGGCTACACACGTGCTACAATGGCGTAA

ACAAAGGGAGGCAATACCGCGAGGTTGAGCAAATCCCAAAAATAACGTCTCAGTTCGGATTGTAGTCTGCAACTCGA

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CTACATGAAGCTGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCG

CCCGTCACACCATGGGAGTTGGTAACGCCCGAAGTCAGTGACCCAACCGTAAGGAGGGAGCTGCCGAAGGCGGGATC

GATAACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTT

> SEQ ID NO: 103|NR_104700.1|*Blautia coccoides* strain JCM 1395 16S ribosomal RNA gene, partial sequence

AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGAAGCGCTAAGACAGAT

TTCTTCGGATTGAAGTCTTTGTGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTCATACAGGGGGA

TAACAGTTAGAAATGACTGCTAATACCGCATAAGCGCACAGGACCGCATGGTCTGGTGTGAAAAACTCCGGTGGTAT

GAGATGGACCCGCGTCTGATTAGCTAGTTGGAGGGGTAACGGCCCACCAAGGCGACGATCAGTAGCCGGCCTGAGAG

GGTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGG

GGAAACCCTGATGCAGCGACGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAACTTCTATCAGCAGGGAAGAAAAT

GACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCG

GATTTACTGGGTGTAAAGGGAGCGTAGACGGAAGAGCAAGTCTGATGTGAAAGGCTGGGGCTTAACCCCAGGACTGC

ATTGGAAACTGTTGTTCTAGAGTGCCGGAGAGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGG

AGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGAT

TAGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTCGGGTGGCAAAGCCATTCGGTGCCGCAGCAAA

CGCAATAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGG

TGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCCTCTGACCGTCCCGTAACGG

GGGCTTCCCTTCGGGGCAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTC

CCGCAACGAGCGCAACCCTTATCCTTAGTAGCCAGCACATGATGGTGGGCACTCTAGGGAGACTGCCGGGGATAACC

CGGAGGAAGGCGGGGACGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAAC

AAAGGGAAGCGAGACAGCGATGTTGAGCGAATCCCAAAAATAACGTCCCAGTTCGGACTGCAGTCTGCAACTCGACT

GCACGAAGCTGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCC

CGTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCTAACCGAAAGGAAGGAGCTGCCGAAGGCGGGACCGA

TAACTGGGGTGAAGTCGTAACAAGGTAACC

> SEQ ID NO: 104|NR_109014.1|*Blautia faecis* strain M25 16S ribosomal RNA gene, partial sequence

ATAACAGCCAGAAATGACTGCTAATACCGCATAAGCGCACAGAACCGCATGGTTCGGTGTGAAAAACTCCGGTGGTA

TAAGATGGACCCGCGTTGGATTAGCTAGTTGGCAGGGCAGCGGCCTACCAAGGCGACGATCCATAGCCGGCCTGAGA

GGGTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGG

GGGAAACCCTGATGCAGCGACGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAACTTCTATCAGCAGGGAAGATAA

TGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCC

GGATTTACTGGGTGTAAAGGGAGCGTAGACGGCGCAGCAAGTCTGATGTGAAAGGCAGGGGCTTAACCCCTGGACTG

CATTGGAAACTGCTGTGCTTGAGTGCCGGAGGGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAG

GAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGA

TTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTCAGGGAGCACAGCTCTTTGGTGCCGCCGCAA

ACGCATTAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCG

GTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAATCTTGACATCCCTCTGACCGGGACTTAACC

GTCCCTTTCCTTCGGGACAGGGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGT

CCCGCAACGAGCGCAACCCCTATCCTTAGTAGCCAGCACGCARTGGTGGGCACTCTGAGGAGACTGCCAGGGATAAC

CTGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAA

CAAAGGGAAGCGAACCCGCGAGGGTGGGCAAATCTCAAAAATAACGTCCCAGTTCGGACTGCAGTCTGCAACTCGAC

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TGCACGAAGCTGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGC

CCGTCACACCATGGGAGTCAGTAACGCCCG

> SEQ ID NO: 105|NR_036928.1|*Clostridium hathewayi* strain 1313 16S ribosomal RNA gene, partial sequence

CTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGAAGCGGTTTCAATGAAGTTTTCGGATGGATT

TGAAATTGACTTAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTTACACTGGGGGATAACAGTTAGAAATG

ACTGCTAATACCGCATAAGCGCACAGGGCCGCATGGNCTGGTGTGAAAAACTCCGGNGGTGTAAGATGGACCCGCGT

CTGATTAGGTAGTTGGNGGGGTAACGGCCCACCAAGCCGACGATCAGTAGCCGACCTGAGAGGGTGACCGGCCACAT

TGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCA

GCGACGCCGCGTGAGTGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGACTA

AGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTA

AAGGGAGCGTAGACGGTTTAGCAAGTCTGAAGTGAAAGCCCGGGGCTCAACCCCGGTACTGCTTTGGAAACTGTTAG

ACTTGAGTGCAGGAGAGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGC

GAAGGCGGCTTACTGGACTGTAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG

TCCACGCCGTAAACGATGAATACTAGGTGTCGGGGGGCAAAGCCCTTCGGTGCCGCCGCAAACGCAATAAGTATTCC

ACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTT

AATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCCACTGAAAACACNTTAACCGTGATCCCTCTTCGGA

GCAGTGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAA

CCCTTATCCTTAGTAGCCAGCGAGTAGAGTCGGGCACTCTGGGGAGACTGCCAGGGATAACCTGGAGGAAGGTGGGG

ATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAACAAAGGGAGGCAAAGG

AGCGATCTGGAGCAAACCCCAAAAATAACGTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCTGGAAT

CGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGA

GTTGGTAACGCCCGAAGTCAGTGACCCAACCGAAAGGAGGGAGCT

> SEQ ID NO: 106|NR_113270.1|*Blautia producta* strain JCM 1471 16S ribosomal RNA gene, partial sequence

AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGAAGCACTAAGACGGAT

TTCTTCGGATTGAAGTCTTTGTGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTCATACAGGGGGA

TAACAGTTAGAAATGACTGCTAATACCGCATAAGCGCACAGGACCGCATGGTCTGGTGTGAAAAACTCCGGTGGTAT

GAGATGGACCCGCGTCTGATTAGCTAGTTGGAGGGGTAACGGCCCACCAAGGCGACGATCAGTAGCCGGCCTGAGAG

GGTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGG

GGAAACCCTGATGCAGCGACGCCGCGTGAAGGAAGAAGTATCTCGGTATGTAAACTTCTATCAGCAGGGAAGAAAAT

GACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCG

GATTTACTGGGTGTAAAGGGAGCGTAGACGGAAGAGCAAGTCTGATGTGAAAGGCTGGGGCTTAACCCCAGGACTGC

ATTGGAAACTGTTGTTCTAGAGTGCCGGAGAGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGG

AGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGAT

TAGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTCGGGTGGCAAAGCCATTCGGTGCCGCAGCAAA

CGCAATAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGG

TGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCCTCTGACCGTCCCGTAACGG

GGACTTCCCTTCGGGGCAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTC

CCGCAACGAGCGCAACCCTTATCCTTAGTAGCCAGCACATGATGGTGGGCACTCTAGGGAGACTGCCGGGGATAACC

CGGAGGAAGGCGGGGACGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAAC

AAAGGGAAGCGAGACAGCGATGTTGAGCGAATCCCAAAAATAACGTCCCAGTTCGGACTGCAGTCTGCAACTCGACT

GCACGAAGCTGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCC

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CGTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCTAACCGAAAGGAAGGAGCTGCCGAAGGCGGGACCGA

TAACTGGGGTGAAGTCGTAACAAGGTAACC

> SEQ ID NO: 107|NR_104799.1|*Anaerostipes hadrus* strain DSM 3319 16S ribosomal RNA gene, partial sequence

TGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAAGCTGCTTAACTGATCTTCTTCGGAAT

TGACGTTTTGTAGACTGAGTGGCGGACGGGTGAGTAACGCGTGGGCAACCTGCCCTGTACAGGGGGATAACAGTCAG

AAATGACTGCTAATACCGCATAAGACCACAGCACCGCATGGTGCAGGGGTAAAAACTCCGGTGGTACAGGATGGACC

CGCGTCTGATTAGCTGGTTGGTGAGGTAACGGCTCACCAAGGCGACGATCAGTAGCCGGCTTGAGAGAGTGAACGGC

CACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTG

ATGCAGCGACGCCGCGTGAGTGAAGAAGTATCTCGGTATGTAAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCT

GACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCGGAATTACTGG

GTGTAAAGGGTGCGTAGGTGGTATGGCAAGTCAGAAGTGAAAACCCAGGGCTTAACTCTGGGACTGCTTTTGAAACT

GTCAGACTGGAGTGCAGGAGAGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACATCA

GTGGCGAAGGCGGCTTACTGGACTGAAACTGACACTGAGGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACCCT

GGTAGTCCACGCCGTAAACGATGAATACTAGGTGTCGGGGCCGTAGAGGCTTCGGTGCCGCAGCCAACGCAGTAAGT

ATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGT

GGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGGTCTTGACATCCTTCTGACCGGTCCTTAACCGGACCTTTCCT

TCGGGACAGGAGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAG

CGCAACCCCTATCTTTAGTAGCCAGCATTTCAGGTGGGCACTCTAGAGAGACTGCCAGGGATAACCTGGAGGAAGGT

GGGGACGACGTCAAATCATCATGCCCCTTATGACCAGGGCTACACACGTGCTACAATGGCGTAAACAGAGGGAAGCA

GCCTCGTGAGAGTGAGCAAATCCCAAAAATAACGTCTCAGTTCGGATTGTAGTCTGCAACTCGACTACATGAAGCTG

GAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCAT

GGGAGTCAGTAACGCCCGAAGTCAGTGACCCAACCGTAAGGAGGGAGCTGCCGAAGGCGGGACCGATAACTGGGGTG

AAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTC

> SEQ ID NO: 108|NR_117142.1|*Eubacterium fissicatena* strain DSM 3598 16S ribosomal RNA gene, partial sequence

GTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGAAGCGCTTTACTTAGATTT

CTTCGGATTGAAGAGTTTTGCGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTCATACAGGGGGAT

AACAGTTAGAAATGACTGCTAATACCGCATAAGACCACAGTACCGCATGGTACAGTGGGAAAAACTCCGGTGGTATG

AGATGGACCCGCGTCTGATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCAACGATCAGTAGCCGACCTGAGAGG

GTGACCGGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGG

GAAACCCTGATGCAGCGACGCCGCGTGAAGGATGAAGTATTTCGGTATGTAAACTTCTATCAGCAGGGAAGAAAATG

ACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCGG

ATTTACTGGGTGTAAAGGGAGCGTAGACGGTTATGTAAGTCTGATGTGAAAACCCGGGGCTCAACCCCGGGACTGCA

TTGGAAACTATGTAACTAGAGTGTCGGAGAGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGA

GGAACACCAGTGGCGAAGGCGGCTTACTGGACGATCACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATT

AGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTCGGGTGGCAAAGCCATTCGGTGCCGCAGCAAAC

GCAATAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGT

GGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGCTCTTGACATCCCACTGACCGGCGTGTAATGGC

GCCTTCCCTTCGGGGCAGTGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCC

CGCAACGAGCGCAACCCTTATCTTTAGTAGCCAGCGGTTTGGCCGGGCACTCTAGAGAGACTGCCAGGGATAACCTG

GAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGAGCAGGGCTACACACGTGCTACAATGGCGTAAACAA

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AGGGAGGCAATACCGCGAGGTTGAGCAAATCCCAAAAATAACGTCTCAGTTCGGATTGTAGTCTGCAACTCGACTAC

ATGAAGCTGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCG

TCACACCATGGGAGTTGGTAACGCCCGAAGTCAGTGACCCAACCGTAAGGAGGGAGCTGCCGAAGGCGGGATCGATA

ACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTT

> SEQ ID NO: 109|NR_117147.1|*Eubacterium contortum* strain DSM 3982 16S ribosomal RNA gene, partial sequence

TTTGATCCTGGCTCAGGATGAACGCTGGCGACGTGCTTAACACATGCAAGTCGAGCGAAGCACTTTACTTTGATTTC

TTCGGAATGAAAGGTTTTGTGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTCATACAGGGGGATA

ACAGTTAGAAATGACTGCTAATACCGCATAAGACCACAGTACCGCATGGTACAGTGGGAAAAACTCCGGTGGTATGA

GATGGACCCGCGTCTGATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCGACGATCAGTAGCCGACCTGAGAGGG

TGACCGGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGG

AAACCCTGATGCAGCGACGCCGCGTGAAGGATGAAGTATTTCGGTATGTAAACTTCTATCAGCAGGGAAGAAAATGA

CGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCGGA

TTTACTGGGTGTAAAGGGAGCGTAGACGGTTATGTAAGTCTGATGTGAAAACCCGGGGCTCAACCCCGGGACTGCAT

TGGAAACTATGTAACTAGAGTGTCGGAGAGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAG

GAACACCAGTGGCGAAGGCGGCTTACTGGACGATGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTA

GATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTCGGGTGGCAAAGCCATTCGGTGCCGCAGCAAACG

CAATAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTG

GAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGCTCTTGACATCCCCCTGACCGGCGTGTAATGGTG

CCTTTCCTTCGGGACAGGGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCC

GCAACGAGCGCAACCCTTATCTTTAGTAGCCAGCGGTTTGGCCGGGCACTCTAGAGAGACTGCCAGGGATAACCTGG

AGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGAGCAGGGCTACACACGTGCTACAATGGCGTAAACAAA

GGGAGGCGAAGCCGTGAGGTGGAGCAAATCCCAAAAATAACGTCTCAGTTCGGATTGTAGTCTGCAACTCGACTACA

TGAAGCTGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGT

CACACCATGGGAGTTGGTAACGCCCGAAGTCAGTGACCCAACCGCAAGGAGGGAGCTGCCGAGGGTGGGACCGATAA

CTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTTCT

> SEQ ID NO: 110|NR_113410.1|*Clostridium bolteae* strain JCM 12243 16S ribosomal RNA gene, partial sequence

TTTTAATTGACTGAGTGGCGGACGGGTGAGTAACGCGTGGATAACCTGCCTCACACTGGGGGATAACAGTTAGAAAT

GACTGCTAATACCGCATAAGCGCACAGTACCGCATGGTACAGTGTGAAAAACTCCGGTGGTGTGAGATGGATCCGCG

TCTGATTAGCCAGTTGGCGGGGTAACGGCCCACCAAAGCGACGATCAGTAGCCGACCTGAGAGGGTGACCGGCCACA

TTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGC

AGCGACGCCGCGTGAGTGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGACT

AAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGT

AAAGGGAGCGTAGACGGCGAAGCAAGTCTGAAGTGAAAACCCAGGGCTCAACCCTGGGACTGCTTTGGAAACTGTTT

TGCTAGAGTGTCGGAGAGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGG

CGAAGGCGGCTTACTGGACGATAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTA

GTCCACGCCGTAAACGATGAATGCTAGGTGTTGGGGGGCAAAGCCCTTCGGTGCCGTCGCAAACGCAGTAAGCATTC

CACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTT

TAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCTCTTGACCGGCGTGTAACGGCGCCTTCCCTTCGG

GGCAAGAGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA

ACCCTTATCCTTAGTAGCCAGCAGGTAAAGCTGGGCACTCTAGGGAGACTGCCAGGGATAACCTGGAGGAAGGTGGG

GATGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAACAAAGGGAAGCAAGA

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CAGTGATGTGGAGCAAATCCCAAAAATAACGTCCCAGTTCGGACTGTAGTCTGCAACCCGACTACACGAAGCTGGAA

TCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGG

AGTCAGCAACGCCCGAAGTCAGTGACCCAACTCGCAAGAGAGGGAGCTGCCGAAGGCGGGGCAGGTAACTGGGGTGA

AGTC

> SEQ ID NO: 111|NR_041960.1|*Blautia luti* strain BInIX 16S ribosomal RNA gene, complete sequence

GTGGGTAACCTGCCTTATACAGGGGGATAACAGTCAGAAATGACTGCTAATACCGCATAAGCGCACAGAGCTGCATG

GCTCCGGTGTGAAAAACTCCGGTGGTATAAGATGGACCCGCGTTGGATTAGCTAGTTGGTGAGGTAACGGCCCACCA

AGGCGACGATCCATAGCCGGCCTGAGAGGGTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAG

GCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGCGACGCCGCGTGAAGGAAGAAGTATCTCGGTAT

GTAAACTTCTATCAGCAGGGAAGAAAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCG

GTAATACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCATGGACAAGTCTGATGT

GAAAGGCTGGGGCTCAACCCCGGGACTGCATTGGAAACTGCCCGTCTTGAGTGCCGGAGAGGTAAGCGGAATTCCTA

GTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGGTAACTGACGTTGA

GGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCGGTAAACGATGAATCCTAGGTGTCGG

GGAGCAAANNNNTTCGGTGCCGCCGCAAACGCATTAAGCATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCA

AAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTC

TTGACATCCCTCTGACCGAGTATGTATGGTACTTTTCCTTCGGGAGAGAGAGGAGACAGGTGGTGCATGGTTGTCGT

CAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCCCCAGTAGCCAGCGGTTCGGCCG

GGCACTCTGAGGAGACTGCCAGGGATAACCTGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTATGATTT

GGGCTACACACGTGCTACAATGGCGTAAACAAAGGGAAGCAAGCCTGCGAGGGTGGGCAAATCCCAAAAATAACGTC

CCAGTTCGGACTGTAGTCTGCAACCCGACTACACGAAGCTGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGGTG

AATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCTAACT

> SEQ ID NO: 112|NR_074306.1|*Acidaminococcus intestini* RyC-MR95 strain RyC-MR95 16S ribosomal RNA, complete sequence

CTGGCGGCGTGCTTAACACATGCAAGTCGAACGGAGAACTTATTTCGGTAAGTTCTTAGTGGCGAACGGGTGAGTAA

CGCGTGGGCAACCTGCCCTCCAGTTGGGGACAACATTCCGAAAGGGATGCTAATACCGAATGTCCTCCCTCCTCCGC

ATGGAGGAGGGAGGAAAGATGGCCTCTGCTTGCAAGCTATCGCTGGAAGATGGGCCCGCGTCTGATTAGCTAGTTGG

TGGGGTAACGGCTCACCAAGGCGATGATCAGTAGCCGGTCTGAGAGGATGAACGGCCACATTGGGACTGAGACACGG

CCCAAACTCCTACGGGAGGCAGCAGTGGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGT

GATGAAGGTCTTCGGATTGTAAAACTCTGTTGTTAGGGACGAAAGCACCGTGTTCGAACAGGTCATGGTGTTGACGG

TACCTAACGAGGAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATT

ATTGGGCGTAAAGAGCATGTAGGCGGGCTTTTAAGTCTGACGTGAAAATGCGGGGCTTAACCCCGTATGGCGTTGGA

TACTGGAAGTCTTGAGTGCAGGAGAGGAAAGGGGAATTCCCAGTGTAGCGGTGAAATGCGTAGATATTGGGAGGAAC

ACCAGTGGCGAAGGCGCCTTTCTGGACTGTGTCTGACGCTGAGATGCGAAAGCCAGGGTAGCAAACGGGATTAGATA

CCCCGGTAGTCCTGGCCGTAAACGATGGATACTAGGTGTAGGAGGTATCGACCCCTTCTGTGCCGGAGTTAACGCAA

TAAGTATCCCGCCTGGGGACTACGATCGCAAGATTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAG

TATGTGGTTTAATTCGACGCAACGCGAAGAACCTTACCAAGGCTTGACATTGAGTGAAAGACCTAGAGATAGGTCCC

TCCCTTCGGGGACACGAAAACAGGTGGTGCATGGCTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCA

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GAAGGCGGGGATGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTACACACGTACTACAATGGTCGGCAACAAAG

GGCAGCGAAACCGCGAGGTGGAGCAAATCCCAGAAACCCGACCCCAGTTCGGATCGTAGGCTGCAACCCGCCTACGT

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ACACCACGAAAGTTGGTAACACCCGAAGCCGGTGAGATAACCTTTTAGGAGTCAGCTGTCTAAGGTGGGGCCGATGA

TTGGGGTGAAGTCGTAACAAGGTAGC

> SEQ ID NO: 113|NR_074399.1|*Ruminococcus albus* strain 7 16S ribosomal RNA gene, complete sequence

AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCACGCTTAACACATGCAAGTCGAACGAGCGAAAGAGTGCTTG

CACTCTCTAGCTAGTGGCGGACGGGTGAGTAACACGTGAGCAATCTGCCTTTCGGAGAGGGATACCAATTGGAAACG

ATTGTTAATACCTCATAACATAACGAAGCCGCATGACTTTGTTATCAAATGAATTTCGCCGAAAGATGAGCTCGCGT

CTGATTAGGTAGTTGGTGAGGTAACGGCCCACCAAGCCGACGATCAGTAGCCGGACTGAGAGGTTGAACGGCCACAT

TGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGATGCA

GCGATGCCGCGTGAGGGAAGAAGGTTTTAGGATTGTAAACCTCTGTCTTTGGGGACGATAATGACGGTACCCAAGGA

GGAAGCTCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTA

AAGGGAGCGTAGGCGGGATTGCAAGTCAGGTGTGAAATTTAGGGGCTTAACCCCTGAACTGCACTTGAAACTGTAGT

TCTTGAGTGAAGTAGAGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACATCAGTGGC

GAAGGCGGCTTACTGGGCTTTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAG

TCCACGCCGTAAACGATGATTACTAGGTGTGGGGGGACTGACCCCTTCCGTGCCGCAGTTAACACAATAAGTAATCC

ACCTGGGGAGTACGGCCGCAAGGCTGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCAGTGGAGTATGTGGTTT

AATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCGTACGCATAGCATAGAGATATGTGAAATCCCTTCGG

GGACGTATAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGGTTAAGTCCCGCAACGAGCGC

AACCCTTACTGTTAGTTGCTACGCAAGAGCACTCTAGCAGGACTGCCGTTGACAAAACGGAGGAAGGTGGGGATGAC

GTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTACTACAATGGCTGTTAACAGAGGGAAGCAAAACAGTG

ATGTGGAGCAAAACCCTAAAAGCAGTCTTAGTTCGGATTGTAGGCTGCAACCCGCCTACATGAAGTCGGAATTGCTA

GTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGCCATGGGAGTCGG

TAACACCCGAAGCCTGTGTTCTAACCGCAAGGAGGAAGCAGTCGAAGGTGGGATTGATGACTGGGGTGAAGTCGTAA

CAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCT

> SEQ ID NO: 114|NR_074634.1|*Eubacterium rectale* strain ATCC 33656 16S ribosomal RNA gene, complete sequence

AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAAGCACTTTATTTGAT

TTCCTTCGGGACTGATTATTTTGTGACTGAGTGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTTGTACAGGGG

GATAACAGTTGGAAACGGCTGCTAATACCGCATAAGCGCACGGCATCGCATGATGCAGTGTGAAAAACTCCGGTGGT

ATAAGATGGACCCGCGTTGGATTAGCTAGTTGGTGAGGTAACGGCCCACCAAGGCGACGATCCATAGCCGACCTGAG

AGGGTGACCGGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATG

GGCGAAAGCCTGATGCAGCGACGCCGCGTGAGCGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGAAGATA

ATGACGGTACCTGACTAAGAAGCACCGGCTAAATACGTGCCAGCAGCCGCGGTAATACGTATGGTGCAAGCGTTATC

CGGATTTACTGGGTGTAAAGGGAGCGCAGGCGGTGCGGCAAGTCTGATGTGAAAGCCCGGGGCTCAACCCCGGTACT

GCATTGGAAACTGTCGTACTAGAGTGTCGGAGGGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTA

GGAGGAACACCAGTGGCGAAGGCGGCTTACTGGACGATAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGG

ATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTTGGGAAGCATTGCTTCTCGGTGCCGTCGCA

AACGCAGTAAGTATTCCACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGC

GGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCTTCTGACCGGTACTTAAC

CGTACCTTCTCTTCGGAGCAGGAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAG

TCCCGCAACGAGCGCAACCCTTATCTTTAGTAGCCAGCGGTTCGGCCGGGCACTCTAGAGAGACTGCCAGGGATAAC

CTGGAGGAAGGCGGGGATGACGTCAAATCATCATGCCCCTTATGACTTGGGCTACACACGTGCTACAATGGCGTAAA

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CAAAGGGAAGCAAAGCTGTGAAGCCGAGCAAATCTCAAAAATAACGTCTCAGTTCGGACTGTAGTCTGCAACCCGAC

TACACGAAGCTGGAATCGCTAGTAATCGCAGATCAGAATGCTGCGGTGAATACGTTCCCGGGTCTTGTACACACCGC

CCGTCACACCATGGGAGTTGGGAATGCCCGAAGCCAGTGACCTAACCGAAAGGAAGGAGCTGTCGAAGGCAGGCTCG

ATAACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCT

> SEQ ID NO: 115|NR_074928.1|*Acidaminococcus fermentans* strain DSM 20731 16S ribosomal RNA gene, complete sequence

AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGAGAACTTTCTTCGGA

ATGTTCTTAGTGGCGAACGGGTGAGTAACGCGTAGGCAACCTGCCCTCTGGTTGGGGACAACATTCCGAAAGGGATG

CTAATACCGAATGAGATCCTCTTTCCGCATGGAGAGAGGATGAAAGATGGCCTCTACTTGTAAGCTATCGCCAGAAG

ATGGGCCTGCGTCTGATTAGCTAGTAGGTGAGGTAACGGCTCACCTAGGCGATGATCAGTAGCCGGTCTGAGAGGAT

GAACGGCCACATTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATCTTCCGCAATGGACGA

AAGTCTGACGGAGCAACGCCGCGTGAGTGATGAAGGCCTTCGGGTTGTAAAACTCTGTTGTCAGGGACGAAAGCACC

GATCTATAATACATTTTGGTGTTGACGGTACCTGACGAGGAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAAT

ACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCATGTAGGCGGGCTTTTAAGTCCGACGTGAAAAT

GCGGGGCTTAACCCCGTATGGCGTTGGATACTGGAAGTCTTGAGTGCAGGAGAGGAAAGGGGAATTCCCAGTGTAGC

GGTGAAATGCGTAGATATTGGGAGGAACACCAGTGGCGAAGGCGCCTTTCTGGACTGTGTCTGACGCTGAGATGCGA

AAGCCAGGGTAGCAAACGGGATTAGATACCCCGGTAGTCCTGGCCGTAAACGATGGGTACTAGGTGTAGGAGGTATC

GACCCCTTCTGTGCCGGAGTTAACGCAATAAGTACCCCGCCTGGGGACTACGATCGCAAGATTGAAACTCAAAGGAA

TTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGACGCAACGCGAAGAACCTTACCAAGGCTTGACA

TTGAGTGAAAGACCCAGAGATGGGTCCCCTTCTTCGGAAGCACGAAAACAGGTGGTGCATGGCTGTCGTCAGCTCGT

GTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATCCTATGTTACCAGCACGTAATGGTGGGGACTC

ATAGGAGACTGCCAGGGATAACCTGGAGGAAGGCGGGGATGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTAC

ACACGTACTACAATGGTCGGCAACAAAGGGCAGCGAAGCCGCGAGGCGGAGCCAATCCCAGAAACCCGACCCCAGTT

CGGATCGCAGGCTGCAACCCGCCTGCGTGAAGTTGGAATCGCTAGTAATCGCAGGTCAGCATACTGCGGTGAATACG

TTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAAAGTTGGTAACACCCGAAGCCGGTGAGATAACCTTTTAGG

AGTCAGCTGTCTAAGGTGGGGCCGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTTCGAGAACGAGCGGCTGGAT

CACCT

> SEQ ID NO: 116|NR_114326.1|*Fusicatenibacter saccharivorans* strain HT03-11 16S ribosomal RNA gene, partial sequence

TGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGAAGCAGTTAAGAAGATTYTTCGGATGAT

TCTTGACTGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGTGACCTGCCCCATACCGGGGGATAACAGCTGGAAAC

GGCTGCTAATACCGCATAAGCGCACAGAGCTGCATGGCTCGGTGTGAAAAACTCCGGTGGTATGGGATGGGCCCGCG

TCTGATTAGGCAGTTGGCGGGGTAACGGCCCACCAAACCGACGATCAGTAGCCGGCCTGAGAGGGCGACCGGCCACA

TTGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGC

AGCGACGCCGCGTGAGCGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGAAGATAATGACGGTACCTGACT

AAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGT

AAAGGGAGCGTAGACGGCAAGGCAAGTCTGATGTGAAAACCCAGGGCTTAACCCTGGGACTGCATTGGAAACTGTCT

GGCTCGAGTGCCGGAGAGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAAGAACACCAGTGG

CGAAGGCGGCTTACTGGACGGTAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTA

GTCCACGCCGTAAACGATGAATGCTAGGTGTTGGGGAGCAAAGCTCTTCGGTGCCGCCGCAAACGCATTAAGCATTC

CACCTGGGGAGTACGTTCGCAAGAATGAAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGAGCATGTGGTT

TAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCGATGACCGGCCCGTAACGGGGCCTTCTCTTCGG

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AGCATTGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCA

ACCCTTATCCTCAGTAGCCAGCAGGTAAAGCTGGGCACTCTGTGGAGACTGCCAGGGATAACCTGGAGGAAGGTGGG

GATGACGTCAAATCATCATGCCCCTTATGATCTGGGCTACACACGTGCTACAATGGCGTAAACAAAGGGAGGCAAAG

CCGCGAGGTGGAGCAAATCCCAAAAATAACGTCTCAGTTCGGACTGCAGTCTGCAACTCGACTGCACGAAGCTGGAA

TCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGG

AGTTGGTAACGCCCGAAGTCAGTGACCCAACCTTTTA

> SEQ ID NO: 117|NR_102884.1|*Ruminococcus champanellensis* strain 18P13 16S ribosomal RNA gene, complete sequence

AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCACGCCTAACACATGCAAGTCGAACGGAGATAAAGACTTCGG

TTTTTATCTTAGTGGCGGACGGGTGAGTAACACGTGAGCAACCTGCCTCTGAGAGAGGGATAGCTTCTGGAAACGGA

TGGTAATACCTCATAACATAGCGGTACCGCATGATACTGCTATCAAAGATTTATCGCTCAGAGATGGGCTCGCGTCT

GATTAGCTAGATGGTGAGGTAACGGCTCACCATGGCGACGATCAGTAGCCGGACTGAGAGGTTGAACGGCCACATTG

GGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGCAGC

GATGCCGCGTGGAGGAAGAAGGTTTTCGGATTGTAAACTCCTGTCTTAAGGGACGATAATGACGGTACCTTAGGAGG

AAGCTCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGAGCGAGCGTTGTCCGGAATTACTGGGTGTAAA

GGGAGCGTAGGCGGGATTGCAAGTCAGATGTGAAAACTATGGGCTTAACCCATAGACTGCATTTGAAACTGTAGTTC

TTGAGTGAAGTAGAGGTAAGCGGAATTCCTAGTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACATCGGTGGCGA

AGGCGGCTTACTGGGCTTTTACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTC

CACGCTGTAAACGATGATTACTAGGTGTGGGGGGACTGACCCCTTCCGTGCCGCAGTTAACACAATAAGTAATCCAC

CTGGGGAGTACGGCCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCAGTGGAGTATGTGGTTTAA

TTCGAAGCAACGCGAAAAACCTTACCAGGTCTTGACATCGAGTGAATGATCTAGAGATAGATCAGTCCTTCGGGACA

CAAAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT

TACCTTTAGTTGCTACGCAAGAGCACTCTAGAGGGACTGCCGTTGACAAAACGGAGGAAGGTGGGGATGACGTCAAA

TCATCATGCCCCTTATGACCTGGGCTACACACGTACTACAATGGCAATGAACAGAGGGAAGCAATACAGTGATGTGG

AGCAAATCCCCAAAAATTGTCCCAGTTCAGATTGTAGGCTGCAACTCGCCTACATGAAGTCGGAATTGCTAGTAATC

GCAGATCAGCATGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCATGGGAGTCGGTAACAC

CCGAAGCCAGTAGCCTAACCGCAAGGAGGGCGCTGTCGAAGGTGGGATTGATGACTGGGGTGAAGTCGTAACAAGGT

AGCCGTATCGGAAGGTGCGGCTGGATCACCT

> SEQ ID NO: 118|NR_102971.1|*Bifidobacterium bifidum* S17 strain S17 16S ribosomal RNA, complete sequence

TTTTTGTGGAGGGTTCGATTCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGGGATCCA

TCGGGCTTTGCTTGGTGGTGAGAGTGGCGAACGGGTGAGTAATGCGTGACCGACCTGCCCCATGCTCCGGAATAGCT

CCTGGAAACGGGTGGTAATGCCGGATGTTCCACATGATCGCATGTGATTGTGGGAAAGATTCTATCGGCGTGGGATG

GGGTCGCGTCCTATCAGCTTGTTGGTGAGGTAACGGCTCACCAAGGCTTCGACGGGTAGCCGGCCTGAGAGGGCGAC

CGGCCACATTGGGACTGAGATACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAG

CCTGATGCAGCGACGCCGCGTGAGGGATGGAGGCCTTCGGGTTGTAAACCTCTTTTGTTTGGGAGCAAGCCTTCGGG

TGAGTGTACCTTTCGAATAAGCGCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGCGCAAGCGTTATCC

GGATTTATTGGGCGTAAAGGGCTCGTAGGCGGCTCGTCGCGTCCGGTGTGAAAGTCCATCGCTTAACGGTGGATCTG

CGCCGGGTACGGGCGGGCTGGAGTGCGGTAGGGGAGACTGGAATTCCCGGTGTAACGGTGGAATGTGTAGATATCGG

GAAGAACACCGATGGCGAAGGCAGGTCTCTGGGCCGTCACTGACGCTGAGGAGCGAAAGCGTGGGGAGCGAACAGGA

TTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGACGCTGGATGTGGGGCACGTTCCACGTGTTCCGTGTCGGAGC

TAACGCGTTAAGCGTCCCGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGAAATTGACGGGGGCCCGCACAAG

CGGCGGAGCATGCGGATTAATTCGATGCAACGCGAAGAACCTTACCTGGGCTTGACATGTTCCCGACGACGCCAGAG

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ATGGCGTTTCCCTTCGGGGCGGGTTCACAGGTGGTGCATGGTCGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAG

TCCCGCAACGAGCGCAACCCTCGCCCCGTGTTGCCAGCACGTTATGGTGGGAACTCACGGGGGACCGCCGGGGTTAA

CTCGGAGGAAGGTGGGGATGACGTCAGATCATCATGCCCCTTACGTCCAGGGCTTCACGCATGCTACAATGGCCGGT

ACAGCGGGATGCGACATGGCGACATGGAGCGGATCCCTGAAAACCGGTCTCAGTTCGGATCGGAGCCTGCAACCCGG

CTCCGTGAAGGCGGAGTCGCTAGTAATCGCGGATCAGCAACGCCGCGGTGAATGCGTTCCCGGGCCTTGTACACACC

GCCCGTCAAGTCATGAAAGTGGGCAGCACCCGAAGCCGGTGGCCTAACCCCTTGTGGGATGGAGCCGTCTAAGGTGA

GGCTCGTGATTGGGACTAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCTGGATCACCTCCTTTCT

> SEQ ID NO: 119|NR_102980.1|*Megasphaera elsdenii* strain DSM 20460 16S ribosomal RNA gene, complete sequence

AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAACGAGAAGAGATGAGAAGC

TTGCTTCTTATCAATTCGAGTGGCAAACGGGTGAGTAACGCGTAAGCAACCTGCCCTTCAGATGGGGACAACAGCTG

GAAACGGCTGCTAATACCGAATACGTTCTTTTTGTCGCATGGCAGAGGGAAGAAAGGGAGGCTCTTCGGAGCTTTCG

CTGAAGGAGGGGCTTGCGTCTGATTAGCTAGTTGGAGGGGTAACGGCCCACCAAGGCGACGATCAGTAGCCGGTCTG

AGAGGATGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATCTTCCGCAA

TGGACGAAAGTCTGACGGAGCAACGCCGCGTGAACGATGACGGCCTTCGGGTTGTAAAGTTCTGTTATACGGGACGA

ATGGCGTAGCGGTCAATACCCGTTACGAGTGACGGTACCGTAAGAGAAAGCCACGGCTAACTACGTGCCAGCAGCCG

CGGTAATACGTAGGTGGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGGGCGCGCAGGCGGCGTCGTAAGTCGGTCT

TAAAAGTGCGGGGCTTAACCCCGTGAGGGGACCGAAACTGCGATGCTAGAGTATCGGAGAGGAAAGCGGAATTCCTA

GTGTAGCGGTGAAATGCGTAGATATTAGGAGGAACACCAGTGGCGAAAGCGGCTTTCTGGACGACAACTGACGCTGA

GGCGCGAAAGCCAGGGGAGCAAACGGGATTAGATACCCCGGTAGTCCTGGCCGTAAACGATGGATACTAGGTGTAGG

AGGTATCGACCCCTTCTGTGCCGGAGTTAACGCAATAAGTATCCCGCCTGGGGAGTACGGCCGCAAGGCTGAAACTC

AAAGGAATTGACGGGGGCCCGCACAAGCGGTGGAGTATGTGGTTTAATTCGACGCAACGCGAAGAACCTTACCAAGC

CTTGACATTGATTGCTATGGATAGAGATATCCAGTTCCTCTTCGGAGGACAAGAAAACAGGTGGTGCACGGCTGTCG

TCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATCTTCTGTTACCAGCGGTTCGGCC

GGGGACTCAGGAGAGACTGCCGCAGACAATGCGGAGGAAGGCGGGGATGACGTCAAGTCATCATGCCCCTTATGGCT

TGGGCTACACACGTACTACAATGGCTCTTAATAGAGGGAAGCGAAGGAGCGATCCGGAGCAAACCCCAAAAACAGAG

TCCCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCAGGAATCGCTAGTAATCGCAGGTCAGCATACTGCGG

TGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAAAGTCATTCACACCCGAAGCCGGTGAGGTAAC

CTTTTGGAGCCAGCCGTCGAAGGTGGGGGCGATGATTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCG

GCTGGATCACCT

> SEQ ID NO: 120|NR_044645.2|*Dorea formicigenerans* strain ATCC 27755 16S ribosomal RNA gene, complete sequence

TTAAACGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGAAGCACATA

AGTTTGATTCTTCGGATGAAGACTTTTGTGACTGAGCGGCGGACGNNNGAGTAACGCGTGGGTAACCTGCCTCATAC

AGGGGGATAACAGYTAGAAATGGCTGCTAATACCGCATAAGACCACAGTACTGCATGGTACAGTGNNNAAAACTCCG

GTGGTATGAGATGGACCCGCGTCTGATTAGGTAGTTGGTGAGGTAACGGCCCACCNAGCCGACGATCAGTAGCCGAC

CTGAGAGGGTGACCGGCCACATTGGGACTGAGACACGGCCNNGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCA

CAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAAGGATGAAGTATTTCGGTATGTAAACTTCTATCAGCAGGGA

AGAAAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGNGGTAATACGTAGGGGGNNAGCG

TTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGCTGTGCAAGTCTGAAGTGAAAGGCATGGGCTCAACCTGT

GGACTGCTTTGGAAACTGTGCAGCTAGAGTGTCGGAGAGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGA

TATTAGGAGGAACACCAGTGGCGAAGGCGGCNTACTGGACGATGACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAA

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ACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGACTGCTAGGTGTCGGGTAGCAAAGCTATTCGGTGCCG

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CAAGCGGTGGAGCATGTGGTTTAATTCGAANNAACGCGAAGAACCTTACCTGATCTTGACATCCCGATGACCGCTTC

GTAATGGAAGYTTTTCTTCGGAACATCGGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGG

TTAAGTCCCGCAACGAGCGCAACCCTTATCTTCAGTAGCCAGCATTTAGGATGGGCACTCTGGAGAGACTGCCAGGG

ATAACCTGGAGGAAGGTGGGGATGACGTNNAATCATCATGCCCCTTATGACCAGGGCTACACACGTGCTACAATGGC

GTAAACAGAGGGAGGCAGAGCCGCGAGGCCGAGCAAATCTCAAAAATAACGTCTCAGTTCGGATTGTAGTCTGCAAC

TCGACTACATGAAGCTGGAATCGCTAGTAATCGCAGATCAGAATGCTGCGGTGAATACGTTCCCGGGTCTTGTACAC

ACCGCCCGTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCCAACCGAAAGGAGGGAGCTGCCGAAGGTGG

GACCGATAACTGGGGT

> SEQ ID NO: 121|NR_118643.1|*Eisenbergiella tayi* strain B086562 16S ribosomal RNA gene, partial sequence

GGTATAACTTAGTGGCGGACGGGTGAGTAACGCGTGGGAAACCTGCCCTGTACCGGGGGATAACACTTAGAAATAGG

TGCTAATACCGCATAAGCGCACGGAACCGCATGGTTCCGTGTGAAAAACTCCGGTGGTACAGGATGGTCCCGCGTCT

GATTAGCCAGTTGGCAGGGTAACGGCCTACCAAAGCGACGATCAGTAGCCGGCCTGAGAGGGTGAACGGCCACATTG

GGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGGGAAACCCTGATGCAGC

GACGCCGCGTGAGTGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGACTAAG

AAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGCAAGCGTTATCCGGATTTACTGGGTGTAAA

GGGAGCGTAGACGGCATGGCAAGCCAGATGTGAAAACCCAGGGCTCAACCTTGGGATTGCATTTGGAACTGCCAGGC

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AGGCGGCTTACTGGACTGTAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTC

CACGCGGTAAACGATGATTGCTAGGTGTAGGTGGGTATGGACCCATCGGTGCCGCAGCTAACGCAATAAGCAATCCA

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CATTGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC

CCTTATTCTTAGTAGCCAGCAGGTAAAGCTGGGCACTCTAAGGAGACTGCCGGGGATAACCCGGAGGAAGGCGGGGA

TGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAACAAAGGGAAGCGAGACA

GTGATGTGGAGCAAATCYCAGAAATAACGTCTCAGTTCGGATTGTAGTCTGCAACTCGACTACATGAAGCTGGAATC

GCTAGTAATCGCGAATCAGCATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCCGTCACACCATGGGAG

TTGGAAATGCCCGAAGTCTGTGACCTAACCGAAAGGGAGGAGCAGCCGAAGGCAGGTCTGATAACTGGGGTGAAGTC

GTAA

> SEQ ID NO: 122|NR_118730.1|*Clostridium symbiosum* strain ATCC 14940 16S ribosomal RNA gene, partial sequence

AAACATGAGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAACACATGCAAGTCGAACGAAGCGATTT

AACGGAAGTTTTCGGATGGAAGTTGAATTGACTGAGTGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTTGTAC

TGGGGGACAACAGTTAGAAATGACTGCTAATACCGCATAAGCGCACAGTATTGCATGATACAGTGTGAAAAACTCCG

GTGGTACAAGATGGACCCGCGTCTGATTAGCTAGTTGGTAAGGTAACGGCTTACCAAGGCGACGATCAGTAGCCGAC

CTGAGAGGGTGACCGGCCACATTGGGACTGAGACACGGCCNNAACTCCTACGGGAGGCAGCAGTGGGGAATATTGCA

CAATGGGCGAAAGCCTGATGCAGCGACGCCGCGTGAGTGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGA

AGAAAATGACGGTACCTGACTAAGAAGCCCCGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGGGGNNAGCG

TTATCCGGATTTACTGGGTGTAAAGGGAGCGTAGACGGTAAAGCAAGTCTGAAGTGAAAGCCCGCGNCTCAACTGCG

GNNCTGCTTTGGAAACTGTTTAACTGGAGTGTCGGAGAGGTAAGTGGAATTCCTAGTGTAGCGGTGAAATGCGTAGA

TATTAGGAGGAACACNAGTGGCGAAGGCGACTTACTGGACGATAACTGACGTTGAGGCTCGAAAGCGTGGGGAGCAA

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ACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGATGAATACTAGGTGTTGGGGAGCAAAGCTCTTCGGTGCCG

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GTAACGTCCCNNTNCCTTCGGGGCGGAGAAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGG

TTNAGTCCCGCAACGAGCGCAACCCTTATTCTAAGTAGCCAGCGGTTCGGCCGGGAACTCTTGGGAGACTGCCAGGG

ATAACCTGGAGGAAGGTGGGGATGACGTCNAATCATCATGCCCCTTATGATCTGGGCTACACACGTGCTACAATGGC

GTAAACANAGAGAAGCAAGACCGCGAGGTGGAGCAAATCTCAAAAATAACGTCTCAGTTCGGACTGCAGGCTGCAAC

TCGCCTGCACGAAGCTGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACAC

ACCGNNCGTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCCAACCGCAAGGAGGGAGCTGCCGAAGGCGG

GACCGANAACNNGGG

> SEQ ID NO: 123|NR_113243.1|*Erysipelatoclostridium ramosum* strain JCM 1298 16S ribosomal RNA gene, partial sequence

AGAGTTTGATCCTGGCTCAGGATGAACGCTGGCGGCGTGCCTAATACATGCAAGTCGAACGCGAGCACTTGTGCTCG

AGTGGCGAACGGGTGAGTAATACATAAGTAACCTGCCCTAGACAGGGGGATAACTATTGGAAACGATAGCTAAGACC

GCATAGGTACGGACACTGCATGGTGACCGTATTAAAAGTGCCTCAAAGCACTGGTAGAGGATGGACTTATGGCGCAT

TAGCTGGTTGGCGGGGTAACGGCCCACCAAGGCGACGATGCGTAGCCGACCTGAGAGGGTGACCGGCCACACTGGGA

CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATTTTCGGCAATGGGGGAAACCCTGACCGAGCAAC

GCCGCGTGAAGGAAGAAGGTTTTCGGATTGTAAACTTCTGTTATAAAGGAAGAACGGCGGCTACAGGAAATGGTAGC

CGAGTGACGGTACTTTATTAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTT

ATCCGGAATTATTGGGCGTAAAGAGGGAGCAGGCGGCAGCAAGGGTCTGTGGTGAAAGCCTGAAGCTTAACTTCAGT

AAGCCATAGAAACCAGGCAGCTAGAGTGCAGGAGAGGATCGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATAT

ATGGAGGAACACCAGTGGCGAAGGCGACGATCTGGCCTGCAACTGACGCTCAGTCCCGAAAGCGTGGGGAGCAAATA

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>SEQ ID NO: 124 |PROKKA_00507 16S ribosomal RNA gene | VE202-7

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>SEQ ID NO: 125 |PROKKA_00709 16S ribosomal RNA gene | VE202-7
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>SEQ ID NO: 126 |PROKKA_01766 16S ribosomal RNA gene | VE202-7
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>SEQ ID NO: 127 |PROKKA_01779 16S ribosomal RNA gene | VE202-7

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>SEQ ID NO: 128 |PROKKA_05926 16S ribosomal RNA gene | VE202-7

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>SEQ ID NO: 129 | PROKKA_01784 16S ribosomal RNA gene
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>SEQ ID NO: 130 | PROKKA_01864 16S ribosomal RNA gene
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>SEQ ID NO: 133 | PROKKA_00991 16S ribosomal RNA gene
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>SEQ ID NO: 134 | PROKKA_01948 16S ribosomal RNA gene
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>SEQ ID NO: 136 | PROKKA_02993 16S ribosomal RNA gene

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>SEQ ID NO: 139 | PROKKA_01171 16S ribosomal RNA gene

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>SEQ ID NO: 145 | PROKKA_04947 16S ribosomal RNA gene
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AGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAAGTCTTGACATCCCTCTGACCGGCCCGT

AACGGGGCCTTCCCTTCGGGGCAGAGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTT

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>SEQ ID NO: 146 | PROKKA_00208 16S ribosomal RNA gene
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>SEQ ID NO: 147 | PROKKA_00340 16S ribosomal RNA gene
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ACCTGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCAGGGCTACACACGTGCTACAATGGCGTA

AACAAAGAGAAGCGAACTCGCGAGGGTAAGCAAATCTCAAAAATAACGTCTCAGTTCGGATTGTAGTCTGCAACTCG

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>SEQ ID NO: 148 | PROKKA_01031 16S ribosomal RNA gene
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>SEQ ID NO: 149 | PROKKA_01840 16S ribosomal RNA gene
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>SEQ ID NO: 150 | PROKKA_02944 16S ribosomal RNA gene
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ACTACATGAAGCTGGAATCGCTAGTAATCGCAGATCAGAATGCTGCGGTGAATACGTTCCCGGGTCTTGTACACACC

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>SEQ ID NO: 151 | PROKKA_04036 16S ribosomal RNA gene

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>SEQ ID NO: 152 | PROKKA_00437 16S ribosomal RNA gene

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>SEQ ID NO: 153 | PROKKA_00896 16S ribosomal RNA gene

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>SEQ ID NO: 155 | PROKKA_04164 16S ribosomal RNA gene
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This invention is not limited in its application to the details of construction and the arrangement of components set forth in the following description or illustrated in the drawings. The invention is capable of other embodiments and of being practiced or of being carried out in various ways. Also, the phraseology and terminology used herein is for the purpose of description and should not be regarded as limiting. The use of "including," "comprising," or "having," "containing," "involving," and variations thereof herein, is meant to encompass the items listed thereafter and equivalents thereof as well as additional items.

Unless otherwise defined herein, scientific and technical terms used in connection with the present disclosure shall have the meanings that are commonly understood by those of ordinary skill in the art. Further, unless otherwise required by context, singular terms shall include pluralities and plural terms hall include the singular. The methods and techniques of the present disclosure are generally performed according to conventional methods well-known in the art. Generally, nomenclatures used in connection with, and techniques of biochemistry, enzymology, molecular and cellular biology, microbiology, virology, cell or tissue culture, genetics and protein and nucleic chemistry described herein are those well-known and commonly used in the art. The methods and techniques of the present disclosure are generally performed according to conventional methods well known in the art and as described in various general and more specific references that are cited and discussed throughout the present specification unless otherwise indicated.

The present invention is further illustrated by the following Examples, which in no way should be construed as further limiting. The entire contents of all of the references (including literature references, issued patents, published patent applications, and co-pending patent applications) cited throughout this application are hereby expressly incorporated by reference, in particular for the teaching that is referenced hereinabove. However, the citation of any reference is not intended to be an admission that the reference is prior art.

EXAMPLES

Example 1: Mouse Model of *C. difficile* Infection

Mouse Husbandry

Experiments were performed using C57BL/6J female mice purchased from Jackson Laboratories (Bar Harbor, Me.) and housed in ventilated sterile cages. All animals were maintained in a specific-pathogen-free facility. Animals were acclimated to the vivarium for at least 3 days prior to study (i.e., commencing antibiotic courses). For experiments involving *C. difficile* infection, mice were administered 10-10^4 *C. difficile* VPI 10463 spores in 200 μl PBS by oral gavage. Experiments were performed in compliance with institutional guidelines and approved by the institution's Institutional Animal Care and Use Committee. Sterile food and drinking water were provided to the animals

Live Biotherapeutic Product (LBP) Preparation

Individual bacterial strains were isolated from fecal material obtained from healthy donors. The individual strains were struck out from 15% glycerol freezer stocks onto EG (Eggerth Gagnon) agar plates containing 5% horse blood in an anaerobic chamber and incubated for 24-48 hours at 37° C. Colonies were inoculated into pre-reduced liquid Peptone Yeast Glucose (PYG) media and grown for 24-48 hours until dense (static in the anaerobic chamber). Optical density (OD_{600}) of the cultures was assessed and live biotherapeutic product (LBP) cocktails were prepared inside an anaerobic chamber adjusting inputs based upon OD_{600} for equal CFU ratio cocktails in PBS (sterile, pre-treated).

C. difficile Colony Forming Unit (CFU) Determination

Fecal pellets were collected, transported to an anaerobic chamber (<2 hours), and manually homogenized in 500 μl, of pre-reduced PBS using a pipette tip and through repeated pipetting. Serial dilutions of fecal homogenates were prepared in pre-reduced PBS, 100 μl, of which was spread onto cycloserine-cefoxitin-fructose agar with sodium taurocholate (TCCFA) plates, and incubated anaerobically at 37° C. *C. difficile* CFUs were enumerated at 48 hours.

Murine Susceptibility to *C. difficile* Infection

Groups of mice were evaluated for susceptibility to *C. difficile* using three antibiotic regimen protocols: (1) an antibiotic cocktail, (2) clindamycin administration, or (3) cefoperazone administration (FIGS. **2** and **3**). The antibiotic cocktail consisted of kanamycin (0.4 mg/ml), gentamicin (0.035 mg/ml), colistin (0.056 mg/ml), metronidazole (0.215 mg/ml), vancomycin (0.045 mg/ml) in the drinking water from day −10 to day −3, followed by a single intraperitoneal clindamycin injection (200 μg/mouse). The clindamycin administration involved a single intraperitoneal injection of clindamycin (200 μg/mouse) on day −1. The notation of days is relative to day 0, the day of *C. difficile* infection.

Mice were treated with the indicated antibiotic regimen as described above and then infected with either 10 or 10^4 *C. difficile* spores by oral gavage on day 0 (FIGS. **2** and **3**). An additional experimental arm was added to the antibiotic treatment model in which mice were treated with vancomycin after *C. difficile* infection (FIG. **4**J; black triangles).

Mice were monitored daily following infection for mortality/survival (FIGS. **4**A-**4**D) and weight (FIGS. **4**E-**4**H). Fecal pellets were also collected daily and used for *C. difficile* CFU enumeration, presented as CFU/gram feces (FIGS. **4**I-**4**L).

The groups of mice that received cefoperazone treatment had a significant change in weight (FIG. **4**H) and substantial *C. difficile* bacterial load in the fecal pellets (FIG. **4**L), even following administration with 10 *C. difficile* spores. These results indicated that the cefoperazone pre-treatment regimen provided a good model for *C. difficile* infection and for evaluating protection and/or treatment of *C. difficile* infection. In the absence of antibiotic treatment prior to infection, *C. difficile* infection was not established (FIG. **4**I) and all mice survived (FIG. **4**A) without significant change in body weight (FIG. **4**E).

Example 2: Live Biotherapeutic Product (LBP) Preparations Protect Against *C. difficile* Infection

The following LBP compositions were evaluated for their capacity to protect and/or treat *C. difficile* infection:

Composition A,

Composition B,

Composition C,

Composition D,

Composition E (See e.g., Narushima et al., Gut Microbes (2014) 5(3) 333-339), and

Composition I: a mixture of *Clostridium scindens, Pseudoflavonifractor capillosus* and *Blautia hansenii* (FIG. **5**).

In general, LBP cocktails were mixed in PYG media, and each mouse was administered a dose by oral gavage in 250 μL pre-reduced PBS (media-free). For composition E, bacteria were mixed in equal volumes (not equal ratios/CFUs) and administered in a 250 μL dose. Each LBP of Compositions A-D contained 10^8 CFUs total in a 250 μL dose, comprised of 10^7 CFU of each of the bacterial strains (FIG. **1**), for a total of 10^8 CFU administered to each animal. Composition I contained a total of 10^6 CFUs in a 250 μL dose (approximately 333,000 of each of the 3 bacteria mixed).

Groups of mice were subjected to cefoperazone treatment, as described in Example 1, and were administered the indicated composition by oral gavage 2 days after the cessation of cefoperazone treatment. Twenty-four hours later, the mice were subjected to infection with 10^4 *C. difficile* spores (FIG. **5**). Mice evaluated for survival/mortality (FIG. **6**), weight (FIGS. **7**A-**7**I, and *C. difficile* CFUs (FIGS. **8**A-**8**C). The results show that administration of Composition B prior to *C. difficile* infection is an effective protection and/or treatment against *C. difficile* infection.

Example 3: Composition B Protects Against and/or Treats *C. difficile* Infection

Groups of 10-12 week old mice were used in the *C. difficile* mouse model (FIG. **9**). Mice were subjected to cefoperazone treatment as described in Example 1. One group of mice was then administered Composition B (10^8 CFU per mouse) administered by oral gavage, as described in Examples 1 and 2, 2 days after the cessation of cefoperazone treatment. The other group of mice did not receive a live biotherapeutic product after cefoperazone treatment (control). Twenty-four hours later, the mice were subjected to *C. difficile* infection (10^4 *C. difficile* spores) and then evaluated for survival/mortality (FIG. **10**), weight (FIG. **11**), and *C. difficile* burden (CFUs per gram feces; FIG. **12**). These results confirm the results of Example 2 that demonstrate treatment with Composition B prior to *C. difficile* infection is an effective protection and/or treatment against *C. difficile* infection.

Example 4: LBP Composition F Protects Against and/or Treat *C. difficile* Infection

FIG. **13** shows the strains of live biotherapeutic product (LBP) Composition F. The genus-species classification indicates the closest species based on the sequence of the isolated strain. FIG. **14** shows the classification by *Clostridium* cluster of the strains in Composition F.

Groups of mice were administered cefoperazone, as described in the Examples above, then administered LBPs or fecal matter transplant (FMT) from mice or human (FIG. **15**). Composition B was administered to the indicated groups on day −1; days −2 and −1; or on days −2, −1, 1, 2, and 3, relative to infection with 10^4 *C. difficile* spores. Composition F was administered to the indicated groups on day −1 or on days −2, −1, 1, 2, and 3, relative to administration of *C. difficile* spores. Additional groups received FMT from mice or from humans (200 μL of a 10% fecal sample s per mouse). Mice were then evaluated for survival/mortality (FIG. **16**), weight (FIGS. **17**A-**17**H), and *C. difficile* burden (CFU/gram feces) on days 1, 3, 8 and 17 after infection (FIGS. **18**A and **18**B). The data demonstrate that Composition B, Composition F, and FMT protect against and/or treat *C. difficile* infection.

Example 5: LBP Compositions Protect Against and/or Treat *C. difficile* Infection

FIG. **19** shows the strains of LBP Composition G. The genus-species notation indicates the closest species based on the sequence of the isolated strain. Composition G includes a subset of the strains of Composition F. Groups of mice were administered cefoperazone, as described in the Examples above, then administered the LBP:

Composition B;

Composition B-1 (Composition B with *Bacteroides* added);

Composition B-2 (Composition B from which *Flavonifractor plautii* was removed and *Bacteroides* added);

Composition F;

Composition G;

Human fecal samples subjected to ethanol treatment;

Composition B subjected to ethanol treatment;

Composition B that had been frozen; or

Composition J: *Clostridium innocuum, Clostridium bolteae* and *Clostridium symbiosum* subjected to ethanol treatment;

(See also FIG. **20**).

The *Bacteroides* strain used in Composition B-1 and B-2 was *Bacteroides ovatus* (strain identifier 211-B; SEQ ID NO: 83).

Mice were challenged with *C. difficile* VPI 10463 spores (10^4) and monitored daily (Day 0 to Day 7 post *C. difficile* infection) for survival/mortality (FIGS. **21** and **23**) and change in weight (FIGS. **22**A-**22**J and **24**). These data show that the compositions protect against and/or treat *C. difficile* infection.

Example 6: LBP Compositions Protect Against and/or Treat *C. difficile* Infection

Groups of mice were subjected to cefoperazone treatment, as described above, then administered human fecal matter transplant, Composition B, Composition B+4 spores, or Composition H (FIG. **25**). "Composition B+4 spores" refers to Composition B plus the following four strains in spore form: *Clostridium bolteae, Anaerotruncus colihominis, Clostridium symbiosum* and *Clostridium innocuum*. Composition H contains the following six strains in spore form: *Clostridium bolteae, Anaerotruncus colihominis, Clostridium symbiosum, Clostridium innocuum, Clostridium disporicum* and *Erysipelatoclostridium ramosum* (FIG. **26**).

Mice were then challenged with *C. difficile* infection with 10^4 *C. difficile* VPI 10463 spores and monitored for survival/mortality (FIGS. **27**A and **28**A), weight (FIGS. **27**B and **28**B). Mice that lost more than 20% body weight relative to baseline were included in mortality numbers in survival

curves. The *C. difficile* burden was assessed by CFU in fecal pellets on days 1, 4 and 19 after infection (FIGS. **29**A-**29**C).

These data indicate that Composition B as well as other compositions can improve survival in the cefoperazone-induced *C. difficile* mouse model and protect against and/or treat *C. difficile* infection.

Example 7: *C. difficile* Toxin Experiment

Vero cells, epithelial cells derived from African Green Monkey kidney epithelium, are sensitive to a variety of bacterial toxins, including *C. difficile* Toxin B. Exposure of cells to *C. difficile* Toxin B results in inhibition of the function of Rho, Rac, and Cdc42 leading to a decline in F-actin, a change in cell morphology (e.g., cell rounding), and eventually apoptosis.

To determine whether administration of bacterial compositions described herein has an effect on the production or activity of *C. difficile* Toxin B, a cellular assay was performed. Briefly, groups of mice were treated with cefoperazone, as described above, and administered human fecal matter transplant (FMT) ("4-3"); Composition B ("5-3"); Composition B plus four strains in spore form: *Clostridium bolteae, Anaerotruncus colihominis, Clostridium symbiosum* and *Clostridium innocuum* ("7-4"), or no treatment. Each of the groups of mice were then exposed to *C. difficile* infection with 10^4 *C. difficile* spores. The groups of mice that did not receive a treatment after cefoperazone administration and prior to *C. difficile* infection are referred to as "2-1 (Cdiff)" and "2-4 (Cdiff)." An additional group of mice was not exposed to *C. difficile* as indicated by "N3 (Healthy)".

Fecal pellets were collected from each of the groups of mice, weighed, and homogenized in PBS and normalized to a fixed concentration (~25 mg/mL). The samples were centrifuged to prepare a clarified supernatant, which was then diluted in 10-fold serial dilutions to produce a range from 1:10 to $1:10^{-6}$ dilutions of clarified pellet supernatant. Vero cell cultures were exposed to the diluted samples for approximately 18 hours, then visualized by phase contract microscopy to assess morphological changes (i.e., cell rounding) associated with *C. difficile* toxin exposure. The cells were scored based on the highest concentration of supernatant that did not yield a change in morphology (FIG. **30**). The samples from mice that had been treated with Composition B prior to *C. difficile* infection had reduced amounts of *C. difficile* Toxin B, as compared to samples from control mice that did not receive a treatment after cefoperazone administration and prior to *C. difficile* infection ("2-1 (Cdiff)" and "2-4 (Cdiff)") as well as compared to samples from mice that received FMT. Notably, the samples from mice that had been treated with Composition B also had reduced amounts of *C. difficile* Toxin B, as compared to samples from mice that had been treated with Composition B with additional spores.

Example 8: In Vitro Competition Between Compositions B and *C. difficile*

Composition B was assessed for its ability to suppress *Clostridium difficile* growth by an in vitro mixed culture competition assay. From glycerol freezer stocks, individual strains of Composition B, *C. difficile* (Cdiff), *Clostridium bifermentans*, and *Bacteroides* thetaiotaomicron were struck out onto Eggerth-Gagnon agar plates with horse blood (EG+HB). Single colonies of each of the strains were subsequently inoculated into brain heart infusion (BHI) liquid media and allowed to grow in pure culture for 24-48 hours. Turbid cultures were sub-cultured then grown to exponential phase and finally diluted and combined to prepare a mixed culture with an optical density (OD_{600}) of 0.1. Exponential phase Cdiff culture was added to the mixed culture at a final concentration with an OD of 0.1. After the cultures were combined and incubated for 2-3 hours, samples were collected, serially diluted, and plated on Taurocholate-Cycloserine-Cefoxitin-Fructose Agar (TCCFA) plates to select for Cdiff growth. After 48-72 hours, the colony forming units (CFUs) of Cdiff in each competition experiment were determined by manual colony counting.

EG+HB agar plates were prepared according to standard procedures and reduced in an anaerobic environment for at least 6-8 hours prior to use. Liquid BHI medium was obtained from BD Biosciences (Catalog #211059, San Jose, Calif.), prepared according to the manufacturer's instructions, and reduced in an anaerobic environment for at least 18-24 hours prior to use. TCCFA plates were prepared according to standard procedures and reduced in an anaerobic environment for at least 6-8 hours prior to use. *Clostridium difficile* strain used in the experiments: American Type Culture Collection (ATCC) 43255.

TABLE 4

Composition B strains Composition B
VE202-7
VE202-13
VE202-14
VE202-16
Strain #16
Strain #170
Strain #189
Strain #211

Strains were struck out onto EG+HB agar plates from frozen glycerol stocks inside an anaerobic chamber for 48-72 hours. Single colonies were inoculated into 10 mL of BHI media and grown 24-48 hours at 37° C. in the anaerobic chamber. Turbid cultures were then diluted to an OD of 0.1 and grown for 2-3 hours at 37° C. in the anaerobic chamber. Exponential phase cultures were diluted and combined at equivalent ODs. For the competition assay, each of the strains of Combination B (Table 4) were combined in equal parts, based on OD_{600}, to reach a final consortium OD_{600} of 0.1. *C. bifermentans* and *B. thetaiotaomicron* were setup to compete with Cdiff individually at an OD of 0.1. The OD600 for Cdiff in each of the mixed culture competition experiments was 0.1. After combination, the cultures were incubated for 2-3 hours at 37° C. in the anaerobic chamber, then prepared for enumerations on Cdiff selective plates.

TCCFA plates are selective for Cdiff growth, and none of the Combination B strains, nor either of the control strains (*C. bifermentans* and *B. thetaiotaomicron*), grow on these plates. Inside an anaerobic chamber, a 100 μL sample of each competition culture was collected and serially diluted 1:10 to reach a final dilution of 1×10^{-6}. Plates for CFU enumeration were prepared by spreading 100 μL of each of the 1×10^{-4} through 1×10^{-6} dilutions on TCCFA plates using sterile spreading loops. CFU plates were incubated for 48-72 hours at 37° C. in the anaerobic chamber. CFU enumeration was completed by manually counting colonies.

To determine the effect of competition, the ratio of CFUs determined for the competition samples and Cdiff alone was calculated and expressed as a percentage. Inhibition of Cdiff growth by the Composition B cocktail was compared to the responses of *B. thetaiotaomicron* (negative control) and *C. bifermentans* (positive control). The results are shown in Table 5 and FIG. **31**.

TABLE 5

Summary Results for In Vitro Competition

Experiment Number	No Competing Strain(s)	Competition with *B. thetaiotaomicron*	Competition with *C. bifermentans*	Competition with Composition B
n = 1	100			33.8
n = 2	100	9.90	0.1	0.5
n = 3	100	115	39.5	33.1
n = 4	100	41.3	0.7	0.7
n = 5	100	105	14.1	20.9
n = 6	100	57.4	4.1	1.6
Mean	100	65.6	11.7	15.1
Std. Dev.	0	43.8	16.5	16.2
Total N	6	5	5	6

Data is expressed as Cdiff CFU as a percentage of control. Each n is representative of a single biological replicate, independent of other measurements.

In in vitro competition, Composition B inhibited Cdiff growth to 15.1±16.2% of control (absence of competing strain(s)). This result is consistent with the inhibition observed by the positive control, *C. bifermentans*, of 11.7±16.5% of control. *B. thetaiotaomicron*, a negative control, yielded a negligible effect on Cdiff growth at 65.6±43.8% of control. Given the variability inherent in the assessment of CFU, inhibition of growth to <25% of control is considered to be significant inhibition and both the positive control and Composition B cocktail meet this threshold of activity. The Composition B consortium attenuated Cdiff growth in vitro comparable to the direct competition observed by *C. bifermentans*. Direct competition with *B. thetaiotaomicron* did not significantly inhibit Cdiff growth.

Example 9: Determination of In Vitro Short-Chain Fatty Acid Production

Each strain of Composition B was assessed for individual short-chain fatty acid (SCFA) production in vitro. Composition B strains were grown in pure cultures inside an anaerobic chamber. Spent supernatant from liquid media cultures was harvested by centrifugation, filter sterilized, and then stored at <−70° C. Frozen clarified supernatant specimens were analyzed for short-chain fatty acids (SCFAs).

EG+HB agar plates (Eggerth-Gagnon agar plates with horse blood) were prepared according to standard methods and reduced in an anaerobic environment for at least 6-8 hours prior to use. Liquid PYG medium (pre-formulated, pre-reduced) was obtained from Anaerobe Systems (Catalog#AS-822; Morgan Hill, Calif.).

Strains were struck out onto EG+HB agar plates from frozen 15% glycerol stocks inside an anaerobic chamber for 48-72 hours. Single colonies were inoculated into 7 mL PYG media and grown 24-48 hours at 37° C. in the anaerobic chamber. Unless otherwise noted, when the optical density (OD) was >0.2, samples were collected for CFU enumeration and filtration. Inside an anaerobic chamber, a 100 µL sample of turbid culture was collected and serially diluted 1:10 to reach a final dilution of 1×10^{-6}. Plates for CFU enumeration were prepared by spreading 100 µL/dilution for the 1×10^{-4} through 1×10^{-6} dilutions on EG+HB agar plates using sterile glass beads. CFU plates were incubated for 48-72 hours in the anaerobic chamber. CFU enumeration was completed using the EasyCount 2 (bioMérieux SA, Marcy-l'Étoile, France). Immediately after samples of turbid cultures were collected for CFU enumeration, the remaining turbid cultures were centrifuged at approximately 1000 RCF for 10 minutes to pellet cellular debris. The clarified supernatants were transferred to a 0.2 µm plate filter and vacuum filtered to remove any remaining particulates prior to bioanalysis. In the event of blockage in the filter plate, clarified supernatants were manually filtered using 0.2 µm syringe filters. Filtered supernatants were aliquoted and stored at <−70° C. prior to bioanalysis of SCFAs.

To facilitate easier comparisons between samples, raw SCFA data (µg/mL) was normalized by the $\log_{10}$ of corresponding determined/estimated CFU for the culture. The results are depicted in Table 6 and Table 7 below.

TABLE 6

Enumerated CFUs for Composition B Strains

Sample ID	OD600	Enumerated CFU (CFU/mL)
VE202-7	>2	6.11E+08
VE202-13	0.8	4.00E+08
VE202-14	>2	1.60E+09
VE202-16	1.92	1.28E+09
#16	1.97	1.69E+08
#170	1.8	1.08E+08
#189	1.03	1.74E+09
#211	0.35	3.71E+08

TABLE 7

SFCAs produced by individual Composition B strains

	Normalized (µg/Log(CFU/mL) * mL)							
Sample ID	Acetate	Propionate	Iso-butyrate	Butyrate	2-Methyl-butyrate	Iso-valerate	Valerate	Hexanoate
VE202-7	123.7	0.077	0.102	0.208	0.015	0.056	BLOQ	0.031
VE202-13	30.1	0.545	0.116	34.452	0.288	0.188	0.097	0.034

TABLE 7-continued

SFCAs produced by individual Composition B strains

	Normalized (μg/Log(CFU/mL) * mL)							
Sample ID	Acetate	Propionate	Iso-butyrate	Butyrate	2-Methyl-butyrate	Iso-valerate	Valerate	Hexanoate
VE202-14	110.5	0.054	0.022	0.248	0.011	0.014	BLOQ	0.009
VE202-16	313.2	0.000	0.000	0.280	0.004	0.000	BLOQ	0.009
#16	104.0	0.005	0.000	50.988	0.014	0.033	BLOQ	0.009
#170	87.1	0.055	0.025	0.215	0.011	0.039	BLOQ	0.016
#189	0.0	BLOQ	0.000	35.751	0.005	0.019	0.359	0.587
#211	57.6	5.289	0.000	78.227	0.028	0.050	0.053	0.095

Seven strains of Composition B were found to produce significant quantities (>1 μg/Log(CFU/mL) * mL) of the 2-carbon SCFA, acetate. One strain, (#211), produced substantial quantities of the 3-carbon SCFA, propionate. Four strains of Composition B produced substantial quantities of the 4-carbon SCFA, butyrate. Trace quantities (<1 μg/Log(CFU/mL) * mL) of other SCFAs were also produced by the Composition B strains.

Example 10: Composition B Induces Regulatory T Cells (Tress)

Each of the bacterial strains of Composition B were grown to log phase, combined to a total dose of ~10^8 cfu per mouse. Germ-free mice were inoculated with Composition B or a negative control by oral gavage and sacrificed following four weeks of colonization. Lamina propria leukocytes were isolated from colonic tissue of individual mice by standard procedures and assessed by flow cytometry. The regulatory T cell content was evaluated as the percentage of Foxp3-positive cells among CD4+ T cells.

As shown in FIG. **32**, mice that were inoculated with Composition B were found to have significantly more regulatory T cells as compared to mice that were inoculated with the control.

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aacgaagcaa ttaaaatgaa gttttcggat ggatttttga ttgactgagt ggcggacggg 120

tgagtaacgc gtggataacc tgcctcacac tgggggataa cagttagaaa tgactgctaa 180

taccgcataa gcgcacagta ccgcatggta cggtgtgaaa aactccggtg gtgtgagatg 240

gatccgcgtc tgattagcca gttggcgggg taacggccca ccaaagcgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatgggcg aaagcctgat gcagcgacgc cgcgtgagtg 420

aagaagtatt tcggtatgta aagctctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggcc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggcgaagca agtctgaagt gaaaacccag 600

ggctcaaccc tgggactgct ttggaaactg ttttgctaga gtgtcggaga ggtaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ttactggacg ataactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgaatg ctaggtgttg gggggcaaag cccttcggtg 840

ccgtcgcaaa cgcagtaagc attccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc aagtcttgac atcctcttga ccggcgtgta acggcgcctt cccttcgggg 1020

caagagagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaaccct tatccttagt agccagcagg taaagctggg cactctaggg 1140

agactgccag ggataacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

gatttgggct acacacgtgc tacaatggcg taaacaaagg gaagcaagac agtgatgtgg 1260

agcaaatccc aaaaataacg tcccagttcg gactgtagtc tgcaacccga ctacacgaag 1320

ctggaatcgc tagtaatcgc gaatcagaat gtcgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagc aacgcccgaa gtcagtgacc caactcgcaa 1440

gagagggagc tgccgaaggc ggggcaggta actggggtga agtcgtaaca aggtagccgt 1500

atcggaaggt gcggctggat cacctccttt 1530

<210> SEQ ID NO 18
<211> LENGTH: 1528
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 18

aacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcttaaca catgcaagtc 60

gagcgaagca ctttggaaga ttcttcggat gaagactttt gtgactgagc ggcggacggg 120

tgagtaacgc gtgggtaacc tgcctcatac agggggataa cagttagaaa tgactgctaa 180

taccgcataa gaccacggta ccgcatggta cagtggtaaa aactccggtg gtatgagatg 240

gacccgcgtc tgattaggta gttggtgggg taacggccta ccaagccgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccagact cctacgggag 360

gcagcagtgg ggaatattgc acaatggagg aaactctgat gcagcgacgc cgcgtgaagg 420

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atgaagtatt tcggtatgta aacttctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtagggggc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggcacggca agccagatgt gaaagcccgg 600

ggctcaaccc cgggactgca tttggaactg ctgagctaga gtgtcggaga ggcaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ttgctggacg atgactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgactg ctaggtgtcg ggtggcaaag ccattcggtg 840

ccgcagctaa cgcaataagc agtccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc tgatcttgac atcccgatga ccgcttcgta atggaagctt ttcttcggaa 1020

catcggtgac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaacccc tatcttcagt agccagcagg ttaagctggg cactctggag 1140

agactgccag ggataacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

gaccagggct acacacgtgc tacaatggcg taaacaaaga gaagcgaact cgcgagggta 1260

agcaaatctc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc agatcagaat gctgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gtcagtgacc caaccgtaag 1440

gagggagctg ccgaaggtgg gaccgataac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 19
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 19

atcagagagt ttgatcctgg ctcaggatga acgctggcgg cgtgcttaac acatgcaagt 60

cgagcgaagc acttaagtgg atctcttcgg attgaaactt atttgactga gcggcggacg 120

ggtgagtaac gcgtgggtaa cctgcctcat acagggggat aacagttaga aatggctgct 180

aataccgcat aagcgcacag gaccgcatgg tctggtgtga aaaactccgg tggtatgaga 240

tggacccgcg tctgattagc tagttggagg ggtaacggcc caccaaggcg acgatcagta 300

gccggcctga gagggtgaac ggccacattg ggactgagac acggcccaga ctcctacggg 360

aggcagcagt ggggaatatt gcacaatggg ggaaaccctg atgcagcgac gccgcgtgaa 420

ggaagaagta tctcggtatg taaacttcta tcagcaggga agaaaatgac ggtacctgac 480

taagaagccc cggctaacta cgtgccagca gccgcggtaa tacgtagggg gcaagcgtta 540

tccggattta ctgggtgtaa agggagcgta gacggaagag caagtctgat gtgaaaggct 600

ggggcttaac cccaggactg cattggaaac tgtttttcta gagtgccgga gaggtaagcg 660

gaattcctag tgtagcggtg aaatgcgtag atattaggag gaacaccagt ggcgaaggcg 720

gcttactgga cggtaactga cgttgaggct cgaaagcgtg gggagcaaac aggattagat 780

accctggtag tccacgccgt aaacgatgaa tactaggtgt cgggtggcaa agccattcgg 840

tgccgcagca aacgcaataa gtattccacc tggggagtac gttcgcaaga atgaaactca 900

aaggaattga cggggacccg cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg 960

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aagaacctta ccaagtcttg acatccctct gaccggcccg taacggggcc ttcccttcgg 1020

ggcagaggag acaggtggtg catggttgtc gtcagctcgt gtcgtgagat gttgggttaa 1080

gtcccgcaac gagcgcaacc cctatcctta gtagccagca ggtgaagctg ggcactctag 1140

ggagactgcc ggggataacc cggaggaagg cggggacgac gtcaaatcat catgcccctt 1200

atgatttggg ctacacacgt gctacaatgg cgtaaacaaa gggaagcgag acagcgatgt 1260

tgagcaaatc ccaaaaataa cgtcccagtt cggactgcag tctgcaactc gactgcacga 1320

agctggaatc gctagtaatc gcgaatcaga atgtcgcggt gaatacgttc ccgggtcttg 1380

tacacaccgc ccgtcacacc atgggagtca gtaacgcccg aagtcagtga cccaacctta 1440

caggagggag ctgccgaagg cgggaccgat aactggggtg aagtcgtaac aaggtagccg 1500

tatcggaagg tgcggctgga tcacctcctt t 1531

<210> SEQ ID NO 20
<211> LENGTH: 1528
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 20

aacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcttaaca catgcaagtc 60

gagcgaagca ctttggaaga ttcttcggat gatttccttt gtgactgagc ggcggacggg 120

tgagtaacgc gtgggtaacc tgcctcatac agggggataa cagttagaaa tgactgctaa 180

taccgcataa gaccacggta ccgcatggta cagtggtaaa aactccggtg gtatgagatg 240

gacccgcgtc tgattaggta gttggtgggg taacggccta ccaagccgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccagact cctacgggag 360

gcagcagtgg ggaatattgc acaatggagg aaactctgat gcagcgacgc cgcgtgaagg 420

atgaagtatt tcggtatgta aacttctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggcc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggcacggca agccagatgt gaaagcccgg 600

ggctcaaccc cgggactgca tttggaactg ctgagctaga gtgtcggaga ggcaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ttgctggacg atgactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgactg ctaggtgtcg ggtggcaaag ccattcggtg 840

ccgcagctaa cgcaataagc agtccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc tgatcttgac atcccgatga ccgcttcgta atggaagctt ttcttcggaa 1020

catcggtgac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaacccc tatcttcagt agccagcagg ttaagctggg cactctggag 1140

agactgccag ggataacctg gaggaaggtg gggatgacgt caaatcatca tgcccttat 1200

gaccagggct acacacgtgc tacaatggcg taaacaaaga gaagcgaact cgcgagggta 1260

agcaaatctc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc agatcagaat gctgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gtcagtgacc caaccgtaag 1440

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gagggagctg ccgaaggtgg gaccgataac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 21
<211> LENGTH: 1537
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 21

atggagagtt tgatcctggc tcaggatgaa cgctggcggc atgcctaata catgcaagtc 60

gaacgaagtt tcgaggaagc ttgcttccaa agagacttag tggcgaacgg gtgagtaaca 120

cgtaggtaac ctgcccatgt gtccgggata actgctggaa acggtagcta aaaccggata 180

ggtatacaga gcgcatgctc agtatattaa agcgcccatc aaggcgtgaa catggatgga 240

cctgcggcgc attagctagt tggtgaggta acggcccacc aaggcgatga tgcgtagccg 300

gcctgagagg gtaaacggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

agcagtaggg aattttcgtc aatgggggaa accctgaacg agcaatgccg cgtgagtgaa 420

gaaggtcttc ggatcgtaaa gctctgttgt aagtgaagaa cggctcatag aggaaatgct 480

atgggagtga cggtagctta ccagaaagcc acggctaact acgtgccagc agccgcggta 540

atacgtaggt ggcaagcgtt atccggaatc attgggcgta aagggtgcgt aggtggcgta 600

ctaagtctgt agtaaaaggc aatggctcaa ccattgtaag ctatggaaac tggtatgctg 660

gagtgcagaa gagggcgatg gaattccatg tgtagcggta aaatgcgtag atatatggag 720

gaacaccagt ggcgaaggcg gtcgcctggt ctgtaactga cactgaggca cgaaagcgtg 780

gggagcaaat aggattagat accctagtag tccacgccgt aaacgatgag aactaagtgt 840

tggaggaatt cagtgctgca gttaacgcaa taagttctcc gcctggggag tatgcacgca 900

agtgtgaaac tcaaaggaat tgacgggggc ccgcacaagc ggtggagtat gtggtttaat 960

tcgaagcaac gcgaagaacc ttaccaggcc ttgacatgga aacaaatacc ctagagatag 1020

ggggataatt atggatcaca caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg 1080

ttgggttaag tcccgcaacg agcgcaaccc ttgtcgcatg ttaccagcat caagttgggg 1140

actcatgcga gactgccggt gacaaaccgg aggaaggtgg ggatgacgtc aaatcatcat 1200

gccccttatg gcctgggcta cacacgtact acaatggcgg ccacaaagag cagcgacaca 1260

gtgatgtgaa gcgaatctca taaaggtcgt ctcagttcgg attgaagtct gcaactcgac 1320

ttcatgaagt cggaatcgct agtaatcgca gatcagcatg ctgcggtgaa tacgttctcg 1380

ggccttgtac acaccgcccg tcaaaccatg ggagtcagta atacccgaag ccggtggcat 1440

aaccgtaagg agtgagccgt cgaaggtagg accgatgact ggggttaagt cgtaacaagg 1500

tatccctacg ggaacgtggg gatggatcac ctccttt 1537

<210> SEQ ID NO 22
<211> LENGTH: 476
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 22

agtaacgcgt gggtaacctg cctcatacag ggggataaca gttagaaatg actgctaata 60

ccgcataaga ccacggtacc gcatggtaca gtggtaaaaa ctccggtggt atgagatgga 120

-continued

cccgcgtctg attaggtagt tggtggggta acggcctacc aagccgacga tcagtagccg 180

acctgagagg gtgaccggcc acattgggac tgagacacgg cccagactcc tacgggaggc 240

agcagtgggg aatattgcac aatggaggaa actctgatgc agcgacgccg cgtgaaggat 300

gaagtatttc ggtatgtaaa cttctatcag cagggaagaa aatgacggta cctgactaag 360

aagccccggc taactacgtg ccagcagccg cggtaatacg taggggcaa gcgttatccg 420

gatttactgg gtgtaaaggg agcgtagacg gcacggcaag ccagatgtga aagccc 476

<210> SEQ ID NO 23
<211> LENGTH: 354
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 23

caggctggag tgcaggagag gtaagcggaa ttcctagtgt agcggtgaaa tgcgtagata 60

ttaggaggaa caccagtggc gaaggcggct tactggactg taactgacgt tgaggctcga 120

aagcgtgggg agcaaacagg attagatacc ctggtagtcc acgcggtaaa cgatgattgc 180

taggtgtagg tgggtatgga cccatcggtg ccgcagctaa cgcaataagc aatccacctg 240

gggagtacgt tcgcaagaat gaaactcaaa ggaattgacg gggacccgca caagcggtgg 300

agcatgtggt ttaattcgaa gcaacgcgaa gaaccttacc aagtcttgac atcc 354

<210> SEQ ID NO 24
<211> LENGTH: 190
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 24

ccggggctca ccccgggact gcatttggaa ctgctgagct agagtgtcgg agaggcaagt 60

ggaattccta gtgtagcggt gaaatgcgta gatattagga ggaacaccag tggcgaaggc 120

ggcttgctgg acgatgactg acgttgaggc tcgaaagcgt ggggagcaaa caggattaga 180

taccctggta 190

<210> SEQ ID NO 25
<211> LENGTH: 190
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 25

agggtcaacc cctggactgc attggaaact gtcaggctgg agtgccggag aggtaagcgg 60

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 120

cttactggac ggtaactgac gttgatgctc gaaagcgtgg ggagcaaaca ggattagata 180

acctggtaaa 190

<210> SEQ ID NO 26
<211> LENGTH: 209
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 26

gggaagtcgg tcttaagtgc ggggcttaac cccgtgaggg gaccgaaact gtgaagctcg 60

agtgtcggag aggaaagcgg aattcctagt gtagcggtga aatgcgtaga tattaggagg 120

aacaccagtg gcgaaagcgg ctttctggac gacaactgac gctgaggcgc gaaagccagg 180

ggagcaaacg ggattagata ccccagtaa 209

<210> SEQ ID NO 27
<211> LENGTH: 203
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 27

tagtctgagt gatgcggggc ttaaccccgt atggcgttgg atactggaag tcttgagtgc 60

aggagaggaa aggggaattc ccagtgtagc ggtgaaatgc gtagatattg ggaggaacac 120

cagtggcgaa ggcgcctttc tggactgtgt ctgacgctga gatgcgaaag ccagggtagc 180

aaacgggatt agataccacg gta 203

<210> SEQ ID NO 28
<211> LENGTH: 207
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 28

gatagtcggt cttaagtgcg gggcttaccc cgtgagggga ccgaaactgt gaagctcgag 60

tgtcggagag gaaagcggaa ttcctagtgt agcggtgaaa tgcgtagata ttaggaggaa 120

caccagtggc gaaagcggct ttctggacga caactgacgc tgaggcgcga aagccagggg 180

agcaaacggg attagatacc acggtaa 207

<210> SEQ ID NO 29
<211> LENGTH: 424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 29

cgtttgctcc acgctttcga gcctcacgtc agttaccgtc cagtaagccg ccttcgccac 60

tggtgttcct cctaatatct acgcatttca ccgctacact aggaattccg cttacctctc 120

cggtactcta gattgacagt ttccaatgca gtcccggggt tgagccccgg gttttcacat 180

cagacttgcc actccgtcta cgctccctttt acacccagta aatccggata acgcttgcac 240

catacgtatt accgcggctg ctggcacgta tttagccggt gcttcttagt caggtaccgt 300

cattttcttc cctgctgata gagctttaca taccgaaata cttcatcgct cacgcggcgt 360

cgctgcatca gggtttcccc cattgtgcaa tattccccac tgctgcctcc cgtaggagtt 420

tgga 424

<210> SEQ ID NO 30
<211> LENGTH: 441
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 30

tgtcacactt tcgagcatca gcgtcagtta cagtccagta agctgccttc gcaatcggag 60

ttcttcgtga tatctaagca tttcaccgct acaccacgaa ttccgcctac ctctactgca 120

ctcaagacga ccagtatcaa ctgcaatttt acggttgagc cgcaaacttt cacagctgac 180

ttaatagtcc gcctacgctc cctttaaacc caataaatcc ggataacgct tggatcctcc 240

gtattaccgc ggctgctggc acggagttag ccgatcctta ttcgtatggt acatacaaaa 300

agccacacgt ggctcacttt attcccatat aaaagaagtt tacaacccat agggcagtca 360

tccttcacgc tacttggctg gttcagactc tcgtccattg accaatattc ctcactgctg 420

cctcccgtag gtagtttgga a 441

<210> SEQ ID NO 31
<211> LENGTH: 422
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 31

ccgttgtcac gctttcgtgc tcagtgtcag tttcagtcca gtaagccgcc ttcgccactg 60

atgttcctcc taatatctac gcatttcacc gctacactag gaattccgct tacctctcct 120

gcactccagt ctgacagttt caaaagcagt cccagagtta agccctgggt tttcacttct 180

gacttgccat accacctacg cacccttttac acccagtaat tccggataac gcttgccccc 240

tacgtattac cgcggctgct ggcacgtagt tagccggggc ttcttagtca ggtaccgtca 300

ttttcttccc tgctgataga gctttacata ccgaaatact tcttcactca cgcggcgtcg 360

ctgcatcagg gttcccccca ttgtgcaata ttccccactg ctgcctcccg tggaagtttg 420

ga 422

<210> SEQ ID NO 32
<211> LENGTH: 424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 32

gcgaatgtca cgcattcgag cctcacgtca gttaccgtcc agtaagccgc cttcgccact 60

ggtgttcctc ctaatatcta cgcatttcac cgctacacta ggaattccgc ttacctctcc 120

ggcactcaag actaacagtt tccaatgcag tccaggggtt gagcccccgc ctttcacatc 180

agacttgcca gtccgtctac gctcccttta cacccagtaa atccggataa cgcttgcccc 240

ctacgtatta ccgcggctgc tggcacgtag ttagccgggg cttcttagtc aggtaccgtc 300

actatcttcc ctgctgatag aagtttacat accgagatac ttcttccttc acgcggcgtc 360

gctgcatcag ggtttccccc attgtgcaat attccccact gctgcctccc gtgggagttt 420

ggaa 424

<210> SEQ ID NO 33
<211> LENGTH: 422
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 33

tgctcacgct ttcgcgctca gcgtcagtta ctgtccagca atccgccttc gccactggtg 60

ttcctccgta tatctacgca tttcaccgct acacacggaa ttccgattgc ctctccagca 120

ctcaagaact acagtttcaa atgcaggctg gaggttgagc ccccagtttt cacatctgac 180

ttgcaatccc gcctacacgc cctttacacc cagtaaatcc ggataacgct tgccacctac 240

gtattaccgc ggctgctggc acgtagttag ccgtggctta ttcgtcaggt accgtcattt 300

gtttcgtccc tgacaaaaga agtttacaac ccgaaagcct tcttccttca cgcggcgttg 360

ctgggtcagg cttgcgccca ttgcccaata ttccccactg ctgcctcccg tggtagtttg 420

ga 422

<210> SEQ ID NO 34
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 34

tgtccacgct ttcgagctca gcgtcagtta tcgtccagta agccgccttc gccactggtg 60

ttcctcctaa tatctacgca tttcaccgct acactaggaa ttccgcttac ccctccgaca 120

ctctagtacg acagtttcca atgcagtacc ggggttgagc cccgggcttt cacatcagac 180

ttgccgcacc gcctgcgctc cctttacacc cagtaaatcc ggataacgct tgcaccatac 240

gtattaccgc ggctgctggc acgtatttag ccggtgcttc ttagtcaggt accgtcatta 300

tcttccctgc tgatagagct ttacataccg aaatacttct tcgctcacgc ggcgtcgctg 360

catcaggctt tcgcccattg tgcaatattc cccactgctg actcccgtag gagtttgga 419

<210> SEQ ID NO 35
<211> LENGTH: 424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 35

cgtttctcca cgcttcgcgc tcagcgtcag ttactgtcca gcaatccgcc ttcgccactg 60

gtgttcctcc gtatatctac gcatttcacc gctacacacg gaattccgat tgcctctcca 120

gcactcaaga actacagttt caaatgcagg ctggaggttg agcccccagt tttcacatct 180

gacttgcaat cccgcctaca cgccctttac acccagtaaa tccggataac gcttgccacc 240

tacgtattac cgcggctgct ggcacgtagt tagccgtggc ttattcgtca ggtaccgtca 300

tttgtttcgt ccccgacaaa agaagtttac aacccgaaag ccttcttcct tcacgcggcg 360

ttgctgggtc aggcttgcgc ccattgccca tattcccca ctgctgcctc cctgggaagt 420

ttgg 424

<210> SEQ ID NO 36
<211> LENGTH: 445
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 36

atgtcctgac ttcgcgcctc agcgtcagtt gtcgtccaga aagccgcttt cgccactggt 60

gttcctccta atatctacgc atttcaccgc tacactagga attccgcttt cctctccgac 120

actcgagctt cacagtttcg gtcccctcac ggggttaagc cccgcacttt taagaccgac 180

ttgcgatgcc gcctgcgcgc cctttacgcc caataattcc ggacaacgct tgccacctac 240

gtattaccgc ggctgctggc acgtagttag ccgtggcttt ctcttacggt accgtcaggg 300

ataacgggta ttgaccgcta tcctgttcgt cccatataac agaactttac aacccgaagg 360

ccgtcatcgt tcacgcggcg ttgctccgtc agactttcgt ccattgcgga agattcccca 420

ctgctgcctc cctgggaagt ttgga 445

<210> SEQ ID NO 37
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 37

gtttgctcac gctttcgagc tcagcgtcag ttatcgtcca gtaagccgcc ttcgccactg 60

gtgttcctcc taatatctac gcatttcacc gctacactag gaattccgct tacccctccg 120

acactctagt acgacagttt ccaatgcagt accggggttg agccccgggc tttcacatca 180

gacttgccgc accgcctgcg ctccctttac acccagtaaa tccggataac gcttgcacca 240

tacgtattac cgcggctgct ggcacgtatt tagccggtgc ttcttagtca ggtaccgtca 300

ttatcttccc tgctgataga gctttacata ccgaaatact tcttcgctca cgcggcgtcg 360

ctgcatcagg ctttcgccca ttgtgcaata ttccccactg ctgcctcccg taggagtttg 420

g 421

<210> SEQ ID NO 38
<211> LENGTH: 424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 38

cgttgctcac gcattcgagc ctcagcgtca gttaagccca gtaagccgcc ttcgccactg 60

atgttcctcc taatatctac gcatttcacc gctacactag gaattccgct tacctctact 120

tcactcaaga accacagttt caaatgcagt ttatgggtta agcccatagt tttcacatct 180

gacttgcgat cccgcctacg ctccctttac acccagtaat tccggacaac gctcgctccc 240

tacgtattac cgcggctgct ggcacgtagt tagccggagc ttcctcctca ggtaccgtct 300

tttttcgtcc ctgaagacag aggtttacaa tcctaaaacc ttcttccctc acgcggcatc 360

gctgcatcag agtttcctcc attgtgcaat attccccact gctgcctccc gtaggagttt 420

ggaa 424

<210> SEQ ID NO 39
<211> LENGTH: 189
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 39

tgggcttacc cataaactgc atttgaaact gtggttcttg agtgaagtag aggtaagcgg 60

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aattcctagt gtagcggtga aatgcgtaga tattaggagg aacatcagtg gcgaaggcgg 120

cttactgggc tttaactgac gctgaggctc gaaagcgtgg ggagcaaaca ggattagata 180

cccaagtaa 189

<210> SEQ ID NO 40
<211> LENGTH: 414
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 40

gtcagcatcg agctcacgtc agttaccgtc cagtaagccg ccttcgccac tggtgttcct 60

cctaatatct acgcatttca ccgctacact aggaattccg cttacctctc cggtactcta 120

gattgacagt ttccaatgca gtcccggggt tgagccccgg gttttcacat cagacttgcc 180

actccgtcta cgctcccttt acacccagta aatccggata acgcttgcac catacgtatt 240

accgcggctg ctggcacgta tttagccggt gcttcttagt caggtaccgt cattttcttc 300

cctgctgata gagctttaca taccgaaata cttcatcgct cacgcggcgt cgctgcatca 360

gggtttcccc cattgtgcaa tattccccac tgctgcctcc cgagggagtt tgga 414

<210> SEQ ID NO 41
<211> LENGTH: 191
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 41

tcatcgctta cggtggatct gcgccgggta cgggcgggct ggagtgcggt aggggagact 60

ggaattcccg gtgtaacggt ggaatgtgta gatatcggga agaacaccga tggcgaaggc 120

aggtctctgg gccgtcactg acgctgagga gcgaaagcgt ggggagcgaa caggattaga 180

tacaacggta a 191

<210> SEQ ID NO 42
<211> LENGTH: 196
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 42

tgaacccagg gcttaactct gggactgctt ttgaactgtc agactggagt gcaggagagg 60

taagcggaat tcctagtgta gcggtgaaat gcgtagatat taggaggaac atcagtggcg 120

aaggcggctt actggactga aactgacact gaggcacgaa agcgtgggga gcaaacagga 180

ttagatacca tggtaa 196

<210> SEQ ID NO 43
<211> LENGTH: 192
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 43

accagggctt aactctggga ctgcttttga actgtcagac tggagtgcag gagaggtaag 60

cggaattcct agtgtagcgg tgaaatgcgt agatattagg aggaacatca gtggcgaagg 120

cggcttactg gactgaaact gacactgagg cacgaaagcg tggggagcaa acaggattag 180

ataccctggt aa 192

<210> SEQ ID NO 44
<211> LENGTH: 195
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 44

gaacccaggg cttaactctg ggactgcttt tgaactgtca gactggagtg caggagaggt 60

aagcggaatt cctagtgtag cggtgaaatg cgtagatatt aggaggaaca tcagtggcga 120

aggcggctta ctggactgaa actgacactg aggcacgaaa gcgtggggag caaacaggat 180

tagatacccc ggtaa 195

<210> SEQ ID NO 45
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 45

gagtcagctt tcgagctcag cgtcagttat cgtccagtaa gccgccttcg ccactggtgt 60

tcctcctaat atctacgcat ttcaccgcta cactaggaat tccgcttacc cctccgacac 120

tctagtacga cagtttccaa tgcagtaccg gggttgagcc ccgggctttc acatcagact 180

tgccgcaccg cctgcgctcc ctttacaccc agtaaatccg gataacgctt gcaccatacg 240

tattaccgcg gctgctggca cgtatttagc cggtgcttct tagtcaggta ccgtcattat 300

cttccctgct gatagagctt tacataccga aatacttctt cgctcacgcg gcgtcgctgc 360

atcaggcttt cgcccattgt gcaatattcc ccactgctgc ctcccgaggg agtttgga 418

<210> SEQ ID NO 46
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 46

tgtcagcttt cgagctcacg tcagttaccg tccagtaagc cgccttcgcc actggtgttc 60

ctcctaatat ctacgcattt caccgctaca ctaggaattc cgcttacctc tccggtactc 120

tagattgaca gtttccaatg cagtcccggg gttgagcccc gggttttcac atcagacttg 180

ccactccgtc tacgctccct ttacacccag taaatccgga taacgcttgc accatacgta 240

ttaccgcggc tgctggcacg tatttagccg gtgcttctta gtcaggtacc gtcattttct 300

tccctgctga tagagcttta cataccgaaa tacttcatcg ctcacgcggc gtcgctgcat 360

cagggtttcc cccattgtgc aatattcccc actgctgcct cccgtaggag tttgga 416

<210> SEQ ID NO 47
<211> LENGTH: 400
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 47

cacgtcagtt accgtccagt aagccgcctt cgccactggt gttcctccta atatctacgc 60

atttcaccgc tacactagga attccgctta cctctccggc actcaagacg ggcagtttcc 120

aatgcagtcc cggggttgag ccccagcctt tcacatcaga cttgtccatc cgtctacgct 180

ccctttacac ccagtaaatc cggataacgc ttgcccccta cgtattaccg cggctgctgg 240

cacgtagtta gccggggctt cttagtcagg taccgtcatt ttcttccctg ctgatagaag 300

tttacatacc gagatacttc ttccttcacg cggcgtcgct gcatcagggt ttcccccatt 360

gtgcaatatt ccccactgct gcctcccgta ggagtttggg 400

<210> SEQ ID NO 48
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 48

gtcagctttc gagctcacgt cagttaccgt ccagtaagcc gccttcgcca ctggtgttcc 60

tcctaatatc tacgcatttc accgctacac taggaattcc gcttacctct ccggtactct 120

agattgacag tttccaatgc agtcccgggg ttgagccccg ggttttcaca tcagacttgc 180

cactccgtct acgctccctt tacacccagt aaatccggat aacgcttgca ccatacgtat 240

taccgcggct gctggcacgt atttagccgg tgcttcttag tcaggtaccg tcattttctt 300

ccctgctgat agagctttac ataccgaaat acttcatcgc tcacgcggcg tcgctgcatc 360

agggtttccc ccattgtgca atattcccca ctgctgcctc ccgtggggag tttgga 416

<210> SEQ ID NO 49
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 49

gatgctcagc tttcgtgctc agtgtcagtt tcagtccagt aagccgcctt cgccactgat 60

gttcctccta atatctacgc atttcaccgc tacactagga attccgctta cctctcctgc 120

actccagtct gacagtttca aaagcagtcc cagagttaag ccctgggttt tcacttctga 180

cttgccatac cacctacgca ccctttacac ccagtaattc cggataacgc ttgccccctа 240

cgtattaccg cggctgctgg cacgtagtta gccggggctt cttagtcagg taccgtcatt 300

ttcttccctg ctgatagagc tttacatacc gagatacttc ttcactcacg cggcgtcgct 360

gcatcagggt ttcccccatt gtgcaatatt ccccactgct gcctcccgaa ggaagtttgg 420

a 421

<210> SEQ ID NO 50
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 50

gtgtcagctt cgtgctcagt gtcagtttca gtccagtaag ccgccttcgc cactgatgtt 60

cctcctaata tctacgcatt tcaccgctac actaggaatt ccgcttacct ctcctgcact 120

ccagtctgac agtttcaaaa gcagtcccag agttaagccc tgggttttca cttctgactt 180

gccataccac ctacgcaccc tttacaccca gtaattccgg ataacgcttg cccctacgt 240

attaccgcgg ctgctggcac gtagttagcc ggggcttctt agtcaggtac cgtcattttc 300

ttccctgctg atagagcttt acataccgag atacttcttc actcacgcgg cgtcgctgca 360

tcagggtttc ccccattgtg caatattccc cactgctgcc tcccgtaggg agtttgga 418

<210> SEQ ID NO 51
<211> LENGTH: 415
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 51

gtcagcttcg agcctcacgt cagttaccgt ccagtaagcc gccttcgcca ctggtgttcc 60

tcctaatatc tacgcatttc accgctacac taggaattcc gcttacctct ccggtactct 120

agattgacag tttccaatgc agtcccgggg ttgagccccg ggttttcaca tcagacttgc 180

cactccgtct acgctccctt tacacccagt aaatccggat aacgcttgca ccatacgtat 240

taccgcggct gctggcacgt atttagccgg tgcttcttag tcaggtaccg tcattttctt 300

ccctgctgat agagctttac ataccgaaat acttcatcgc tcacgcggcg tcgctgcatc 360

agggtttccc ccattgtgca atattcccca ctgctgcctc gcgtaggagt ttgga 415

<210> SEQ ID NO 52
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 52

tgtcagcttt cgagctcagc gtcagttatc gtccagtaag ccgccttcgc cactggtgtt 60

cctcctaata tctacgcatt tcaccgctac actaggaatt ccgcttaccc ctccgacact 120

ctagtacgac agtttccaat gcagtaccgg ggttgagccc cgggctttca catcagactt 180

gccgcaccgc ctgcgctccc tttacaccca gtaaatccgg ataacgcttg caccatacgt 240

attaccgcgg ctgctggcac gtatttagcc ggtgcttctt agtcaggtac cgtcattatc 300

ttccctgctg atagagcttt acataccgaa atacttcttc gctcacgcgg cgtcgctgca 360

tcaggctttc gcccattgtg caatattccc cactgctgcc tcccgaaggg agtttgga 418

<210> SEQ ID NO 53
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 53

ttcagctttc gagctcagcg tcagttatcg tccagtaagc cgccttcgcc actggtgttc 60

ctcctaatat ctacgcattt caccgctaca ctaggaattc cgcttacccc tccgacactc 120

tagtacgaca gtttccaatg cagtaccggg gttgagcccc gggctttcac atcagacttg 180

ccgcaccgcc tgcgctccct ttacacccag taaatccgga taacgcttgc accatacgta 240

ttaccgcggc tgctggcacg tatttagccg gtgcttctta gtcaggtacc gtcattatct 300

-continued

tccctgctga tagagcttta cataccgaaa tacttcttcg ctcacgcggc gtcgctgcat 360

caggctttcg cccattgtgc aatattcccc actgctgcct cccgagggga gtttgg 416

<210> SEQ ID NO 54
<211> LENGTH: 435
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 54

ttcggtctgc tttccccttc tcgcgcctca gtgtcagttt ctgtctagta agccgccttc 60

gccactgatg ttcctcctaa tatctacgca cttcaccgct ccacaatgaa ttccgcttac 120

ccctcccgcg ctctagtctg acagttttaa aaaaactccc cgagagaaac cctgggtttt 180

ttcttctgac atgcgatatc ccacccccac cctttataca cccaaaaatc ggataaaagg 240

tgcgacctac gtattatacc ggctgctggg gcgtagatag ccgggggttc ttatacaggg 300

accgtcattt tctttcccgc tgatacagct ttacataccg aaatacttct ttctcacgcg 360

gcgtcgctgc atcagggttt cccccattgt gcaatattcc ccactgctgc ctcccgaagg 420

ggaagttggg ggaaa 435

<210> SEQ ID NO 55
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 55

gttcagcttt cgagcctcac gtcagttacc gtccagtaag ccgccttcgc cactggtgtt 60

cctcctaata tctacgcatt tcaccgctac actaggaatt ccgcttacct ctccggtact 120

ctagattgac agtttccaat gcagtcccgg ggttgagccc cgggttttca catcagactt 180

gccactccgt ctacgctccc tttacaccca gtaaatccgg ataacgcttg caccatacgt 240

attaccgcgg ctgctggcac gtatttagcc ggtgcttctt agtcaggtac cgtcattttc 300

ttccctgctg atagagcttt acataccgaa atacttcatc gctcacgcgg cgtcgctgca 360

tcagggtttc ccccattgtg caatattccc cactgctgcc tcccgagggg agtttgga 418

<210> SEQ ID NO 56
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 56

gtcagctttc gagctcacgt cagttaccgt ccagtaagcc gccttcgcca ctggtgttcc 60

tcctaatatc tacgcatttc accgctacac taggaattcc gcttacctct ccggtactct 120

agattgacag tttccaatgc agtcccgggg ttgagccccg ggttttcaca tcagacttgc 180

cactccgtct acgctccctt tacacccagt aaatccggat aacgcttgca ccatacgtat 240

taccgcggct gctggcacgt atttagccgg tgcttcttag tcaggtaccg tcattttctt 300

ccctgctgat agagctttac ataccgaaat acttcatcgc tcacgcggcg tcgctgcatc 360

agggtttccc ccattgtgca atattcccca ctgctgcctc ccgaggggag tttgga 416

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<210> SEQ ID NO 57
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 57

tctcacgctt tcgagctcac gtcagtcatc gtccagcaag ccgccttcgc cactggtgtt 60

cctcctaata tctacgcatt tcaccgctac actaggaatt ccacttgcct ctccgacact 120

ctagctcagc agttccaaat gcagtcccgg ggttgagccc cgggctttca catctggctt 180

gccgtgccgt ctacgctccc tttacaccca gtaaatccgg ataacgcttg ccccctacgt 240

attaccgcgg ctgctggcac gtagttagcc ggggcttctt agtcaggtac cgtcattttc 300

ttccctgctg atagaagttt acataccgaa atacttcatc cttcacgcgg cgtcgctgca 360

tcagagtttc ctccattgtg caatattccc cactgctgcc tcccgtaggg agtttgg 417

<210> SEQ ID NO 58
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 58

gtcagctttc gagctcagcg tcagttatcg tccagtaagc cgccttcgcc actggtgttc 60

ctcctaatat ctacgcattt caccgctaca ctaggaattc cacttacccc tccgacactc 120

tagtacgaca gtttccaatg cagtaccggg gttgagcccc gggctttcac atcagacttg 180

ccgcaccgcc tgcgctccct ttacacccag taaatccgga taacgcttgc accatacgta 240

ttaccgcggc tgctggcacg tatttagccg gtgcttctta gtcaggtacc gtcattcttc 300

ttccctgctg atagagcttt acataccgaa atacttcttc gctcacgcgg cgtcgctgca 360

tcagggtttc ccccattgtg caatattccc cactgctgcc tcccgaggga gtttgga 417

<210> SEQ ID NO 59
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 59

agccccgctt tcgagcctca cgtcagttac cgtccagtaa gccgccttcg ccactggtgt 60

tcctcctaat atctacgcat ttcaccgcta cactaggaat tccgcttacc tctccggcac 120

tcaagacggg cagtttccaa tgcagtcccg gggttgagcc ccagcctttc acatcagact 180

tgtccatccg tctacgctcc ctttacaccc agtaaatccg gataacgctt gccccctacg 240

tattaccgcg gctgctggca cgtagttagc cggggcttct tagtcaggta ccgtcatttt 300

cttccctgct gatagaagtt tacataccga gatacttctt ccttcacgcg gcgtcgctgc 360

atcagggttt cccccattgt gcaatattcc ccactgctgc ctcccgaagg aagtttgga 419

<210> SEQ ID NO 60
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 60

tgctcagctt tcgagcctca cgtcagttac cgtccagtaa gccgccttcg ccactggtgt 60

tcttcctaat atctacgcat ttcaccgcta cactaggaat tccgcttacc tctccggcac 120

tcgagccaga cagtttccaa tgcagtccca gggttaagcc ctgggttttc acatcagact 180

tgccttgccg tctacgctcc ctttacaccc agtaaatccg gataacgctt gccccctacg 240

tattaccgcg gctgctggca cgtagttagc cggggcttct tagtcaggta ccgtcattat 300

cttccctgct gatagagctt tacataccga aatacttctt cgctcacgcg gcgtcgctgc 360

atcagggttt cccccattgt gcaatattcc ccactgctgc ctcccgaagg gagtttgga 419

<210> SEQ ID NO 61
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 61

gttgctcagc tttcgagctc acgtcagtta ccgtccagta agccgccttc gccactggtg 60

ttcttcctaa tatctacgca tttcaccgct acactaggaa ttccgcttac ctctccggca 120

ctcgagccag acagtttcca atgcagtccc agggttaagc cctgggtttt cacatcagac 180

ttgccttgcc gtctacgctc cctttacacc cagtaaatcc ggataacgct tgccccctac 240

gtattaccgc ggctgctggc acgtagttag ccggggcttc ttagtcaggt accgtcatta 300

tcttccctgc tgatagagct ttacataccg aaatacttct tcgctcacgc ggcgtcgctg 360

catcagggtt tcccccattg tgcaatattc cccactgctg cctcccgaag gaaagtttgg 420

a 421

<210> SEQ ID NO 62
<211> LENGTH: 420
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 62

tgctcagctt tcgagctcag cgtcagttat cgtccagtaa gccgccttcg ccactggtgt 60

tcctcctaat atctacgcat ttcaccgcta cactaggaat tccacttacc cctccgacac 120

tctagtacga cagtttccaa tgcagtaccg gggttgagcc ccgggctttc acatcagact 180

tgccgcaccg cctgcgctcc ctttacaccc agtaaatccg gataacgctt gcaccatacg 240

tattaccgcg gctgctggca cgtatttagc cggtgcttct tagtcaggta ccgtcattct 300

tcttccctgc tgatagagct ttacataccg aaatacttct tcgctcacgc ggcgtcgctg 360

catcagggtt tcccccattg tgcaatattc cccactgctg cctcccgaag ggagtttgga 420

<210> SEQ ID NO 63
<211> LENGTH: 446
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 63

gatgccctgg cttcgcgctc agcgtcagtt gtcgtccaga aagccgcttt cgccactggt 60

gttcctccta atatctacgc atttcaccgc tacactagga attccgcttt cctctccgac 120

actcgagctt cacagtttcg gtcccctcac ggggttaagc cccgcacttt taagaccgac 180

ttgcgatgcc gcctgcgcgc cctttacgcc caataattcc ggacaacgct tgccacctac 240

gtattaccgc ggctgctggc acgtagttag ccgtggcttt ctcttacggt accgtcaggg 300

ataacgggta ttgaccgcta tcctgttcgt cccatataac agaactttac aacccgaagg 360

ccgtcatcgt tcacgcggcg ttgctccgtc agactttcgt ccattgcgga agattcccca 420

ctgctgcctc ccgggggggag tttgga 446

<210> SEQ ID NO 64
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 64

gtcccgcttt cgagcctcag cgtcagttat cgtccagtaa gccgccttcg ccactggtgt 60

tcctcctaat atctacgcat ttcaccgcta cactaggaat tccgcttacc cctccgacac 120

tctagtacga cagtttccaa tgcagtaccg gggttgagcc ccgggctttc acatcagact 180

tgccgcaccg cctgcgctcc ctttacaccc agtaaatccg gataacgctt gcaccatacg 240

tattaccgcg gctgctggca cgtatttagc cggtgcttct tagtcaggta ccgtcattat 300

cttccctgct gatagagctt tacataccga aatacttctt cgctcacgcg gcgtcgctgc 360

atcaggcttt cgcccattgt gcaatattcc ccactgctgc ctcccgaagg gaagtttgg 419

<210> SEQ ID NO 65
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 65

tgtcagcttt cgagctcagc gtcagttatc gtccagtaag ccgccttcgc cactggtgtt 60

cctcctaata tctacgcatt tcaccgctac actaggaatt ccgcttaccc ctccgacact 120

ctagtacgac agtttccaat gcagtaccgg ggttgagccc cgggctttca catcagactt 180

gccgcaccgc ctgcgctccc tttacaccca gtaaatccgg ataacgcttg caccatacgt 240

attaccgcgg ctgctggcac gtatttagcc ggtgcttctt agtcaggtac cgtcattatc 300

ttccctgctg atagagcttt acataccgaa atacttcttc gctcacgcgg cgtcgctgca 360

tcaggctttc gcccattgtg caatattccc cactgctgcc tcccgaaggg agtttgga 418

<210> SEQ ID NO 66
<211> LENGTH: 420
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 66

tgctcagctt tcgagctcag cgtcagttat cgtccagtaa gccgccttcg ccactggtgt 60

tcctcctaat atctacgcat ttcaccgcta cactaggaat tccacttacc cctccgacac 120

tctagtacga cagtttccaa tgcagtaccg gggttgagcc ccgggctttc acatcagact 180

tgccgcaccg cctgcgctcc ctttacaccc agtaaatccg gataacgctt gcaccatacg 240

-continued

tattaccgcg gctgctggca cgtatttagc cggtgcttct tagtcaggta ccgtcattct 300

tcttccctgc tgatagagct ttacataccg aaatacttct tcgctcacgc ggcgtcgctg 360

catcagggtt tcccccattg tgcaatattc cccactgctg cctcccgaag ggagtttgga 420

<210> SEQ ID NO 67
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 67

attcagcttt cgagctcacg tcagttaccg tccagtaagc cgccttcgcc actggtgttc 60

ctcctaatat ctacgcattt caccgctaca ctaggaattc cgcttacccc tccggcactc 120

aagcatacca gtttccaatg cagtccaggg gttaagcccc tgcctttcac atcagacttg 180

atacgccgtc tacgctccct ttacacccag taaatccgga taacgctcgc cccctacgta 240

ttaccgcggc tgctggcacg tagttagccg gggcttctta gtcaggtacc gtcattatct 300

tccctgctga tagaagttta cataccgaga tacttcttcc ttcacgcggc gtcgctgcat 360

cagggtttcc cccattgtgc aatattcccc actgctgcct cccgagggaa gtttgga 417

<210> SEQ ID NO 68
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 68

gtgtcagctt tcgagctcac gtcagttacc gtccagtaag ccgccttcgc cactggtgtt 60

cttcctaata tctacgcatt tcaccgctac actaggaatt ccgcttacct ctccggcact 120

cgagccagac agtttccaat gcagtcccag ggttaagccc tgggttttca catcagactt 180

gccttgccgt ctacgctccc tttacaccca gtaaatccgg ataacgcttg ccccctacgt 240

attaccgcgg ctgctggcac gtagttagcc ggggcttctt agtcaggtac cgtcattatc 300

ttccctgctg atagagcttt acataccgaa atacttcttc gctcacgcgg cgtcgctgca 360

tcagggtttc ccccattgtg caatattccc cactgctgcc tcccgaggga gtttgg 416

<210> SEQ ID NO 69
<211> LENGTH: 416
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 69

gccagcttcg agcctcacgt cagtcatcgt ccagtaagcc gccttcgcca ctggtgttcc 60

tcctaatatc tacgcatttc accgctacac taggaattcc acttacctct ccgacactct 120

agctgcacag tttccaaagc agtccacagg ttgagcccat gcctttcact tcagacttgc 180

acagccgtct acgctccctt tacacccagt aaatccggat aacgcttgcc ccctacgtat 240

taccgcggct gctggcacgt agttagccgg ggcttcttag tcaggtaccg tcattttctt 300

ccctgctgat agaagtttac ataccgaaat acttcatcct tcacgcggcg tcgctgcatc 360

aggctttcgc ccattgtgca atattcccca ctgctgcctc ccgagggaag tttgga 416

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<210> SEQ ID NO 70
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 70

tgatcagctt tcgagctcac gtcagttacc gtccagtaag ccgccttcgc cactggtgtt 60

cctcctaata tctacgcatt tcaccgctac actaggaatt ccgcttacct ctccggtact 120

ctagattgac agtttccaat gcagtcccgg ggttgagccc cgggttttca catcagactt 180

gccactccgt ctacgctccc tttacaccca gtaaatccgg ataacgcttg caccatacgt 240

attaccgcgg ctgctggcac gtatttagcc ggtgcttctt agtcaggtac cgtcattttc 300

ttccctgctg atagagcttt acataccgaa atacttcatc gctcacgcgg cgtcgctgca 360

tcagggtttc ccccattgtg caatattccc cactgctgcc tcccgggggg agtttgga 418

<210> SEQ ID NO 71
<211> LENGTH: 420
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 71

gatgatcagc tttcgagctc acgtcagtta ccgtccagta agccgccttc gccactggtg 60

ttcctcctaa tatctacgca tttcaccgct acactaggaa ttccgcttac ctctccggca 120

ctctagaaaa acagtttcca atgcagtcct ggggttaagc cccagccttt cacatcagac 180

ttgctcttcc gtctacgctc cctttacacc cagtaaatcc ggataacgct tgccccctac 240

gtattaccgc ggctgctggc acgtagttag ccggggcttc ttagtcaggt accgtcattt 300

tcttccctgc tgatagaagt ttacataccg agatacttct tccttcacgc ggcgtcgctg 360

catcagggtt tcccccattg tgcaatattc cccactgctg cctcccgggg gaagtttgga 420

<210> SEQ ID NO 72
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 72

ttgatcagct ttcgagctca cgtcagttac cgtccagtaa gccgccttcg ccactggtgt 60

tcctcctaat atctacgcat ttcaccgcta cactaggaat tccgcttacc tctccggcac 120

tctagaaaaa cagtttccaa tgcagtcctg gggttaagcc ccagcctttc acatcagact 180

tgctcttccg tctacgctcc ctttacaccc agtaaatccg gataacgctt gccccctacg 240

tattaccgcg gctgctggca cgtagttagc cggggcttct tagtcaggta ccgtcatttt 300

cttccctgct gatagaagtt tacataccga gatacttctt ccttcacgcg gcgtcgctgc 360

atcagggttt cccccattgt gcaatattcc ccactgctgc ctcccgaagg gagtttgg 418

<210> SEQ ID NO 73
<211> LENGTH: 421
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

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<400> SEQUENCE: 73

gtatttcagc tttcgagctc agcgtcagtt atcgtccagt aagccgcctt cgccactggt 60

gttcctccta atatctacgc atttcaccgc tacactagga attccgctta cccctccgac 120

actctagtac gacagtttcc aatgcagtac cggggttgag ccccgggctt tcacatcaga 180

cttgccgcac cgcctgcgct ccctttacac ccagtaaatc cggataacgc ttgcaccata 240

cgtattaccg cggctgctgg cacgtattta gccggtgctt cttagtcagg taccgtcatt 300

atcttccctg ctgatagagc tttacatacc gaaatacttc ttcgctcacg cggcgtcgct 360

gcatcaggct ttcgcccatt gtgcaatatt ccccactgct gcctcccgaa gggagtttgg 420

a 421

<210> SEQ ID NO 74
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 74

gctcagcttt cgagctcagc gtcagttatc gtccagtaag ccgccttcgc cactggtgtt 60

cctcctaata tctacgcatt tcaccgctac actaggaatt ccacttaccc ctccgacact 120

ctagtacgac agtttccaat gcagtaccgg ggttgagccc cgggctttca catcagactt 180

gccgcaccgc ctgcgctccc tttacaccca gtaaatccgg ataacgcttg caccatacgt 240

attaccgcgg ctgctggcac gtatttagcc ggtgcttctt agtcaggtac cgtcattctt 300

cttccctgct gatagagctt tacataccga aatacttctt cgctcacgcg gcgtcgctgc 360

atcagggttt cccccattgt gcaatattcc ccactgctgc ctcccgaggg gagtttgga 419

<210> SEQ ID NO 75
<211> LENGTH: 417
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 75

tttcagcttc gagcctcagc gtcagttatc gtccagtaag ccgccttcgc cactggtgtt 60

cctcctaata tctacgcatt tcaccgctac actaggaatt ccgcttaccc ctccgacact 120

ctagtacgac agtttccaat gcagtaccgg ggttgagccc cgggctttca catcagactt 180

gccgcaccgc ctgcgctccc tttacaccca gtaaatccgg ataacgcttg caccatacgt 240

attaccgcgg ctgctggcac gtatttagcc ggtgcttctt agtcaggtac cgtcattatc 300

ttccctgctg atagagcttt acataccgaa atacttcttc gctcacgcgg cgtcgctgca 360

tcaggctttc gcccattgtg caatattccc cactgctagc tcccgaagga gtttgga 417

<210> SEQ ID NO 76
<211> LENGTH: 419
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 76

agctcagctt tcgagctcag cgtcagttat cgtccagtaa gccgccttcg ccactggtgt 60

tcctcctaat atctacgcat ttcaccgcta cactaggaat tccgcttacc cctccgacac 120

-continued

tctagtacga cagtttccaa tgcagtaccg gggttgagcc ccgggctttc acatcagact 180

tgccgcaccg cctgcgctcc ctttacaccc agtaaatccg gataacgctt gcaccatacg 240

tattaccgcg gctgctggca cgtatttagc cggtgcttct tagtcaggta ccgtcattat 300

cttccctgct gatagagctt tacataccga aatacttctt cgctcacgcg gcgtcgctgc 360

atcaggcttt cgcccattgt gcaatattcc ccactgctgc ctcccgaagg gagtttgga 419

<210> SEQ ID NO 77
<211> LENGTH: 418
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 77

gtccagcttt cgagcctcag cgtcagttat cgtccagtaa gccgccttcg ccactggtgt 60

tcctcctaat atctacgcat ttcaccgcta cactaggaat tccgcttacc cctccgacac 120

tctagtacga cagtttccaa tgcagtaccg gggttgagcc ccgggctttc acatcagact 180

tgccgcaccg cctgcgctcc ctttacaccc agtaaatccg gataacgctt gcaccatacg 240

tattaccgcg gctgctggca cgtatttagc cggtgcttct tagtcaggta ccgtcattat 300

cttccctgct gatagagctt tacataccga aatacttctt cgctcacgcg gcgtcgctgc 360

atcaggcttt cgcccattgt gcaatattcc ccactgctgc ctcccgaggg agtttgga 418

<210> SEQ ID NO 78
<211> LENGTH: 193
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 78

tgagccgggc tcaccccggt actgcattgg aactgtcgta ctagagtgtc ggaggggtaa 60

gcggaattcc tagtgtagcg gtgaaatgcg tagatattag gaggaacacc agtggcgaag 120

gcggcttact ggacgataac tgacgctgag gctcgaaagc gtggggagca aacaggatta 180

gatacaccgg taa 193

<210> SEQ ID NO 79
<211> LENGTH: 424
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 79

cacgatgtca gctttcgagc tcagcgtcag ttatcgtcca gtaagccgcc ttcgccactg 60

gtgttcctcc taatatctac gcatttcacc gctacactag gaattccact tacccctccg 120

acactctagt acgacagttt ccaatgcagt accggggttg agccccgggc tttcacatca 180

gacttgccgc accgcctgcg ctccctttac acccagtaaa tccggataac gcttgcacca 240

tacgtattac cgcggctgct ggcacgtatt tagccggtgc ttcttagtca ggtaccgtca 300

ttcttcttcc ctgctgatag agctttacat accgaaatac ttcttcgctc acgcggcgtc 360

gctgcatcag ggtttccccc attgtgcaat attccccact gctgcctccc gaggggagtt 420

tgga 424

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<210> SEQ ID NO 80
<211> LENGTH: 1524
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 80

atggagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcctaata catgcaagtc 60

gaacgcgagc acttgtgctc gagtggcgaa cgggtgagta atacataagt aacctgccct 120

agacaggggg ataactattg gaaacgatag ctaagaccgc ataggtacgg acactgcatg 180

gtgaccgtat taaaagtgcc tcaaagcact ggtagaggat ggacttatgg cgcattagct 240

ggttggcggg gtaacggccc accaaggcga cgatgcgtag ccgacctgag agggtgaccg 300

gccacactgg gactgagaca cggcccagac tcctacggga ggcagcagta gggaattttc 360

ggcaatgggg gaaaccctga ccgagcaacg ccgcgtgaag gaagaaggtt ttcggattgt 420

aaacttctgt tataaaggaa gaacggcggc tacaggaaat ggtagccgag tgacggtact 480

ttattagaaa gccacggcta actacgtgcc agcagccgcg gtaatacgta ggtggcaagc 540

gttatccgga attattgggc gtaaagaggg agcaggcggc agcaagggtc tgtggtgaaa 600

gcctgaagct taacttcagt aagccataga aaccaggcag ctagagtgca ggagaggatc 660

gtggaattcc atgtgtagcg gtgaaatgcg tagatatatg gaggaacacc agtggcgaag 720

gcgacgatct ggcctgcaac tgacgctcag tcccgaaagc gtggggagca aataggatta 780

gataccctag tagtccacgc cgtaaacgat gagtactaag tgttggatgt caaagttcag 840

tgctgcagtt aacgcaataa gtactccgcc tgagtagtac gttcgcaaga atgaaactca 900

aaggaattga cgggggcccg cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg 960

aagaacctta ccaggtcttg acatactcat aaaggctcca gagatggaga gatagctata 1020

tgagatacag gtggtgcatg gttgtcgtca gctcgtgtcg tgagatgttg ggttaagtcc 1080

cgcaacgagc gcaaccctta tcgttagtta ccatcattaa gttggggact ctagcgagac 1140

tgccagtgac aagctggagg aaggcgggga tgacgtcaaa tcatcatgcc ccttatgacc 1200

tgggctacac acgtgctaca atggatggtg cagagggaag cgaagccgcg aggtgaagca 1260

aaacccataa aaccattctc agttcggatt gtagtctgca actcgactac atgaagttgg 1320

aatcgctagt aatcgcgaat cagcatgtcg cggtgaatac gttctcgggc cttgtacaca 1380

ccgcccgtca caccacgaga gttgataaca cccgaagccg gtggcctaac cgcaaggaag 1440

gagctgtcta aggtgggatt gatgattggg gtgaagtcgt aacaaggtat ccctacggga 1500

acgtggggat ggatcacctc cttt 1524

<210> SEQ ID NO 81
<211> LENGTH: 1528
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 81

atgagagttt gatcctggct caggatgaac gctggcggcg tgcctaacac atgcaagtcg 60

aacgaagcaa ttgaaggaag ttttcggatg gaattcgatt gactgagtgg cggacgggtg 120

agtaacgcgt ggataacctg cctcacactg ggggataaca gttagaaatg actgctaata 180

ccgcataagc gcacagtacc gcatggtaca gtgtgaaaaa ctccggtggt gtgagatgga 240

tccgcgtctg attagccagt tggcggggta acggcccacc aaagcgacga tcagtagccg 300

acctgagagg gtgaccggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

agcagtgggg aatattgcac aatgggcgaa agcctgatgc agcgacgccg cgtgagtgaa 420

gaagtatttc ggtatgtaaa gctctatcag cagggaagaa aatgacggta cctgactaag 480

aagccccggc taactacgtg ccagcagccg cggtaatacg taggggcaa gcgttatccg 540

gatttactgg gtgtaaaggg agcgtagacg gcgaagcaag tctgaagtga aaacccaggg 600

ctcaaccctg ggactgcttt ggaaactgtt ttgctagagt gtcggagagg taagtggaat 660

tcctagtgta gcggtgaaat gcgtagatat taggaggaac accagtggcg aaggcggctt 720

actggacgat aactgacgtt gaggctcgaa agcgtgggga gcaaacagga ttagataccc 780

tggtagtcca cgccgtaaac gatgaatgct aggtgttggg gggcaaagcc cttcggtgcc 840

gtcgcaaacg cagtaagcat tccacctggg gagtacgttc gcaagaatga aactcaaagg 900

aattgacggg gacccgcaca agcggtggag catgtggttt aattcgaagc aacgcgaaga 960

accttaccaa gtcttgacat cctcttgacc ggcgtgtaac ggcgccttcc cttcggggca 1020

agagagacag gtggtgcatg gttgtcgtca gctcgtgtcg tgagatgttg ggttaagtcc 1080

cgcaacgagc gcaaccctta tccttagtag ccagcaggta aagctgggca ctctagggag 1140

actgccaggg ataacctgga ggaaggtggg gatgacgtca aatcatcatg ccccttatga 1200

tttgggctac acacgtgcta caatggcgta aacaaaggga agcaagacag tgatgtggag 1260

caaatcccaa aaataacgtc ccagttcgga ctgtagtctg caacccgact acacgaagct 1320

ggaatcgcta gtaatcgcga atcagaatgt cgcggtgaat acgttcccgg gtcttgtaca 1380

caccgcccgt cacaccatgg gagtcagcaa cgcccgaagt cagtgaccca actcgcaaga 1440

gagggagctg ccgaaggcgg ggcaggtaac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 82
<211> LENGTH: 385
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 82

aattcgacgt tgtccggatt actgggcgta aagggagcgt aggcggactt ttaagtgaga 60

tgtgaaatac ccgggctcaa cttgggtgct gcatttcaaa ctggaagtct agagtgcagg 120

agaggagaat ggaattccta gtgtagcggt gaaatgcgta gagattagga agaacaccag 180

tggcgaaggc gattctctgg actgtaactg acgctgaggc tcgaaagcgt ggggagcaaa 240

caggattaga taccctggta gtccacgccg taaacgatga atactaggtg taggggttgt 300

catgacctct gtgccgccgc taacgcatta agtattccgc ctggggagta cggtcgcaag 360

attaaaactc aaagaaattg acgga 385

<210> SEQ ID NO 83
<211> LENGTH: 434
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 83

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acgagcgtat cggattattg ggtttaaggg agcgtaggtg gattgttaag tcagttgtga 60

aagtttgcgg ctcaaccgta aaattgcagt tgaaactggc agtcttgagt acagtagagg 120

tgggcggaat tcgtggtgta gcggtgaaat gcttagatat cacgaagaac tccgattgcg 180

aaggcagctc actagactgt cactgacact gatgctcgaa agtgtgggta tcaaacagga 240

ttagataccc tggtagtcca cacagtaaac gatgaatact cgctgtttgc gatatacagt 300

aagcggccaa gcgaaagcat taagtattcc acctggggag tacgccggca acggtgaaac 360

tcaaagaaat tgacggaagc ccgcccaggg gggaaaaaca tggggtttag ttggatgata 420

cggggaggaa cctc 434

<210> SEQ ID NO 84
<211> LENGTH: 1457
<212> TYPE: DNA
<213> ORGANISM: Ruminococcus obeum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (65)..(66)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (960)..(960)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 84

ggcggcgtgc ttaacacatg caagtcgaac gggaaacctt tcattgaagc ttcggcagat 60

ttggnntgtt tctagtggcg gacgggtgag taacgcgtgg gtaacctgcc ttatacaggg 120

ggataacaac cagaaatggt tgctaatacc gcataagcgc acaggaccgc atggtctggt 180

gtgaaaaact ccggtggtat aagatggacc cgcgttggat tagctagttg gcagggtaac 240

ggcctaccaa ggcgacgatc catagccggc ctgagagggt gaacggccac attgggactg 300

agacacggcc cagactccta cgggaggcag cagtggggaa tattgcacaa tgggggaaac 360

cctgatgcag cgacgccgcg tgaaggaaga agtatctcgg tatgtaaact tctatcagca 420

gggaagatag tgacggtacc tgactaagaa gccccggcta actacgtgcc agcagccgcg 480

gtaatacgta gggggcaagc gttatccgga tttactgggt gtaaagggag cgtagacgga 540

ctggcaagtc tgatgtgaaa ggcgggggct caacccctgg actgcattgg aaactgttag 600

tcttgagtgc cggagaggta agcggaattc ctagtgtagc ggtgaaatgc gtagatatta 660

ggaggaacac cagtggcgaa ggcggcttac tggacggtaa ctgacgttga ggctcgaaag 720

cgtggggagc aaacaggatt agataccctg gtagtccacg ccgtaaacga tgattactag 780

gtgttgggga gcaaagctct tcggtgccgc cgcaaacgca ttaagtattc cacctgggga 840

gtacgttcgc aagaatgaaa ctcaaaggaa ttgacgggga cccgcacaag cggtggagca 900

tgtggtttaa ttcgaagcaa cgcgaagaac cttaccaagt cttgacatcc ctctgaccgn 960

cccttaaccg gatctttcct tcgggacagg ggagacaggt ggtgcatggt tgtcgtcagc 1020

tcgtgtcgtg agatgttggg ttaagtcccg caacgagcgc aacccctatc cccagtagcc 1080

agcagtccgg ctgggcactc tgaggagact gccagggata acctggagga aggcggggat 1140

gacgtcaaat catcatgccc cttatgattt gggctacaca cgtgctacaa tggcgtaaac 1200

aaagggaagc aagcctgcga aggtaagcaa atcccaaaaa taacgtccca gttcggactg 1260

cagtctgcaa ctcgactgca cgaagctgga atcgctagta atcgcggatc agaatgccgc 1320

ggtgaatacg ttcccgggtc ttgtacacac cgcccgtcac accatgggag tcagtaacgc 1380

ccgaagtcag tgacctaact gcaaagaagg agctgccgaa ggcgggaccg atgactgggg 1440

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tgaagtcgta acaaggt 1457

<210> SEQ ID NO 85
<211> LENGTH: 1398
<212> TYPE: DNA
<213> ORGANISM: Ruminococcus obeum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1083)..(1083)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1207)..(1207)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1233)..(1233)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 85

ggcgtgctta acacatgcaa gtcgaacggg aaacttttca ttgaagcttc ggcagatttg 60

gtctgtttct agtggcggac gggtgagtaa cgcgtgggta acctgcctta tacaggggga 120

taacaaccag aaatggttgc taataccgca taagcgcaca ggaccgcatg gtctggtgtg 180

aaaaactccg gtggtataag atggacccgc gttggattag ctagttggca gggtaacggc 240

ctaccaaggc gacgatccat agccggcctg agagggtgaa cggccacatt gggactgaga 300

cacgccccag actcctcggg aggcagcagt ggggaatatt gcacaatggg ggaaaccctg 360

atgcagcgac gccgcgtgaa ggaagaagta tctcggtatg taaacttcta tcagcaggga 420

agatagtgac ggtacctgac taagaagccc cgkctaacta cgtgccagca gccgcggtaa 480

tacgtagggg gcaagcgtta tccggattta ctgggtgtaa agggagcgta gacggactgg 540

caagtctgat gtgaaaggcg ggggctcaac ccctggactg cattggaaac tgttagtctt 600

gagtgccgga gaggtaagcg gaattcctag tgtagcggtg aaatgcgtag atattaggag 660

gaacaccagt ggcgaaggcg gcttactgga cggtaactga cgttgaggct cgaaagcgtg 720

gggagcaaac aggattagat accctggtag tccacgccgc aaacgatgaa tactaggtgt 780

tggggagcaa agctcttcgg tgccgccgca aacgcattaa gtattccacc tggggagtac 840

gttcgcaaga atgaaactca aaggaattga cggggacccg cacaagcggt ggagcatgtg 900

gtttaattcg aagcaacgcg aagaacctta ccaagtcttg acatccctct gaccgtccct 960

taaccggatc tttccttcgg gacaggggag acaggtggtg catggttgtc gtcagctcgt 1020

gtcgtgagat gttgggttaa gtcccgcaac gagcgcaacc cctatcccca gtagccagca 1080

gtncggctgg gcactctgag gagactgcca gggataacct ggaggaaggc ggggatgacg 1140

tcaaatcatc atgcccctta tgatttgggc tacacacgtg ctacaatggc gtaaacaaag 1200

ggaagcnagc ctkcgraggt aagcaaatcc canaaataac gtcccagttc ggactgcagt 1260

ctgcaactcg actgcacgaa gctggaatcg ctagtaatcg cggatcagaa tgccgcggtg 1320

aatacgttcc cgggtcttgt acacaccgcc cgtcacacca tgggagtcag taacgcccga 1380

agtcagtgac ctaactgc 1398

<210> SEQ ID NO 86
<211> LENGTH: 1472
<212> TYPE: DNA
<213> ORGANISM: Clostridium disporicum

<400> SEQUENCE: 86

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gctcaggacg aacgctggcg gcgtgcctaa cacatgcaag tcgagcgagt tgattctctt 60

cggagatgaa gctagcggcg gacgggtgag taacacgtgg gcaacctgcc tcatagaggg 120

gaatagcctc ccgaaaggga gattaatacc gcataagatt gtagcttcgc atgaagtagc 180

aattaaagga gcaatccgct atgagatggg cccgcggcgc attagctagt tggtgaggta 240

acggctcacc aaggcgacga tgcgtagccg acctgagagg gtgatcggcc acattgggac 300

tgagacacgg cccagactcc tacgggaggc agcagtgggg aatattgcac aatgggggaa 360

accctgatgc agcaacgccg cgtgagtgat gacggccttc gggttgtaaa gctctgtctt 420

cagggacgat aatgacggta cctgaggagg aagccacggc taactacgtg ccagcagccg 480

cggtaatacg taggtggcga gcgttgtccg gatttactgg gcgtaaaggg agcgtaggcg 540

gacttttaag tgagatgtga aatacccggg ctcaacttgg gtgctgcatt tcaaactgga 600

agtctagagt gcaggagagg agaatggaat tcctagtgta gcggtgaaat gcgtagagat 660

taggaagaac accagtggcg aaggcgattc tctggactgt aactgacgct gaggctcgaa 720

agcgtgggga gcaaacagga ttagataccc tggtagtcca cgccgtaaac gatgaatact 780

aggtgtaggg gttgtcatga cctctgtgcc gccgctaacg cattaagtat tccgcctggg 840

gagtacggtc gcaagattaa aactcaaagg aattgacggg ggcccgcaca agcagcggag 900

catgtggttt aattcgaagc aacgcgaaga accttaccta gacttgacat ctcctgaatt 960

acccgtaact ggggaagcca cttcggtggc aggaagacag gtggtgcatg gttgtcgtca 1020

gctcgtgtcg tgagatgttg ggttaagtcc cgcaacgagc gcaaccctta ttgttagttg 1080

ctaccattta gttgagcact ctagcgagac tgcccgggtt aaccgggagg aaggtgggga 1140

tgacgtcaaa tcatcatgcc ccttatgtct agggctacac acgtgctaca atggcaagta 1200

caaagagaag caagaccgcg aggtggagca aaactcaaaa acttgtctca gttcggattg 1260

taggctgaaa ctcgcctaca tgaagctgga gttgctagta atcgcgaatc agcatgtcgc 1320

ggtgaatacg ttcccgggcc ttgtacacac cgcccgtcac accatgagag ttggcaatac 1380

ccaacgtacg tgatctaacc cgcaagggag gaagcgtcct aaggtagggt cagcgattgg 1440

ggtgaagtcg taacaaggta gccgtaggag aa 1472

<210> SEQ ID NO 87
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Clostridium scindens

<400> SEQUENCE: 87

gagagtttga tcctggctca ggatgaacgc tggcggcgtg cctaacacat gcaagtcgaa 60

cgaagcgcct ggccccgact tcttcggaac gaggagcctt gcgactgagt ggcggacggg 120

tgagtaacgc gtgggcaacc tgccttgcac tgggggataa cagccagaaa tggctgctaa 180

taccgcataa gaccgaagcg ccgcatggcg cggcggccaa agccccggcg gtgcaagatg 240

ggcccgcgtc tgattaggta gttggcgggg taacggccca ccaagccgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccagact cctacgggag 360

gcagcagtgg ggaatattgc acaatggggg aaaccctgat gcagcgacgc cgcgtgaagg 420

atgaagtatt tcggtatgta aacttctatc agcagggaag aagatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggggc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggcgatgca agccagatgt gaaagcccgg 600

ggctcaaccc cgggactgca tttggaactg cgtggctgga gtgtcggaga ggcaggcgga 660

-continued

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ctgctggacg atgactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgacta ctaggtgtcg ggtggcaagg ccattcggtg 840

ccgcagcaaa cgcaataagt agtccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc tgatcttgac atcccgatgc caaagcgcgt aacgcgctct ttcttcggaa 1020

catcggtgac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaacccc tatcttcagt agccagcatt ttggatgggc actctggaga 1140

gactgccagg gagaacctgg aggaaggtgg ggatgacgtc aaatcatcat gccccttatg 1200

accagggcta cacacgtgct acaatggcgt aaacaaaggg aggcgaaccc gcgagggtgg 1260

gcaaatccca aaaataacgt ctcagttcgg attgtagtct gcaactcgac tacatgaagt 1320

tggaatcgct agtaatcgcg aatcagaatg tcgcggtgaa tacgttcccg ggtcttgtac 1380

acaccgcccg tcacaccatg ggagtcagta acgcccgaag ccggtgaccc aacccgtaag 1440

ggagggagcc gtcgaaggtg ggaccgataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttc 1529

<210> SEQ ID NO 88
<211> LENGTH: 1456
<212> TYPE: DNA
<213> ORGANISM: Anaerostipes caccae

<400> SEQUENCE: 88

gcgcttaata catgtcaagt cgaacgaagc atttaggatt gaagttttcg gatggatttc 60

ctatatgact gagtggcgga cgggtgagta acgcgtgggg aacctgccct atacaggggg 120

ataacagctg gaaacggctg ctaataccgc ataagcgcac agaatcgcat gattcagtgt 180

gaaaagccct ggcagtatag gatggtcccg cgtctgatta gctggttggt gaggtaacgg 240

ctcaccaagg cgacgatcag tagccggctt gagagagtga acggccacat tgggactgag 300

acacggccca aactcctacg ggaggcagca gtggggaata ttgcacaatg ggggtaaacc 360

ctgatgcagc gacgccgcgt gagtgaagaa gtatttcggt atgtaaagct ctatcagcag 420

ggaagaaaac agacggtacc tgactaagaa gccccggcta actacgtgcc agcagccgcg 480

gtaatacgta gggggcaagc gttatccgga attactgggt gtaaagggtg cgtaggtggc 540

atggtaagtc agaagtgaaa gcccggggct taaccccggg actgcttttg aaactgtcat 600

gctggagtgc aggagaggta agcggaattc ctagtgtagc ggtgaaatgc gtagatatta 660

ggaggaacac cagtggcgaa ggcggcttac tggactgtca ctgacactga tgcacgaaag 720

cgtggggagc aaacaggatt agataccctg gtagtccacg ccgtaaacga tgaatactag 780

gtgtcggggc cgtagaggct tcggtgccgc agcaaacgca gtaagtattc cacctgggga 840

gtacgttcgc aagaatgaaa ctcaaaggaa ttgacgggga cccgcacaag cggtggagca 900

tgtggtttaa ttcgaagcaa cgcgaagaac cttacctggt cttgacatcc caatgaccga 960

accttaaccg gtttttttctt tcgagacatt ggagacaggt ggtgcatggt tgtcgtcagc 1020

tcgtgtcgtg agatgttggg ttaagtcccg caacgagcgc aacccctatc tttagtagcc 1080

agcatttaag gtgggcactc tagagagact gccagggata acctggagga aggtggggac 1140

gacgtcaaat catcatgccc cttatggcca gggctacaca cgtgctacaa tggcgtaaac 1200

-continued

aaagggaagc gaagtcgtga ggcgaagcaa atcccagaaa taacgtctca gttcggattg 1260

tagtctgcaa ctcgactaca tgaagctgga atcgctagta atcgtgaatc agaatgtcac 1320

ggtgaatacg ttcccgggtc ttgtacacac cgcccgtcac accatgggag tcagtaacgc 1380

ccgaagtcag tgacccaacc gcaaggaggg agctgccgaa ggtgggaccg ataactgggg 1440

tgaagtcgta acaagg 1456

<210> SEQ ID NO 89
<211> LENGTH: 1456
<212> TYPE: DNA
<213> ORGANISM: Marvinbryantia formatexigens

<400> SEQUENCE: 89

tggcggcgtg cttaacacat gcaagtcgag cgaagcattt taaatgaagt tttcggacgg 60

aatttaaaat gactgagcgg cggacgggtg agtaacgcgt ggataacctg ccttatacag 120

ggggataaca gccagaaatg gctgctaata ccgcataagc gcacggtacc gcatggtaca 180

gtgtgaaaaa ctccggtggt ataagatggg tccgcgttgg attaggcagt tggcggggta 240

aaggcccacc aaaccgacga tccatagccg gcctgagagg gtggacggcc acattgggac 300

tgagacacgg cccagactcc tacgggaggc agcagtgggg aatattgcac aatgggggaa 360

accctgatgc agcgacgccg cgtgggtgaa gaagtatttc ggtatgtaaa gccctatcag 420

cagggaagaa aatgacggta cctgaccaag aagccccggc taactacgtg ccagcagccg 480

cggtaatacg taggggggcaa gcgttatccg gatttactgg gtgtaaaggg agcgtagacg 540

gccatgcaag tctggtgtga aaggcggggg ctcaaccccc ggactgcatt ggaaactgta 600

tggcttgagt gccggagagg taagcggaat tcctggtgta gcggtgaaat gcgtagatat 660

caggaggaac accagtggcg aaggcggctt actggacggt aactgacgtt gaggctcgaa 720

agcgtgggga gcaaacagga ttagataccc tggtagtcca cgccgtaaac gatgaatacc 780

aggtgtcggg ggacacggtc cttcggtgcc gcagcaaacg cactaagtat tccacctggg 840

gagtacgttc gcaagaatga aactcaaagg aattgacggg gacccgcaca agcggtggag 900

catgtggttt aattcgaagc aacgcgaaga accttaccag gtcttgacat ccggacgacc 960

ggacagtaac gtgtccttcc cttcggggcg tccgagacag gtggtgcatg gttgtcgtca 1020

gctcgtgtcg tgagatgttg ggttaagtcc cgcaacgagc gcaacccctg ttcccagtag 1080

ccagcattca ggatgggcac tctggggaga ctgccaggga taacctggag gaaggcgggg 1140

atgacgtcaa atcatcatgc cccttatgat ctgggctaca cacgtgctac aatggcgtga 1200

acagagggaa gcgaacccgc gaggggagc aaatcccaga aataacgtcc cagttcggat 1260

tgtagtctgc aacccggcta catgaagctg gaatcgctag taatcgcgga tcagcatgcc 1320

gcggtgaata cgttcccggg tcttgtacac accgcccgtc acaccatggg agtcggaaat 1380

gcccgaagtc agtgacccaa ccggaaggag ggagctgccg aaggcggggc cggtaactgg 1440

ggtgaagtcg taacaa 1456

<210> SEQ ID NO 90
<211> LENGTH: 1568
<212> TYPE: DNA
<213> ORGANISM: Lactobacillus mucosae

<400> SEQUENCE: 90

agagtttgat cctggctcag gatgaacgcc ggcggtgtgc ctaatacatg caagtcgaac 60

gcgttggccc aactgattga acgtgcttgc acggacttga cgttggttta ccagcgagtg 120

-continued

gcggacgggt gagtaacacg taggtaacct gccccaaagc gggggataac atttggaaac 180

agatgctaat accgcataac aatttgaatc gcatgattca aatttaaaag atggcttcgg 240

ctatcacttt gggatggacc tgcggcgcat tagcttgttg gtagggtaac ggcctaccaa 300

ggctgtgatg cgtagccgag ttgagagact gatcggccac aatggaactg agacacggtc 360

catactccta cgggaggcag cagtagggaa tcttccacaa tgggcgcaag cctgatggag 420

caacaccgcg tgagtgaaga agggtttcgg ctcgtaaagc tctgttgtta gagaagaacg 480

tgcgtgagag caactgttca cgcagtgacg gtatctaacc agaaagtcac ggctaactac 540

gtgccagcag ccgcggtaat acgtaggtgg caagcgttat ccggatttat tgggcgtaaa 600

gcgagcgcag gcggtttgat aagtctgatg tgaaagcctt tggcttaacc aaagaagtgc 660

atcggaaact gtcagacttg agtgcagaag aggacagtgg aactccatgt gtagcggtgg 720

aatgcgtaga tatatggaag aacaccagtg gcgaaggcgg ctgtctggtc tgcaactgac 780

gctgaggctc gaaagcatgg gtagcgaaca ggattagata ccctggtagt ccatgccgta 840

aacgatgagt gctaggtgtt ggagggtttc cgcccttcag tgccgcagct aacgcattaa 900

gcactccgcc tggggagtac gaccgcaagg ttgaaactca aaggaattga cgggggcccg 960

cacaagcggt ggagcatgtg gtttaattcg aagctacgcg aagaacctta ccaggtcttg 1020

acatcttgcg ccaaccctag agatagggcg tttccttcgg gaacgcaatg acaggtggtg 1080

catggtcgtc gtcagctcgt gtcgtgagat gttgggttaa gtcccgcaac gagcgcaacc 1140

cttgttacta gttgccagca ttcagttggg cactctagtg agactgccgg tgacaaaccg 1200

gaggaaggtg gggacgacgt cagatcatca tgccccttat gacctgggct acacacgtgc 1260

tacaatggac ggtacaacga gtcgcgaact cgcgagggca agctaatctc ttaaaaccgt 1320

tctcagttcg gactgcaggc tgcaactcgc ctgcacgaag tcggaatcgc tagtaatcgc 1380

ggatcagcat gccgcggtga atacgttccc gggccttgta cacaccgccc gtcacaccat 1440

gagagtttgc aacacccaaa gtcggtgggg taacccttcg gggagctagc cgcctaaggt 1500

ggggcagatg attagggtga agtcgtaaca aggtagccgt aggagaacct gcggctggat 1560

cacctcct 1568

<210> SEQ ID NO 91
<211> LENGTH: 1508
<212> TYPE: DNA
<213> ORGANISM: Turicibacter sanguinis

<400> SEQUENCE: 91

agagtttgat catggctcag gatgaacgct ggcggcgtgc ctaatacatg caagtcgagc 60

gaaccacttc ggtggtgagc ggcgaacggg tgagtaacac gtaggttatc tgcccatcag 120

acggggacaa cgattggaaa cgatcgctaa taccggatag gacgaaagtt taaaggtgct 180

tcggcaccac tgatggatga gcctgcggcg cattagctag ttggtagggt aaaggcctac 240

caaggcgacg atgcgtagcc gacctgagag ggtgaacggc cacactggga ctgagacacg 300

gcccagactc ctacgggagg cagcagtagg gaatcttcgg caatgggcga aagcctgacc 360

gagcaacgcc gcgtgaatga tgaaggcctt cgggttgtaa aattctgtta taagggaaga 420

atggctctag taggaaatgg ctagagtgtg acggtacctt atgagaaagc cacggctaac 480

tacgtgccag cagccgcggt aatacgtagg tggcgagcgt tatccggaat tattgggcgt 540

aaagagcgcg caggtggttg attaagtctg atgtgaaagc ccacggctta accgtggagg 600

-continued

gtcattggaa actggtcaac ttgagtgcag aagagggaag tggaattcca tgtgtagcgg 660

tgaaatgcgt agagatatgg aggaacacca gtggcgaagg cggcttcctg gtctgtaact 720

gacactgagg cgcgaaagcg tggggagcaa acaggattag ataccctggt agtccacgcc 780

gtaaacgatg agtgctaagt gttgggggtc gaacctcagt gctgaagtta acgcattaag 840

cactccgcct ggggagtacg gtcgcaagac tgaaactcaa aggaattgac ggggacccgc 900

acaagcggtg gagcatgtgg tttaattcga agcaacgcga agaaccttac caggtcttga 960

cataccagtg accgtcctag agataggatt ttcccttcgg ggacaatgga tacaggtggt 1020

gcatggttgt cgtcagctcg tgtcgtgaga tgttgggtta agtcccgcaa cgagcgcaac 1080

ccctgtcgtt agttgccagc attcagttgg ggactctaac gagactgcca gtgacaaact 1140

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ctacaatggt tggtacaaag agaagcgaag cggtgacgtg gagcaaacct cataaagcca 1260

atctcagttc ggattgtagg ctgcaactcg cctacatgaa gttggaatcg ctagtaatcg 1320

cgaatcagca tgtcgcggtg aatacgttcc cgggtcttgt acacaccgcc cgtcacacca 1380

cgagagttta caacacccga agtcagtggc ctaaccgcaa ggagggagct gcctaaggtg 1440

gggtagatga ttggggtgaa gtcgtaacaa ggtatcccta ccggaaggtg gggttggatc 1500

acctcctt 1508

<210> SEQ ID NO 92
<211> LENGTH: 1456
<212> TYPE: DNA
<213> ORGANISM: Roseburia faecis

<400> SEQUENCE: 92

gatgaacgct ggcggcgtgc ttaacacatg caagtcgaac gaagcactct atttgatttt 60

cttcggaaat gaagattttg tgactgagtg gcggacgggt gagtaacgcg tgggtaacct 120

gcctcataca gggggataac agttggaaac gactgctaat accgcataag cgcacaggat 180

cgcatgatcc ggtgtgaaaa actccggtgg tatgagatgg acccgcgtct gattagccag 240

ttggcagggt aacggcctac caaagcgacg atcagtagcc gacctgagag ggtgaccggc 300

cacattggga ctgagacacg gcccaaactc ctacgggagg cagcagtggg gaatattgca 360

caatgggggа aaccctgatg cagcgacgcc gcgtgagcga agaagtattt cggtatgtaa 420

agctctatca gcagggaaga agaatgacgg tacctgacta agaagcaccg gctaaatacg 480

tgccagcagc cgcggtaata cgtatggtgc aagcgttatc cggatttact gggtgtaaag 540

ggagcgcagg cggtgcggca agtctgatgt gaaagcccgg ggctcaaccc cggtactgca 600

ttggaaactg tcgtactaga gtgtcggagg ggtaagtgga attcctagtg tagcggtgaa 660

atgcgtagat attaggagga acaccagtgg cgaaggcggc ttactggacg ataactgacg 720

ctgaggctcg aaagcgtggg gagcaaacag gattagatac cctggtagtc cacgccgtaa 780

acgatgaata ctaggtgtcg gggagcattg ctcttcggtg ccgcagcaaa cgcaataagt 840

attccacctg gggagtacgt tcgcaagaat gaaactcaaa ggaattgacg gggacccgca 900

caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa gaaccttacc aagtcttgac 960

atcccgatga cagagtatgt aatgtacytt ctcttcggag catcggtgac aggtggtgca 1020

tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt cccgcaacga gcgcaacccc 1080

tgtccttagt agccagcggt tcggccgggc actctaggga gactgccagg gataacctgg 1140

aggaaggcgg ggatgacgtc aaatcatcat gccccttatg acttgggcta cacacgtgct 1200

acaatggcgt aaacaaaggg aagcggagcc gtgaggccga gcaaatctca aaaataacgt 1260

ctcagttcgg actgtagtct gcaacccgac tacacgaagc tggaatcgct agtaatcgca 1320

gatcagaatg ctgcggtgaa tacgttcccg ggtcttgtac acaccgcccg tcacaccatg 1380

ggagttggaa atgcccgaag tcagtgaccc aaccgcaagg agggagctgc cgaaggcagg 1440

ttcgataact ggggtg 1456

<210> SEQ ID NO 93
<211> LENGTH: 1465
<212> TYPE: DNA
<213> ORGANISM: Flavonifractor plautii

<400> SEQUENCE: 93

cgctggcggc gtgcttaaca catgcaagtc gaacggggtg ctcatgacgg aggattcgtc 60

caatggattg agttacctag tggcggacgg gtgagtaacg cgtgaggaac ctgccttgga 120

gaggggaata acactccgaa aggagtgcta ataccgcatg aagcagttgg gtcgcatggc 180

tctgactgcc aaagatttat cgctctgaga tggcctcgcg tctgattagc tagtaggcgg 240

ggtaacggcc cacctaggcg acgatcagta gccggactga gaggttgacc ggccacattg 300

ggactgagac acggcccaga ctcctacggg aggcagcagt ggggaatatt gggcaatggg 360

cgcaagcctg acccagcaac gccgcgtgaa ggaagaaggc tttcgggttg taaacttctt 420

ttgtcgggga cgaaacaaat gacggtaccc gacgaataag ccacggctaa ctacgtgcca 480

gcagccgcgg taatacgtag gtggcaagcg ttatccggat ttactgggtg taaagggcgt 540

gtaggcggga ttgcaagtca gatgtgaaaa ctgggggctc aacctccagc ctgcatttga 600

aactgtagtt cttgagtgct ggagaggcaa tcggaattcc gtgtgtagcg gtgaaatgcg 660

tagatatacg gaggaacacc agtggcgaag gcggattgct ggacagtaac tgacgctgag 720

gcgcgaaagc gtggggagca aacaggatta gataccctgg tagtccacgc cgtaaacgat 780

ggatactagg tgtggggggt ctgacccccc ccgtgccgca gttaacacaa taagtatccc 840

acctggggag tacgatcgca aggttgaaac tcaaaggaat tgacgggggc ccgcacaagc 900

ggtggagtat gtggtttaat tcgaagcaac gcgaagaacc ttaccagggc ttgacatccc 960

actaacgagg cagagatgcg ttaggtgccc ttcggggaaa gtggagacag gtggtgcatg 1020

gttgtcgtca gctcgtgtcg tgagatgttg ggttaagtcc cgcaacgagc gcaaccctta 1080

ttgttagttg ctacgcaaga gcactctagc gagactgccg ttgacaaaac ggaggaaggt 1140

ggggacgacg tcaaatcatc atgcccctta tgtcctgggc cacacacgta ctacaatggt 1200

ggttaacaga gggaggcaat accgcgaggt ggagcaaatc cctaaaagcc atcccagttc 1260

ggattgcagg ctgaaacccg cctgtatgaa gttggaatcg ctagtaatcg cggatcagca 1320

tgccgcggtg aatacgttcc cgggccttgt acacaccgcc cgtcacacca tgagagtcgg 1380

gaacacccga agtccgtagc ctaaccgcaa ggagggcgcg gccgaaggtg ggttcgataa 1440

ttggggtgaa gtcgtaacaa ggtag 1465

<210> SEQ ID NO 94
<211> LENGTH: 1438
<212> TYPE: DNA
<213> ORGANISM: Blautia wexlerae
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (19)..(19)
<223> OTHER INFORMATION: n is a, c, g, t or u

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<400> SEQUENCE: 94

caagtcgaac gggaattant ttattgaaac ttcggtcgat ttaatttaat tctagtggcg 60

gacgggtgag taacgcgtgg gtaacctgcc ttatacaggg ggataacagt cagaaatggc 120

tgctaatacc gcataagcgc acagagctgc atggctcagt gtgaaaaact ccggtggtat 180

aagatggacc cgcgttggat tagcttgttg gtggggtaac ggcccaccaa ggcgacgatc 240

catagccggc ctgagagggt gaacggccac attgggactg agacacggcc cagactccta 300

cgggaggcag cagtggggaa tattgcacaa tgggggaaac cctgatgcag cgacgccgcg 360

tgaaggaaga agtatctcgg tatgtaaact tctatcagca gggaagatag tgacggtacc 420

tgactaagaa gccccggcta actacgtgcc agcagccgcg gtaatacgta gggggcaagc 480

gttatccgga tttactgggt gtaaagggag cgtagacggt gtggcaagtc tgatgtgaaa 540

ggcatgggct caacctgtgg actgcattgg aaactgtcat acttgagtgc cggaggggta 600

agcggaattc ctagtgtagc ggtgaaatgc gtagatatta ggaggaacac cagtggcgaa 660

ggcggcttac tggacggtaa ctgacgttga ggctcgaaag cgtggggagc aaacaggatt 720

agataccctg gtagtccacg ccgtaaacga tgaataacta ggtgtcgggt ggcaaagcca 780

ttcggtgccg tcgcaaacgc agtaagtatt ccacctgggg agtacgttcg caagaatgaa 840

actcaaagga attgacgggg acccgcacaa gcggtggagc atgtggttta attcgaagca 900

acgcgaagaa ccttaccaag tcttgacatc cgcctgaccg atccttaacc ggatctttcc 960

ttcgggacag gcgagacagg tggtgcatgg ttgtcgtcag ctcgtgtcgt gagatgttgg 1020

gttaagtccc gcaacgagcg caacccctat cctcagtagc cagcatttaa ggtgggcact 1080

ctggggagac tgccagggat aacctggagg aaggcgggga tgacgtcaaa tcatcatgcc 1140

ccttatgatt tgggctacac acgtgctaca atggcgtaaa caaagggaag cgagattgtg 1200

agatggagca aatcccaaaa ataacgtccc agttcggact gtagtctgca acccgactac 1260

acgaagctgg aatcgctagt aatcgcggat cagaatgccg cggtgaatac gttcccgggt 1320

cttgtacaca ccgcccgtca caccatggga gtcagtaacg cccgaagtca gtgacctaac 1380

tgcaaagaag gagctgccga aggcgggacc gatgactggg gtgaagtcgt aacaaggt 1438

<210> SEQ ID NO 95
<211> LENGTH: 1365
<212> TYPE: DNA
<213> ORGANISM: Anaerotruncus colihominis

<400> SEQUENCE: 95

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gagtaacacg tgagcaacct gcctttcaga gggggataac agccggaaac ggctgctaat 120

accgcatgat gttgcggggg cacatgcccc tgcaaccaaa ggagcaatcc gctgaaagat 180

gggctcgcgt ccgattagcc agttggcggg gtaacggccc accaaagcga cgatcggtag 240

ccggactgag aggttgaacg gccacattgg gactgagaca cggcccagac tcctacggga 300

ggcagcagtg ggggatattg cacaatgggc gaaagcctga tgcagcgacg ccgcgtgagg 360

gaagacggtc ttcggattgt aaacctctgt ctttggggaa gaaaatgacg gtacccaaag 420

aggaagctcc ggctaactac gtgccagcag ccgcggtaat acgtagggag caagcgttgt 480

ccggaattac tgggtgtaaa gggagcgtag gcgggatggc aagtagaatg ttaaatccat 540

cggctcaacc ggtggctgcg ttctaaactg ccgttcttga gtgaagtaga ggcaggcgga 600

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 660

-continued

ctgctgggct ttaactgacg ctgaggctcg aaagcgtggg gagcaaacag gattagatac 720

cctggtagtc cacgccgtaa acgatgatta ctaggtgtgg ggggactgac cccttccgtg 780

ccgcagttaa cacaataagt aatccacctg gggagtacgg ccgcaaggtt gaaactcaaa 840

ggaattgacg ggggcccgca caagcagtgg agtatgtggt ttaattcgaa gcaacgcgaa 900

gaaccttacc aggtcttgac atcggcgtaa tagcctagag agtaggtgaa gcccttcggg 960

gcatccagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1020

cccgcaacga gcgcaaccct tattattagt tgctacgcaa gagcactcta atgagactgc 1080

cgttgacaaa acggaggaag gtggggatga cgtcaaatca tcatgcccct tatgacctgg 1140

gctacacacg tactacaatg gcactaaaac agagggcggc gacaccgcga ggtgaagcga 1200

atcccagaaa aagtgtctca gttcagattg caggctgcaa cccgcctgca tgaagtcgga 1260

attgctagta atcgcggatc agcatgccgc ggtgaatacg ttcccgggcc ttgtacacac 1320

cgcccgtcac accatgggag tccgggtaac acccgaagcc agtag 1365

<210> SEQ ID NO 96
<211> LENGTH: 1404
<212> TYPE: DNA
<213> ORGANISM: Ruminococcus faecis

<400> SEQUENCE: 96

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ggcggacggg tgagtaacgc gtgggtaacc tgcctcatac aggggataa cagttagaaa 120

tgactgctaa taccgcataa gaccacagca ccgcatggtg caggggtaaa aactccggtg 180

gtatgagatg gacccgcgtc tgattaggta gttggtgggg taacggccta ccaagccgac 240

gatcagtagc cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact 300

cctacgggag gcagcagtgg ggaatattgc acaatggggg aaaccctgat gcagcgacgc 360

cgcgtgagcg atgaagtatt tcggtatgta aagctctatc agcagggaag aaaatgacgg 420

tacctgacta agaagcaccg gctaaatacg tgccagcagc cgcggtaata cgtatggtgc 480

aagcgttatc cggatttact gggtgtaaag ggagcgtaga cggagtggca agtctgatgt 540

gaaaacccgg ggctcaaccc cgggactgca ttggaaactg tcaatctaga gtaccggaga 600

ggtaagcgga attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg 660

cgaaggcggc ttactggacg gtaactgacg ttgaggctcg aaagcgtggg gagcaaacag 720

gattagatac cctggtagtc cacgccgtaa acgatgacta ctaggtgtcg ggcagcaaag 780

ctgttcggtg ccgcagcaaa cgcaataagt agtccacctg gggagtacgt tcgcaagaat 840

gaaactcaaa ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa 900

gcaacgcgaa gaaccttacc tgctcttgac atctccctga ccggcaagta atgttgcctt 960

tccttcggga cagggatgac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt 1020

tgggttaagt cccgcaacga gcgcaacccc tatctttagt agccagcggt ttggccgggc 1080

actctagaga gactgccagg gataacctgg aggaaggtgg ggatgacgtc aaatcatcat 1140

gccccttatg agcagggcta cacacgtgct acaatggcgt aaacaaaggg aggcagaacc 1200

gcgaggtcga gcaaatccca aaaataacgt ctcagttcgg attgtagtct gcaactcgac 1260

tacatgaagc tggaatcgct agtaatcgcg aatcagaatg tcgcggtgaa tacgttcccg 1320

ggtcttgtac acaccgcccg tcacaccatg ggagtcagta acgcccgaag tcagtgaccc 1380

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aaccgtaagg aggagctgcc gaag 1404

<210> SEQ ID NO 97
<211> LENGTH: 1316
<212> TYPE: DNA
<213> ORGANISM: Dorea longicatena

<400> SEQUENCE: 97

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gcataagacc acgtaccgca tggtacagtg gtaaaaactc cggtggtatg agatggaccc 120

gcgtctgatt aggtagttgg tggggtaacg gcctaccaag ccgacgatca gtagccgacc 180

tgagagggtg accggccaca ttgggactga gacacggccc agactcctac gggaggcagc 240

agtggggaat attgcacaat ggaggaaact ctgatgcagc gacgccgcgt gaaggatgaa 300

gtatttcggt atgtaaactt ctatcagcag ggaagaaaat gacggtacct gactaagaag 360

ccccggctaa ctacgtgcca gcagccgcgg taatacgtag ggggcaagcg ttatccggat 420

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caaccccggg actgcatttg gaactgctga gctagagtgt cggagaggca agtggaattc 540

ctagtgtagc ggtgaaatgc gtagatatta ggaggaacac cagtggcgaa ggcggcttgc 600

tggacgatga ctgacgttga ggctcgaaag cgtggggagc aaacaggatt agataccctg 660

gtagtccacg ccgtaaacga tgactgctag gtgtcgggtg gcaaagccat tcggtgccgc 720

agctaacgca ataagcagtc cacctgggga gtacgttcgc aagaatgaaa ctcaaaggaa 780

ttgacgggga cccgcacaag cggtggagca tgtggtttaa ttcgaagcaa cgcgaagaac 840

cttacctgat cttgacatcc cgatgaccgc ttcgtaatgg aagtttttct tcggaacatc 900

ggtgacaggt ggtgcatggt tgtcgtcagc tcgtgtcgtg agatgttggg ttaagtcccg 960

caacgagcgc aacccctatc ttcagtagcc agcaggttaa gctgggcact ctggagagac 1020

tgccagggat aacctggagg aaggtgggga tgacgtcaaa tcatcatgcc ccttatgacc 1080

agggctacac acgtgctaca atggcgtaaa caaagagaag cgaactcgcg agggtaagca 1140

aatctcaaaa ataacgtctc agttcggatt gtagtctgca actcgactac atgaagctgg 1200

aatcgctagt aatcgcagat cagaatgctg cggtgaatac gttcccgggt cttgtacaca 1260

ccgcccgtca caccatggga gtcataacgc ccgaagtcag tgacccaacc gtaagg 1316

<210> SEQ ID NO 98
<211> LENGTH: 1475
<212> TYPE: DNA
<213> ORGANISM: Clostridium innocuum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (905)..(905)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (942)..(942)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 98

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gaacgaagtc ttcaggaagc ttgcttccaa aaagacttag tggcgaacgg gtgagtaaca 120

cgtaggtaac ctgcccatgt gtccgggata actgctggaa acggtagcta aaaccggata 180

ggtatacgga gcgcatgctc tgtatattaa agcgcccttc aaggcgtgaa catggatgga 240

cctgcgacgc attagctagt tggtgaggta acggcccacc aaggcgatga tgcgtagccg 300

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gcctgagagg gtaaacggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

agcagtaggg aattttcgtc aatgggggaa accctgaacg agcaatgccg cgtgagtgaa 420

gaaggtcttc ggatcgtaaa gctctgttgt aagtgaagaa cggctcatag aggaaatgct 480

atgggagtga cggtagctta ccagaaagcc acggctaact acgtgccagy agccgcggta 540

atacgtaggt ggcaagcgtt atccggaatc attgggcgta aagggtgcgt aggtggcgta 600

ctaagtctgt agtaaaaggc aatggctcaa ccattgtaag ctatggaaac tggtatgctg 660

gagtgcagaa gagggcgatg gaattccatg tgtagcggta aaatgcgtag atatatggag 720

gaacaccagt ggcgaaggcg gtcgcctggt ctgtaactga cactgaggca cgaaagcgtg 780

gggagcaaat aggattagat accctagtag tccacgccgt aaacgatgag aactaagtgt 840

tggagaaatt cagtgctgca gttaacgcaa taagttctcc gcctggggag tatgcacgca 900

agttngaaac tcaaaggaat tgacgggggc ccgcacaagc gntggagtat gtggtttaat 960

tcgaagcaac gcgaagaacc ttaccaggcc ttgacatgga aacaaatacc ctagagatag 1020

ggggataatt atggatcaca caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg 1080

ttgggttaag tcccgcaacg agcgcaaccc ttgtcgcatg ttaccagcat caagttgggg 1140

actcatgcga gactgccggt gacaaaccgg aggaaggtgg ggatgacgtc aaatcatcat 1200

gccccttatg gcctgggcta cacacgtact acaatggcga ccacaaagag cagcgacttg 1260

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ttcatgaagt cggaatcgct agtaatcgca gatcagcatg ctgcggtgaa tacgttctcg 1380

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aaccgtaagg agtgagccgt cgaaggtagg accga 1475

<210> SEQ ID NO 99
<211> LENGTH: 1492
<212> TYPE: DNA
<213> ORGANISM: Blautia hansenii

<400> SEQUENCE: 99

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gaagcactta tcattgactc ttcggaagat ttgatatttg actgagcggc ggacgggtga 120

gtaacgcgtg ggtaacctgc ctcatacagg ggaataacag ttagaaatgg ctgctaatgc 180

cgcataagcg cacaggaccg catggtctgg tgtgaaaaac tgaggtggta tgagatggac 240

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cctgagaggg tgaacggcca cattgggact gagacacggc ccagactcct acgggaggca 360

gcagtgggga atattgcaca atgggggaaa ccctgatgca gcgacgccgc gtgaaggaag 420

aagtatctcg gtatgtaaac ttctatcagc agggaagaaa atgacggtac ctgactaaga 480

agccccggct aactacgtgc cagcagccgc ggtaatacgt aggggcaag cgttatccgg 540

atttactggg tgtaaaggga gcgtagacgg aagagcaagt ctgatgtgaa aggctggggc 600

ttaaccccag gactgcattg gaaactgttt ttctagagtg ccggagaggt aagcggaatt 660

cctagtgtag cggtgaaatg cgtagatatt aggaggaaca ccagtggcga aggcggctta 720

ctggacggta actgacgttg aggctcgaaa gcgtggggag caaacaggat tagataccct 780

ggtagtccac gccgtaaacg atgaatacta ggtgtcgggg tgcaaagcag ttcggtgccg 840

cagcaaacgc aataagtatt ccacctgggg agtacgttcg caagaatgaa actcaaagga 900

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attgacgggg acccgcacaa gcggtggagc atgtggttta attcgaagca acgcgaagaa 960

ccttaccaag tcttgacatc tgcctgaccg ttccttaacc ggagctttcc ttcgggacag 1020

gcaagacagg tggtgcatgg ttgtcgtcag ctcgtgtcgt gagatgttgg gttaagtccc 1080

gcaacgagcg caacccctat ccttagtagc cagcagtccg gctgggcact ctagggagac 1140

tgccggggat aacccggagg aaggcgggga cgacgtcaaa tcatcatgcc ccttatgatt 1200

tgggctacac acgtgctaca atggcgtaaa caaagggaag cgaagcggtg acgcttagca 1260

aatctcaaaa ataacgtccc agttcggact gcagtctgca actcgactgc acgaagctgg 1320

aatcgctagt aatcgcgaat cagaatgtcg cggtgaatac gttcccgggt cttgtacaca 1380

ccgcccgtca caccatggga gtcagtaacg cccgaagtca gtgacccaac cttatggagg 1440

gagctgccga aggcgggacc gataactggg gtgaagtcgt aacaaggtaa cc 1492

<210> SEQ ID NO 100
<211> LENGTH: 1473
<212> TYPE: DNA
<213> ORGANISM: Bacteroides cellulosilyticus

<400> SEQUENCE: 100

agagtttgat cctggctcag gatgaacgct agctacaggc ttaacacatg caagtcgagg 60

ggcagcatga cctagcaata ggttgatggc gaccggcgca cgggtgagta acacgtatcc 120

aacctaccgg ttattccggg atagcctttc gaaagaaaga ttaataccgg atagtataac 180

gagaaggcat ctttttgtta ttaaagaatt tcgataaccg atggggatgc gttccattag 240

tttgttggcg gggtaacggc ccaccaagac atcgatggat aggggttctg agaggaaggt 300

cccccacatt ggaactgaga cacggtccaa actcctacgg gaggcagcag tgaggaatat 360

tggtcaatgg acgagagtct gaaccagcca agtagcgtga aggatgactg ccctatgggt 420

tgtaaacttc ttttatatgg gaataaagtg agccacgtgt ggctttttgt atgtaccata 480

cgaataagga tcggctaact ccgtgccagc agccgcggta atacggagga tccgagcgtt 540

atccggattt attgggttta aagggagcgt aggcggacta ttaagtcagc tgtgaaagtt 600

tgcggctcaa ccgtaaaatt gcagttgata ctggtcgtct tgagtgcagt agaggtaggc 660

ggaattcgtg gtgtagcggt gaaatgctta gatatcacga agaactccga ttgcgaaggc 720

agcttactgg actgtaactg acgctgatgc tcgaaagtgt gggtatcaaa caggattaga 780

taccctggta gtccacacag taaacgatga atactcgctg tttgcgatat acagcaagcg 840

gccaagcgaa agcattaagt attccacctg gggagtacgc cggcaacggt gaaactcaaa 900

ggaattgacg ggggcccgca caagcggagg aacatgtggt ttaattcgat gatacgcgag 960

gaaccttacc cgggcttaaa ttgcatctga ataatttgga aacagattag ccgcaaggca 1020

gatgtgaagg tgctgcatgg ttgtcgtcag ctcgtgccgt gaggtgtcgg cttaagtgcc 1080

ataacgagcg caacccttat ctttagttac taacaggtca tgctgaggac tctagagaga 1140

ctgccgtcgt aagatgtgag gaaggtgggg atgacgtcaa atcagcacgg cccttacgtc 1200

cggggctaca cacgtgttac aatgggggt acagaaggca gctacacagc gatgtgatgc 1260

taatcccaaa agcctctctc agttcggatt ggagtctgca acccgactcc atgaagctgg 1320

attcgctagt aatcgcgcat cagccacggc gcggtgaata cgttcccggg ccttgtacac 1380

accgcccgtc aagccatgaa agccgggggt acctgaagtc cgtaaccgca aggagcggcc 1440

tagggtaaaa ctggtaattg gggctaagtc gta 1473

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<210> SEQ ID NO 101
<211> LENGTH: 1459
<212> TYPE: DNA
<213> ORGANISM: Bacteroides ovatus

<400> SEQUENCE: 101

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tttgcttgca aactgaagat ggcgaccggc gcacgggtga gtaacacgta tccaacctgc 120

cgataactcc ggaatagcct ttcgaaagaa agattaatac cggatagcat acgaatatcg 180

catgatattt ttattaaaga atttcggtta tcgatgggga tgcgttccat tagtttgttg 240

gcggggtaac ggcccaccaa gactacgatg gatagggggtt ctgagaggaa ggtcccccac 300

attggaactg agacacggtc caaactccta cgggaggcag cagtgaggaa tattggtcaa 360

tgggcgagag cctgaaccag ccaagtagcg tgaaggatga aggctctatg ggtcgtaaac 420

ttcttttata tgggaataaa gttttccacg tgtggaattt tgtatgtacc atatgaataa 480

ggatcggcta actccgtgcc agcagccgcg gtaatacgga ggatccgagc gttatccgga 540

tttattgggt ttaaagggag cgtaggtgga ttgttaagtc agttgtgaaa gtttgcggct 600

caaccgtaaa attgcagttg aaactggcag tcttgagtac agtagaggtg ggcggaattc 660

gtggtgtagc ggtgaaatgc ttagatatca cgaagaactc cgattgcgaa ggcagctcac 720

tagactgtta ctgacactga tgctcgaaag tgtgggtatc aaacaggatt agataccctg 780

gtagtccaca cagtaaacga tgaatactcg ctgtttgcga tatacagtaa gcggccaagc 840

gaaagcatta agtattccac ctggggagta cgccggcaac ggtgaaactc aaaggaattg 900

acgggggccc gcacaagcgg aggaacatgt ggtttaattc gatgatacgc gaggaacctt 960

acccgggctt aaattgcaac agaatatatt ggaaacagta tagccgtaag gctgttgtga 1020

aggtgctgca tggttgtcgt cagctcgtgc cgtgaggtgt cggcttaagt gccataacga 1080

gcgcaaccct tatctttagt tactaacagg ttatgctgag gactctagag agactgccgt 1140

cgtaagatgt gaggaaggtg gggatgacgt caaatcagca cggcccttac gtccggggct 1200

acacacgtgt tacaatgggg ggtacagaag gcagctacct ggcgacagga tgctaatccc 1260

aaaaacctct ctcagttcgg atcgaagtct gcaacccgac ttcgtgaagc tggattcgct 1320

agtaatcgcg catcagccat ggcgcggtga atacgttccc gggccttgta cacaccgccc 1380

gtcaagccat gaaagccggg ggtacctgaa gtacgtaacc gcaaggagcg tcctagggta 1440

aaactggtaa ttggggcta 1459

<210> SEQ ID NO 102
<211> LENGTH: 1526
<212> TYPE: DNA
<213> ORGANISM: Eubacterium fissicatena

<400> SEQUENCE: 102

tagagtttga tcctggctca ggatgaacgc tggcggcgtg cttaacacat gcaagtcgag 60

cgaagcgctt tacttagatt tcttcggatt gaagagtttt gcgactgagc ggcggacggg 120

tgagtaacgc gtgggtaacc tgcctcatac agggggataa cagttagaaa tgactgctaa 180

taccgcataa gaccacagta ccgcatggta cagtgggaaa aactccggtg gtatgagatg 240

gacccgcgtc tgattagcta gttggtaagg taacggctta ccaaggcgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatggggg aaaccctgat gcagcgacgc cgcgtgaagg 420

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atgaagtatt tcggtatgta aacttctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggcc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggttatgta agtctgatgt gaaaacccgg 600

ggctcaaccc cgggactgca ttggaaacta tgtaactaga gtgtcggaga ggtaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ttactggacg atcactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgaata ctaggtgtcg ggtggcaaag ccattcggtg 840

ccgcagcaaa cgcaataagt attccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc tgctcttgac atcccactga ccggcgtgta atggcgcctt cccttcgggg 1020

cagtggagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaaccct tatctttagt agccagcggt ttggccgggc actctagaga 1140

gactgccagg gataacctgg aggaaggtgg ggatgacgtc aaatcatcat gccccttatg 1200

agcagggcta cacacgtgct acaatggcgt aaacaaaggg aggcaatacc gcgaggttga 1260

gcaaatccca aaaataacgt ctcagttcgg attgtagtct gcaactcgac tacatgaagc 1320

tggaatcgct agtaatcgcg aatcagaatg tcgcggtgaa tacgttcccg ggtcttgtac 1380

acaccgcccg tcacaccatg ggagttggta acgcccgaag tcagtgaccc aaccgtaagg 1440

agggagctgc cgaaggcggg atcgataact ggggtgaagt cgtaacaagg tagccgtatc 1500

ggaaggtgcg gctggatcac ctccttt 1526

<210> SEQ ID NO 103
<211> LENGTH: 1493
<212> TYPE: DNA
<213> ORGANISM: Blautia coccoides

<400> SEQUENCE: 103

agagtttgat cctggctcag gatgaacgct ggcggcgtgc ttaacacatg caagtcgagc 60

gaagcgctaa gacagatttc ttcggattga agtctttgtg actgagcggc ggacgggtga 120

gtaacgcgtg ggtaacctgc ctcatacagg gggataacag ttagaaatga ctgctaatac 180

cgcataagcg cacaggaccg catggtctgg tgtgaaaaac tccggtggta tgagatggac 240

ccgcgtctga ttagctagtt ggaggggtaa cggcccacca aggcgacgat cagtagccgg 300

cctgagaggg tgaacggcca cattgggact gagacacggc ccagactcct acgggaggca 360

gcagtgggga atattgcaca atgggggaaa ccctgatgca gcgacgccgc gtgaaggaag 420

aagtatctcg gtatgtaaac ttctatcagc agggaagaaa atgacggtac ctgactaaga 480

agccccggct aactacgtgc cagcagccgc ggtaatacgt aggggcaag cgttatccgg 540

atttactggg tgtaaaggga gcgtagacgg aagagcaagt ctgatgtgaa aggctggggc 600

ttaaccccag gactgcattg gaaactgttg ttctagagtg ccggagaggt aagcggaatt 660

cctagtgtag cggtgaaatg cgtagatatt aggaggaaca ccagtggcga aggcggctta 720

ctggacggta actgacgttg aggctcgaaa gcgtggggag caaacaggat tagataccct 780

ggtagtccac gccgtaaacg atgaatacta ggtgtcgggt ggcaaagcca ttcggtgccg 840

cagcaaacgc aataagtatt ccacctgggg agtacgttcg caagaatgaa actcaaagga 900

attgacgggg acccgcacaa gcggtggagc atgtggttta attcgaagca acgcgaagaa 960

ccttaccaag tcttgacatc cctctgaccg tcccgtaacg ggggcttccc ttcggggcag 1020

aggagacagg tggtgcatgg ttgtcgtcag ctcgtgtcgt gagatgttgg gttaagtccc 1080

gcaacgagcg caacccttat ccttagtagc cagcacatga tggtgggcac tctagggaga 1140

ctgccgggga taacccggag gaaggcgggg acgacgtcaa atcatcatgc cccttatgat 1200

ttgggctaca cacgtgctac aatggcgtaa acaaagggaa gcgagacagc gatgttgagc 1260

gaatcccaaa aataacgtcc cagttcggac tgcagtctgc aactcgactg cacgaagctg 1320

gaatcgctag taatcgcgga tcagaatgcc gcggtgaata cgttcccggg tcttgtacac 1380

accgcccgtc acaccatggg agtcagtaac gcccgaagtc agtgacctaa ccgaaaggaa 1440

ggagctgccg aaggcgggac cgataactgg ggtgaagtcg taacaaggta acc 1493

<210> SEQ ID NO 104
<211> LENGTH: 1262
<212> TYPE: DNA
<213> ORGANISM: Blautia faecis

<400> SEQUENCE: 104

ataacagcca gaaatgactg ctaataccgc ataagcgcac agaaccgcat ggttcggtgt 60

gaaaaactcc ggtggtataa gatggacccg cgttggatta gctagttggc agggcagcgg 120

cctaccaagg cgacgatcca tagccggcct gagagggtga acggccacat tgggactgag 180

acacggccca gactcctacg ggaggcagca gtggggaata ttgcacaatg ggggaaaccc 240

tgatgcagcg acgccgcgtg aaggaagaag tatctcggta tgtaaacttc tatcagcagg 300

gaagataatg acggtacctg actaagaagc cccggctaac tacgtgccag cagccgcggt 360

aatacgtagg gggcaagcgt tatccggatt tactgggtgt aaagggagcg tagacggcgc 420

agcaagtctg atgtgaaagg caggggctta acccctggac tgcattggaa actgctgtgc 480

ttgagtgccg gaggggtaag cggaattcct agtgtagcgg tgaaatgcgt agatattagg 540

aggaacacca gtggcgaagg cggcttactg gacggtaact gacgttgagg ctcgaaagcg 600

tggggagcaa acaggattag ataccctggt agtccacgcc gtaaacgatg aatactaggt 660

gtcagggagc acagctcttt ggtgccgccg caaacgcatt aagtattcca cctggggagt 720

acgttcgcaa gaatgaaact caaaggaatt gacggggacc cgcacaagcg gtggagcatg 780

tggtttaatt cgaagcaacg cgaagaacct taccaaatct tgacatccct ctgaccggga 840

cttaaccgtc cctttccttc gggacagggg agacaggtgg tgcatggttg tcgtcagctc 900

gtgtcgtgag atgttgggtt aagtcccgca acgagcgcaa cccctatcct tagtagccag 960

cacgcartgg tgggcactct gaggagactg ccagggataa cctggaggaa ggcggggatg 1020

acgtcaaatc atcatgcccc ttatgatttg ggctacacac gtgctacaat ggcgtaaaca 1080

aagggaagcg aacccgcgag ggtgggcaaa tctcaaaaat aacgtcccag ttcggactgc 1140

agtctgcaac tcgactgcac gaagctggaa tcgctagtaa tcgcggatca gaatgccgcg 1200

gtgaatacgt tcccgggtct tgtacacacc gcccgtcaca ccatgggagt cagtaacgcc 1260

cg 1262

<210> SEQ ID NO 105
<211> LENGTH: 1431
<212> TYPE: DNA
<213> ORGANISM: Clostridium hathewayi
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (191)..(191)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:

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<221> NAME/KEY: misc_feature
<222> LOCATION: (211)..(211)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (248)..(248)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (979)..(979)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 105

ctcaggatga acgctggcgg cgtgcttaac acatgcaagt cgagcgaagc ggtttcaatg 60

aagttttcgg atggatttga aattgactta gcggcggacg ggtgagtaac gcgtgggtaa 120

cctgccttac actgggggat aacagttaga aatgactgct aataccgcat aagcgcacag 180

ggccgcatgg nctggtgtga aaaactccgg nggtgtaaga tggacccgcg tctgattagg 240

tagttggngg ggtaacggcc caccaagccg acgatcagta gccgacctga gagggtgacc 300

ggccacattg ggactgagac acggcccaaa ctcctacggg aggcagcagt ggggaatatt 360

ggacaatggg cgaaagcctg atccagcgac gccgcgtgag tgaagaagta tttcggtatg 420

taaagctcta tcagcaggga agaaaatgac ggtacctgac taagaagccc cggctaacta 480

cgtgccagca gccgcggtaa tacgtagggg gcaagcgtta tccggattta ctgggtgtaa 540

agggagcgta gacggtttag caagtctgaa gtgaaagccc ggggctcaac cccggtactg 600

ctttggaaac tgttagactt gagtgcagga gaggtaagtg gaattcctag tgtagcggtg 660

aaatgcgtag atattaggag gaacaccagt ggcgaaggcg gcttactgga ctgtaactga 720

cgttgaggct cgaaagcgtg gggagcaaac aggattagat accctggtag tccacgccgt 780

aaacgatgaa tactaggtgt cgggggggcaa agcccttcgg tgccgccgca aacgcaataa 840

gtattccacc tggggagtac gttcgcaaga atgaaactca aaggaattga cggggacccg 900

cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg aagaacctta ccaagtcttg 960

acatcccact gaaaacacnt taaccgtgat ccctcttcgg agcagtggag acaggtggtg 1020

catggttgtc gtcagctcgt gtcgtgagat gttgggttaa gtcccgcaac gagcgcaacc 1080

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tggaggaagg tggggatgac gtcaaatcat catgcccctt atgatttggg ctacacacgt 1200

gctacaatgg cgtaaacaaa gggaggcaaa ggagcgatct ggagcaaacc ccaaaaataa 1260

cgtctcagtt cggattgcag gctgcaactc gcctgcatga agctggaatc gctagtaatc 1320

gcgaatcaga atgtcgcggt gaatacgttc ccgggtcttg tacacaccgc ccgtcacacc 1380

atgggagttg gtaacgcccg aagtcagtga cccaaccgaa aggagggagc t 1431

<210> SEQ ID NO 106
<211> LENGTH: 1493
<212> TYPE: DNA
<213> ORGANISM: Blautia producta

<400> SEQUENCE: 106

agagtttgat cctggctcag gatgaacgct ggcggcgtgc ttaacacatg caagtcgagc 60

gaagcactaa gacggatttc ttcggattga agtctttgtg actgagcggc ggacgggtga 120

gtaacgcgtg ggtaacctgc ctcatacagg gggataacag ttagaaatga ctgctaatac 180

cgcataagcg cacaggaccg catggtctgg tgtgaaaaac tccggtggta tgagatggac 240

ccgcgtctga ttagctagtt ggaggggtaa cggcccacca aggcgacgat cagtagccgg 300

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cctgagaggg tgaacggcca cattgggact gagacacggc ccagactcct acgggaggca 360

gcagtgggga atattgcaca atgggggaaa ccctgatgca gcgacgccgc gtgaaggaag 420

aagtatctcg gtatgtaaac ttctatcagc agggaagaaa atgacggtac ctgactaaga 480

agccccggct aactacgtgc cagcagccgc ggtaatacgt aggggggcaag cgttatccgg 540

atttactggg tgtaaaggga gcgtagacgg aagagcaagt ctgatgtgaa aggctggggc 600

ttaaccccag gactgcattg gaaactgttg ttctagagtg ccggagaggt aagcggaatt 660

cctagtgtag cggtgaaatg cgtagatatt aggaggaaca ccagtggcga aggcggctta 720

ctggacggta actgacgttg aggctcgaaa gcgtggggag caaacaggat tagataccct 780

ggtagtccac gccgtaaacg atgaatacta ggtgtcgggt ggcaaagcca ttcggtgccg 840

cagcaaacgc aataagtatt ccacctgggg agtacgttcg caagaatgaa actcaaagga 900

attgacgggg acccgcacaa gcggtggagc atgtggttta attcgaagca acgcgaagaa 960

ccttaccaag tcttgacatc cctctgaccg tcccgtaacg gggacttccc ttcggggcag 1020

aggagacagg tggtgcatgg ttgtcgtcag ctcgtgtcgt gagatgttgg gttaagtccc 1080

gcaacgagcg caacccttat ccttagtagc cagcacatga tggtgggcac tctagggaga 1140

ctgccgggga taacccggag gaaggcgggg acgacgtcaa atcatcatgc cccttatgat 1200

ttgggctaca cacgtgctac aatggcgtaa acaaagggaa gcgagacagc gatgttgagc 1260

gaatcccaaa aataacgtcc cagttcggac tgcagtctgc aactcgactg cacgaagctg 1320

gaatcgctag taatcgcgga tcagaatgcc gcggtgaata cgttcccggg tcttgtacac 1380

accgcccgtc acaccatggg agtcagtaac gcccgaagtc agtgacctaa ccgaaaggaa 1440

ggagctgccg aaggcgggac cgataactgg ggtgaagtcg taacaaggta acc 1493

<210> SEQ ID NO 107
<211> LENGTH: 1515
<212> TYPE: DNA
<213> ORGANISM: Anaerostipes hadrus

<400> SEQUENCE: 107

tggctcagga tgaacgctgg cggcgtgctt aacacatgca agtcgaacga agctgcttaa 60

ctgatcttct tcggaattga cgttttgtag actgagtggc ggacgggtga gtaacgcgtg 120

ggcaacctgc cctgtacagg gggataacag tcagaaatga ctgctaatac cgcataagac 180

cacagcaccg catggtgcag gggtaaaaac tccggtggta caggatggac ccgcgtctga 240

ttagctggtt ggtgaggtaa cggctcacca aggcgacgat cagtagccgg cttgagagag 300

tgaacggcca cattgggact gagacacggc ccaaactcct acgggaggca gcagtgggga 360

atattgcaca atgggggaaa ccctgatgca gcgacgccgc gtgagtgaag aagtatctcg 420

gtatgtaaag ctctatcagc agggaagaaa atgacggtac ctgactaaga agccccggct 480

aactacgtgc cagcagccgc ggtaatacgt aggggggcaag cgttatccgg aattactggg 540

tgtaaagggt gcgtaggtgg tatggcaagt cagaagtgaa aacccagggc ttaactctgg 600

gactgctttt gaaactgtca gactggagtg caggagaggt aagcggaatt cctagtgtag 660

cggtgaaatg cgtagatatt aggaggaaca tcagtggcga aggcggctta ctggactgaa 720

actgacactg aggcacgaaa gcgtggggag caaacaggat tagataccct ggtagtccac 780

gccgtaaacg atgaatacta ggtgtcgggg ccgtagaggc ttcggtgccg cagccaacgc 840

agtaagtatt ccacctgggg agtacgttcg caagaatgaa actcaaagga attgacgggg 900

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tcttgacatc cttctgaccg gtccttaacc ggacctttcc ttcgggacag gagagacagg 1020

tggtgcatgg ttgtcgtcag ctcgtgtcgt gagatgttgg gttaagtccc gcaacgagcg 1080

caacccctat ctttagtagc cagcatttca ggtgggcact ctagagagac tgccagggat 1140

aacctggagg aaggtgggga cgacgtcaaa tcatcatgcc ccttatgacc agggctacac 1200

acgtgctaca atggcgtaaa cagagggaag cagcctcgtg agagtgagca aatcccaaaa 1260

ataacgtctc agttcggatt gtagtctgca actcgactac atgaagctgg aatcgctagt 1320

aatcgcgaat cagaatgtcg cggtgaatac gttcccgggt cttgtacaca ccgcccgtca 1380

caccatggga gtcagtaacg cccgaagtca gtgacccaac cgtaaggagg gagctgccga 1440

aggcgggacc gataactggg gtgaagtcgt aacaaggtag ccgtatcgga aggtgcggct 1500

ggatcacctc ctttc 1515

<210> SEQ ID NO 108
<211> LENGTH: 1523
<212> TYPE: DNA
<213> ORGANISM: Eubacterium fissicatena

<400> SEQUENCE: 108

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gcgctttact tagatttctt cggattgaag agttttgcga ctgagcggcg gacgggtgag 120

taacgcgtgg gtaacctgcc tcatacaggg ggataacagt tagaaatgac tgctaatacc 180

gcataagacc acagtaccgc atggtacagt gggaaaaact ccggtggtat gagatggacc 240

cgcgtctgat tagctagttg gtaaggtaac ggcttaccaa ggcaacgatc agtagccgac 300

ctgagagggt gaccggccac attgggactg agacacggcc caaactccta cgggaggcag 360

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agtatttcgg tatgtaaact tctatcagca gggaagaaaa tgacggtacc tgactaagaa 480

gccccggcta actacgtgcc agcagccgcg gtaatacgta gggggcaagc gttatccgga 540

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ctagtgtagc ggtgaaatgc gtagatatta ggaggaacac cagtggcgaa ggcggcttac 720

tggacgatca ctgacgttga ggctcgaaag cgtggggagc aaacaggatt agataccctg 780

gtagtccacg ccgtaaacga tgaatactag gtgtcgggtg gcaaagccat tcggtgccgc 840

agcaaacgca ataagtattc cacctgggga gtacgttcgc aagaatgaaa ctcaaaggaa 900

ttgacgggga cccgcacaag cggtggagca tgtggtttaa ttcgaagcaa cgcgaagaac 960

cttacctgct cttgacatcc cactgaccgg cgtgtaatgg cgccttccct tcggggcagt 1020

ggagacaggt ggtgcatggt tgtcgtcagc tcgtgtcgtg agatgttggg ttaagtcccg 1080

caacgagcgc aacccttatc tttagtagcc agcggtttgg ccgggcactc tagagagact 1140

gccagggata acctggagga aggtggggat gacgtcaaat catcatgccc cttatgagca 1200

gggctacaca cgtgctacaa tggcgtaaac aaagggaggc aataccgcga ggttgagcaa 1260

atcccaaaaa taacgtctca gttcggattg tagtctgcaa ctcgactaca tgaagctgga 1320

atcgctagta atcgcgaatc agaatgtcgc ggtgaatacg ttcccgggtc ttgtacacac 1380

cgcccgtcac accatgggag ttggtaacgc ccgaagtcag tgacccaacc gtaaggaggg 1440

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ggtgcggctg gatcacctcc ttt 1523

<210> SEQ ID NO 109
<211> LENGTH: 1524
<212> TYPE: DNA
<213> ORGANISM: Eubacterium contortum

<400> SEQUENCE: 109

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cactttactt tgatttcttc ggaatgaaag gttttgtgac tgagcggcgg acgggtgagt 120

aacgcgtggg taacctgcct catacagggg gataacagtt agaaatgact gctaataccg 180

cataagacca cagtaccgca tggtacagtg ggaaaaactc cggtggtatg agatggaccc 240

gcgtctgatt agctagttgg taaggtaacg gcttaccaag gcgacgatca gtagccgacc 300

tgagagggtg accggccaca ttgggactga gacacggccc aaactcctac gggaggcagc 360

agtggggaat attgcacaat gggggaaacc ctgatgcagc gacgccgcgt gaaggatgaa 420

gtatttcggt atgtaaactt ctatcagcag ggaagaaaat gacggtacct gactaagaag 480

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aaccccggga ctgcattgga aactatgtaa ctagagtgtc ggagaggtaa gtggaattcc 660

tagtgtagcg gtgaaatgcg tagatattag gaggaacacc agtggcgaag gcggcttact 720

ggacgatgac tgacgttgag gctcgaaagc gtggggagca aacaggatta gataccctgg 780

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gcaaacgcaa taagtattcc acctggggag tacgttcgca agaatgaaac tcaaaggaat 900

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ggctacacac gtgctacaat ggcgtaaaca aagggaggcg aagccgtgag gtggagcaaa 1260

tcccaaaaat aacgtctcag ttcggattgt agtctgcaac tcgactacat gaagctggaa 1320

tcgctagtaa tcgcgaatca gaatgtcgcg gtgaatacgt tcccgggtct tgtacacacc 1380

gcccgtcaca ccatgggagt tggtaacgcc cgaagtcagt gacccaaccg caaggaggga 1440

gctgccgagg gtgggaccga taactggggt gaagtcgtaa caaggtagcc gtatcggaag 1500

gtgcggctgg atcacctcct ttct 1524

<210> SEQ ID NO 110
<211> LENGTH: 1390
<212> TYPE: DNA
<213> ORGANISM: Clostridium bolteae

<400> SEQUENCE: 110

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gtgaaaaact ccggtggtgt gagatggatc cgcgtctgat tagccagttg gcggggtaac 180

ggcccaccaa agcgacgatc agtagccgac ctgagagggt gaccggccac attgggactg 240

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gggaagaaaa tgacggtacc tgactaagaa gccccggcta actacgtgcc agcagccgcg 420

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gaagcaagtc tgaagtgaaa acccagggct caaccctggg actgctttgg aaactgtttt 540

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cgtggggagc aaacaggatt agataccctg gtagtccacg ccgtaaacga tgaatgctag 720

gtgttggggg gcaaagccct tcggtgccgt cgcaaacgca gtaagcattc cacctgggga 780

gtacgttcgc aagaatgaaa ctcaaaggaa ttgacgggga cccgcacaag cggtggagca 840

tgtggtttaa ttcgaagcaa cgcgaagaac cttaccaagt cttgacatcc tcttgaccgg 900

cgtgtaacgg cgccttccct tcggggcaag agagacaggt ggtgcatggt tgtcgtcagc 960

tcgtgtcgtg agatgttggg ttaagtcccg caacgagcgc aacccttatc cttagtagcc 1020

agcaggtaaa gctgggcact ctagggagac tgccagggat aacctggagg aaggtgggga 1080

tgacgtcaaa tcatcatgcc ccttatgatt tgggctacac acgtgctaca atggcgtaaa 1140

caaagggaag caagacagtg atgtggagca aatcccaaaa ataacgtccc agttcggact 1200

gtagtctgca acccgactac acgaagctgg aatcgctagt aatcgcgaat cagaatgtcg 1260

cggtgaatac gttcccgggt cttgtacaca ccgcccgtca caccatggga gtcagcaacg 1320

cccgaagtca gtgacccaac tcgcaagaga gggagctgcc gaaggcgggg caggtaactg 1380

gggtgaagtc 1390

<210> SEQ ID NO 111
<211> LENGTH: 1308
<212> TYPE: DNA
<213> ORGANISM: Blautia luti
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (702)..(705)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 111

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tggattagct agttggtgag gtaacggccc accaaggcga cgatccatag ccggcctgag 180

agggtgaacg gccacattgg gactgagaca cggcccagac tcctacggga ggcagcagtg 240

gggaatattg cacaatgggg gaaaccctga tgcagcgacg ccgcgtgaag gaagaagtat 300

ctcggtatgt aaacttctat cagcagggaa gaaaatgacg gtacctgact aagaagcccc 360

ggctaactac gtgccagcag ccgcggtaat acgtaggggg caagcgttat ccggatttac 420

tgggtgtaaa gggagcgtag acggcatgga caagtctgat gtgaaaggct ggggctcaac 480

cccgggactg cattggaaac tgcccgtctt gagtgccgga gaggtaagcg gaattcctag 540

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cggtaactga cgttgaggct cgaaagcgtg gggagcaaac aggattagat accctggtag 660

tccacgcggt aaacgatgaa tcctaggtgt cggggagcaa annnnttcgg tgccgccgca 720

aacgcattaa gcattccacc tggggagtac gttcgcaaga atgaaactca aaggaattga 780

cggggacccg cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg aagaacctta 840

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ccaagtcttg acatccctct gaccgagtat gtatggtact tttccttcgg gagagagagg 900

agacaggtgg tgcatggttg tcgtcagctc gtgtcgtgag atgttgggtt aagtcccgca 960

acgagcgcaa cccctatccc cagtagccag cggttcggcc gggcactctg aggagactgc 1020

cagggataac ctggaggaag gcggggatga cgtcaaatca tcatgcccct tatgatttgg 1080

gctacacacg tgctacaatg gcgtaaacaa agggaagcaa gcctgcgagg gtgggcaaat 1140

cccaaaaata acgtcccagt tcggactgta gtctgcaacc cgactacacg aagctggaat 1200

cgctagtaat cgcggatcag aatgccgcgg tgaatacgtt cccgggtctt gtacacaccg 1260

cccgtcacac catgggagtc agtaacgccc gaagtcagtg acctaact 1308

<210> SEQ ID NO 112
<211> LENGTH: 1489
<212> TYPE: DNA
<213> ORGANISM: Acidaminococcus intestini

<400> SEQUENCE: 112

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ggcgaacggg tgagtaacgc gtgggcaacc tgccctccag ttggggacaa cattccgaaa 120

gggatgctaa taccgaatgt cctccctcct ccgcatggag gagggaggaa agatggcctc 180

tgcttgcaag ctatcgctgg aagatgggcc cgcgtctgat tagctagttg gtggggtaac 240

ggctcaccaa ggcgatgatc agtagccggt ctgagaggat gaacggccac attgggactg 300

agacacggcc caaactccta cgggaggcag cagtggggaa tcttccgcaa tggacgaaag 360

tctgacggag caacgccgcg tgagtgatga aggtcttcgg attgtaaaac tctgttgtta 420

gggacgaaag caccgtgttc gaacaggtca tggtgttgac ggtacctaac gaggaagcca 480

cggctaacta cgtgccagca gccgcggtaa tacgtaggtg gcaagcgttg tccggaatta 540

ttgggcgtaa agagcatgta ggcgggcttt taagtctgac gtgaaaatgc ggggcttaac 600

cccgtatggc gttggatact ggaagtcttg agtgcaggag aggaaagggg aattcccagt 660

gtagcggtga aatgcgtaga tattgggagg aacaccagtg gcgaaggcgc ctttctggac 720

tgtgtctgac gctgagatgc gaaagccagg gtagcaaacg ggattagata ccccggtagt 780

cctggccgta aacgatggat actaggtgta ggaggtatcg acccccttctg tgccggagtt 840

aacgcaataa gtatcccgcc tggggactac gatcgcaaga ttgaaactca aaggaattga 900

cgggggcccg cacaagcggt ggagtatgtg gtttaattcg acgcaacgcg aagaacctta 960

ccaaggcttg acattgagtg aaagacctag agataggtcc ctcccttcgg ggacacgaaa 1020

acaggtggtg catggctgtc gtcagctcgt gtcgtgagat gttgggttaa gtcccgcaac 1080

gagcgcaacc cctatcctat gttaccagcg cgtaaaggcg gggactcata ggagactgcc 1140

agggataact tggaggaagg cggggatgac gtcaagtcat catgcccctt atgtcttggg 1200

ctacacacgt actacaatgg tcggcaacaa agggcagcga aaccgcgagg tggagcaaat 1260

cccagaaacc cgaccccagt tcggatcgta ggctgcaacc cgcctacgtg aagttggaat 1320

cgctagtaat cgcaggtcag catactgcgg tgaatacgtt cccgggcctt gtacacaccg 1380

cccgtcacac cacgaaagtt ggtaacaccc gaagccggtg agataacctt ttaggagtca 1440

gctgtctaag gtggggccga tgattggggt gaagtcgtaa caaggtagc 1489

<210> SEQ ID NO 113
<211> LENGTH: 1500
<212> TYPE: DNA

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<213> ORGANISM: Ruminococcus albus

<400> SEQUENCE: 113

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tctgcctttc ggagagggat accaattgga aacgattgtt aatacctcat aacataacga 180

agccgcatga ctttgttatc aaatgaattt cgccgaaaga tgagctcgcg tctgattagg 240

tagttggtga ggtaacggcc caccaagccg acgatcagta gccggactga gaggttgaac 300

ggccacattg ggactgagac acggcccaga ctcctacggg aggcagcagt ggggaatatt 360

gcacaatggg cgaaagcctg atgcagcgat gccgcgtgag ggaagaaggt tttaggattg 420

taaacctctg tctttgggga cgataatgac ggtacccaag gaggaagctc cggctaacta 480

cgtgccagca gccgcggtaa tacgtaggga gcgagcgttg tccggaatta ctgggtgtaa 540

agggagcgta ggcgggattg caagtcaggt gtgaaattta ggggcttaac ccctgaactg 600

cacttgaaac tgtagttctt gagtgaagta gaggtaagcg gaattcctag tgtagcggtg 660

aaatgcgtag atattaggag gaacatcagt ggcgaaggcg gcttactggg ctttaactga 720

cgctgaggct cgaaagcgtg gggagcaaac aggattagat accctggtag tccacgccgt 780

aaacgatgat tactaggtgt gggggggactg acccccttccg tgccgcagtt aacacaataa 840

gtaatccacc tggggagtac ggccgcaagg ctgaaactca aaggaattga cggggacccg 900

cacaagcagt ggagtatgtg gtttaattcg aagcaacgcg aagaacctta ccaggtcttg 960

acatcgtacg catagcatag agatatgtga aatcccttcg gggacgtata gacaggtggt 1020

gcatggttgt cgtcagctcg tgtcgtgaga tgttggggtt aagtcccgca acgagcgcaa 1080

cccttactgt tagttgctac gcaagagcac tctagcagga ctgccgttga caaaacggag 1140

gaaggtgggg atgacgtcaa atcatcatgc cccttatgac ctgggctaca cacgtactac 1200

aatggctgtt aacagaggga agcaaaacag tgatgtggag caaaacccta aaagcagtct 1260

tagttcggat tgtaggctgc aacccgccta catgaagtcg gaattgctag taatcgcgga 1320

tcagcatgcc gcggtgaata cgttcccggg ccttgtacac accgcccgtc acgccatggg 1380

agtcggtaac acccgaagcc tgtgttctaa ccgcaaggag gaagcagtcg aaggtgggat 1440

tgatgactgg ggtgaagtcg taacaaggta gccgtatcgg aaggtgcggc tggatcacct 1500

<210> SEQ ID NO 114
<211> LENGTH: 1521
<212> TYPE: DNA
<213> ORGANISM: Eubacterium rectale

<400> SEQUENCE: 114

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gagtaacgcg tgggtaacct gccttgtaca gggggataac agttggaaac ggctgctaat 180

accgcataag cgcacggcat cgcatgatgc agtgtgaaaa actccggtgg tataagatgg 240

acccgcgttg gattagctag ttggtgaggt aacggcccac caaggcgacg atccatagcc 300

gacctgagag ggtgaccggc cacattggga ctgagacacg gcccaaactc ctacgggagg 360

cagcagtggg gaatattgca caatgggcga aagcctgatg cagcgacgcc gcgtgagcga 420

agaagtattt cggtatgtaa agctctatca gcagggaaga taatgacggt acctgactaa 480

gaagcaccgg ctaaatacgt gccagcagcc gcggtaatac gtatggtgca agcgttatcc 540

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gctcaacccc ggtactgcat tggaaactgt cgtactagag tgtcggaggg gtaagcggaa 660

ttcctagtgt agcggtgaaa tgcgtagata ttaggaggaa caccagtggc gaaggcggct 720

tactggacga taactgacgc tgaggctcga aagcgtgggg agcaaacagg attagatacc 780

ctggtagtcc acgccgtaaa cgatgaatac taggtgttgg gaagcattgc ttctcggtgc 840

cgtcgcaaac gcagtaagta ttccacctgg ggagtacgtt cgcaagaatg aaactcaaag 900

gaattgacgg ggacccgcac aagcggtgga gcatgtggtt taattcgaag caacgcgaag 960

aaccttacca agtcttgaca tccttctgac cggtacttaa ccgtaccttc tcttcggagc 1020

aggagtgaca ggtggtgcat ggttgtcgtc agctcgtgtc gtgagatgtt gggttaagtc 1080

ccgcaacgag cgcaaccctt atctttagta gccagcggtt cggccgggca ctctagagag 1140

actgccaggg ataacctgga ggaaggcggg gatgacgtca aatcatcatg ccccttatga 1200

cttgggctac acacgtgcta caatggcgta aacaaaggga agcaaagctg tgaagccgag 1260

caaatctcaa aaataacgtc tcagttcgga ctgtagtctg caacccgact acacgaagct 1320

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gaaggtgcgg ctggatcacc t 1521

<210> SEQ ID NO 115
<211> LENGTH: 1545
<212> TYPE: DNA
<213> ORGANISM: Acidaminococcus fermentans

<400> SEQUENCE: 115

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ccctctggtt ggggacaaca ttccgaaagg gatgctaata ccgaatgaga tcctctttcc 180

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cgtctgatta gctagtaggt gaggtaacgg ctcacctagg cgatgatcag tagccggtct 300

gagaggatga acggccacat tgggactgag acacggccca aactcctacg ggaggcagca 360

gtggggaatc ttccgcaatg gacgaaagtc tgacggagca acgccgcgtg agtgatgaag 420

gccttcgggt tgtaaaactc tgttgtcagg gacgaaagca ccgatctata atacattttg 480

gtgttgacgg tacctgacga ggaagccacg gctaactacg tgccagcagc cgcggtaata 540

cgtaggtggc aagcgttgtc cggaattatt gggcgtaaag agcatgtagg cgggctttta 600

agtccgacgt gaaaatgcgg ggcttaaccc cgtatggcgt tggatactgg aagtcttgag 660

tgcaggagag gaaaggggaa ttcccagtgt agcggtgaaa tgcgtagata ttgggaggaa 720

caccagtggc gaaggcgcct ttctggactg tgtctgacgc tgagatgcga aagccagggt 780

agcaaacggg attagatacc ccggtagtcc tggccgtaaa cgatgggtac taggtgtagg 840

aggtatcgac cccttctgtg ccggagttaa cgcaataagt accccgcctg gggactacga 900

tcgcaagatt gaaactcaaa ggaattgacg ggggcccgca caagcggtgg agtatgtggt 960

ttaattcgac gcaacgcgaa gaaccttacc aaggcttgac attgagtgaa agacccagag 1020

atgggtcccc ttcttcggaa gcacgaaaac aggtggtgca tggctgtcgt cagctcgtgt 1080

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cgtgagatgt tgggttaagt cccgcaacga gcgcaaccct tatcctatgt taccagcacg 1140

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agccggtgag ataacctttt aggagtcagc tgtctaaggt ggggccgatg attggggtga 1500

agtcgtaaca aggtagccgt tcgagaacga gcggctggat cacct 1545

<210> SEQ ID NO 116
<211> LENGTH: 1423
<212> TYPE: DNA
<213> ORGANISM: Fusicatenibacter saccharivorans

<400> SEQUENCE: 116

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aagattyttc ggatgattct tgactgactg agcggcggac gggtgagtaa cgcgtgggtg 120

acctgcccca taccgggggga taacagctgg aaacggctgc taataccgca taagcgcaca 180

gagctgcatg gctcggtgtg aaaaactccg gtggtatggg atgggcccgc gtctgattag 240

gcagttggcg gggtaacggc ccaccaaacc gacgatcagt agccggcctg agagggcgac 300

cggccacatt gggactgaga cacggcccaa actcctacgg gaggcagcag tggggaatat 360

tgcacaatgg gggaaaccct gatgcagcga cgccgcgtga gcgaagaagt atttcggtat 420

gtaaagctct atcagcaggg aagataatga cggtacctga ctaagaagcc ccggctaact 480

acgtgccagc agccgcggta atacgtaggg ggcaagcgtt atccggattt actgggtgta 540

aagggagcgt agacggcaag gcaagtctga tgtgaaaacc cagggcttaa ccctgggact 600

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gcacaagcgg tggagcatgt ggtttaattc gaagcaacgc gaagaacctt accaggtctt 960

gacatcccga tgaccggccc gtaacggggc cttctcttcg gagcattgga gacaggtggt 1020

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acgtctcagt tcggactgca gtctgcaact cgactgcacg aagctggaat cgctagtaat 1320

cgcgaatcag aatgtcgcgg tgaatacgtt cccgggtctt gtacacaccg cccgtcacac 1380

catgggagtt ggtaacgccc gaagtcagtg acccaacctt tta 1423

<210> SEQ ID NO 117
<211> LENGTH: 1494
<212> TYPE: DNA
<213> ORGANISM: Ruminococcus champanellensis

<400> SEQUENCE: 117

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ccacattggg actgagacac ggcccagact cctacgggag gcagcagtgg ggaatattgc 360

acaatgggcg caagcctgat gcagcgatgc cgcgtggagg aagaaggttt tcggattgta 420

aactcctgtc ttaagggacg ataatgacgg taccttagga ggaagctccg gctaactacg 480

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agattgtagg ctgcaactcg cctacatgaa gtcggaattg ctagtaatcg cagatcagca 1320

tgctgcggtg aatacgttcc cgggccttgt acacaccgcc cgtcacacca tgggagtcgg 1380

taacacccga agccagtagc ctaaccgcaa ggagggcgct gtcgaaggtg ggattgatga 1440

ctggggtgaa gtcgtaacaa ggtagccgta tcggaaggtg cggctggatc acct 1494

<210> SEQ ID NO 118
<211> LENGTH: 1533
<212> TYPE: DNA
<213> ORGANISM: Bifidobacterium bifidum

<400> SEQUENCE: 118

tttttgtgga gggttcgatt ctggctcagg atgaacgctg gcggcgtgct taacacatgc 60

aagtcgaacg ggatccatcg ggctttgctt ggtggtgaga gtggcgaacg ggtgagtaat 120

gcgtgaccga cctgccccat gctccggaat agctcctgga aacgggtggt aatgccggat 180

gttccacatg atcgcatgtg attgtgggaa agattctatc ggcgtgggat ggggtcgcgt 240

cctatcagct tgttggtgag gtaacggctc accaaggctt cgacgggtag ccggcctgag 300

agggcgaccg gccacattgg gactgagata cggcccagac tcctacggga ggcagcagtg 360

gggaatattg cacaatgggc gcaagcctga tgcagcgacg ccgcgtgagg gatggaggcc 420

ttcgggttgt aaacctcttt tgtttgggag caagccttcg ggtgagtgta cctttcgaat 480

aagcgccggc taactacgtg ccagcagccg cggtaatacg tagggcgcaa gcgttatccg 540

gatttattgg gcgtaaaggg ctcgtaggcg gctcgtcgcg tccggtgtga aagtccatcg 600

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cttaacggtg gatctgcgcc gggtacgggc gggctggagt gcggtagggg agactggaat 660

tcccggtgta acggtggaat gtgtagatat cgggaagaac accgatggcg aaggcaggtc 720

tctgggccgt cactgacgct gaggagcgaa agcgtgggga gcgaacagga ttagataccc 780

tggtagtcca cgccgtaaac ggtggacgct ggatgtgggg cacgttccac gtgttccgtg 840

tcggagctaa cgcgttaagc gtcccgcctg gggagtacgg ccgcaaggct aaaactcaaa 900

gaaattgacg ggggcccgca caagcggcgg agcatgcgga ttaattcgat gcaacgcgaa 960

gaaccttacc tgggcttgac atgttcccga cgacgccaga gatggcgttt cccttcgggg 1020

cgggttcaca ggtggtgcat ggtcgtcgtc agctcgtgtc gtgagatgtt gggttaagtc 1080

ccgcaacgag cgcaaccctc gccccgtgtt gccagcacgt tatggtggga actcacgggg 1140

gaccgccggg gttaactcgg aggaaggtgg ggatgacgtc agatcatcat gcccccttacg 1200

tccagggctt cacgcatgct acaatggccg gtacagcggg atgcgacatg gcgacatgga 1260

gcggatccct gaaaaccggt ctcagttcgg atcggagcct gcaacccggc tccgtgaagg 1320

cggagtcgct agtaatcgcg gatcagcaac gccgcggtga atgcgttccc gggccttgta 1380

cacaccgccc gtcaagtcat gaaagtgggc agcacccgaa gccggtggcc taacccccttg 1440

tgggatggag ccgtctaagg tgaggctcgt gattgggact aagtcgtaac aaggtagccg 1500

taccggaagg tgcggctgga tcacctcctt tct 1533

<210> SEQ ID NO 119
<211> LENGTH: 1552
<212> TYPE: DNA
<213> ORGANISM: Megasphaera elsdenii

<400> SEQUENCE: 119

agagtttgat cctggctcag gacgaacgct ggcggcgtgc ttaacacatg caagtcgaac 60

gagaagagat gagaagcttg cttcttatca attcgagtgg caaacgggtg agtaacgcgt 120

aagcaacctg cccttcagat ggggacaaca gctggaaacg gctgctaata ccgaatacgt 180

tctttttgtc gcatggcaga gggaagaaag ggaggctctt cggagctttc gctgaaggag 240

gggcttgcgt ctgattagct agttggaggg gtaacggccc accaaggcga cgatcagtag 300

ccggtctgag aggatgaacg gccacattgg gactgagaca cggcccagac tcctacggga 360

ggcagcagtg gggaatcttc cgcaatggac gaaagtctga cggagcaacg ccgcgtgaac 420

gatgacggcc ttcgggttgt aaagttctgt tatacgggac gaatggcgta gcggtcaata 480

cccgttacga gtgacggtac cgtaagagaa agccacggct aactacgtgc cagcagccgc 540

ggtaatacgt aggtggcaag cgttgtccgg aattattggg cgtaaagggc gcgcaggcgg 600

cgtcgtaagt cggtcttaaa agtgcggggc ttaaccccgt gaggggaccg aaactgcgat 660

gctagagtat cggagaggaa agcggaattc ctagtgtagc ggtgaaatgc gtagatatta 720

ggaggaacac cagtggcgaa agcggctttc tggacgacaa ctgacgctga ggcgcgaaag 780

ccaggggagc aaacgggatt agataccccg gtagtcctgg ccgtaaacga tggatactag 840

gtgtaggagg tatcgacccc ttctgtgccg gagttaacgc aataagtatc ccgcctgggg 900

agtacggccg caaggctgaa actcaaagga attgacgggg gcccgcacaa gcggtggagt 960

atgtggttta attcgacgca acgcgaagaa ccttaccaag ccttgacatt gattgctatg 1020

gatagagata tccagttcct cttcggagga caagaaaaca ggtggtgcac ggctgtcgtc 1080

agctcgtgtc gtgagatgtt gggttaagtc ccgcaacgag cgcaacccct atcttctgtt 1140

accagcggtt cggccgggga ctcaggagag actgccgcag acaatgcgga ggaaggcggg 1200

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gatgacgtca agtcatcatg ccccttatgg cttgggctac acacgtacta caatggctct 1260

taatagaggg aagcgaagga gcgatccgga gcaaacccca aaaacagagt cccagttcgg 1320

attgcaggct gcaactcgcc tgcatgaagc aggaatcgct agtaatcgca ggtcagcata 1380

ctgcggtgaa tacgttcccg ggccttgtac acaccgcccg tcacaccacg aaagtcattc 1440

acacccgaag ccggtgaggt aacctttttgg agccagccgt cgaaggtggg ggcgatgatt 1500

ggggtgaagt cgtaacaagg tagccgtatc ggaaggtgcg gctggatcac ct 1552

<210> SEQ ID NO 120
<211> LENGTH: 1479
<212> TYPE: DNA
<213> ORGANISM: Dorea formicigenerans
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (123)..(125)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (220)..(222)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (287)..(287)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (349)..(350)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (517)..(517)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (534)..(535)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (725)..(725)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (918)..(918)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (921)..(921)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (955)..(956)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1184)..(1185)
<223> OTHER INFORMATION: n is a, c, g, t or u

<400> SEQUENCE: 120

ttaaacgaga gtttgatcct ggctcaggat gaacgctggc ggcgtgctta acacatgcaa 60

gtcgagcgaa gcacataagt ttgattcttc ggatgaagac ttttgtgact gagcggcgga 120

cgnnngagta acgcgtgggt aacctgcctc atacaggggg ataacagyta gaaatggctg 180

ctaataccgc ataagaccac agtactgcat ggtacagtgn nnaaaactcc ggtggtatga 240

gatggacccg cgtctgatta ggtagttggt gaggtaacgg cccaccnagc cgacgatcag 300

tagccgacct gagagggtga ccggccacat tgggactgag acacggccnn gactcctacg 360

ggaggcagca gtggggaata ttgcacaatg ggcgaaagcc tgatgcagcg acgccgcgtg 420

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aaggatgaag tatttcggta tgtaaacttc tatcagcagg gaagaaaatg acggtacctg 480

actaagaagc cccggctaac tacgtgccag cagccgnggt aatacgtagg gggnnagcgt 540

tatccggatt tactgggtgt aaagggagcg tagacggctg tgcaagtctg aagtgaaagg 600

catgggctca acctgtggac tgctttggaa actgtgcagc tagagtgtcg gagaggtaag 660

tggaattcct agtgtagcgg tgaaatgcgt agatattagg aggaacacca gtggcgaagg 720

cggcntactg gacgatgact gacgttgagg ctcgaaagcg tggggagcaa acaggattag 780

ataccctggt agtccacgcc gtaaacgatg actgctaggt gtcgggtagc aaagctattc 840

ggtgccgcag ctaacgcaat aagcagtcca cctggggagt acgttcgcaa gaatgaaact 900

caaaggaatt gacggggncc ngcacaagcg gtggagcatg tggtttaatt cgaannaacg 960

cgaagaacct tacctgatct tgacatcccg atgaccgctt cgtaatggaa gytttttcttc 1020

ggaacatcgg tgacaggtgg tgcatggttg tcgtcagctc gtgtcgtgag atgttgggtt 1080

aagtcccgca acgagcgcaa cccttatctt cagtagccag catttaggat gggcactctg 1140

gagagactgc cagggataac ctggaggaag gtggggatga cgtnnaatca tcatgcccct 1200

tatgaccagg gctacacacg tgctacaatg gcgtaaacag agggaggcag agccgcgagg 1260

ccgagcaaat ctcaaaaata acgtctcagt tcggattgta gtctgcaact cgactacatg 1320

aagctggaat cgctagtaat cgcagatcag aatgctgcgg tgaatacgtt cccgggtctt 1380

gtacacaccg cccgtcacac catgggagtc agtaacgccc gaagtcagtg acccaaccga 1440

aaggagggag ctgccgaagg tgggaccgat aactggggt 1479

<210> SEQ ID NO 121
<211> LENGTH: 1390
<212> TYPE: DNA
<213> ORGANISM: Eisenbergiella tayi

<400> SEQUENCE: 121

ggtataactt agtggcggac gggtgagtaa cgcgtgggaa acctgccctg taccggggga 60

taacacttag aaataggtgc taataccgca taagcgcacg gaaccgcatg gttccgtgtg 120

aaaaactccg gtggtacagg atggtcccgc gtctgattag ccagttggca gggtaacggc 180

ctaccaaagc gacgatcagt agccggcctg agagggtgaa cggccacatt gggactgaga 240

cacggcccaa actcctacgg gaggcagcag tggggaatat tgcacaatgg gggaaaccct 300

gatgcagcga cgccgcgtga gtgaagaagt atttcggtat gtaaagctct atcagcaggg 360

aagaaaatga cggtacctga ctaagaagcc ccggctaact acgtgccagc agccgcggta 420

atacgtaggg ggcaagcgtt atccggattt actgggtgta aagggagcgt agacggcatg 480

gcaagccaga tgtgaaaacc cagggctcaa ccttgggatt gcatttggaa ctgccaggct 540

ggagtgcagg agaggtaagc ggaattccta gtgtagcggt gaaatgcgta gatattagga 600

ggaacaccag tggcgaaggc ggcttactgg actgtaactg acgttgaggc tcgaaagcgt 660

ggggagcaaa caggattaga taccctggta gtccacgcgg taaacgatga ttgctaggtg 720

taggtgggta tggacccatc ggtgccgcag ctaacgcaat aagcaatcca cctggggagt 780

acgttcgcaa gaatgaaact caaaggaatt gacggggacc cgcacaagcg gtggagcatg 840

tggtttaatt cgaagcaacg cgaagaacct taccaagtct tgacatccca atgacgcacc 900

tgtaaagagg tgttcccttc ggggcattgg agacaggtgg tgcatggttg tcgtcagctc 960

gtgtcgtgag atgttgggtt aagtcccgca acgagcgcaa cccttattct tagtagccag 1020

caggtaaagc tgggcactct aaggagactg ccggggataa cccggaggaa ggcggggatg 1080

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acgtcaaatc atcatgcccc ttatgatttg ggctacacac gtgctacaat ggcgtaaaca 1140

aagggaagcg agacagtgat gtggagcaaa tcycagaaat aacgtctcag ttcggattgt 1200

agtctgcaac tcgactacat gaagctggaa tcgctagtaa tcgcgaatca gcatgtcgcg 1260

gtgaatacgt tcccgggtct tgtacacacc gcccgtcaca ccatgggagt tggaaatgcc 1320

cgaagtctgt gacctaaccg aaagggagga gcagccgaag gcaggtctga taactggggt 1380

gaagtcgtaa 1390

<210> SEQ ID NO 122
<211> LENGTH: 1478
<212> TYPE: DNA
<213> ORGANISM: Clostridium symbiosum
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (349)..(350)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (534)..(535)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (606)..(606)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (618)..(619)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (709)..(709)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (921)..(921)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (955)..(956)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1012)..(1013)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1015)..(1015)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1081)..(1081)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1185)..(1185)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1240)..(1240)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1391)..(1392)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1470)..(1470)
<223> OTHER INFORMATION: n is a, c, g, t or u
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (1474)..(1475)
<223> OTHER INFORMATION: n is a, c, g, t or u

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<400> SEQUENCE: 122

aaacatgaga gtttgatcct ggctcaggat gaacgctggc ggcgtgccta acacatgcaa 60

gtcgaacgaa gcgatttaac ggaagttttc ggatggaagt tgaattgact gagtggcgga 120

cgggtgagta acgcgtgggt aacctgcctt gtactggggg acaacagtta gaaatgactg 180

ctaataccgc ataagcgcac agtattgcat gatacagtgt gaaaaactcc ggtggtacaa 240

gatggacccg cgtctgatta gctagttggt aaggtaacgg cttaccaagg cgacgatcag 300

tagccgacct gagagggtga ccggccacat tgggactgag acacggccnn aactcctacg 360

ggaggcagca gtggggaata ttgcacaatg ggcgaaagcc tgatgcagcg acgccgcgtg 420

agtgaagaag tatttcggta tgtaaagctc tatcagcagg gaagaaaatg acggtacctg 480

actaagaagc cccggctaac tacgtgccag cagccgcggt aatacgtagg gggnnagcgt 540

tatccggatt tactgggtgt aaagggagcg tagacggtaa agcaagtctg aagtgaaagc 600

ccgcgnctca actgcggnnc tgctttggaa actgtttaac tggagtgtcg gagaggtaag 660

tggaattcct agtgtagcgg tgaaatgcgt agatattagg aggaacacna gtggcgaagg 720

cgacttactg gacgataact gacgttgagg ctcgaaagcg tggggagcaa acaggattag 780

ataccctggt agtccacgcc gtaaacgatg aatactaggt gttggggagc aaagctcttc 840

ggtgccgtcg caaacgcagt aagtattcca cctggggagt acgttcgcaa gaatgaaact 900

caaaggaatt gacggggacc ngcacaagcg gtggagcatg tggtttaatt cgaannaacg 960

cgaagaacct taccaggtct tgacatcgac tcgacggggg agtaacgtcc cnntnccttc 1020

ggggcggaga agacaggtgg tgcatggttg tcgtcagctc gtgtcgtgag atgttgggtt 1080

nagtcccgca acgagcgcaa cccttattct aagtagccag cggttcggcc gggaactctt 1140

gggagactgc cagggataac ctggaggaag gtggggatga cgtcnaatca tcatgcccct 1200

tatgatctgg gctacacacg tgctacaatg gcgtaaacan agagaagcaa gaccgcgagg 1260

tggagcaaat ctcaaaaata acgtctcagt tcggactgca ggctgcaact cgcctgcacg 1320

aagctggaat cgctagtaat cgcgaatcag aatgtcgcgg tgaatacgtt cccgggtctt 1380

gtacacaccg nncgtcacac catgggagtc agtaacgccc gaagtcagtg acccaaccgc 1440

aaggagggag ctgccgaagg cgggaccgan aacnnggg 1478

<210> SEQ ID NO 123
<211> LENGTH: 1488
<212> TYPE: DNA
<213> ORGANISM: Erysipelatoclostridium ramosum

<400> SEQUENCE: 123

agagtttgat cctggctcag gatgaacgct ggcggcgtgc ctaatacatg caagtcgaac 60

gcgagcactt gtgctcgagt ggcgaacggg tgagtaatac ataagtaacc tgccctagac 120

agggggataa ctattggaaa cgatagctaa gaccgcatag gtacggacac tgcatggtga 180

ccgtattaaa agtgcctcaa agcactggta gaggatggac ttatggcgca ttagctggtt 240

ggcggggtaa cggcccacca aggcgacgat gcgtagccga cctgagaggg tgaccggcca 300

cactgggact gagacacggc ccagactcct acgggaggca gcagtaggga attttcggca 360

atgggggaaa ccctgaccga gcaacgccgc gtgaaggaag aaggttttcg gattgtaaac 420

ttctgttata aaggaagaac ggcggctaca ggaaatggta gccgagtgac ggtactttat 480

tagaaagcca cggctaacta cgtgccagca gccgcggtaa tacgtaggtg gcaagcgtta 540

tccggaatta ttgggcgtaa agagggagca ggcggcagca agggtctgtg gtgaaagcct 600

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gaagcttaac ttcagtaagc catagaaacc aggcagctag agtgcaggag aggatcgtgg 660

aattccatgt gtagcggtga aatgcgtaga tatatggagg aacaccagtg gcgaaggcga 720

cgatctggcc tgcaactgac gctcagtccc gaaagcgtgg ggagcaaata ggattagata 780

ccctagtagt ccacgccgta aacgatgagt actaagtgtt ggatgtcaaa gttcagtgct 840

gcagttaacg caataagtac tccgcctgag tagtacgttc gcaagaatga aactcaaagg 900

aattgacggg ggcccgcaca agcggtggag catgtggttt aattcgaagc aacgcgaaga 960

accttaccag gtcttgacat actcataaag gctccagaga tggagagata gctatatgag 1020

atacaggtgg tgcatggttg tcgtcagctc gtgtcgtgag atgttgggtt aagtcccgca 1080

acgagcgcaa cccttatcgt tagttaccat cattaagttg gggactctag cgagactgcc 1140

agtgacaagc tggaggaagg cggggatgac gtcaaatcat catgcccctt atgacctggg 1200

ctacacacgt gctacaatgg atggtgcaga gggaagcgaa gccgcgaggt gaagcaaaac 1260

ccataaaacc attctcagtt cggattgtag tctgcaactc gactacatga agttggaatc 1320

gctagtaatc gcgaatcagc atgtcgcggt gaatacgttc tcgggccttg tacacaccgc 1380

ccgtcacacc acgagagttg ataacacccg aagccggtgg cctaaccgca aggaaggagc 1440

tgtctaaggt gggattgatg attggggtga agtcgtaaca aggtaacc 1488

<210> SEQ ID NO 124
<211> LENGTH: 1528
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 124

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aacgaagcaa ttaaaggaag ttttcggatg gaatttgatt gactgagtgg cggacgggtg 120

agtaacgcgt ggataacctg cctcacactg ggggataaca gttagaaatg actgctaata 180

ccgcataagc gcacagtacc gcatggtacg gtgtgaaaaa ctccggtggt gtgagatgga 240

tccgcgtctg attagccagt tggcggggta acggcccacc aaagcgacga tcagtagccg 300

acctgagagg gtgaccggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

agcagtgggg aatattgcac aatgggcgaa agcctgatgc agcgacgccg cgtgagtgaa 420

gaagtatttc ggtatgtaaa gctctatcag cagggaagaa aatgacggta cctgactaag 480

aagccccggc taactacgtg ccagcagccg cggtaatacg taggggcaa gcgttatccg 540

gattcactgg gtgtaaaggg agcgtagacg gcgaagcaag tctgaagtga aaacccaggg 600

ctcaaccctg ggactgcttt ggaaactgtt ttgctagagt gtcggagagg taagtggaat 660

tcctagtgta gcggtgaaat gcgtagatat taggaggaac accagtggcg aaggcggctt 720

actggacgat aactgacgtt gaggctcgaa agcgtgggga gcaaacagga ttagataccc 780

tggtagtcca cgccgtaaac gatgaatgct aggtgttggg gggcaaagcc cttcggtgcc 840

gtcgcaaacg cagtaagcat tccacctggg gagtacgttc gcaagaatga aactcaaagg 900

aattgacggg gacccgcaca agcggtggag catgtggttt aattcgaagc aacgcgaaga 960

accttaccaa gtcttgacat cctcttgacc ggcgtgtaac ggcgccttcc cttcggggca 1020

agagagacag gtggtgcatg gttgtcgtca gctcgtgtcg tgagatgttg ggttaagtcc 1080

cgcaacgagc gcaaccctta tccttagtag ccagcaggta gagctgggca ctctagggag 1140

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actgccaggg ataacctgga ggaaggtggg gatgacgtca aatcatcatg ccccttatga 1200

tttgggctac acacgtgcta caatggcgta aacaaaggga agcaagacag tgatgtggag 1260

caaatcccaa aaataacgtc ccagttcgga ctgtagtctg caacccgact acacgaagct 1320

ggaatcgcta gtaatcgcga atcagaatgt cgcggtgaat acgttcccgg gtcttgtaca 1380

caccgcccgt cacaccatgg gagtcagcaa cgcccgaagt cagtgaccca actcgcaaga 1440

gagggagctg ccgaaggcgg ggcaggtaac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 125
<211> LENGTH: 1530
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 125

atgagagttt gatcctggct caggatgaac gctggcggcg tgcctaacac atgcaagtcg 60

aacgaagcaa ttaaaatgaa gttttcggat ggatttttga ttgactgagt ggcggacggg 120

tgagtaacgc gtggataacc tgcctcacac tgggggataa cagttagaaa tgactgctaa 180

taccgcataa gcgcacagta ccgcatggta cggtgtgaaa aactccggtg gtgtgggatg 240

gatccgcgtc tgattagcca gttggcgggg taacggccca ccaaagcgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatgggcg aaagcctgat gcagcgacgc cgcgtgagtg 420

aagaagtatt tcggtatgta aagctctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggcc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggcgaagca agtctgaagt gaaaacccag 600

ggctcaaccc tgggactgct ttggaaactg ttttgctaga gtgtcggaga ggtaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ttactggacg ataactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgaatg ctaggtgttg gggggcaaag cccttcggtg 840

ccgtcgcaaa cgcagtaagc attccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc aagtcttgac atcctcttga ccggcgtgta acggcgcctt cccttcgggg 1020

caagagagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaaccct tatccttagt agccagcagg taaagctggg cactctaggg 1140

agactgccag ggataacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

gatttgggct acacacgtgc tacaatggcg taaacaaagg gaagcaagac agtgatgtgg 1260

agcaaatccc aaaaataacg tcccagttcg gactgtagtc tgcaacccga ctacacgaag 1320

ctggaatcgc tagtaatcgc gaatcagaat gtcgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagc aacgcccgaa gtcagtgacc caactcgcaa 1440

gagagggagc tgccgaaggc ggggcaggta actggggtga agtcgtaaca aggtagccgt 1500

atcggaaggt gcggctggat cacctccttt 1530

<210> SEQ ID NO 126
<211> LENGTH: 1528

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 126

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aacgaagcaa ttaaaatgaa gttttcggat ggatttttga ttgactgagt ggcggacggg 120

tgagtaacgc gtggataacc tgcctcacac tgggggataa cagttagaaa tgactgctaa 180

taccgcataa gcgcacagta ccgcatggta cggtgtgaaa aactccggtg gtgtgagatg 240

gatccgcgtc tgattagcca gttggcgggg taacggccca ccaaagcgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatgggcg aaagcctgat gcagcgacgc cgcgtgagtg 420

aagaagtatt tcggtatgta aagctctatc agcagggaag aaatgacggt acctgactaa 480

gaagccccgg ctaactacgt gccagcagcc gcggtaatac gtaggggcga agcgttatcc 540

ggatttactg ggtgtaaagg gagcgtagac ggcgaagcaa gtctgaagtg aaaacccagg 600

gctcaaccct gggactgctt tggaaactgt tttgctagag tgtcggagag gtaagtggaa 660

ttcctagtgt agcggtgaaa tgcgtagata ttaggaggaa caccagtggc gaaggcggct 720

tactggacga taactgacgt tgaggctcga aagcgtgggg agcaaacagg attagatacc 780

ctggtagtcc acgccgtaaa cgatgaatgc taggtgttgg gggcaaagcc cttcggtgcc 840

gtcgcaaacg cagtaagcat tccacctggg gagtacgttc gcaagaatga aactcaaagg 900

aattgacggg gacccgcaca agcggtggag catgtggttt aattcgaagc aacgcgaaga 960

accttaccaa gtcttgacat cctcttgacc ggcgtgtaac ggcgccttcc cttcggggca 1020

agagagacag gtggtgcatg gttgtcgtca gctcgtgtcg tgagatgttg ggttaagtcc 1080

cgcaacgagc gcaaccctta tccttagtag ccagcaggta aagctgggca ctctagggag 1140

actgccaggg ataacctgga ggaaggtggg gatgacgtca aatcatcatg ccccttatga 1200

tttgggctac acacgtgcta caatggcgta aacaaaggga agcaagacag tgatgtggag 1260

caaatcccaa aaataacgtc ccagttcgga ctgtagtctg caacccgact acacgaagct 1320

ggaatcgcta gtaatcgcga atcagaatgt cgcggtgaat acgttcccgg gtcttgtaca 1380

caccgcccgt cacaccatgg gagtcagcaa cgcccgaagt cagtgaccca actcgcaaga 1440

gagggagctg ccgaaggcgg ggcaggtaac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 127
<211> LENGTH: 1528
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 127

atgagagttt gatcctggct caggatgaac gctggcggcg tgcctaacac atgcaagtcg 60

aacgaagcaa ttaaaatgaa gttttcggat ggatttttga ttgactgagt ggcggacggg 120

tgagtaacgc gtggataacc tgcctcacac tgggggataa cagttagaaa tgactgctaa 180

taccgcataa gcgcacagta ccgcatggta cggtgtgaaa aactccggtg gtgtgagatg 240

gatccgcgtc tgattagcca gttggcgggg taacggccca ccaaagcgac gatcagtagc 300

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cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatgggcg aaagcctgat gcagcgacgc cgcgtgagtg 420

aagaagtatt tcggtatgta aagctctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtagggggc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggcgaagca agtctgaagt gaaaacccag 600

ggctcaaccc tgggactgct ttggaaactg ttttgctaga gtgtcggaga ggtaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ttactggacg ataactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgaatg ctaggtgttg ggggcaaagc ccttcggtgc 840

cgtcgcaaac gcagtaagca ttccacctgg ggagtacgtt cgcaagaatg aaactcaaag 900

gaattgacgg ggacccgcac aagcggtgga gcatgtggtt taattcgaag caacgcgaag 960

aaccttacca agtcttgaca tcctcttgac cggcgtgtaa cggcgccttc ccttcggggc 1020

aggagagaca ggtggtgcat ggttgtcgtc agctcgtgtc gtgagatgtt gggttaagtc 1080

ccgcaacgag cgcaaccctt atccttagta gccagcaggt agagctgggc actctaggga 1140

gactgccagg gataacctgg aggaaggtgg ggatgacgtc aaatcatcat gccccttatg 1200

atttgggcta cacacgtgct acaatggcgt aaacaaaggg aagcaagaca gtgatgtgga 1260

gcaaatccca aaataacgtc ccagttcgga ctgtagtctg caacccgact acacgaagct 1320

ggaatcgcta gtaatcgcga atcagaatgt cgcggtgaat acgttcccgg gtcttgtaca 1380

caccgcccgt cacaccatgg gagtcagcaa cgcccgaagt cagtgaccca actcgcaaga 1440

gagggagctg ccgaaggcgg ggcaggtaac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 128
<211> LENGTH: 1528
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 128

atgagagttt gatcctggct caggatgaac gctggcggcg tgcctaacac atgcaagtcg 60

aacgaagcaa ttaaaatgaa gttttcggat ggattttaat tgactgagtg gcggacgggt 120

gagtaacgcg tggataacct gcctcacact gggggataac agttagaaat gactgctaat 180

accgcataag cgcacagtac cgcatggtac ggtgtgaaaa actccggtgg tgtgagatgg 240

atccgcgtct gattagccag ttggcggggt aacggcccac caaagcgacg atcagtagcc 300

gacctgagag ggtgaccggc cacattggga ctgagacacg gcccaaactc ctacgggagg 360

cagcagtggg gaatattgca caatgggcga aagcctgatg cagcgacgcc gcgtgagtga 420

agaagtattt cggtatgtaa agctctatca gcagggaaga aaatgacggt acctgactaa 480

gaagccccgg ctaactacgt gccagcagcc gcggtaatac gtaggggggca agcgttatcc 540

ggatttactg ggtgtaaagg gagcgtagac ggcgaagcaa gtctgaagtg aaaacccagg 600

gctcaaccct gggactgctt tggaaactgt tttgctagag tgtcggagag gtaagtggaa 660

ttcctagtgt agcggtgaaa tgcgtagata ttaggaggaa caccagtggc gaaggcggct 720

tactggacga taactgacgt tgaggctcga aagcgtgggg agcaaacagg attagatacc 780

ctggtagtcc acgccgtaaa cgatgaatgc taggtgttgg ggggcaaagc ccttcggtgc 840

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cgtcgcaaac gcagtaagca ttccacctgg ggagtacgtt cgcaagaatg aaactcaaag 900

gaattgacgg ggacccgcac aagcggtgga gcatgtggtt taattcgaag caacgcgaag 960

aaccttacca agtcttgaca tcctcttgac cggcgtgtaa cggcgccttc ccttcggggc 1020

aagagagaca ggtggtgcat ggttgtcgtc agctcgtgtc gtgagatgtt gggttaagtc 1080

ccgcaacgag cgcaaccctt atccttagta gccagcaggt aaagctgggc actctaggga 1140

gactgccagg gataacctgg aggaaggtgg ggatgacgtc aaatcatcat gccccttatg 1200

atttgggcta cacacgtgct acaatggcgt aaacaaaggg aagcaagaca gtgatgtgga 1260

gcaaatccca aaataacgtc ccagttcgga ctgtagtctg caacccgact acacgaagct 1320

ggaatcgcta gtaatcgcga atcagaatgt cgcggtgaat acgttcccgg gtcttgtaca 1380

caccgcccgt cacaccatgg gagtcagcaa cgcccgaagt cagtgaccca actcgcaaga 1440

gagggagctg ccgaaggcgg ggcaggtaac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 129
<211> LENGTH: 1522
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 129

tcaaagagtt tgatcctggc tcaggacgaa cgctggcggc gcgcctaaca catgcaagtc 60

gaacggagct tacgttttga agttttcgga tggatgaatg taagcttagt ggcggacggg 120

tgagtaacac gtgagcaacc tgcctttcag agggggataa cagccggaaa cggctgctaa 180

taccgcatga tgttgcgggg gcacatgccc ctgcaaccaa aggagcaatc cgctgaaaga 240

tgggctcgcg tccgattagc cagttggcgg ggtaacggcc caccaaagcg acgatcggta 300

gccggactga gaggttgaac ggccacattg ggactgagac acggcccaga ctcctacggg 360

aggcagcagt gggggatatt gcacaatggg cgaaagcctg atgcagcgac gccgcgtgag 420

ggaagacggt cttcggattg taaacctctg tctttgggga agaaaatgac ggtacccaaa 480

gaggaagctc cggctaacta cgtgccagca gccgcggtaa tacgtaggga gcaagcgttg 540

tccggaatta ctgggtgtaa agggagcgta ggcgggatgg caagtagaat gttaaatcca 600

tcggctcaac cggtggctgc gttctaaact gccgttcttg agtgaagtag aggcaggcgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cctgctgggc tttaactgac gctgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgatt actaggtgtg gggggactga ccccttccgt 840

gccgcagtta acacaataag taatccacct ggggagtacg gccgcaaggt tgaaactcaa 900

aggaattgac gggggcccgc acaagcagtg gagtatgtgg tttaattcga agcaacgcga 960

agaaccttac caggtcttga catcggatgc atagcctaga gataggtgaa gcccttcggg 1020

gcatccagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaaccct tattattagt tgctacgcaa gagcactcta atgagactgc 1140

cgttgacaaa acggaggaag gtggggatga cgtcaaatca tcatgcccct tatgacctgg 1200

gctacacacg tactacaatg gcactaaaac agagggcggc gacaccgcga ggtgaagcga 1260

atcccgaaaa agtgtctcag ttcagattgc aggctgcaac ccgcctgcat gaagtcggaa 1320

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ttgctagtaa tcgcggatca gcatgccgcg gtgaatacgt tcccgggcct tgtacacacc 1380

gcccgtcaca ccatgggagt cggtaacacc cgaagccagt agcctaaccg caaggggggc 1440

gctgtcgaag gtgggattga tgactggggt gaagtcgtaa caaggtagcc gtatcggaag 1500

gtgcggctgg atcacctcct tt 1522

<210> SEQ ID NO 130
<211> LENGTH: 1521
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 130

tcaaagagtt tgatcctggc tcaggacgaa cgctggcggc gcgcctaaca catgcaagtc 60

gaacggagct tacgttttga agttttcgga tggacgaatg taagcttagt ggcggacggg 120

tgagtaacac gtgagcaacc tgcctttcag aggggataac agccggaaac ggctgctaat 180

accgcatgat gttgcggggg cacatgcccc tgcaaccaaa ggagcaatcc gctgaaagat 240

gggctcgcgt ccgattagcc agttggcggg gtaacggccc accaaagcga cgatcggtag 300

ccggactgag aggttgaacg gccacattgg gactgagaca cggcccagac tcctacggga 360

ggcagcagtg ggggatattg cacaatgggc gaaagcctga tgcagcgacg ccgcgtgagg 420

gaagacggtc ttcggattgt aaacctctgt ctttggggaa gaaaatgacg gtacccaaag 480

aggaagctcc ggctaactac gtgccagcag ccgcggtaat acgtagggag caagcgttgt 540

ccggaattac tgggtgtaaa gggagcgtag gcgggatggc aagtagaatg ttaaatccat 600

cggctcaacc ggtggctgcg ttctaaactg ccgttcttga gtgaagtaga ggcaggcgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ctgctgggct ttaactgacg ctgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgatta ctaggtgtgg ggggactgac cccttccgtg 840

ccgcagttaa cacaataagt aatccacctg gggagtacgg ccgcaaggtt gaaactcaaa 900

ggaattgacg ggggcccgca caagcagtgg agtatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc aggtcttgac atcggatgca tagcctagag ataggtgaag cccttcgggg 1020

catccagaca ggtggtgcat ggttgtcgtc agctcgtgtc gtgagatgtt gggttaagtc 1080

ccgcaacgag cgcaaccctt attattagtt gctacgcaag agcactctaa tgagactgcc 1140

gttgacaaaa cggaggaagg tggggatgac gtcaaatcat catgcccctt atgacctggg 1200

ctacacacgt actacaatgg cactaaaaca gagggcggcg acaccgcgag gtgaagcgaa 1260

tcccgaaaaa gtgtctcagt tcagattgca ggctgcaacc cgcctgcatg aagtcggaat 1320

tgctagtaat cgcggatcag catgccgcgg tgaatacgtt cccgggcctt gtacacaccg 1380

cccgtcacac catgggagtc ggtaacaccc gaagccagta gcctaaccgc aaggggggcg 1440

ctgtcgaagg tgggattgat gactggggtg aagtcgtaac aaggtagccg tatcggaagg 1500

tgcggctgga tcacctcctt t 1521

<210> SEQ ID NO 131
<211> LENGTH: 1522
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 131

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tcaaagagtt tgatcctggc tcaggacgaa cgctggcggc gcgcctaaca catgcaagtc 60

gaacggagct tacgttttga agttttcgga tggatgaatg taagcttagt ggcggacggg 120

tgagtaacac gtgagcaacc tgcctttcag aggggggataa cagccggaaa cggctgctaa 180

taccgcatga tgttgcgggg gcacatgccc ctgcaaccaa aggagcaatc cgctgaaaga 240

tgggctcgcg tccgattagc cagttggcgg ggtaacggcc caccaaagcg acgatcggta 300

gccggactga gaggttgaac ggccacattg ggactgagac acggcccaga ctcctacggg 360

aggcagcagt gggggatatt gcacaatggg cgaaagcctg atgcagcgac gccgcgtgag 420

ggaagacggt cttcggattg taaacctctg tctttgggga agaaaatgac ggtacccaaa 480

gaggaagctc cggctaacta cgtgccagca gccgcggtaa tacgtaggga gcaagcgttg 540

tccggaatta ctgggtgtaa agggagcgta ggcgggatgg caagtagaat gttaaatcca 600

tcggctcaac cggtggctgc gttctaaact gccgttcttg agtgaagtag aggcaggcgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cctgctgggc tttaactgac gctgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgatt actaggtgtg gggggactga ccccttccgt 840

gccgcagtta acacaataag taatccacct ggggagtacg gccgcaaggt tgaaactcaa 900

aggaattgac gggggcccgc acaagcagtg gagtatgtgg tttaattcga agcaacgcga 960

agaaccttac caggtcttga catcggatgc atagcctaga gataggtgaa gcccttcggg 1020

gcatccagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

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gctacacacg tactacaatg gcactaaaac agagggcggc gacaccgcga ggtgaagcga 1260

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ttgctagtaa tcgcggatca gcatgccgcg gtgaatacgt tcccgggcct tgtacacacc 1380

gcccgtcaca ccatgggagt cggtaacacc cgaagccagt agcctaaccg caaggggggc 1440

gctgtcgaag gtgggattga tgactggggt gaagtcgtaa caaggtagcc gtatcggaag 1500

gtgcggctgg atcacctcct tt 1522

<210> SEQ ID NO 132
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 132

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gagcgaagcg ctgttttcag aatcttcgga ggaagaggac agtgactgag cggcggacgg 120

gtgagtaacg cgtgggcaac ctgcctcata caggggggata acagttagaa atgactgcta 180

ataccgcata agcgcacagg accgcatggt gtagtgtgaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaaaggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccaaac tcctacggga 360

ggcagcagtg gggaatattg cacaatgggg gaaaccctga tgcagcgacg ccgcgtgaag 420

gaagaagtat ttcggtatgt aaacttctat cagcagggaa gaaaatgacg gtacctgagt 480

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aagaagcacc ggctaaatac gtgccagcag ccgcggtaat acgtatggtg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggataggc aagtctggag tgaaaaccca 600

gggctcaacc ctgggactgc tttggaaact gcagatctgg agtgccggag aggtaagcgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cttactggac ggtgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact actaggtgtc ggtgtgcaaa gcacatcggt 840

gccgcagcaa acgcaataag tagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctggtcttga catccggatg acgggcgagt aatgtcgccg tcccttcggg 1020

gcgtccgaga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ttatcttcag tagccagcat ataaggtggg cactctggag 1140

agactgccag ggagaacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

ggccagggct acacacgtgc tacaatggcg taaacaaagg gaagcgagag ggtgacctgg 1260

agcgaatccc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc ggatcagcat gccgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gccagtgacc caaccttaga 1440

ggagggagct gtcgaaggcg ggacggataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttt 1529

<210> SEQ ID NO 133
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 133

tacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcctaaca catgcaagtc 60

gagcgaagcg ctgttttcag aatcttcgga ggaagaggac agtgactgag cggcggacgg 120

gtgagtaacg cgtgggcaac ctgcctcata cagggggata acagttagaa atgactgcta 180

ataccgcata agcgcacagg accgcatggt gtagtgtgaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaaaggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccaaac tcctacggga 360

ggcagcagtg gggaatattg cacaatgggg gaaaccctga tgcagcgacg ccgcgtgaag 420

gaagaagtat ttcggtatgt aaacttctat cagcagggaa gaagatgacg gtacctgagt 480

aagaagcacc ggctaaatac gtgccagcag ccgcggtaat acgtatggtg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggataggc aagtctggag tgaaaaccca 600

gggctcaacc ctgggactgc tttggaaact gcagatctgg agtgccggag aggtaagcgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cttactggac ggtgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact actaggtgtc ggtgtgcaaa gcacatcggt 840

gccgcagcaa acgcaataag tagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctggtcttga catccggatg acgggcgagt aatgtcgccg tcccttcggg 1020

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gcatccgaga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ttatcttcag tagccagcat ataaggtggg cactctggag 1140

agactgccag ggagaacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

ggccagggct acacacgtgc tacaatggcg taaacaaagg gaagcgagag ggtgacctga 1260

agcgaatccc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc ggatcagcat gccgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gccagtgacc caaccttaga 1440

ggagggagct gtcgaaggcg ggacggataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttt 1529

<210> SEQ ID NO 134
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 134

tacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcctaaca catgcaagtc 60

gagcgaagcg ctgttttcag aatcttcgga ggaagaggac agtgactgag cggcggacgg 120

gtgagtaacg cgtgggcaac ctgcctcata cagggggata acagttagaa atgactgcta 180

ataccgcata agcgcacagg accgcatggt gtagtgtgaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaaaggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccaaac tcctacggga 360

ggcagcagtg gggaatattg cacaatgggg gaaaccctga tgcagcgacg ccgcgtgaag 420

gaagaagtat ttcggtatgt aaacttctat cagcagggaa gaagatgacg gtacctgagt 480

aagaagcacc ggctaaatac gtgccagcag ccgcggtaat acgtatggtg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggataggc aagtctggag tgaaaaccca 600

gggctcaacc ctgggactgc tttggaaact gcagatctgg agtgccggag aggtaagcgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cttactggac ggtgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact actaggtgtc ggtgtgcaaa gcacatcggt 840

gccgcagcaa acgcaataag tagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctggtcttga catccggatg acgggcgagt aatgtcgccg tcccttcggg 1020

gcatccgaga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ttatcttcag tagccagcat ataaggtggg cactctggag 1140

agactgccag ggagaacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

ggccagggct acacacgtgc tacaatggcg taaacaaagg gaagcgagag ggtgacctgg 1260

agcgaatccc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc ggatcagcat gccgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gccagtgacc caaccttaga 1440

ggagggagct gtcgaaggcg ggacggataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

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tcggaaggtg cggctggatc acctccttt 1529

<210> SEQ ID NO 135
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 135

tacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcctaaca catgcaagtc 60

gagcgaagcg ctgttttcag aatcttcgga ggaagaggac agtgactgag cggcggacgg 120

gtgagtaacg cgtgggcaac ctgcctcata cagggggata acagttagaa atgactgcta 180

ataccgcata agcgcacagg accgcatggt gtagtgtgaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaaaggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccaaac tcctacggga 360

ggcagcagtg gggaatattg cacaatgggg gaaaccctga tgcagcgacg ccgcgtgaag 420

gaagaagtat ttcggtatgt aaacttctat cagcagggaa gaagatgacg gtacctgagt 480

aagaagcacc ggctaaatac gtgccagcag ccgcggtaat acgtatggtg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggataggc aagtctggag tgaaaaccca 600

gggctcaacc ctgggactgc tttggaaact gcagatctgg agtgccggag aggtaagcgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cttactggac ggtgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact actaggtgtc ggtgtgcaaa gcacatcggt 840

gccgcagcaa acgcaataag tagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctggtcttga catccggatg acgggcgagt aatgtcgccg tcccttcggg 1020

gcatccgaga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ttatcttcag tagccagcat ataaggtggg cactctggag 1140

agactgccag ggagaacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

ggccagggct acacacgtgc tacaatggcg taaacaaagg gaagcgagag ggtgacctga 1260

agcgaatccc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc ggatcagcat gccgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gccagtgacc caaccttaga 1440

ggagggagct gtcgaaggcg ggacggataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttt 1529

<210> SEQ ID NO 136
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 136

tacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcctaaca catgcaagtc 60

gagcgaagcg ctgttttcag aatcttcgga ggaagaggac agtgactgag cggcggacgg 120

gtgagtaacg cgtgggcaac ctgcctcata cagggggata acagttagaa atgactgcta 180

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ataccgcata agcgcacagg accgcatggt gtagtgtgaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaaaggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccaaac tcctacggga 360

ggcagcagtg gggaatattg cacaatgggg gaaaccctga tgcagcgacg ccgcgtgaag 420

gaagaagtat ttcggtatgt aaacttctat cagcagggaa gaagatgacg gtacctgagt 480

aagaagcacc ggctaaatac gtgccagcag ccgcggtaat acgtatggtg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggataggc aagtctggag tgaaaaccca 600

gggctcaacc ctgggactgc tttggaaact gcagatctgg agtgccggag aggtaagcgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cttactggac ggtgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact actaggtgtc ggtgtgcaaa gcacatcggt 840

gccgcagcaa acgcaataag tagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctggtcttga catccggatg acgggcgagt aatgtcgccg tcccttcggg 1020

gcatccgaga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ttatcttcag tagccagcat ataaggtggg cactctggag 1140

agactgccag ggagaacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

ggccagggct acacacgtgc tacaatggcg taaacaaagg gaagcgagag ggtgacctgg 1260

agcgaatccc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc ggatcagcat gccgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gccagtgacc caaccttaga 1440

ggagggagct gtcgaaggcg ggacggataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttt 1529

<210> SEQ ID NO 137
<211> LENGTH: 1527
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 137

atgagagttt gatcctagct caggatgaac gctggcggcg tgcctaacac atgcaagtcg 60

aacgaagcaa tttaacggaa gttttcggat ggaagttgaa ttgactgagt ggcggacggg 120

tgagtaacgc gtgggtaacc tgccttgtac tgggggacaa cagttagaaa tgactgctaa 180

taccgcataa gcgcacagta tcgcatgata cagtgtgaaa aactccggtg gtacaagatg 240

gacccgcgtc tgattagcta gttggtaagg taacggctta ccaaggcgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatgggcg aaagcctgat gcagcgacgc cgcgtgagtg 420

aagaagtatt tcggtatgta aagctctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggcc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggtaaagca agtctgaagt gaaagcccgc 600

ggctcaactg cgggactgct ttggaaactg tttaactgga gtgtcggaga ggtaagtgga 660

-continued

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcgac 720

ttactggacg ataactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgaata ctaggtgttg gggagcaaag ctcttcggtg 840

ccgtcgcaaa cgcagtaagt attccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc aggtcttgac atcgatccga cgggggagta acgtcccctt cccttcgggg 1020

cggagaagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaaccct tattctaagt agccagcggt tcggccggga actcttggga 1140

gactgccagg gataacctgg aggaaggtgg ggatgacgtc aaatcatcat gccccttatg 1200

atctgggcta cacacgtgct acaatggcgt aaacaaagag aagcaagacc gcgaggtgga 1260

gcaaatctca aaaataacgt ctcagttcgg actgcaggct gcaactcgcc tgcacgaagc 1320

tggaatcgct agtaatcgcg aatcagaatg tcgcggtgaa tacgttcccg ggtcttgtac 1380

acaccgcccg tcacaccatg ggagtcagta acgcccgaag tcagtgaccc aaccgcaagg 1440

agggagctgc cgaaggcggg accgataact ggggtgaagt cgtaacaagg tagccgtatc 1500

ggaaggtgcg gctggatcac ctccttt 1527

<210> SEQ ID NO 138
<211> LENGTH: 1527
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 138

atgagagttt gatcctggct caggatgaac gctggcggcg tgcctaacac atgcaagtcg 60

aacgaagcga tttaacggaa attttcggat ggaagttgaa ttgactgagt ggcggacggg 120

tgagtaacgc gtgggtaacc tgccttgtac tgggggacaa cagttagaaa tgactgctaa 180

taccgcataa gcgcacagta tcgcatgata cagtgtgaaa aactccggtg gtacaagatg 240

gacccgcgtc tgattagcta gttggtaagg taacggctta ccaaggcgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatgggcg aaagcctgat gcagcgacgc cgcgtgagtg 420

aagaagtatt tcggtatgta aagctctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggcc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggtaaagca agtctgaagt gaaagcccgc 600

ggctcaactg cgggactgct ttggaaactg tttaactgga gtgtcggaga ggtaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcgac 720

ttactggacg ataactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgaata ctaggtgttg gggagcaaag ctcttcggtg 840

ccgtcgcaaa cgcagtaagt attccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc aggtcttgac atcgatccga cgggggagta acgtcccctt cccttcgggg 1020

cggagaagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaaccct tattctaagt agccagcggt tcggccggga actcttggga 1140

gactgccagg gataacctgg aggaaggtgg ggatgacgtc aaatcatcat gccccttatg 1200

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atctgggcta cacacgtgct acaatggcgt aaacaaagag aagcaagacc gcgaggtgga 1260

gcaaatctca aaaataacgt ctcagttcgg actgcaggct gcaactcgcc tgcacgaagc 1320

tggaatcgct agtaatcgcg aatcagaatg tcgcggtgaa tacgttcccg ggtcttgtac 1380

acaccgcccg tcacaccatg ggagtcagta acgcccgaag tcagtgaccc aaccgcaagg 1440

agggagctgc cgaaggcggg accgataact ggggtgaagt cgtaacaagg tagccgtatc 1500

ggaaggtgcg gctggatcac ctccttt 1527

<210> SEQ ID NO 139
<211> LENGTH: 1527
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 139

atgagagttt gatcctggct caggatgaac gctggcggcg tgcctaacac atgcaagtcg 60

aacgaagcga tttaacggaa gttttcggat ggaagttgaa ttgactgagt ggcggacggg 120

tgagtaacgc gtgggtaacc tgccttgtac tgggggacaa cagttagaaa tgactgctaa 180

taccgcataa gcgcacagta tcgcatgata cagtgtgaaa aactccggtg gtacaagatg 240

gacccgcgtc tgattagcta gttggtaagg taacggctta ccaaggcgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatgggcg aaagcctgat gcagcgacgc cgcgtgagtg 420

aagaagtatt tcggtatgta aagctctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggcc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggtaaagca agtctgaagt gaaagcccgc 600

ggctcaactg cgggactgct ttggaaactg tttaactgga gtgtcggaga ggtaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcgac 720

ttactggacg ataactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgaata ctaggtgttg gggagcaaag ctcttcggtg 840

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gaaccttacc aggtcttgac atcgatccga cgggggagta acgtcccctt cccttcgggg 1020

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cccgcaacga gcgcaaccct tattctaagt agccagcggt tcggccggga actcttggga 1140

gactgccagg gataacctgg aggaaggtgg ggatgacgtc aaatcatcat gccccttatg 1200

atctgggcta cacacgtgct acaatggcgt aaacaaagag aagcaagacc gcgaggtgga 1260

gcaaatctca aaaataacgt ctcagttcgg actgcaggct gcaactcgcc tgcacgaagc 1320

tggaatcgct agtaatcgcg aatcagaatg tcgcggtgaa tacgttcccg ggtcttgtac 1380

acaccgcccg tcacaccatg ggagtcagta acgcccgaag tcagtgaccc aaccgcaagg 1440

agggagctgc cgaaggcggg accgataact ggggtgaagt cgtaacaagg tagccgtatc 1500

ggaaggtgcg gctggatcac ctccttt 1527

<210> SEQ ID NO 140
<211> LENGTH: 1527
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 140

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aacgaagcga tttaacggaa gttttcggat ggaagttgga ttgactgagt ggcggacggg 120

tgagtaacgc gtgggtaacc tgccttgtac tgggggacaa cagttagaaa tgactgctaa 180

taccgcataa gcgcacagta tcgcatgata cagtgtgaaa aactccggtg gtacaagatg 240

gacccgcgtc tgattagcta gttggtaagg taacggctta ccaaggcgac gatcagtagc 300

cgacctgaga gggtgaccgg ccacattggg actgagacac ggcccaaact cctacgggag 360

gcagcagtgg ggaatattgc acaatgggcg aaagcctgat gcagcgacgc cgcgtgagtg 420

aagaagtatt tcggtatgta aagctctatc agcagggaag aaaatgacgg tacctgacta 480

agaagccccg gctaactacg tgccagcagc cgcggtaata cgtaggggcc aagcgttatc 540

cggatttact gggtgtaaag ggagcgtaga cggtaaagca agtctgaagt gaaagcccgc 600

ggctcaactg cgggactgct ttggaaactg tttaactgga gtgtcggaga ggtaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcgac 720

ttactggacg ataactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgaata ctaggtgttg gggagcaaag ctcttcggtg 840

ccgtcgcaaa cgcagtaagt attccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc aggtcttgac atcgatccga cgggggagta acgtcccctt cccttcgggg 1020

cggagaagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaaccct tattctaagt agccagcggt tcggccggga actcttggga 1140

gactgccagg gataacctgg aggaaggtgg ggatgacgtc aaatcatcat gccccttatg 1200

atctgggcta cacacgtgct acaatggcgt aaacaaagag aagcaagacc gcgaggtgga 1260

gcaaatctca aaaataacgt ctcagttcgg actgcaggct gcaactcgcc tgcacgaagc 1320

tggaatcgct agtaatcgcg aatcagaatg tcgcggtgaa tacgttcccg ggtcttgtac 1380

acaccgcccg tcacaccatg ggagtcagta acgcccgaag tcagtgaccc aaccgcaagg 1440

agggagctgc cgaaggcggg accgataact ggggtgaagt cgtaacaagg tagccgtatc 1500

ggaaggtgcg gctggatcac ctccttt 1527

<210> SEQ ID NO 141
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 141

atcagagagt ttgatcctgg ctcaggatga acgctggcgg cgtgcttaac acatgcaagt 60

cgagcgaagc acttaagtgg atctcttcgg attgaaactt atttgactga gcggcggacg 120

ggtgagtaac gcgtgggtaa cctgcctcat acagggggat aacagttaga aatggctgct 180

aataccgcat aagcgcacag gaccgcatgg tctggtgtga aaaactccgg tggtatgaga 240

tggacccgcg tctgattagc tagttggagg ggtaacggcc caccaaggcg acgatcagta 300

gccggcctga gagggtgaac ggccacattg ggactgagac acggcccaga ctcctacggg 360

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aggcagcagt ggggaatatt gcacaatggg ggaaaccctg atgcagcgac gccgcgtgaa 420

ggaagaagta tctcggtatg taaacttcta tcagcaggga agaaaatgac ggtacctgac 480

taagaagccc cggctaacta cgtgccagca gccgcggtaa tacgtagggg gcaagcgtta 540

tccggattta ctgggtgtaa agggagcgta gacggaagag caagtctgat gtgaaaggct 600

ggggcttaac cccaggactg cattggaaac tgtttttcta gagtgccgga gaggtaagcg 660

gaattcctag tgtagcggtg aaatgcgtag atattaggag gaacaccagt ggcgaaggcg 720

gcttactgga cggtaactga cgttgaggct cgaaagcgtg gggagcaaac aggattagat 780

accctggtag tccacgccgt aaacgatgaa tactaggtgt cgggtggcaa agccattcgg 840

tgccgcagca aacgcaataa gtattccacc tggggagtac gttcgcaaga atgaaactca 900

aaggaattga cggggacccg cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg 960

aagaacctta ccaagtcttg acatccctct gaccggcccg taacggggcc ttcccttcgg 1020

ggcagaggag acaggtggtg catggttgtc gtcagctcgt gtcgtgagat gttgggttaa 1080

gtcccgcaac gagcgcaacc cctatcctta gtagccagca ggtgaagctg ggcactctag 1140

ggagactgcc ggggataacc cggaggaagg cggggacgac gtcaaatcat catgcccctt 1200

atgatttggg ctacacacgt gctacaatgg cgtaaacaaa gggaagcgag acagcgatgt 1260

tgagcaaatc ccaaaaataa cgtcccagtt cggactgcag tctgcaactc gactgcacga 1320

agctggaatc gctagtaatc gcgaatcaga atgtcgcggt gaatacgttc ccgggtcttg 1380

tacacaccgc ccgtcacacc atgggagtca gtaacgcccg aagtcagtga cccaaccttt 1440

taggagggag ctgccgaagg cgggaccgat aactggggtg aagtcgtaac aaggtagccg 1500

tatcggaagg tgcggctgga tcacctcctt t 1531

<210> SEQ ID NO 142
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 142

atcagagagt ttgatcctgg ctcaggatga acgctggcgg cgtgcttaac acatgcaagt 60

cgagcgaagc acttaagtgg atctcttcgg attgaaactt atttgactga gcggcggacg 120

ggtgagtaac gcgtgggtaa cctgcctcat acaggggat aacagttaga aatggctgct 180

aataccgcat aagcgcacag gaccgcatgg tctggtgtga aaaactccgg tggtatgaga 240

tggacccgcg tctgattagc tagttggagg ggtaacggcc caccaaggcg acgatcagta 300

gccggcctga gagggtgaac ggccacattg ggactgagac acggcccaga ctcctacggg 360

aggcagcagt ggggaatatt gcacaatggg ggaaaccctg atgcagcgac gccgcgtgaa 420

ggaagaagta tctcggtatg taaacttcta tcagcaggga agaaaatgac ggtacctgac 480

taagaagccc cggctaacta cgtgccagca gccgcggtaa tacgtagggg gcaagcgtta 540

tccggattta ctgggtgtaa agggagcgta gacggaagag caagtctgat gtgaaaggct 600

ggggcttaac cccaggactg cattggaaac tgtttttcta gagtgccgga gaggtaagtg 660

gaattcctag tgtagcggtg aaatgcgtag atattaggag gaacaccagt ggcgaaggcg 720

gcttactgga cggtaactga cgttgaggct cgaaagcgtg gggagcaaac aggattagat 780

accctggtag tccacgccgt aaacgatgaa tactaggtgt cgggtggcaa agccattcgg 840

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tgccgcagca aacgcaataa gtattccacc tggggagtac gttcgcaaga atgaaactca 900

aaggaattga cggggacccg cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg 960

aagaacctta ccaagtcttg acatccctct gaccggcccg taacggggcc ttcccttcgg 1020

ggcagaggag acaggtggtg catggttgtc gtcagctcgt gtcgtgagat gttgggttaa 1080

gtcccgcaac gagcgcaacc cctatcctta gtagccagca ggtgaagctg ggcactctag 1140

ggagactgcc ggggataacc cggaggaagg cggggacgac gtcaaatcat catgcccctt 1200

atgatttggg ctacacacgt gctacaatgg cgtaaacaaa gggaagcggg acagcgatgt 1260

tgagcaaatc ccaaaaataa cgtcccagtt cggactgcag tctgcaactc gactgcacga 1320

agctggaatc gctagtaatc gcgaatcaga atgtcgcggt gaatacgttc ccgggtcttg 1380

tacacaccgc ccgtcacacc atgggagtca gtaacgcccg aagtcagtga cccaacctta 1440

caggagggag ctgccgaagg cgggaccgat aactggggtg aagtcgtaac aaggtagccg 1500

tatcggaagg tgcggctgga tcacctcctt t 1531

<210> SEQ ID NO 143
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 143

atcagagagt ttgatcctgg ctcaggatga acgctggcgg cgtgcttaac acatgcaagt 60

cgagcgaagc acttaagtgg atctcttcgg attgaagctt atttgactga gcggcggacg 120

ggtgagtaac gcgtgggtaa cctgcctcat acaggggat aacagttaga aatggctgct 180

aataccgcat aagcgcacag gaccgcatgg tctggtgtga aaaactccgg tggtatgaga 240

tggacccgcg tctgattagc tagttggagg ggtaacggcc caccaaggcg acgatcagta 300

gccggcctga gagggtgaac ggccacattg ggactgagac acggcccaga ctcctacggg 360

aggcagcagt ggggaatatt gcacaatggg ggaaaccctg atgcagcgac gccgcgtgaa 420

ggaagaagta tctcggtatg taaacttcta tcagcaggga agaaaatgac ggtacctgac 480

taagaagccc cggctaacta cgtgccagca gccgcggtaa tacgtagggg gcaagcgtta 540

tccggattta ctgggtgtaa agggagcgta gacggaagag caagtctgat gtgaaaggct 600

ggggcttaac cccaggactg cattggaaac tgtttttcta gagtgccgga gaggtaagcg 660

gaattcctag tgtagcggtg aaatgcgtag atattaggag gaacaccagt ggcgaaggcg 720

gcttactgga cggtaactga cgttgaggct cgaaagcgtg gggagcaaac aggattagat 780

accctggtag tccacgccgt aaacgatgaa tactaggtgt cgggtggcaa agccattcgg 840

tgccgcagca aacgcaataa gtattccacc tggggagtac gttcgcaaga atgaaactca 900

aaggaattga cggggacccg cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg 960

aagaacctta ccaagtcttg acatccctct gaccggcccg taacggggcc ttcccttcgg 1020

ggcagaggag acaggtggtg catggttgtc gtcagctcgt gtcgtgagat gttgggttaa 1080

gtcccgcaac gagcgcaacc cctatcctta gtagccagca ggtgaagctg ggcactctag 1140

ggagactgcc ggggataacc cggaggaagg cggggacgac gtcaaatcat catgcccctt 1200

atgatttggg ctacacacgt gctacaatgg cgtaaacaaa gggaagcgag acagcgatgt 1260

tgagcaaatc ccaaaaataa cgtcccagtt cggactgcag tctgcaactc gactgcacga 1320

agctggaatc gctagtaatc gcgaatcaga atgtcgcggt gaatacgttc ccgggtcttg 1380

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tacacaccgc ccgtcacacc atgggagtca gtaacgcccg aagtcagtga cccaacctta 1440

caggagggag ctgccgaagg cgggaccgat aactggggtg aagtcgtaac aaggtagccg 1500

tatcggaagg tgcggctgga tcacctcctt t 1531

<210> SEQ ID NO 144
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 144

atcagagagt ttgatcctgg ctcaggatga acgctggcgg cgtgcttaac acatgcaagt 60

cgagcgaagc acttaagcgg atctcttcgg attgaaactt atttgactga gcggcggacg 120

ggtgagtaac gcgtgggtaa cctgcctcat acaggggat aacagttaga aatggctgct 180

aataccgcat aagcgcacag gaccgcatgg tctggtgtga aaaactccgg tggtatgaga 240

tggacccgcg tctgattagc tagttggagg ggtaacggcc caccaaggcg acgatcagta 300

gccggcctga gagggtgaac ggccacattg ggactgagac acggcccaga ctcctacggg 360

aggcagcagt ggggaatatt gcacaatggg ggaaaccctg atgcagcgac gccgcgtgaa 420

ggaagaagta tctcggtatg taaacttcta tcagcaggga agaaaatgac ggtacctgac 480

taagaagccc cggctaacta cgtgccagca gccgcggtaa tacgtagggg gcaagcgtta 540

tccggattta ctgggtgtaa agggagcgta gacggaagag caagtctgat gtgaaaggct 600

ggggcttaac cccaggactg cattggaaac tgtttttcta gagtgccgga gaggtaagcg 660

gaattcctag tgtagcggtg aaatgcgtag atattaggag gaacaccagt ggcgaaggcg 720

gcttactgga cggtaactga cgttgaggct cgaaagcgtg gggagcaaac aggattagat 780

accctggtag tccacgccgt aaacgatgaa tactaggtgt cgggtggcaa agccattcgg 840

tgccgcagca aacgcaataa gtattccacc tggggagtac gttcgcaaga atgaaactca 900

aaggaattga cggggacccg cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg 960

aagaacctta ccaagtcttg acatccctct gaccggcccg taacggggcc ttcccttcgg 1020

ggcagaggag acaggtggtg catggttgtc gtcagctcgt gtcgtgagat gttgggttaa 1080

gtcccgcaac gagcgcaacc cctatcctta gtagccagca ggtgaagctg ggcactctag 1140

ggagactgcc ggggataacc cggaggaagg cggggacgac gtcaaatcat catgcccctt 1200

atgatttggg ctacacacgt gctacaatgg cgtaaacaaa gggaagcgag acagcgatgt 1260

tgagcaaatc ccaaaaataa cgtcccagtt cggactgcag tctgcaactc gactgcacga 1320

agctggaatc gctagtaatc gcgaatcaga atgtcgcggt gaatacgttc ccgggtcttg 1380

tacacaccgc ccgtcacacc atgggagtca gtaacgcccg aagtcagtga cccaacctta 1440

caggagggag ctgccgaagg cgggaccgat aactggggtg aagtcgtaac aaggtagccg 1500

tatcggaagg tgcggctgga tcacctcctt t 1531

<210> SEQ ID NO 145
<211> LENGTH: 1531
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 145

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atcagagagt ttgatcctgg ctcaggatga acgctggcgg cgtgcttaac acatgcaagt 60

cgagcgaagc acttaagtgg atctcttcgg attgaaactt atttgactga gcggcggacg 120

ggtgagtaac gcgtgggtaa cctgcctcat acaggggat aacagttaga aatggctgct 180

aataccgcat aagcgcacag gaccgcatgg tctggtgtga aaaactccgg tggtatgaga 240

tggacccgcg tctgattagc tagttggagg ggtaacggcc caccaaggcg acgatcagta 300

gccggcctga gagggtgaac ggccacattg ggactgagac acggcccaga ctcctacggg 360

aggcagcagt ggggaatatt gcacaatggg ggaaaccctg atgcagcgac gccgcgtgaa 420

ggaagaagta tctcggtatg taaacttcta tcagcaggga agaaaatgac ggtacctgac 480

taagaagccc cggctaacta cgtgccagca gccgcggtaa tacgtagggg gcaagcgtta 540

tccggattta ctgggtgtaa agggagcgta gacggaagag caagtctgat gtgaaaggct 600

ggggcttaac cccaggactg cattggaaac tgtttttcta gagtgccgga gaggtaagcg 660

gaattcctag tgtagcggtg aaatgcgtag atattaggag gaacatcagt ggcgaaggcg 720

gcttactgga cggtaactga cgttgaggct cgaaagcgtg gggagcaaac aggattagat 780

accctggtag tccacgccgt aaacgatgaa tactaggtgt cgggtggcaa agccattcgg 840

tgccgcagca aacgcaataa gtattccacc tggggagtac gttcgcaaga atgaaactca 900

aaggaattga cggggacccg cacaagcggt ggagcatgtg gtttaattcg aagcaacgcg 960

aagaacctta ccaagtcttg acatccctct gaccggcccg taacggggcc ttcccttcgg 1020

ggcagaggag acaggtggtg catggttgtc gtcagctcgt gtcgtgagat gttgggttaa 1080

gtcccgcaac gagcgcaacc cctatcctta gtagccagca ggtgaagctg ggcactctag 1140

ggagactgcc ggggataacc cggaggaagg cggggacgac gtcaaatcat catgcccctt 1200

atgatttggg ctacacacgt gctacaatgg cgtaaacaaa gggaagcgag acagcgatgt 1260

tgagcaaatc ccaaaaataa cgtcctagtt cggactgcag tctgcaactc gactgcacga 1320

agctggaatc gctagtaatc gcgaatcaga atgtcgcggt gaatacgttc ccgggtcttg 1380

tacacaccgc ccgtcacacc atgggagtca gtaacgcccg aagtcagtga cccaacctta 1440

caggagggag ctgccgaagg cgggaccgat aactggggtg aagtcgtaac aaggtagccg 1500

tatcggaagg tgcggctgga tcacctcctt t 1531

<210> SEQ ID NO 146
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 146

aacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcttaaca catgcaagtc 60

gagcgaagca cttaagtttg attcttcgga tgaagacttt tgtgactgag cggcggacgg 120

gtgagtaacg cgtgggtaac ctgcctcata caggggata acagttagaa atgactgcta 180

ataccgcata agaccacggt accgcatggt acagtggtaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaacggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccagac tcctacggga 360

ggcagcagtg gggaatattg cacaatggag gaaactctga tgcagcgacg ccgcgtgaag 420

gatgaagtat ttcggtatgt aaacttctat cagcagggaa gaaaatgacg gtacctgact 480

aagaagcccc ggctaactac gtgccagcag ccgcggtaat acgtaggggg caagcgttat 540

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ccggatttac tgggtgtaaa gggagcgtag acggcacggc aagccagatg tgaaagcccg 600

gggctcaacc ccgggactgc atttggaact gctgagctag agtgtcggag aggcaagtgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cttgctggac gatgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact gctaggtgtc gggtggcaaa gccattcggt 840

gccgcagcta acgcaataag cagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctgatcttga catcccgatg accgcttcgt aatggaagtt tttcttcgga 1020

acatcggtga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ctatcttcag tagccagcag gttaagctgg gcactctgga 1140

gagactgcca gggataacct ggaggaaggt ggggatgacg tcaaatcatc atgcccctta 1200

tgaccagggc tacacacgtg ctacaatggc gtaaacaaag agaagcgaac tcgcgagggt 1260

aagcaaatct caaaaataac gtctcagttc ggattgtagt ctgcaactcg actacatgaa 1320

gctggaatcg ctagtaatcg cagatcagaa tgctgcggtg aatacgttcc cgggtcttgt 1380

acacaccgcc cgtcacacca tgggagtcag taacgcccga agtcagtgac ccaaccgtaa 1440

ggagggagct gccgaaggtg ggaccgataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttt 1529

<210> SEQ ID NO 147
<211> LENGTH: 1528
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 147

aacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcttaaca catgcaagtc 60

gagcgaagca ctttggaaag attcttcgga tgatttcctt tgtgactgag cggcggacgg 120

gtgagtaacg cgtgggtaac ctgcctcata cagggggata acagttagaa atgactgcta 180

ataccgcata agaccacggt accgcatggt acagtggtaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaacggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccagac tcctacggga 360

ggcagcagtg gggaatattg cacaatggag gaaactctga tgcagcgacg ccgcgtgaag 420

gatgaagtat ttcggtatgt aaacttctat cagcagggaa gaaaatgacg gtacctgact 480

aagaagcccc ggctaactac gtgccagcag ccgcggtaat acgtaggggg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggcacggc aagccagatg tgaaagcccg 600

gggctcaacc ccggactgca tttggaactg ctgagctaga gtgtcggaga ggcaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ttgctggacg atgactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgactg ctaggtgtcg ggtggcaaag ccattcggtg 840

ccgcagctaa cgcaataagc agtccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc tgatcttgac atcccgatga ccgcttcgta atggaagctt ttcttcggaa 1020

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catcggtgac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaacccc tatcttcagt agccagcagg ttaagctggg cactctggag 1140

agactgccag ggataacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

gaccagggct acacacgtgc tacaatggcg taaacaaaga gaagcgaact cgcgagggta 1260

agcaaatctc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc agatcagaat gctgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gtcagtgacc caaccgtaag 1440

gagggagctg ccgaaggtgg gaccgataac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 148
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 148

aacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcttaaca catgcaagtc 60

gagcgaagca cttaagtttg attcttcgga tgaagacttt tgtgactgag cggcggacgg 120

gtgagtaacg cgtgggtaac ctgcctcata cagggggata acagttagaa atgactgcta 180

ataccgcata agaccacggt accgcatggt acagtggtaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaacggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccagac tcctacggga 360

ggcagcagtg gggaatattg cacaatggag gaaactctga tgcagcgacg ccgcgtgaag 420

gatgaagtat ttcggtatgt aaacttctat cagcagggaa gaaaatgacg gtacctgact 480

aagaagcccc ggctaactac gtgccagcag ccgcggtaat acgtaggggg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggcacggc aagccagatg tgaaagcccg 600

gggctcaacc ccgggactgc atttggaact gctgagctag agtgtcggag aggcaagtgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cttgctggac gatgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact gctaggtgtc gggtggcaaa gccattcggt 840

gccgcagcta acgcaataag cagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctgatcttga catcccgatg accgcttcgt aatggaagct tttcttcgga 1020

acatcggtga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ctatcttcag tagccagcag gttaagctgg gcactctgga 1140

gagactgcca gggataacct ggaggaaggt ggggatgacg tcaaatcatc atgcccctta 1200

tgaccagggc tacacacgtg ctacaatggc gtaaacaaag agaagcgaac tcgcgagggt 1260

aagcaaatct caaaaataac gtctcagttc ggattgtagt ctgcaactcg actacatgaa 1320

gctggaatcg ctagtaatcg cagatcagaa tgctgcggtg aatacgttcc cgggtcttgt 1380

acacaccgcc cgtcacacca tgggagtcag taacgcccga agtcagtgac ccaaccgtaa 1440

ggagggagct gccgaaggtg ggaccgataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttt 1529

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<210> SEQ ID NO 149
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 149

aacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcttaaca catgcaagtc 60

gagcgaagca ctttggaaag attcttcgga tgatttcctt tgtgactgag cggcggacgg 120

gtgagtaacg cgtgggtaac ctgcctcata cagggggata acagttagaa atgactgcta 180

ataccgcata agaccacggt accgcatggt acagtggtaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaacggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccagac tcctacggga 360

ggcagcagtg gggaatattg cacaatggag gaaactctga tgcagcgacg ccgcgtgaag 420

gatgaagtat ttcggtatgt aaacttctat cagcagggaa gaaaatgacg gtacctgact 480

aagaagcccc ggctaactac gtgccagcag ccgcggtaat acgtaggggg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggcacggc aagccagatg tgaaagcccg 600

gggctcaacc ccgggactgc atttggaact gctgagctag agtgtcggag aggcaagtgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

cttgctggac gatgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact gctaggtgtc gggtggcaaa gccattcggt 840

gccgcagcta acgcaataag cagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctgatcttga catcccgatg accgcttcgt aatggaagct tttcttcgga 1020

acatcggtga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ctatcttcag tagccagcag gttaagctgg gcactctgga 1140

gagactgcca gggataacct ggaggaaggt ggggatgacg tcaaatcatc atgcccctta 1200

tgaccagggc tacacacgtg ctacaatggc gtaaacaaag agaagcgaac tcgcgagggt 1260

aagcaaatct caaaaataac gtctcagttc ggattgtagt ctgcaactcg actacatgaa 1320

gctggaatcg ctagtaatcg cagatcagaa tgctgcggtg aatacgttcc cgggtcttgt 1380

acacaccgcc cgtcacacca tgggagtcag taacgcccga agtcagtgac ccaaccgtaa 1440

ggagggagct gccgaaggtg ggaccgataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttt 1529

<210> SEQ ID NO 150
<211> LENGTH: 1528
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 150

aacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcttaaca catgcaagtc 60

gagcgaagcg cttaagtttg attcttcgga tgaagacttt tgtgactgag cggcggacgg 120

gtgagtaacg cgtgggtaac ctgcctcata cagggggata acagttagaa atgactgcta 180

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ataccgcata agaccacggt accgcatggt acagtggtaa aaactccggt ggtatgagat 240

ggacccgcgt ctgattaggt agttggtggg gtaacggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccagac tcctacggga 360

ggcagcagtg gggaatattg cacaatggag gaaactctga tgcagcgacg ccgcgtgaag 420

gatgaagtat ttcggtatgt aaacttctat cagcagggaa gaaaatgacg gtacctgact 480

aagaagcccc ggctaactac gtgccagcag ccgcggtaat acgtaggggg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggcacggc aagccagatg tgaaagcccg 600

ggctcaaccc cgggactgca tttggaactg ctgagctaga gtgtcggaga ggcaagtgga 660

attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc 720

ttgctggacg atgactgacg ttgaggctcg aaagcgtggg gagcaaacag gattagatac 780

cctggtagtc cacgccgtaa acgatgactg ctaggtgtcg ggtggcaaag ccattcggtg 840

ccgcagctaa cgcaataagc agtccacctg gggagtacgt tcgcaagaat gaaactcaaa 900

ggaattgacg gggacccgca caagcggtgg agcatgtggt ttaattcgaa gcaacgcgaa 960

gaaccttacc tgatcttgac atcccgatga ccgcttcgta atggaagttt ttcttcggaa 1020

catcggtgac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt 1080

cccgcaacga gcgcaacccc tatcttcagt agccagcagg ttaagctggg cactctggag 1140

agactgccag ggataacctg gaggaaggtg gggatgacgt caaatcatca tgccccttat 1200

gaccagggct acacacgtgc tacaatggcg taaacaaaga gaggcaaact cgcgagggta 1260

agcaaatctc aaaaataacg tctcagttcg gattgtagtc tgcaactcga ctacatgaag 1320

ctggaatcgc tagtaatcgc agatcagaat gctgcggtga atacgttccc gggtcttgta 1380

cacaccgccc gtcacaccat gggagtcagt aacgcccgaa gtcagtgacc caaccgtaag 1440

gagggagctg ccgaaggtgg gaccgataac tggggtgaag tcgtaacaag gtagccgtat 1500

cggaaggtgc ggctggatca cctccttt 1528

<210> SEQ ID NO 151
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 151

aacgagagtt tgatcctggc tcaggatgaa cgctggcggc gtgcttaaca catgcaagtc 60

gagcgaagcg ctttgggaag attcttcgga tgatttcctt tgtgactgag cggcggacgg 120

gtgagtaacg cgtgggtaac ctgcctcata cagggggata acagttagaa atgactgcta 180

ataccgcata agaccacggt accgcatggt acagtggtaa aaactccggt ggtatgagat 240

ggacccgcgt ttgattaggt agttggtggg gtaacggcct accaagccga cgatcagtag 300

ccgacctgag agggtgaccg gccacattgg gactgagaca cggcccagac tcctacggga 360

ggcagcagtg gggaatattg cacaatggag gaaactctga tgcagcgacg ccgcgtgaag 420

gatgaagtat ttcggtatgt aaacttctat cagcagggaa gaaaatgacg gtacctgact 480

aagaagcccc ggctaactac gtgccagcag ccgcggtaat acgtaggggg caagcgttat 540

ccggatttac tgggtgtaaa gggagcgtag acggcacggc aagccagatg tgaaagcccg 600

gggctcaacc ccgggactgc atttggaact gctgagctag agtgtcggag aggcaagtgg 660

aattcctagt gtagcggtga aatgcgtaga tattaggagg aacaccagtg gcgaaggcgg 720

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cttgctggac gatgactgac gttgaggctc gaaagcgtgg ggagcaaaca ggattagata 780

ccctggtagt ccacgccgta aacgatgact gctaggtgtc gggtggcaaa gccattcggt 840

gccgcagcta acgcaataag cagtccacct ggggagtacg ttcgcaagaa tgaaactcaa 900

aggaattgac ggggacccgc acaagcggtg gagcatgtgg tttaattcga agcaacgcga 960

agaaccttac ctgatcttga catcccgatg actgcttcgt aatggaagtt tttcttcgga 1020

acatcggtga caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg ttgggttaag 1080

tcccgcaacg agcgcaaccc ctatcttcag tagccagcag gttaagctgg gcactctgga 1140

gagactgcca gggataacct ggaggaaggt ggggatgacg tcaaatcatc atgcccctta 1200

tgaccagggc tacacacgtg ctacaatggc gtaaacaaag agaagcgaac tcgcgagggt 1260

aagcaaatct caaaaataac gtctcagttc ggattgtagt ctgcaactcg actacatgaa 1320

gctggaatcg ctagtaatcg cagatcagaa tgctgcggtg aatacgttcc cgggtcttgt 1380

acacaccgcc cgtcacacca tgggagtcag taacgcccga agtcagtgac ccaaccgtaa 1440

ggagggagct gccgaaggtg ggaccgataa ctggggtgaa gtcgtaacaa ggtagccgta 1500

tcggaaggtg cggctggatc acctccttt 1529

<210> SEQ ID NO 152
<211> LENGTH: 1537
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 152

atggagagtt tgatcctggc tcaggatgaa cgctggcggc atgcctaata catgcaagtc 60

gaacgaagtt tcgaggaagc ttgcttccaa agagacttag tggcgaacgg gtgagtaaca 120

cgtaggtaac ctgcccatgt gtccgggata actgctggaa acggtagcta aaaccggata 180

ggtatacaga gcgcatgctc agtatattaa agcgcccatc aaggcgtgaa catggatgga 240

cctgcggcgc attagctagt tggtgaggta acggctcacc aaggcgatga tgcgtagccg 300

gcctgagagg gtaaacggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

agcagtaggg aattttcgtc aatgggggaa accctgaacg agcaatgccg cgtgagtgaa 420

gaaggtcttc ggatcgtaaa gctctgttgt aagtgaagaa cggctcatag aggaaatgct 480

atgggagtga cggtagctta ccagaaagcc acggctaact acgtgccagc agccgcggta 540

atacgtaggt ggcaagcgtt atccggaatc attgggcgta aagggtgcgt aggtggcgta 600

ctaagtctgt agtaaaaggc aatggctcaa ccattgtaag ctatggaaac tggtatgctg 660

gagtgcagaa gagggcgatg gaattccatg tgtagcggta aaatgcgtag atatatggag 720

gaacaccagt ggcgaaggcg gtcgcctggt ctgtaactga cactgaggca cgaaagcgtg 780

gggagcaaat aggattagat accctagtag tccacgccgt aaacgatgag aactaagtgt 840

tggaggaatt cagtgctgca gttaacgcaa taagttctcc gcctggggag tatgcacgca 900

agtgtgaaac tcaaaggaat tgacgggggc ccgcacaagc ggtggagtat gtggtttaat 960

tcgaagcaac gcgaagaacc ttaccaggcc ttgacatgga aacaaatacc ctagagatag 1020

ggggataatt atggatcaca caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg 1080

ttgggttaag tcccgcaacg agcgcaaccc ttgtcgcatg ttaccagcat caagttgggg 1140

actcatgcga gactgccggt gacaaaccgg aggaaggtgg ggatgacgtc aaatcatcat 1200

-continued

gcccttatg gcctgggcta cacacgtact acaatggcgg ccacaaagag cagcgacaca 1260

gtgatgtgaa gcgaatctca taaaggtcgt ctcagttcgg attgaagtct gcaactcgac 1320

ttcatgaagt cggaatcgct agtaatcgca gatcagcatg ctgcggtgaa tacgttctcg 1380

ggccttgtac acaccgcccg tcaaaccatg ggagtcagta atacccgaag ccggtggcat 1440

aaccgtaagg agtgagccgt cgaaggtagg accgatgact ggggttaagt cgtaacaagg 1500

tatccctacg ggaacgtggg gatggatcac ctccttt 1537

<210> SEQ ID NO 153
<211> LENGTH: 1537
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 153

atggagagtt tgatcctggc tcaggatgaa cgctggcggc atgcctaata catgcaagtc 60

gaacgaagtt tcgaggaagc ttgcttccaa agagacttag tggcgaacgg gtgagtaaca 120

cgtaggtaac ctgcccatgt gtccgggata actgctggaa acggtagcta aaaccggata 180

ggtatacaga gcgcatgctc agtatattaa agcgcccatc aaggcgtgaa catggatgga 240

cctgcggcgc attagctagt tggtgaggta acggcccacc aaggcgatga tgcgtagccg 300

gcctgagagg gtaaacggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

agcagtaggg aattttcgtc aatgggggaa accctgaacg agcaatgccg cgtgagtgaa 420

gaaggtcttc ggatcgtaaa gctctgttgt aagtgaagaa cggctcatag aggaaatgct 480

atgggagtga cggtagctta ccagaaagcc acggctaact acgtgccagc agccgcggta 540

atacgtaggt ggcaagcgtt atccggaatc attgggcgta aagggtgcgt aggtggcgta 600

ctaagtctgt agtaaaaggc aatggctcaa ccattgtaag ctatggaaac tggtatgctg 660

gagtgcagaa gagggcgatg gaattccatg tgtagcggta aaatgcgtag atatatggag 720

gaacaccagt ggcgaaggcg gtcgcctggt ctgtaactga cactgaggca cgaaagcgtg 780

gggagcaaat aggattagat accctagtag tccacgccgt aaacgatgag aactaagtgt 840

tggaggaatt cagtgctgca gttaacgcaa taagttctcc gcctggggag tatgcacgca 900

agtgtgaaac tcaaaggaat tgacgggggc ccgcacaagc ggtggagtat gtggtttaat 960

tcgaagcaac gcgaagaacc ttaccaggcc ttgacatgga aacaaatacc ctagagatag 1020

ggggataatt atggatcaca caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg 1080

ttgggttaag tcccgcaacg agcgcaaccc ttgtcgcatg ttaccagcat caagttgggg 1140

actcatgcga gactgccggt gacaaaccgg aggaaggtgg ggatgacgtc aaatcatcat 1200

gcccttatg gcctgggcta cacacgtact acaatggcgg ccacaaagag cagcgacaca 1260

gtgatgtgaa gcgaatctca taaaggtcgt ctcagttcgg attgaagtct gcaactcgac 1320

ttcatgaagt cggaatcgct agtaatcgca gatcagcatg ctgcggtgaa tacgttctcg 1380

ggccttgtac acaccgcccg tcaaaccatg ggagtcagta atacccgaag ccggtggcat 1440

aaccgtaagg agtgagccgt cgaaggtagg accgatgact ggggttaagt cgtaacaagg 1500

tatccctacg ggaacgtggg gatggatcac ctccttt 1537

<210> SEQ ID NO 154
<211> LENGTH: 1537
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 154

atggagagtt tgatcctggc tcaggatgaa cgctggcggc atgcctaata catgcaagtc 60

gaacgaagtt tcgaggaagc ttgcttccaa agagacttag tggcgaacgg gtgagtaaca 120

cgtaggtaac ctgcccatgt gtccgggata actgctggaa acggtagcta aaaccggata 180

ggtatacaga gcgcatgctc agtatattaa agcgcccatc aaggcgtgaa catggatgga 240

cctgcggcgc attagctagt tggtgaggta acggctcacc aaggcgatga tgcgtagccg 300

gcctgagagg gtaaacggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

agcagtaggg aattttcgtc aatgggggaa accctgaacg agcaatgccg cgtgagtgaa 420

gaaggtcttc ggatcgtaaa gctctgttgt aagtgaagaa cggctcatag aggaaatgct 480

atgggagtga cggtagctta ccagaaagcc acggctaact acgtgccagc agccgcggta 540

atacgtaggt ggcaagcgtt atccggaatc attgggcgta aagggtgcgt aggtggcgta 600

ctaagtctgt agtaaaaggc aatggctcaa ccattgtaag ctatggaaac tggtatgctg 660

gagtgcagaa gagggcgatg gaattccatg tgtagcggta aaatgcgtag atatatggag 720

gaacaccagt ggcgaaggcg gtcgcctggt ctgtaactga cactgaggca cgaaagcgtg 780

gggagcaaat aggattagat accctagtag tccacgccgt aaacgatgag aactaagtgt 840

tggaggaatt cagtgctgca gttaacgcaa taagttctcc gcctggggag tatgcacgca 900

agtgtgaaac tcaaaggaat tgacgggggc ccgcacaagc ggtggagtat gtggtttaat 960

tcgaagcaac gcgaagaacc ttaccaggcc ttgacatgga aacaaatacc ctagagatag 1020

ggggataatt atggatcaca caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg 1080

ttgggttaag tcccgcaacg agcgcaaccc ttgtcgcatg ttaccagcat caagttgggg 1140

actcatgcga gactgccggt gacaaaccgg aggaaggtgg ggatgacgtc aaatcatcat 1200

gccccttatg gcctgggcta cacacgtact acaatggcgg ccacaaagag cagcgacaca 1260

gtgatgtgaa gcgaatctca taaaggtcgt ctcagttcgg attgaagtct gcaactcgac 1320

ttcatgaagt cggaatcgct agtaatcgca gatcagcatg ctgcggtgaa tacgttctcg 1380

ggccttgtac acaccgcccg tcaaaccatg ggagtcagta atacccgaag ccggtggcat 1440

aaccgtaagg agtgagccgt cgaaggtagg accgatgact ggggttaagt cgtaacaagg 1500

tatccctacg ggaacgtggg gatggatcac ctccttt 1537

<210> SEQ ID NO 155
<211> LENGTH: 1537
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 155

atggagagtt tgatcctggc tcaggatgaa cgctggcggc atgcctaata catgcaagtc 60

gaacgaagtt tcgaggaagc ttgcttccaa agagacttag tggcgaacgg gtgagtaaca 120

cgtaggtaac ctgcccatgt gtccgggata actgctggaa acggtagcta aaaccggata 180

ggtatacaga gcgcatgctc agtatattaa agcgcccatc aaggcgtgaa catggatgga 240

cctgcggcgc attagctagt tggtgaggta acggcccacc aaggcgatga tgcgtagccg 300

gcctgagagg gtaaacggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

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agcagtaggg aattttcgtc aatgggggaa accctgaacg agcaatgccg cgtgagtgaa 420

gaaggtcttc ggatcgtaaa gctctgttgt aagtgaagaa cggctcatag aggaaatgct 480

atgggagtga cggtagctta ccagaaagcc acggctaact acgtgccagc agccgcggta 540

atacgtaggt ggcaagcgtt atccggaatc attgggcgta aagggtgcgt aggtggcgta 600

ctaagtctgt agtaaaaggc aatggctcaa ccattgtaag ctatggaaac tggtatgctg 660

gagtgcagaa gagggcgatg gaattccatg tgtagcggta aaatgcgtag atatatggag 720

gaacaccagt ggcgaaggcg gtcgcctggt ctgtaactga cactgaggca cgaaagcgtg 780

gggagcaaat aggattagat accctagtag tccacgccgt aaacgatgag aactaagtgt 840

tggaggaatt cagtgctgca gttaacgcaa taagttctcc gcctggggag tatgcacgca 900

agtgtgaaac tcaaaggaat tgacgggggc ccgcacaagc ggtggagtat gtggtttaat 960

tcgaagcaac gcgaagaacc ttaccaggcc ttgacatgga aacaaatacc ctagagatag 1020

ggggataatt atggatcaca caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg 1080

ttgggttaag tcccgcaacg agcgcaaccc ttgtcgcatg ttaccagcat caagttgggg 1140

actcatgcga gactgccggt gacaaaccgg aggaaggtgg ggatgacgtc aaatcatcat 1200

gccccttatg gcctgggcta cacacgtact acaatggcga ccacaaagag cagcgacaca 1260

gtgatgtgaa gcgaatctca taaaggtcgt ctcagttcgg attgaagtct gcaactcgac 1320

ttcatgaagt cggaatcgct agtaatcgca gatcagcatg ctgcggtgaa tacgttctcg 1380

ggccttgtac acaccgcccg tcaaaccatg ggagtcagta atacccgaag ccggtggcat 1440

aaccgcaagg agtgagccgt cgaaggtagg accgatgact ggggttaagt cgtaacaagg 1500

tatccctacg ggaacgtggg gatggatcac ctccttt 1537

<210> SEQ ID NO 156
<211> LENGTH: 1537
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 156

atggagagtt tgatcctggc tcaggatgaa cgctggcggc atgcctaata catgcaagtc 60

gaacgaagtt tcgaggaagc ttgcttccaa agagacttag tggcgaacgg gtgagtaaca 120

cgtaggtaac ctgcccatgt gtccgggata actgctggaa acggtagcta aaaccggata 180

ggtatacaga gcgcatgctc agtatattaa agcgcccatc aaggcgtgaa catggatgga 240

cctgcggcgc attagctagt tggtgaggta acggcccacc aaggcgatga tgcgtagccg 300

gcctgagagg gtaaacggcc acattgggac tgagacacgg cccaaactcc tacgggaggc 360

agcagtaggg aattttcgtc aatgggggaa accctgaacg agcaatgccg cgtgagtgaa 420

gaaggtcttc ggatcgtaaa gctctgttgt aagtgaagaa cggctcatag aggaaatgct 480

atgggagtga cggtagctta ccagaaagcc acggctaact acgtgccagc agccgcggta 540

atacgtaggt ggcaagcgtt atccggaatc attgggcgta aagggtgcgt aggtggcgta 600

ctaagtctgt agtaaaaggc aatggctcaa ccattgtaag ctatggaaac tggtatgctg 660

gagtgcagaa gagggcgatg gaattccatg tgtagcggta aaatgcgtag atatatggag 720

gaacaccagt ggcgaaggcg gtcgcctggt ctgtaactga cactgaggca cgaaagcgtg 780

gggagcaaat aggattagat accctagtag tccacgccgt aaacgatgag aactaagtgt 840

tggaggaatt cagtgctgca gttaacgcaa taagttctcc gcctggggag tatgcacgca 900

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agtgtgaaac tcaaaggaat tgacgggggc ccgcacaagc ggtggagtat gtggtttaat 960

tcgaagcaac gcgaagaacc ttaccaggcc ttgacatgga aacaaatacc ctagagatag 1020

ggggataatt atggatcaca caggtggtgc atggttgtcg tcagctcgtg tcgtgagatg 1080

ttgggttaag tcccgcaacg agcgcaaccc ttgtcgcatg ttaccagcat caagttgggg 1140

actcatgcga gactgccggt gacaaaccgg aggaaggtgg ggatgacgtc aaatcatcat 1200

gccccttatg gcctgggcta cacacgtact acaatggcgg ccacaaagag cagcgacaca 1260

gtgatgtgaa gcgaatctca taaaggtcgt ctcagttcgg attgaagtct gcaactcgac 1320

ttcatgaagt cggaatcgct agtaatcgca gatcagcatg ctgcggtgaa tacgttctcg 1380

ggccttgtac acaccgcccg tcaaaccatg ggagtcagta atacccgaag ccggtggcat 1440

aaccgtaagg agtgagccgt cgaaggtagg accgatgact ggggttaagt cgtaacaagg 1500

tatccctacg ggaacgtggg gatggatcac ctccttt 1537

<210> SEQ ID NO 157
<211> LENGTH: 1529
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Polynucleotide

<400> SEQUENCE: 157

tattgagagt ttgatcctgg ctcaggatga acgctggcgg cgtgcttaac acatgcaagt 60

cgaacggggt gctcatgacg gaggattcgt ccaacggatt gagttaccta gtggcggacg 120

ggtgagtaac gcgtgaggaa cctgccttgg agaggggaat aacactccga aaggagtgct 180

aataccgcat gatgcagttg ggtcgcatgg ctctgactgc caaagattta tcgctctgag 240

atggcctcgc gtctgattag ctagtaggcg gggtaacggc ccacctaggc gacgatcagt 300

agccggactg agaggttgac cggccacatt gggactgaga cacggcccag actcctacgg 360

gaggcagcag tggggaatat tgggcaatgg gcgcaagcct gacccagcaa cgccgcgtga 420

aggaagaagg ctttcgggtt gtaaacttct tttgtcgggg acgaaacaaa tgacggtacc 480

cgacgaataa gccacggcta actacgtgcc agcagccgcg gtaatacgta ggtggcaagc 540

gttatccgga tttactgggt gtaaagggcg tgtaggcggg attgcaagtc agatgtgaaa 600

actgggggct caacctccag cctgcatttg aaactgtagt tcttgagtgc tggagaggca 660

atcggaattc cgtgtgtagc ggtgaaatgc gtagatatac ggaggaacac cagtggcgaa 720

ggcggattgc tggacagtaa ctgacgctga ggcgcgaaag cgtggggagc aaacaggatt 780

agataccctg gtagtccacg ccgtaaacga tggatactag gtgtgggggt ctgacccccct 840

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tcggaaggtg cggctggatc acctccttt                                     1529
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What is claimed is:

1. A pharmaceutical composition comprising a purified bacterial mixture consisting of bacterial strains comprising 16S rDNA sequences of at least 97% sequence identity to SEQ ID NO:10, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:20, and SEQ ID NO:21; wherein the bacterial strains are lyophilized.

2. The pharmaceutical composition of claim **1**, wherein one or more of the bacterial strains are spore-formers.

3. The pharmaceutical composition of claim **1**, wherein the bacterial strains originate from more than one human donor.

4. The pharmaceutical composition of claim **1**, further comprising a pharmaceutically acceptable excipient.

5. The pharmaceutical composition of claim **1**, wherein the pharmaceutical composition is formulated for oral administration.

6. The pharmaceutical composition of claim **1**, wherein the pharmaceutical composition is in the form of a capsule.

7. The pharmaceutical composition of claim **1**, wherein the pharmaceutical composition is formulated for delivery to the colon.

8. The pharmaceutical composition of claim **1**, wherein the pharmaceutical composition further comprises one or more enteric polymers.

* * * * *