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

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(58) **Field of Classification Search**

CPC A23L 5/00; A23L 33/135

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.

20 Claims, 41 Drawing Sheets

Specification includes a Sequence Listing.

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Figure 1

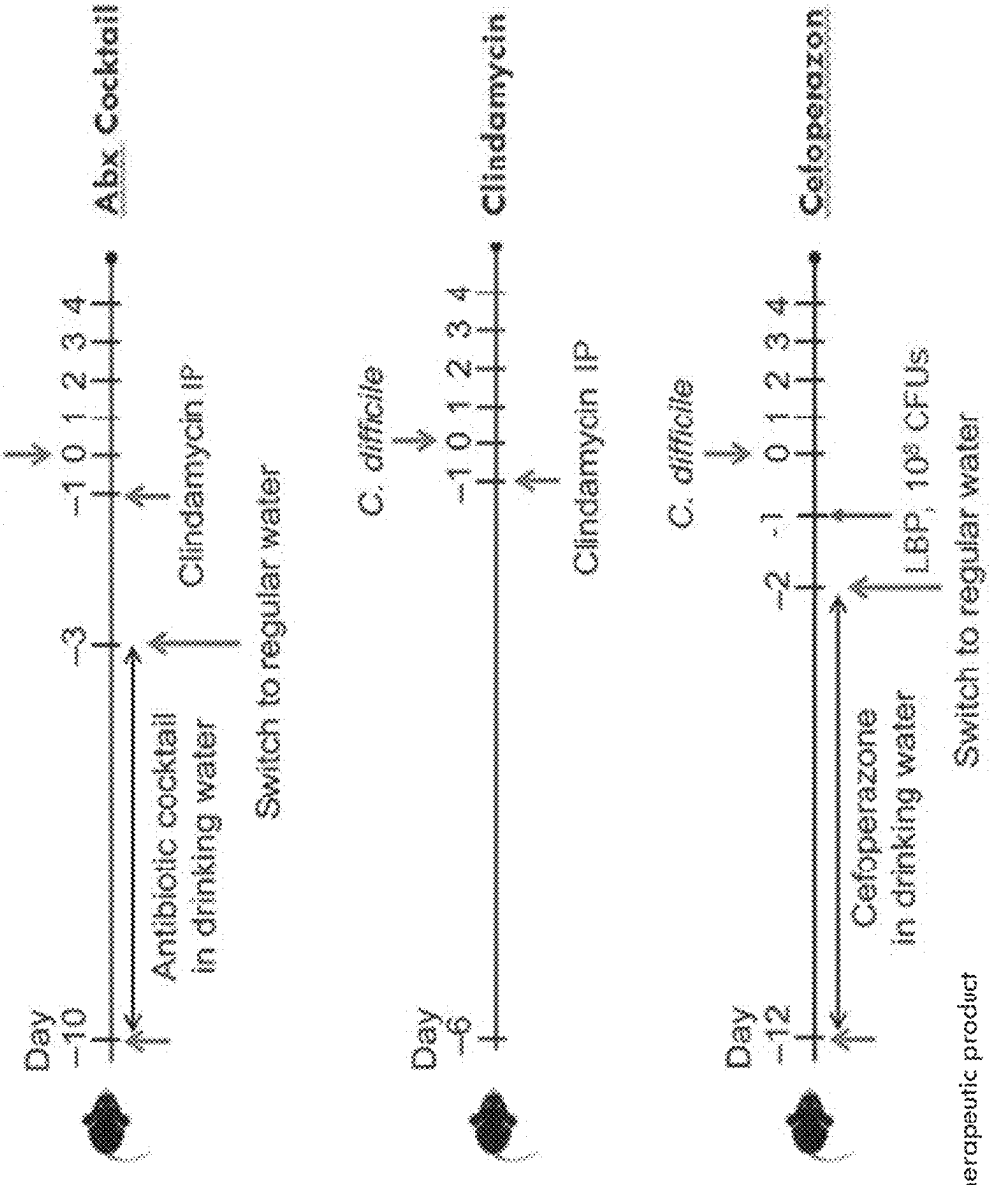
Composition A	Composition B	Composition C	Composition D
SEQ_03 - 5 - Clostridium_hathewayi (XIVa)*	**SEQ_10 - 211 - Flavonifractor_plautii (IV)**	SEQ_12 - VE202-26 - Clostridium_scindens (XIVa)*	SEQ_12 - VE202-26 - Clostridium_scindens (XIVa)*
SEQ_04 - 7 - Blautia_hansenii (XIVa)*	**SEQ_14 - VE202-13 - 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_boteae (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

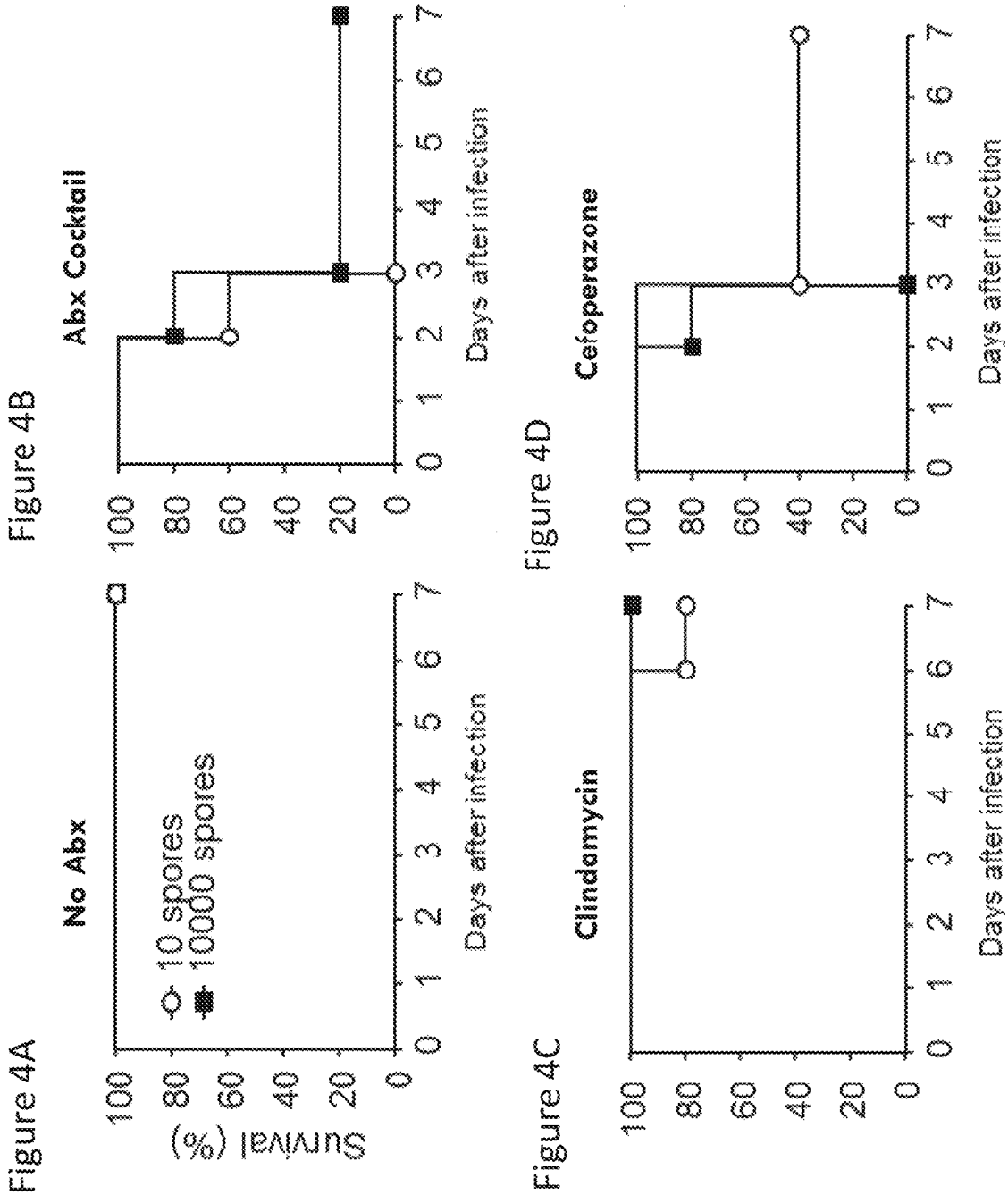


Figure 4A
No Abx
10 spores
10000 spores
Survival (%)
100
80
60
40
20
0
0 1 2 3 4 5 6 7
Days after infection
Figure 4B
Abx Cocktail
100
80
60
40
20
0
0 1 2 3 4 5 6 7
Days after infection
Figure 4C
Clindamycin
100
80
60
40
20
0
0 1 2 3 4 5 6 7
Days after infection
Figure 4D
Cefoperazone
100
80
60
40
20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

Figure 4E

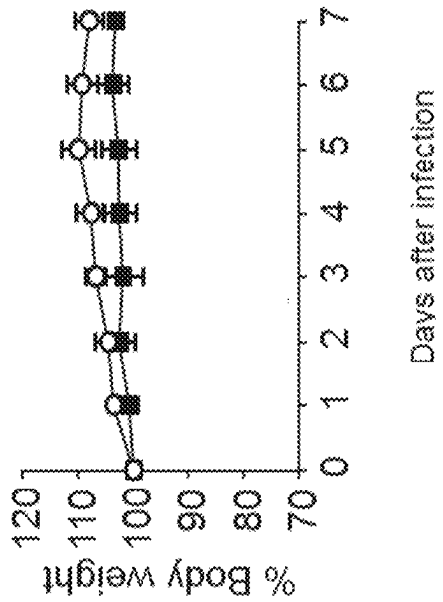


Figure 4F

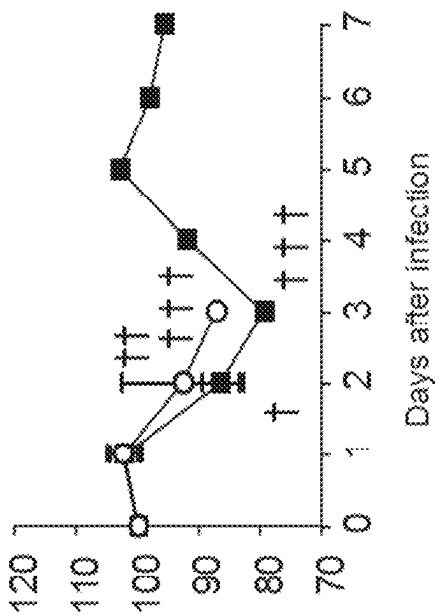


Figure 4G

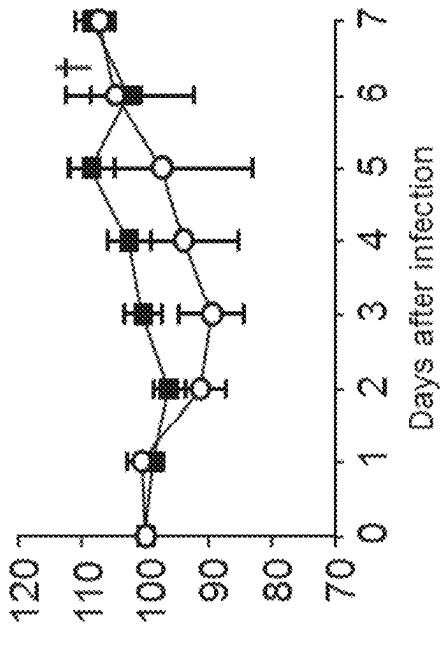


Figure 4H

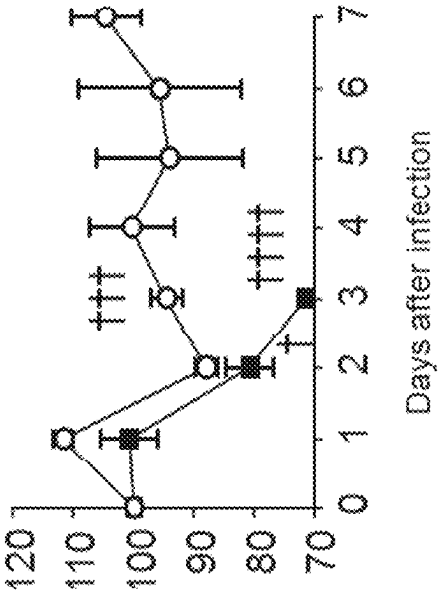


Figure 4I

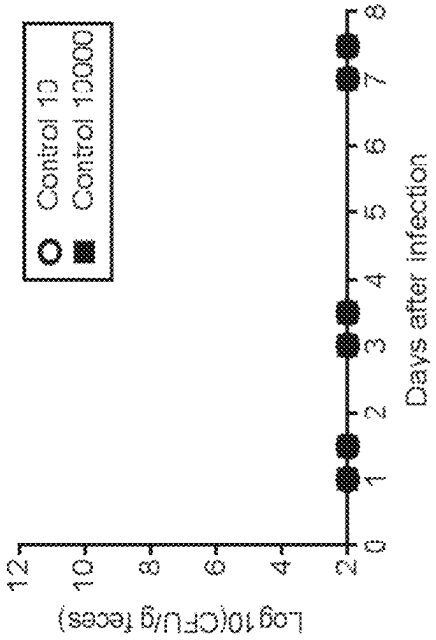


Figure 4J

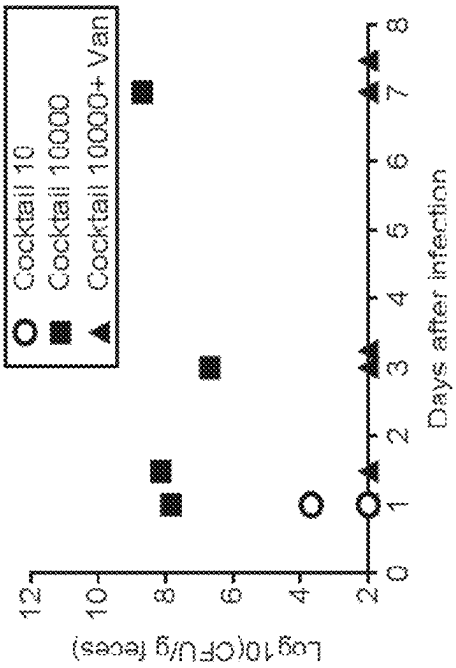


Figure 4K

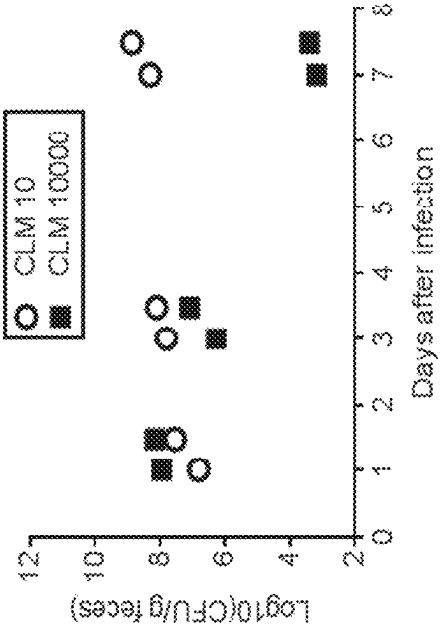


Figure 4L

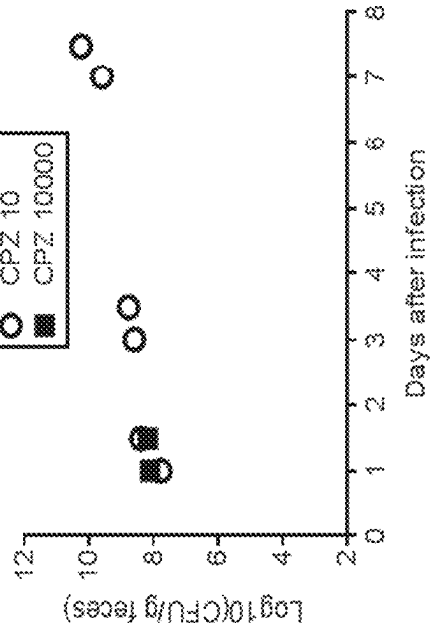


Figure 5

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

Figure 6

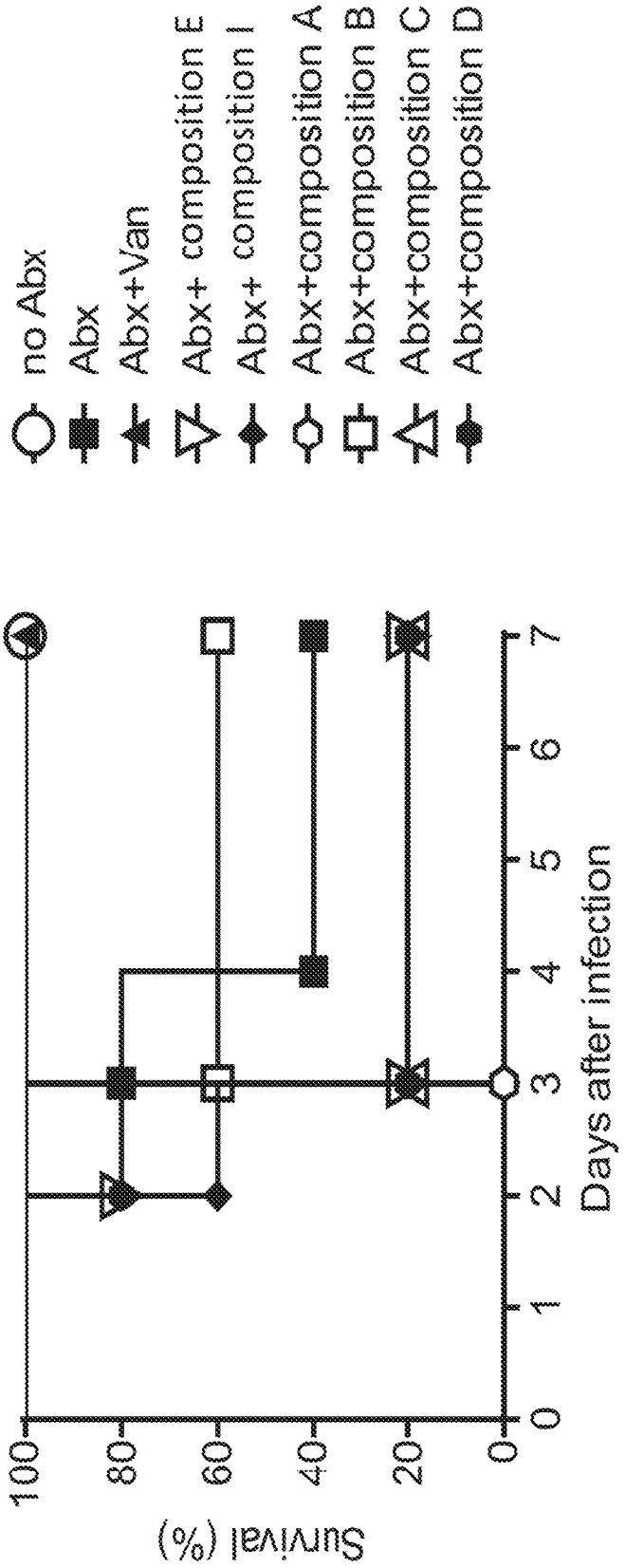

Survival (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
7
Days after infection
no Abx
Abx
Abx+Van
Abx+ composition E
Abx+ composition I
Abx+composition A
Abx+composition B
Abx+composition C
Abx+composition D

Figure 7A

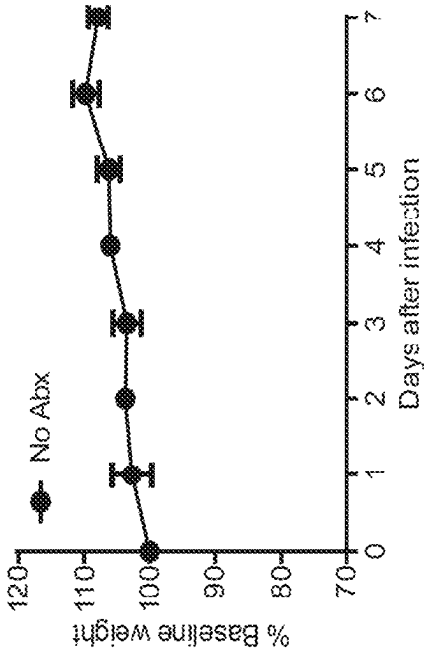


Figure 7B

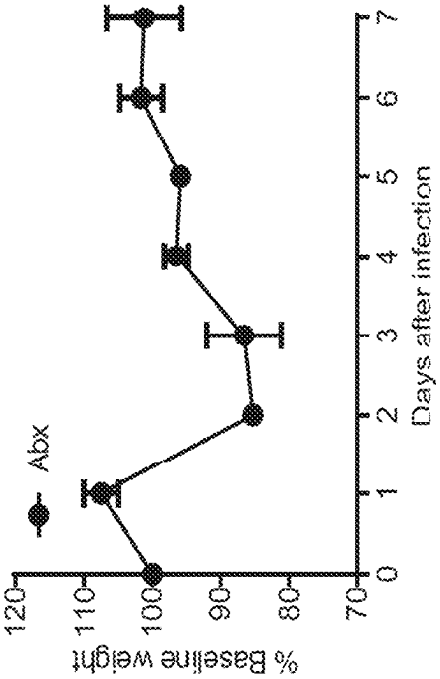


Figure 7C

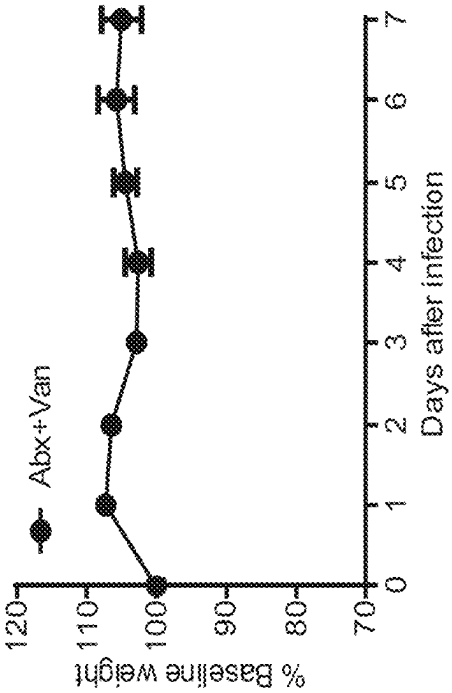


Figure 7D

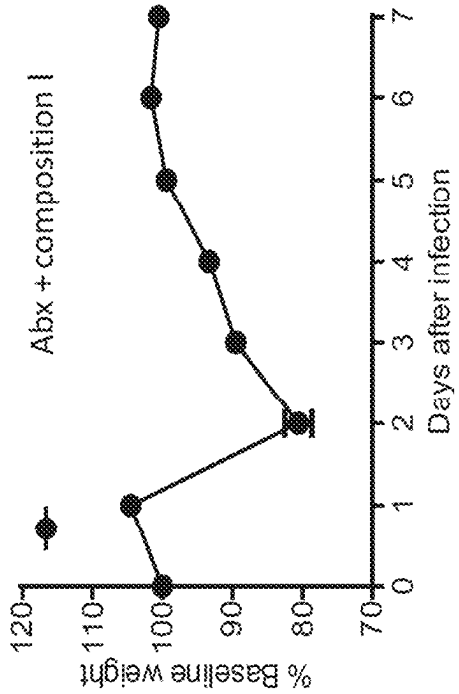


Figure 7E

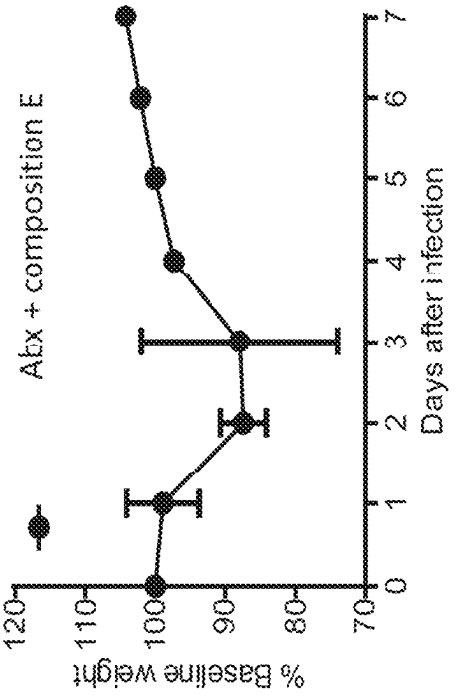


Figure 7F

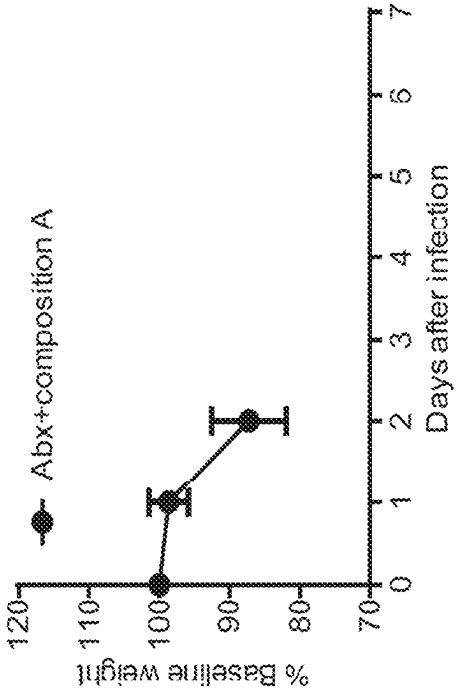


Figure 7G

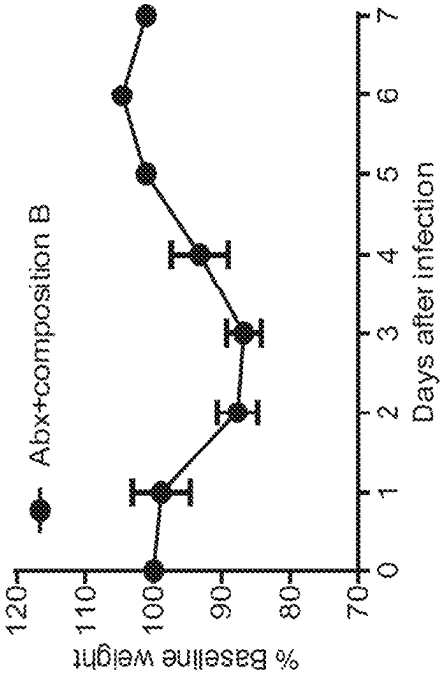


Figure 7H

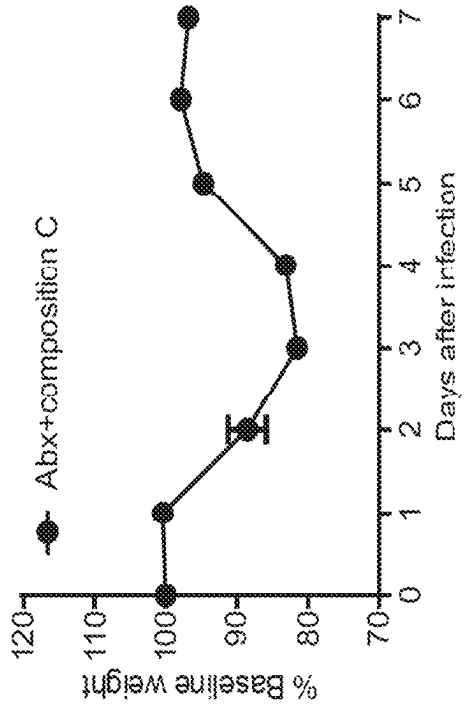
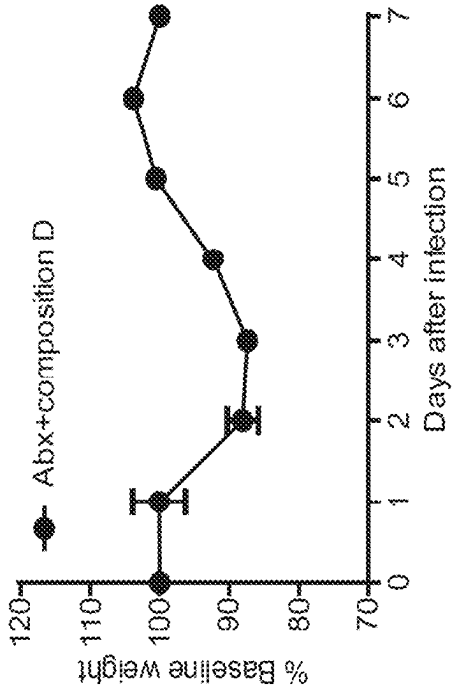


Figure 7I



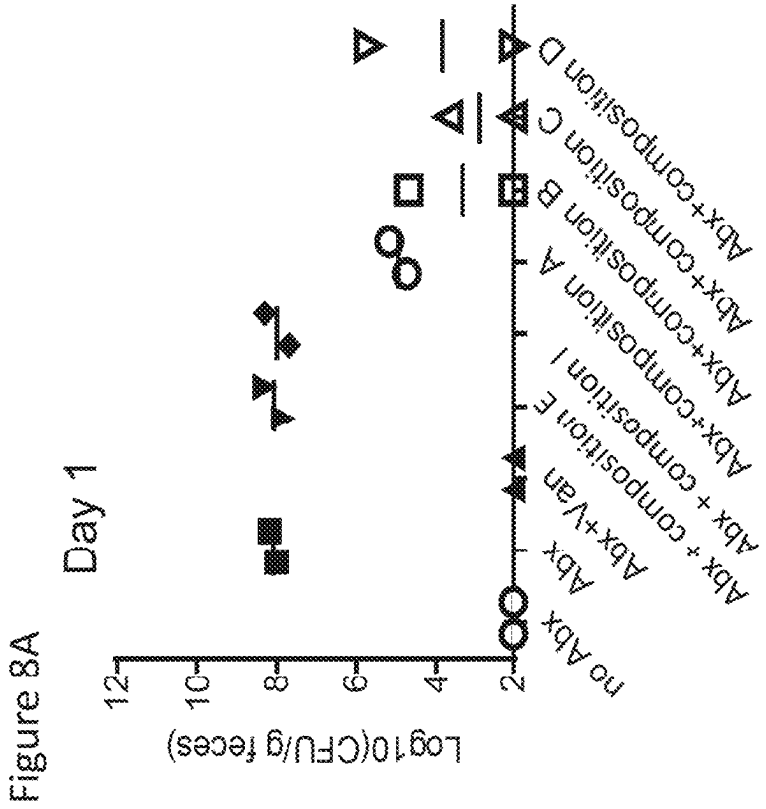


Figure 8A
Day 1
Log10(CFU/g feces)
12
10
8
6
4
2
no Abx
Abx
Abx+Van
Abx + composition E
Abx + composition I
Abx+composition A
Abx+composition B
Abx+composition C
Abx+composition D

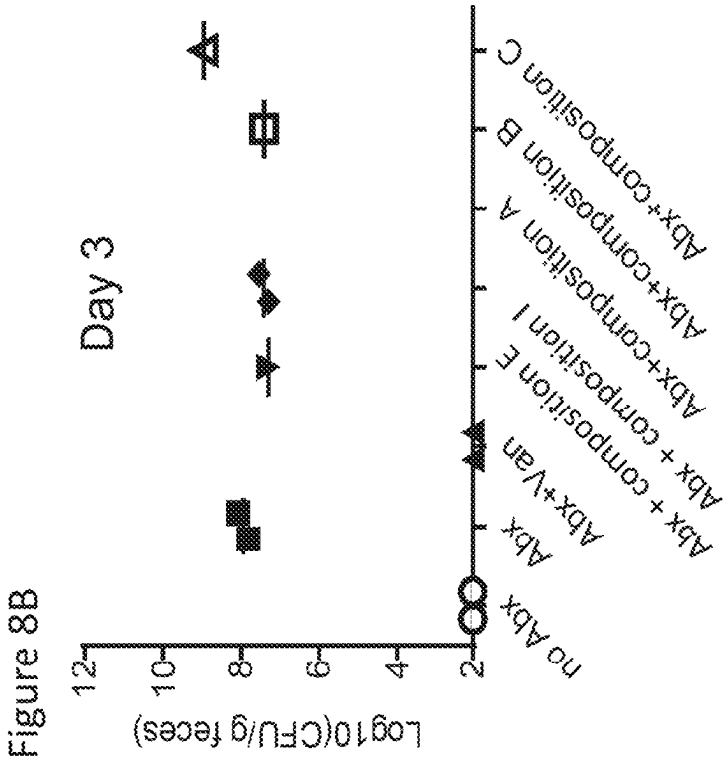


Figure 8B
Day 3
Log10(CFU/g feces)
12
10
8
6
4
2
no Abx
Abx
Abx+Van
Abx + composition E
Abx + composition I
Abx+composition A
Abx+composition B
Abx+composition C

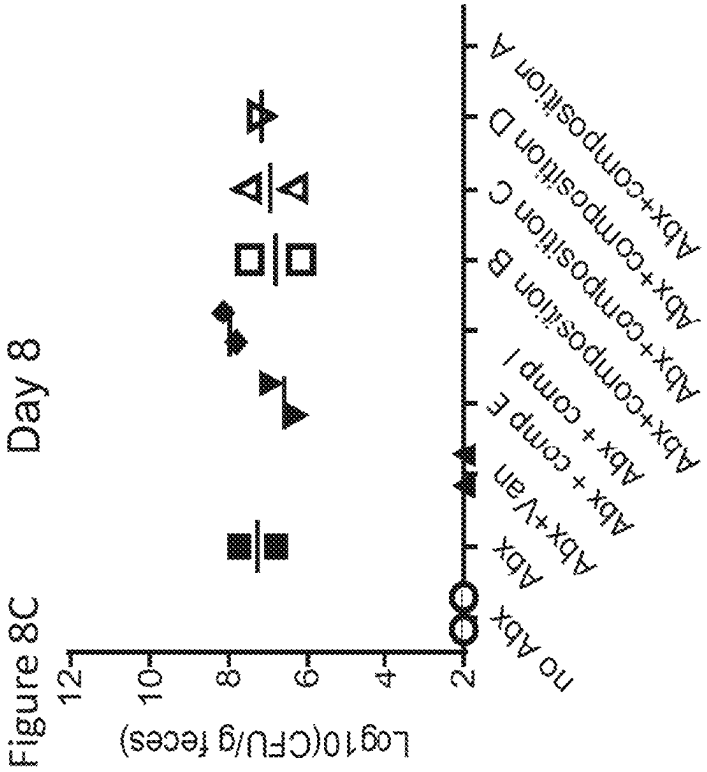
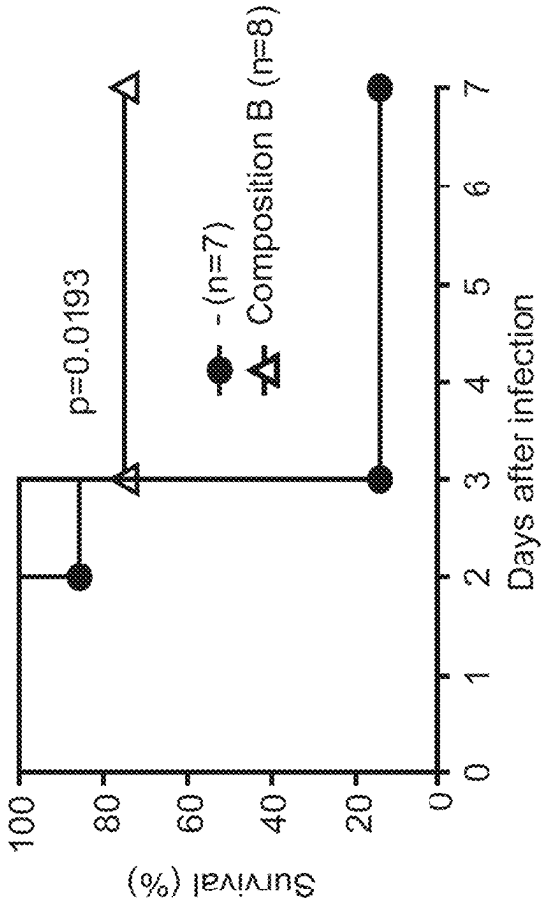


Figure 8C
Day 8
Log10(CFU/g feces)
12
10
8
6
4
2
no Abx
Abx
Abx+Van
Abx + comp E
Abx + comp I
Abx+composition B
Abx+composition C
Abx+composition D
Abx+composition A

Figure 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

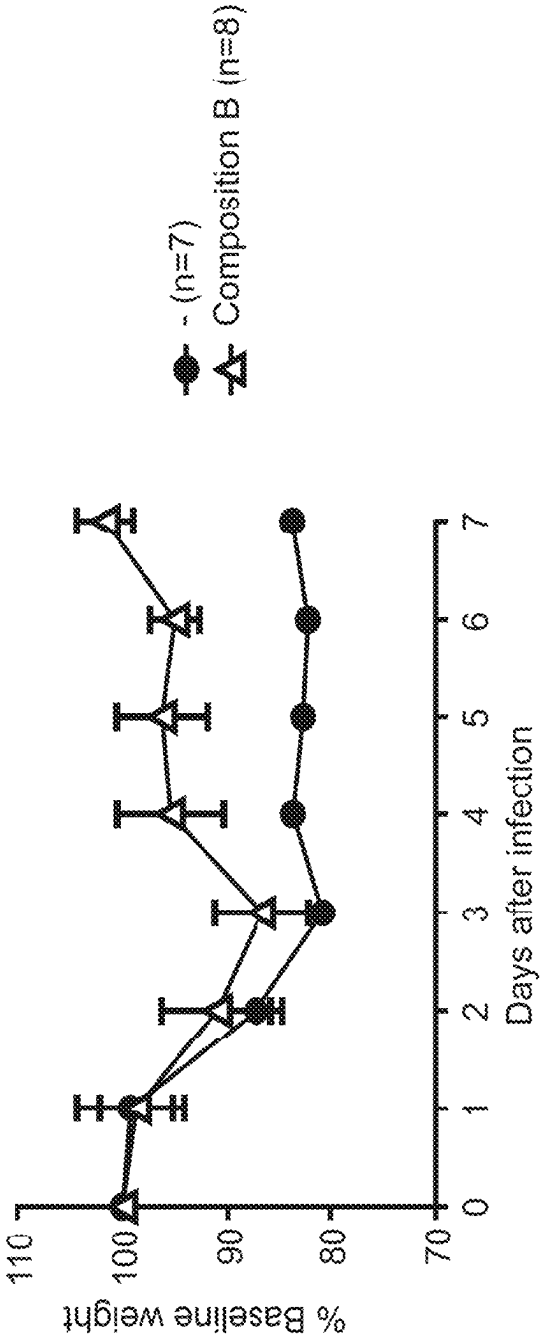

- (n=7)
Composition B (n=8)
% Baseline weight
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

Figure 12

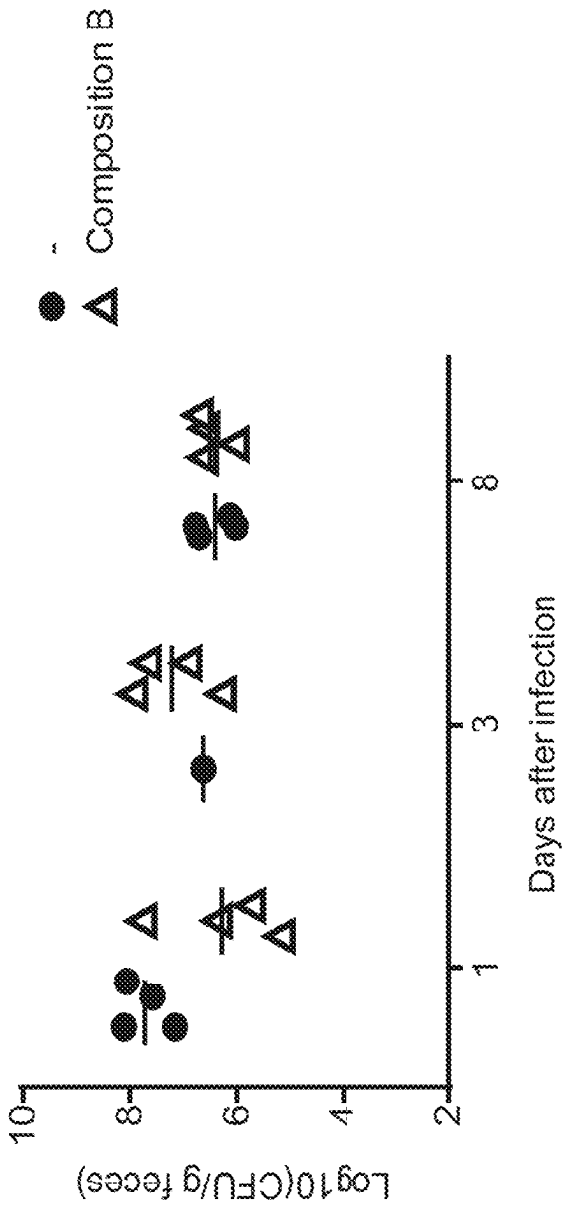

-
Composition B
10
8
6
4
2
Log10(CFU/g feces)
1
3
8
Days after infection

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

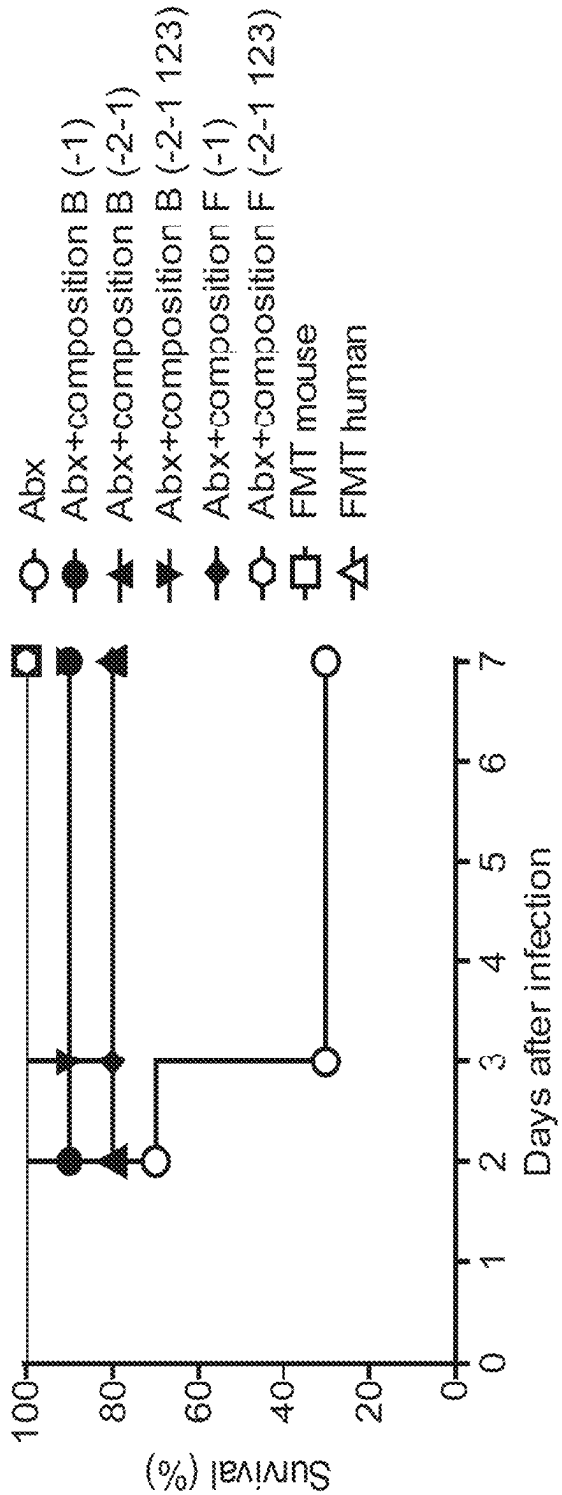
Cluster	Composition F	SCFAs
XIVa	*Eubacterium rectale* 12	A, B, L
	Ruminococcus faecis 8	A, L
	Ruminococcus obeum 2	A, L
	Blautia faecis 1	A, L
	Blautia hansenii 2	A, L
	Blautia luti 2	A, L
	Anaerostipes hadrus 7	B
	Roseburia faecis 5	A, B
	Fusicatenibacter saccharivorans 3	A, L
	Dorea formicigenerans 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

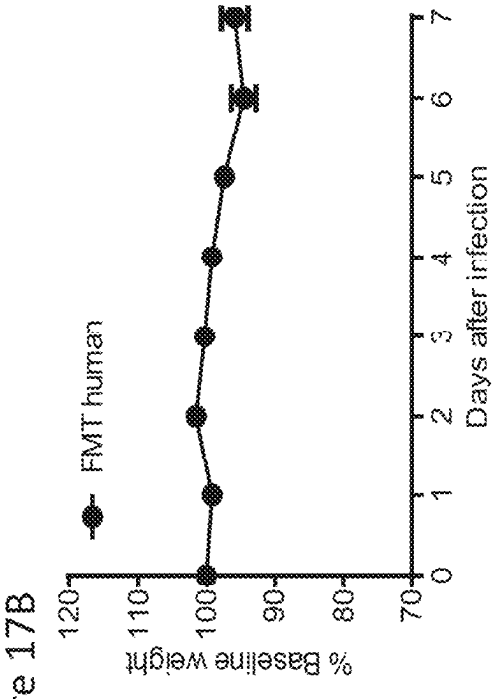


Figure 17B
FMT human
% Baseline weight
120
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

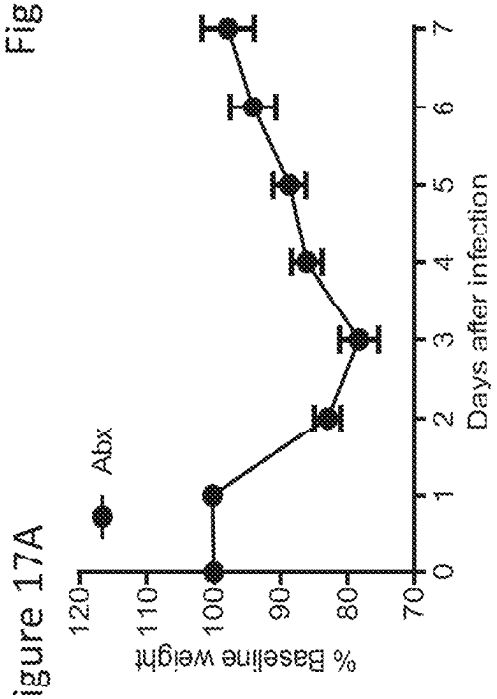


Figure 17A
Abx
% Baseline weight
120
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

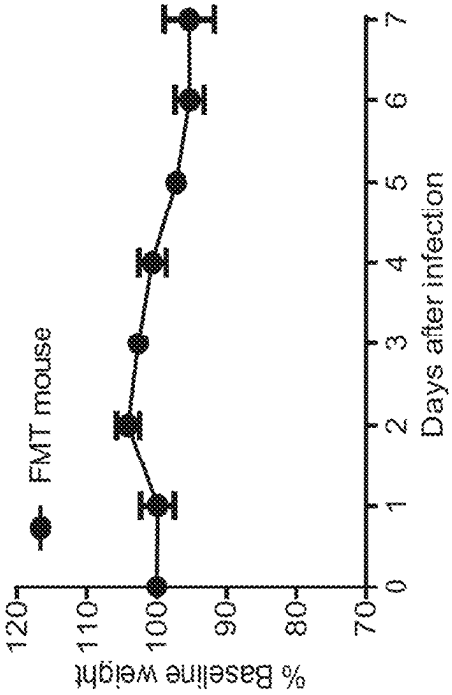


Figure 17C
FMT mouse
% Baseline weight
120
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

Figure 17D

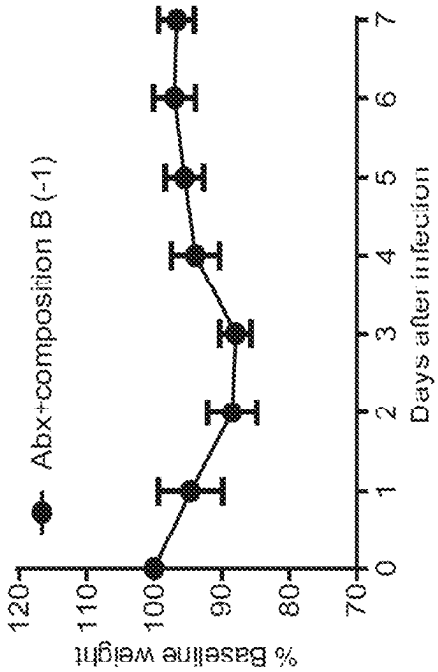


Figure 17E

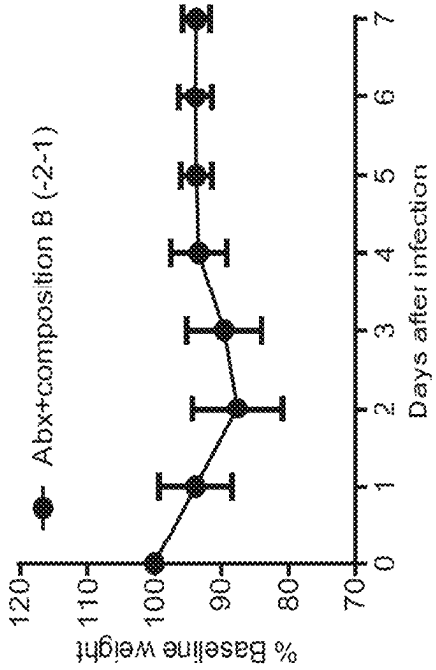


Figure 17F

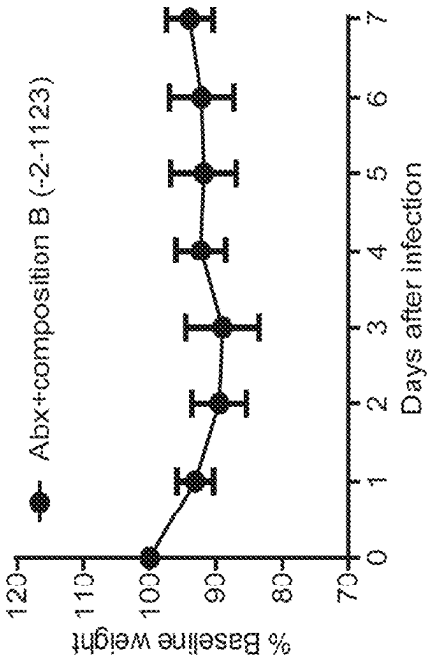


Figure 17G

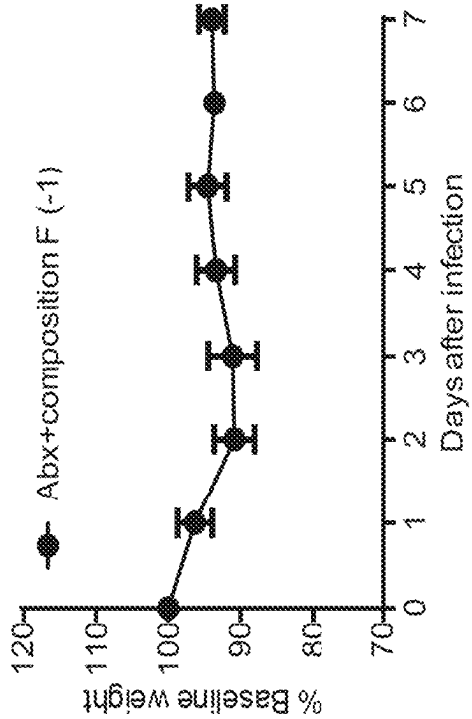
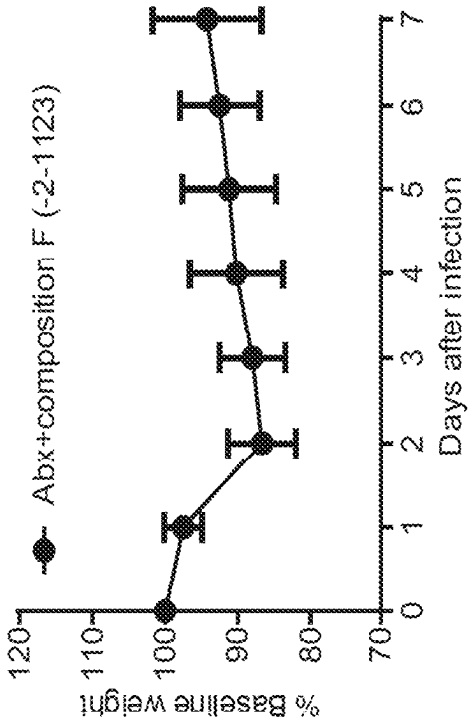


Figure 17H



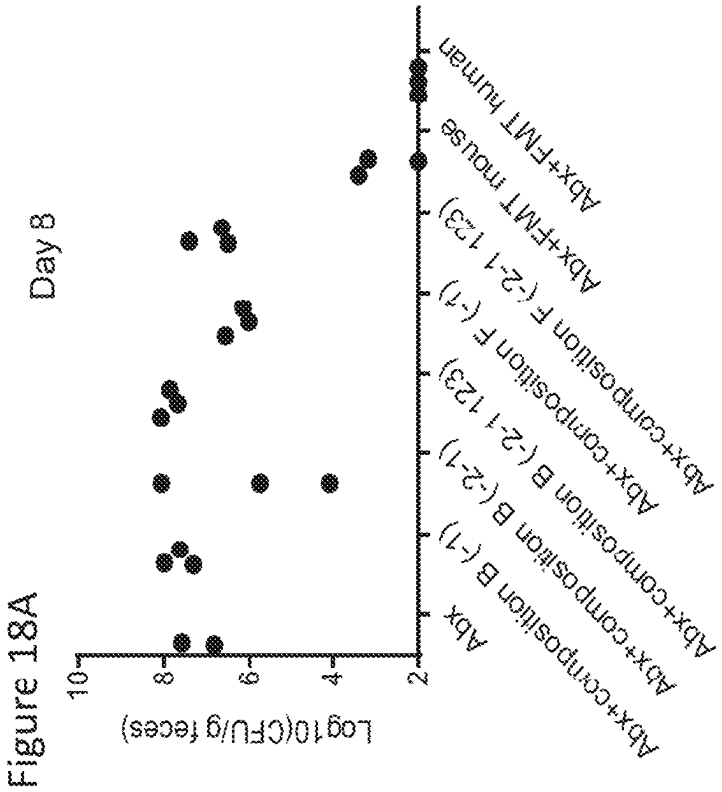


Figure 18A
Day 8
Log10(CFU/g feces)
10
8
6
4
2
Abx
Abx+composition B (-1)
Abx+composition B (-2-1)
Abx+composition B (-2-1 123)
Abx+composition F (-1)
Abx+composition F (-2-1 123)
Abx+FMT mouse
Abx+FMT human

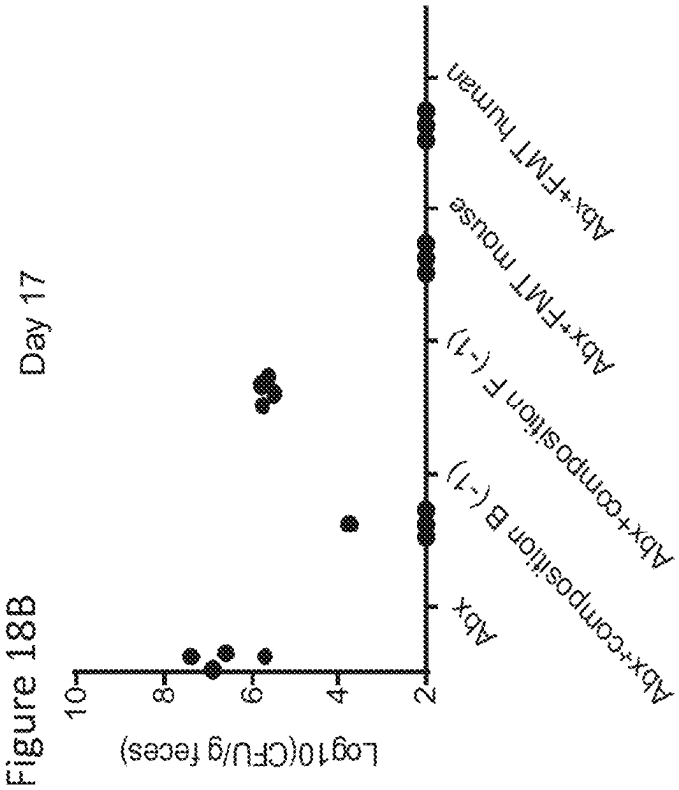


Figure 18B
Day 17
Log10(CFU/g feces)
10
8
6
4
2
Abx
Abx+composition B (-1)
Abx+composition F (-1)
Abx+FMT mouse
Abx+FMT human

Figure 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/Rumirococcus_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

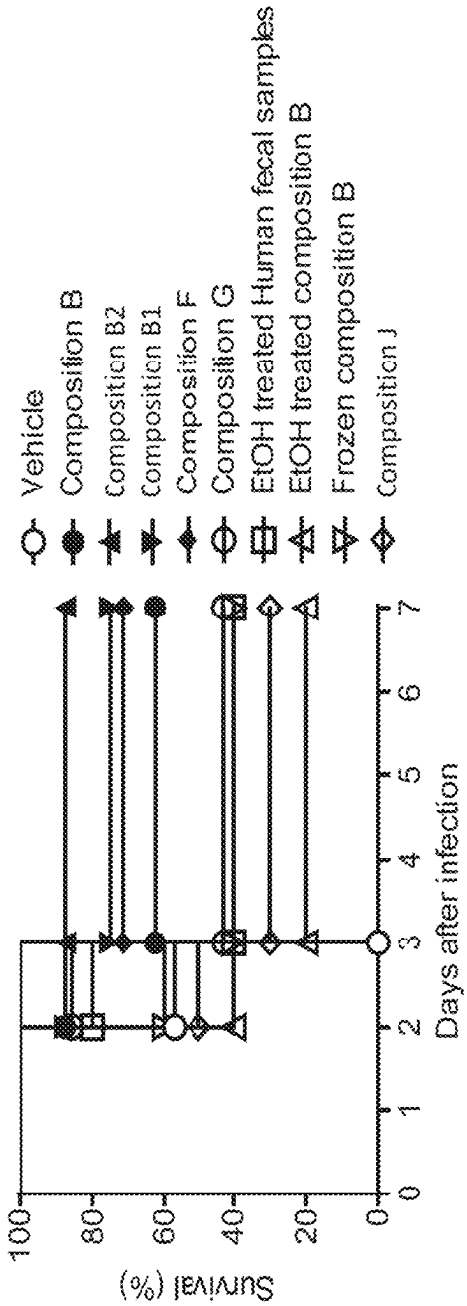

Survival (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
7
Days after infection
Vehicle
Composition B
Composition B2
Composition B1
Composition F
Composition G
EtOH treated Human fecal samples
EtOH treated composition B
Frozen composition B
Composition J

Figure 22A

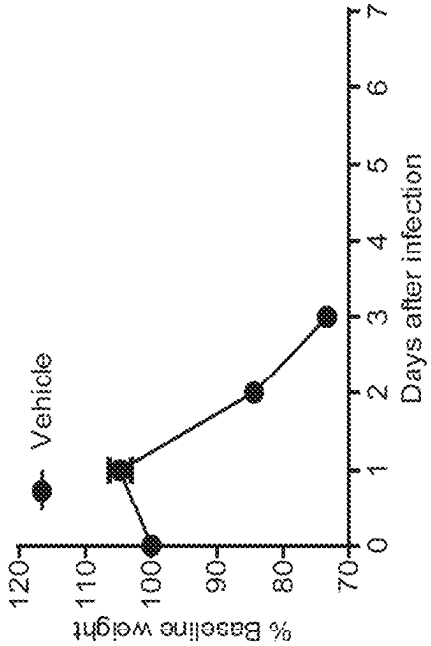


Figure 22B

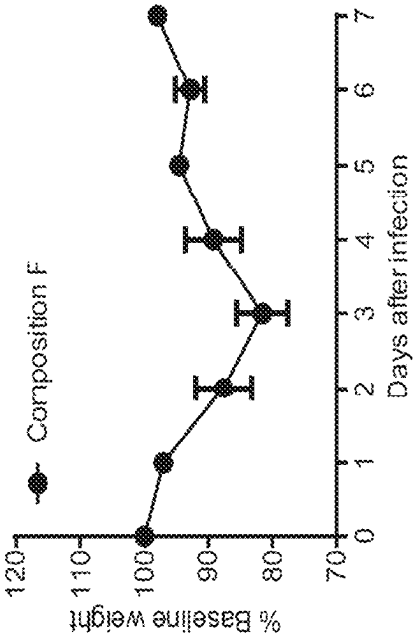


Figure 22C

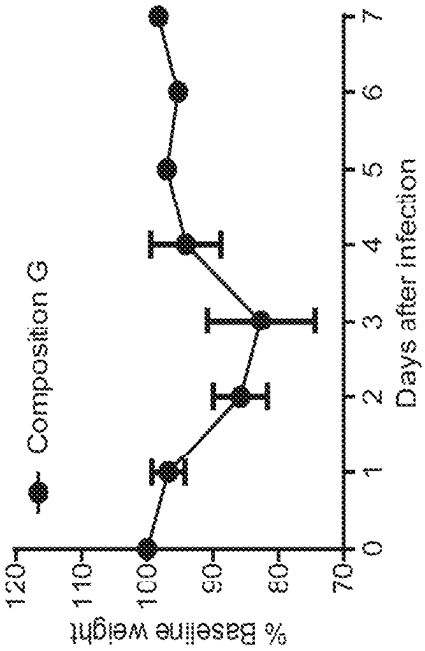


Figure 22D

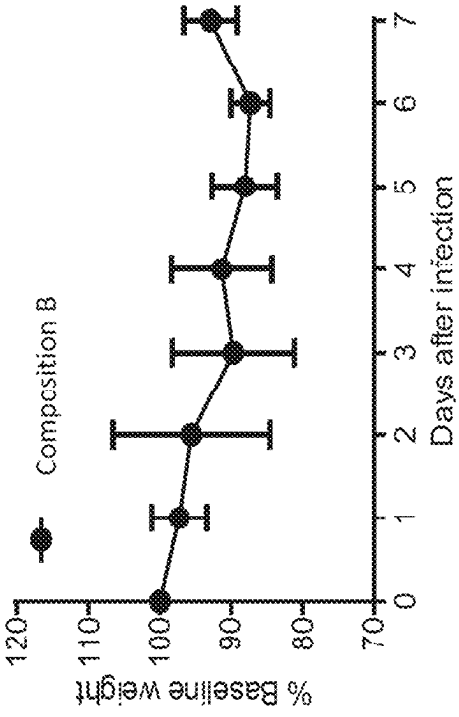


Figure 22E

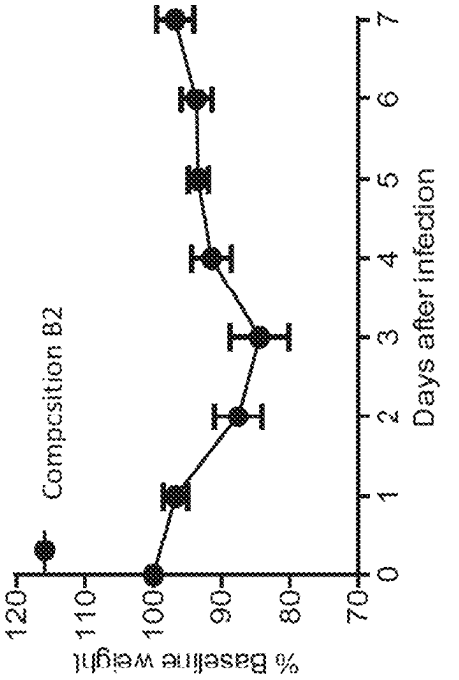


Figure 22F

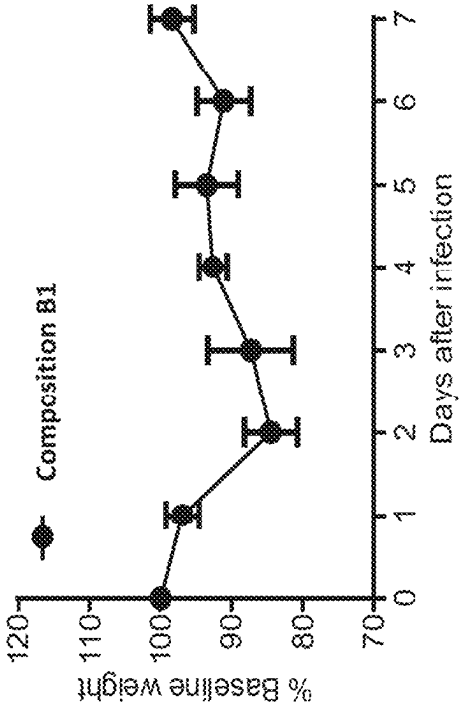


Figure 22G

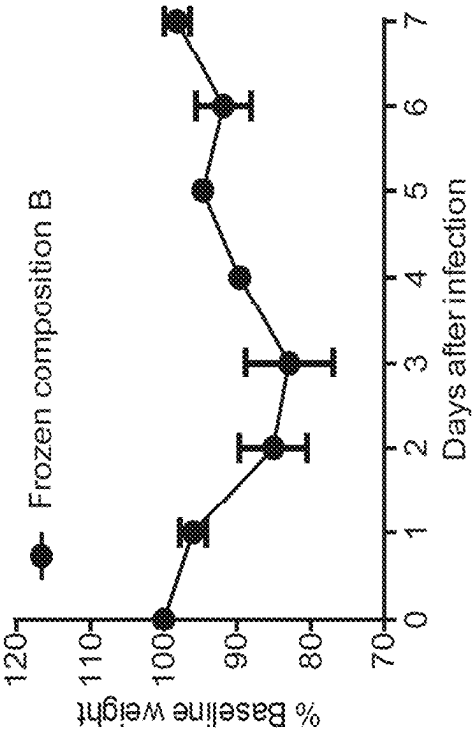


Figure 22I

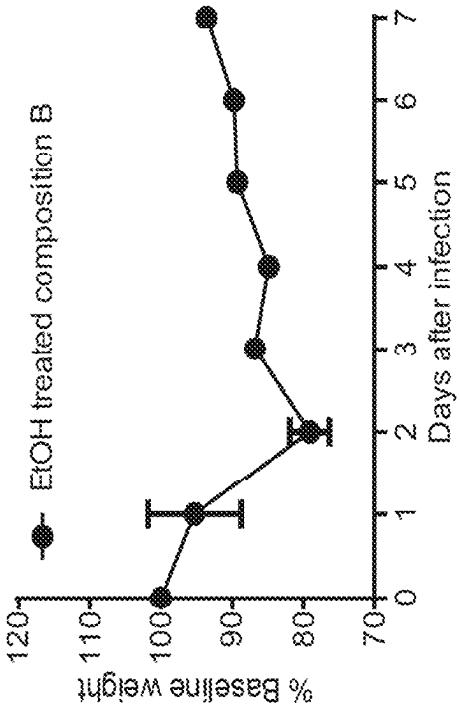


Figure 22H

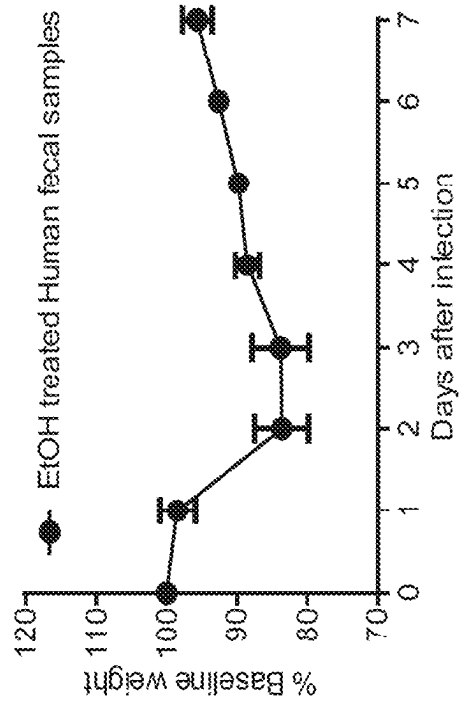
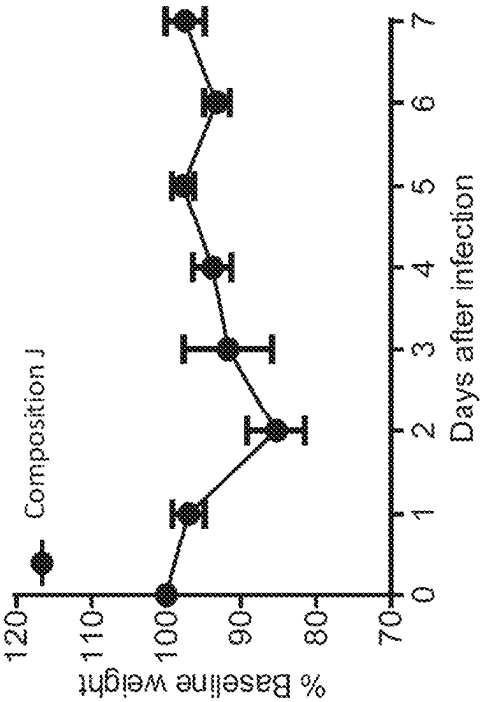


Figure 22J



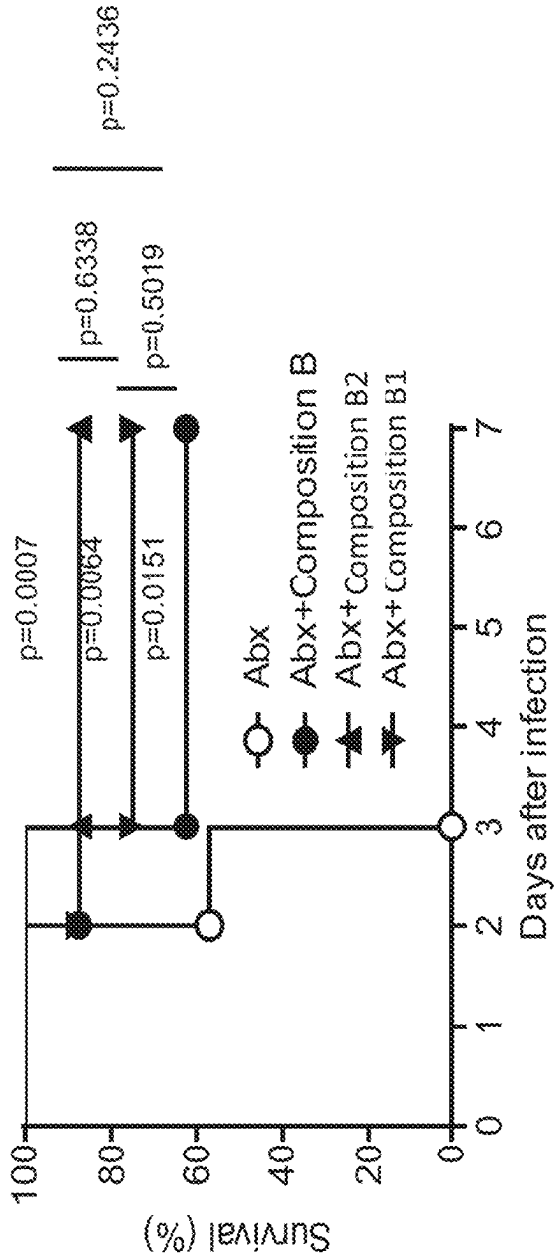


Figure 23
p=0.0007
p=0.0064
p=0.0151
p=0.6338
p=0.5019
p=0.2436
Abx
Abx+Composition B
Abx+Composition B2
Abx+Composition B1
Survival (%)
100
80
60
40
20
0
0
1
2
3
4
5
6
7
Days after infection

Figure 24

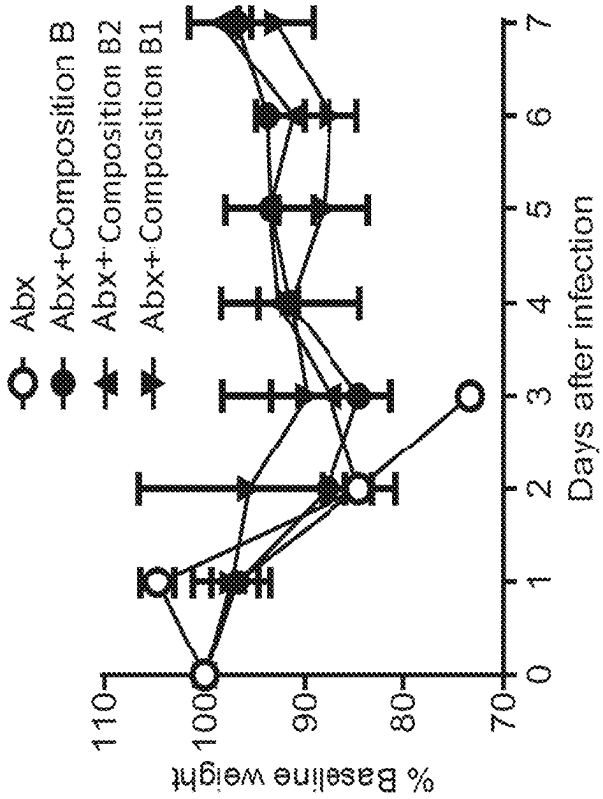

Abx
Abx+Composition B
Abx+Composition B2
Abx+Composition B1
% Baseline weight
110
100
90
80
70
0
1
2
3
4
5
6
7
Days after infection

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

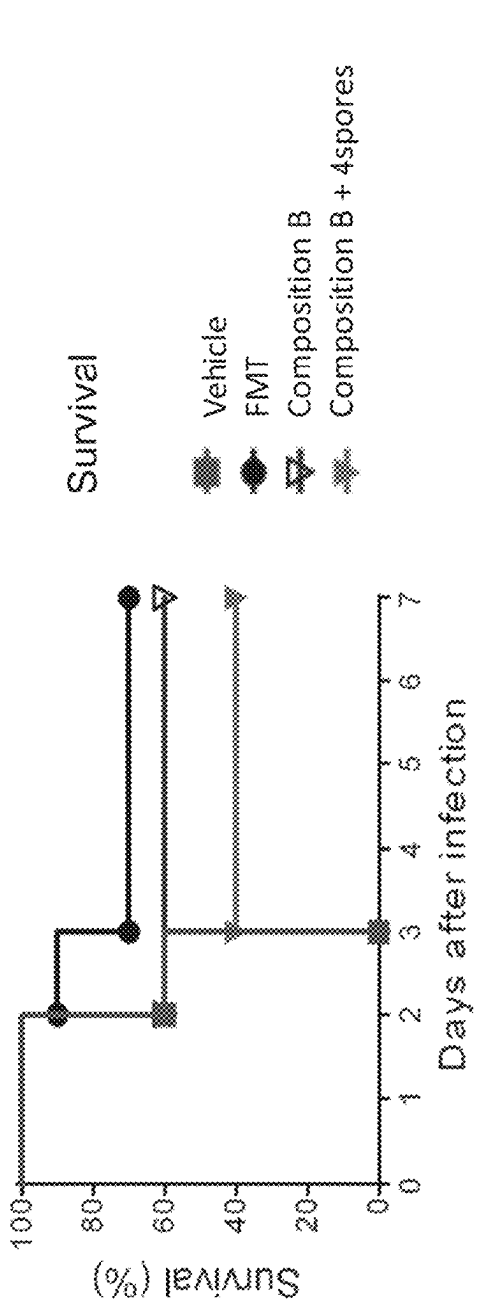


Figure 27B

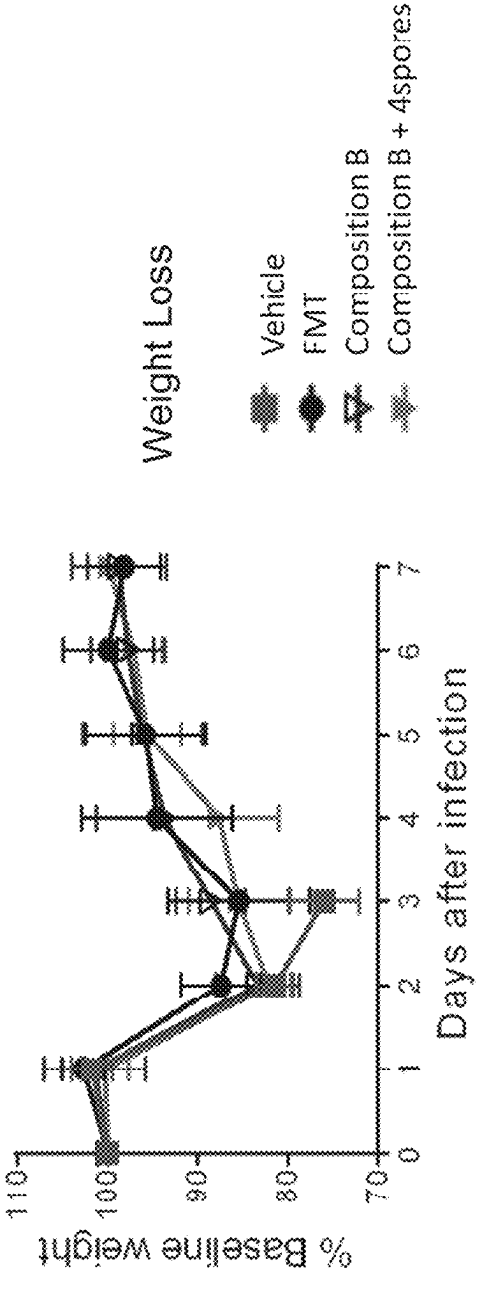


Figure 28A

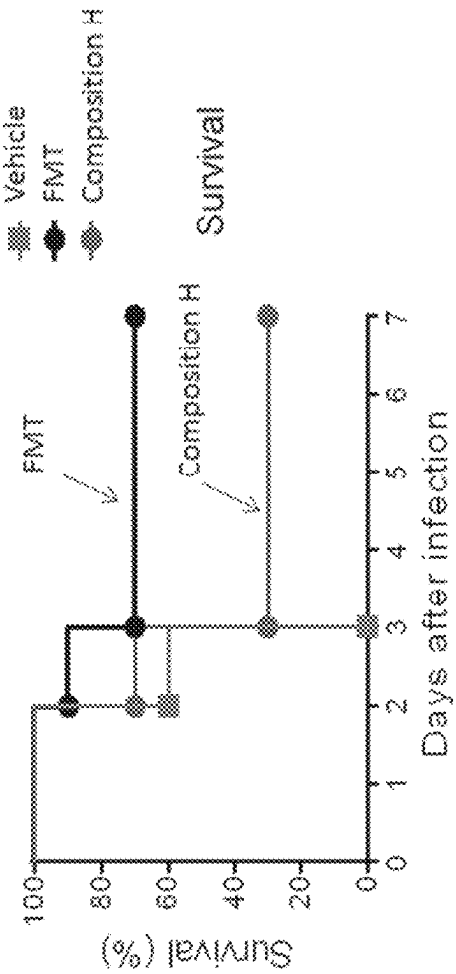
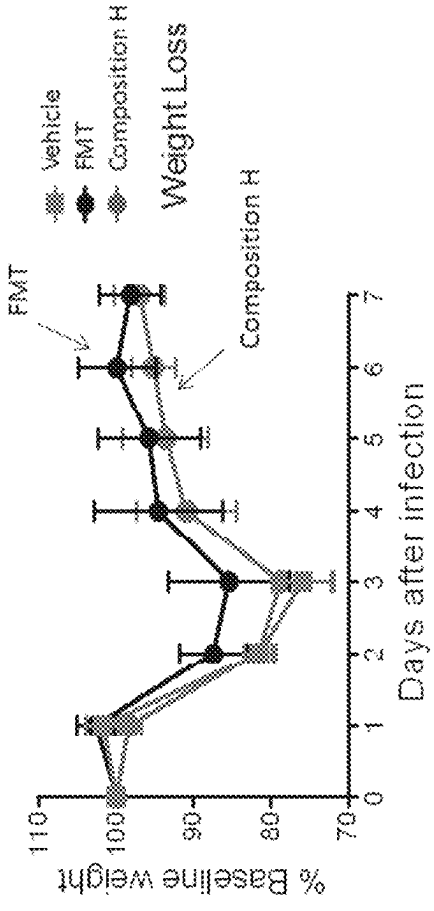


Figure 28B



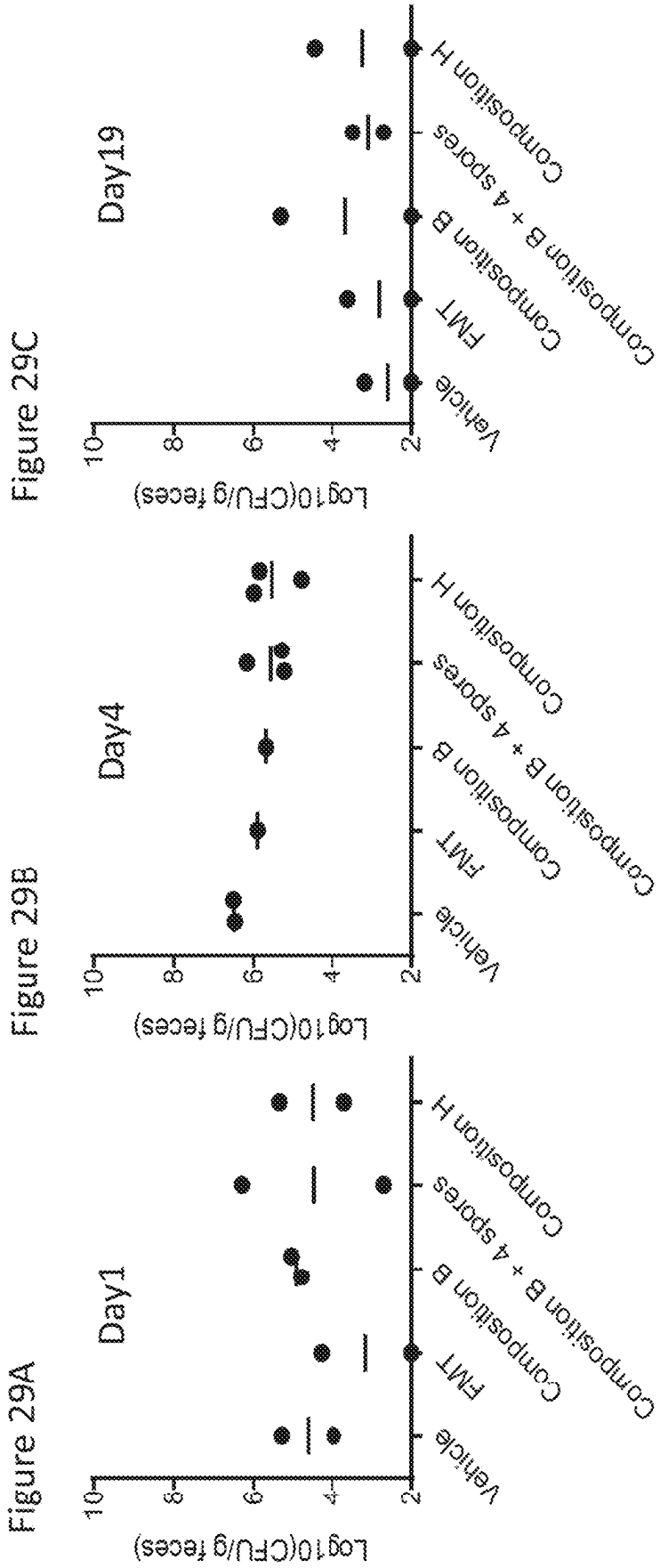


Figure 29A
Day1
Figure 29B
Day4
Figure 29C
Day19
Log10(CFU/g feces)
10
8
6
4
2
Vehicle
FMT
Composition B
Composition B + 4 spores
Composition H

Figure 30

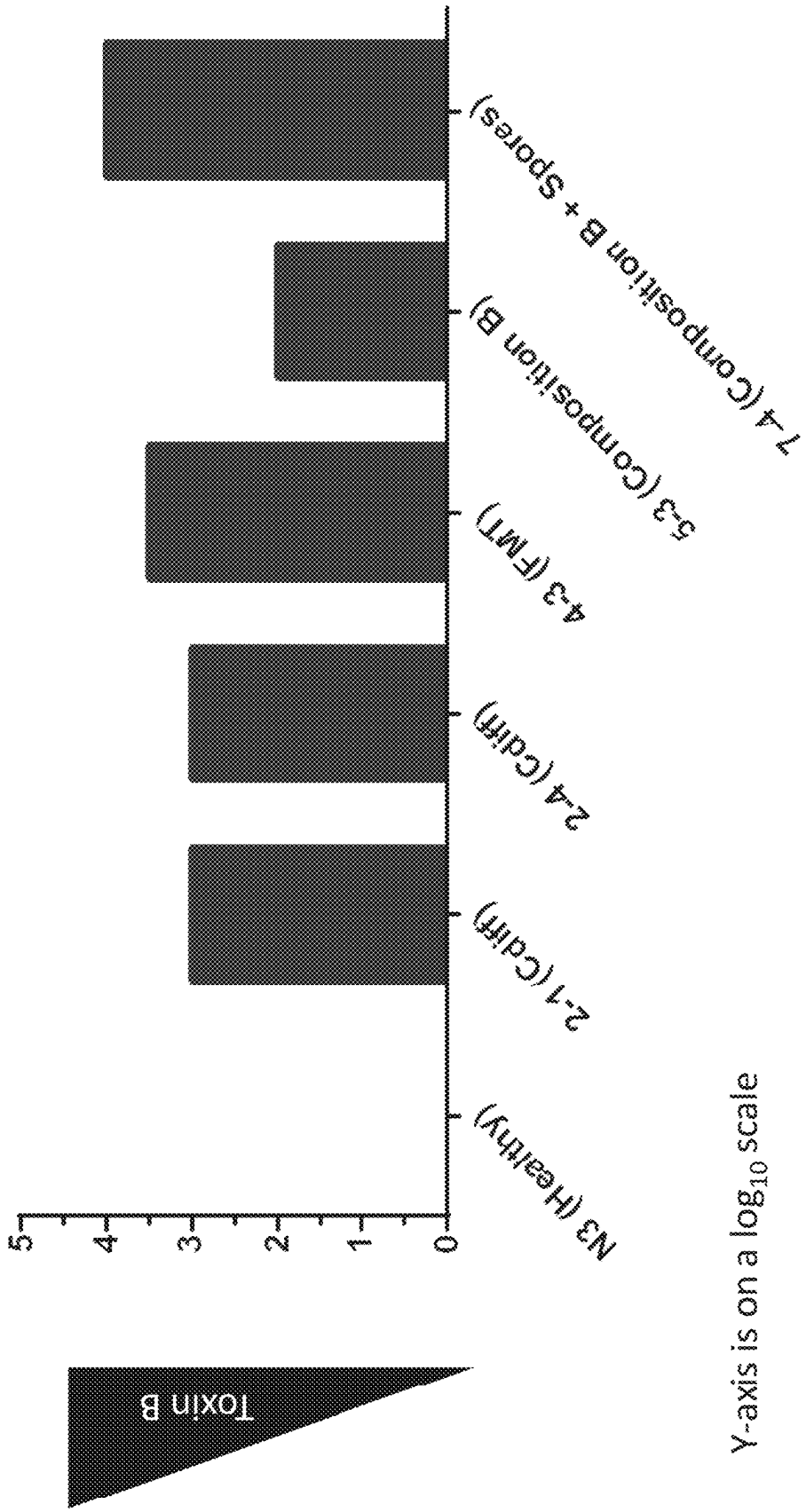

Toxin B
5
4
3
2
1
0
N3 (Healthy)
2-1 (Cdiff)
2-4 (Cdiff)
4-3 (FMT)
5-3 (Composition B)
7-4 (Composition B + Spores)
Y-axis is on a log_{10} scale

Figure 31

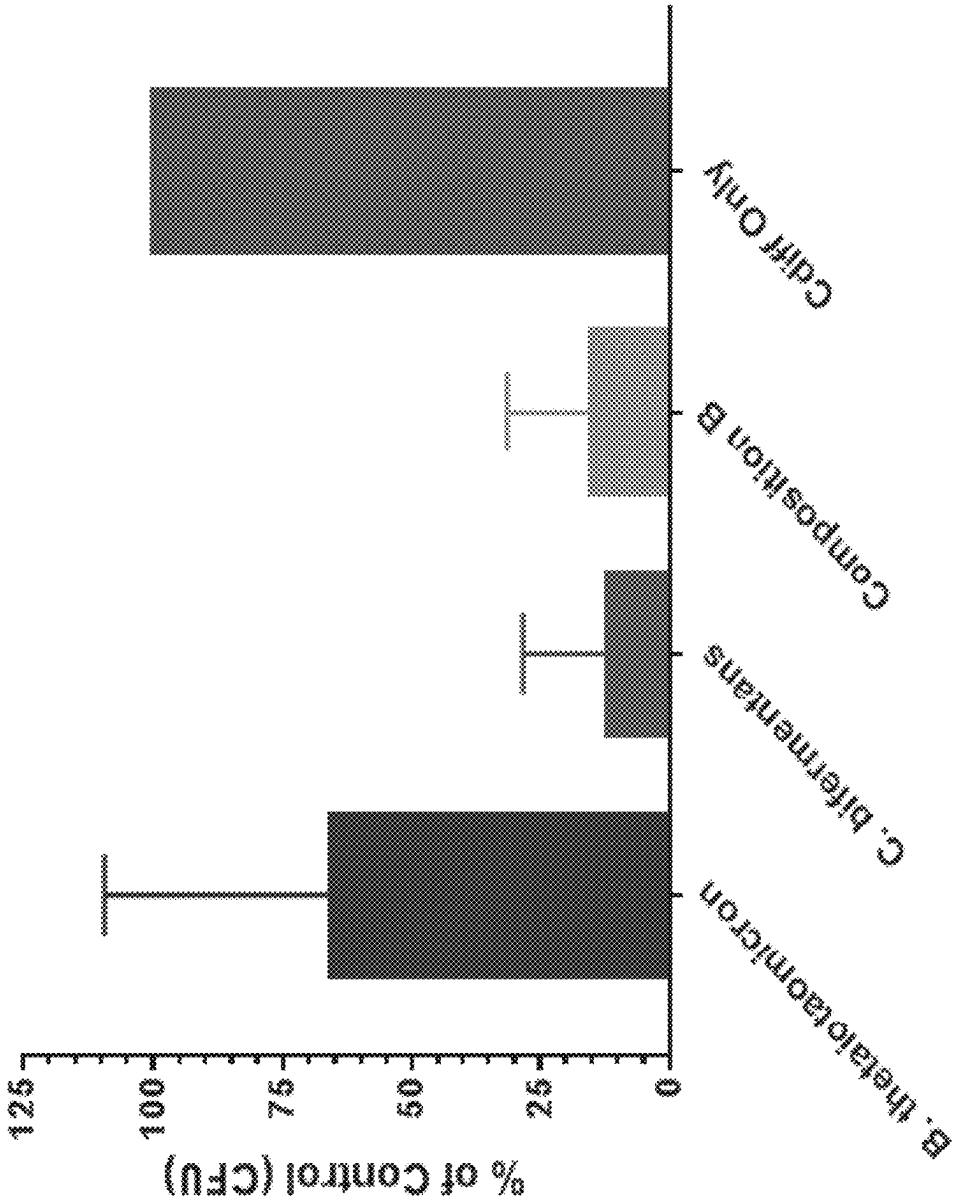
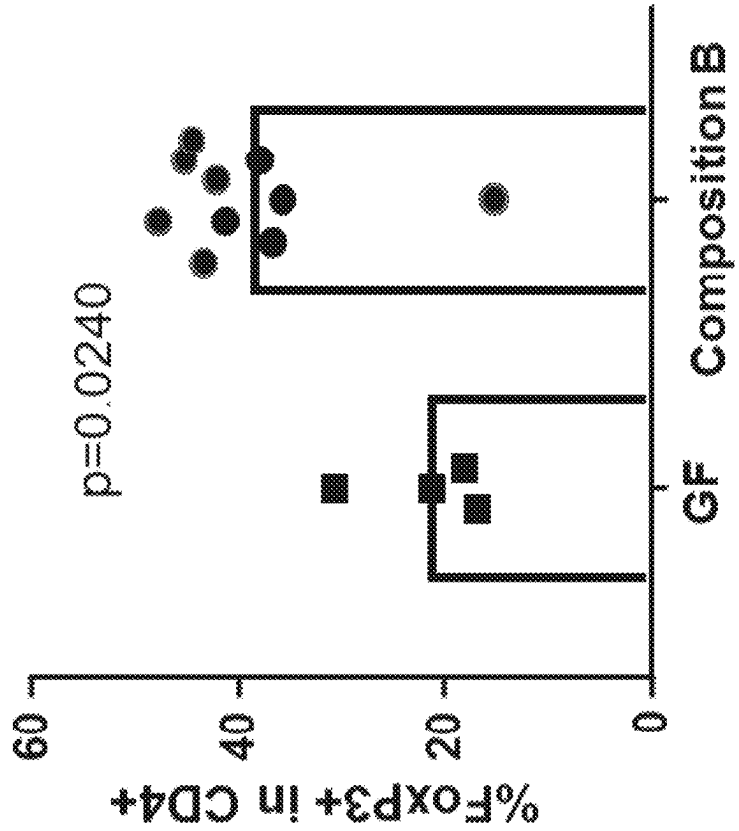

% of Control (CFU)
125
100
75
50
25
0
B. thetaiotaomicron
C. difficile
Composition B
Cdiff Only

Figure 32



TREATMENT OF CLOSTRIDIUM DIFFICILE INFECTION

RELATED APPLICATIONS

This application is a continuation of U.S. application Ser. No. 16/702,659, filed Dec. 4, 2019, which is a continuation of U.S. application Ser. No. 16/423,487, filed May 28, 2019, now issued as U.S. Pat. No. 10,555,980, which is a continuation of U.S. application Ser. No. 16/157,640, filed Oct. 11, 2018, now issued as U.S. Pat. No. 10,456,431, which is a continuation of U.S. application Ser. No. 15/993,037, filed May 30, 2018, now issued as U.S. Pat. No. 10,350,250, which is a continuation of U.S. application Ser. No. 15/630,088, filed Jun. 22, 2017, now issued as U.S. Pat. No. 9,999,641, which 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.

REFERENCE TO AN ELECTRONIC SEQUENCE LISTING

The contents of the electronic sequence listing (P074570006US07-SEQ-NTJ.xml; Size: 340,528 bytes; and Date of Creation: May 15, 2023) is herein incorporated by reference 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_50 AFAA, *Lachnospiraceae bacterium* 7_1_58 FAA, *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, 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 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_50 AFAA, *Lachnospiraceae bacterium* 7_1_58 FAA, *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_50 AFAA, *Lachnospiraceae bacterium* 7_1_58 FAA, *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_50 AFAA, *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_50 AFAA, *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_50 AFAA, *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_50 AFAA, *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_58 FAA, *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_50 AFAA, *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_58 FAA. 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_50 AFAA, 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_58 FAA, *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_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, Anaerotruncus colihominis, Dorea longicatena, Clostridium innocuum, Erysipelotrichaceae_bacterium*_21-3, *Flavinofractor plautii, Lachnospiraceae bacterium* 7-_1_58 FAA, *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_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: *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 embodi-

ments 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 follow-

ing 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 B*2=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_50 AFAA, *Lachnospiraceae bacterium* 7_1_58 FAA, *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_50 AFAA, *Lachnospiraceae bacterium* 7_1_58 FAA, *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_50 AFAA, *Lachnospiraceae bacterium* 7_1_58 FAA, *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*. 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_50 AFAA, *Lachnospiraceae bacterium* 7_1_58 FAA, *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 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 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, and 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_58 FAA, *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, CA) 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_50 AFAA (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_58 FAA, *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: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 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_50 AFAA, *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58 FAA. In some embodiments, the compositions disclosed herein do not include *Clostridium orbiscindens* 1_3_50 AFAA. In some embodiments, the compositions disclosed herein do not include *Flavinofractor plautii*. In some embodiments, the compositions disclosed herein do not include *Subdoligranulum*. In some embodiments, the compositions disclosed herein do not include *Lachnospiraceae bacterium* 7_1_58 FAA.

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_50 AFAA, *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58 FAA. (Composition B2, See e.g., Table B2). In some embodiments, the compositions include *Bacteroides ovatus* and do not include *Clostridium orbiscindens* 1_3_50 AFAA, *Flavinofractor plautii, Subdoligranulum* or *Lachnospiraceae bacterium* 7_1_58 FAA.

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_58 FAA, *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_58 FAA, *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_58 FAA. 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_58 FAA, *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_58 FAA, *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_58 FAA, *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_58 FAA. 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 F2-continued

Composition F, strain groupings		
Cluster	Composition F	*SCFAs
	Dorea formicigenerans 1	A
	Dorea longicatena 2	A
IV	*Flavomfractor_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

TABLE F1

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*

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

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*

TABLE G-continued

Composition G		
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. WI), 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 7α 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 *Clostridium* 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 dispori-*

cum. In some embodiments, the compositions provided herein do not include strains belonging to *Clostridium* 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 embodi-

ments 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 Microbiol*. (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 regulatory 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. Nos. 3,261,761; 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 com-

position 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 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 soy-bean 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

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: 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
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

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: 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
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*

TABLE 2-continued

Bacterial species with a high degree of homology based on whole genome analysis:	
Strain	Whole genome homology
SEQ_17 - VE202-7	*Clostridium_bolteae*
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
1	VE202-7	17	*Clostridium bolteae*	124, 125, 126, 127, 128	124
2	VE202-13	14	*Anaerotruncus colihominis*	129,130, 131	129
3	VE202-14	15	*Eubacterium fissicatena*	132, 133, 134, 135, 136	132
4	VE202-16	16	*Clostridium symbiosum*	137, 138, 139, 140	137
5	strain #16	19	*Blautia producta*	141, 142, 143, 144, 145	141
6	strain #170	20	*Dorea longicatena*	146, 147, 148, 149, 150, 151	146
7	strain #189	21	*Clostridium innocuum*	152, 153, 154, 155, 156	152
8	strain #211	10	*Flavinofractor plautii*	157, 158, 159	157

Composition B strain number	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	*Clostridium bolteae*	*Clostridium bolteae* 90A9		XIVa
2	*Anaerotruncus colihominis*	*Anaerotruncus colihominis* DSM 17241		IV
3	*Dracourtella massiliensis*	*Dracourtella massiliensis* GD1	*Ruminococcus torques*; *Sellimonas intestinalis*	XIVa
4	*Clostridium symbiosum*	*Clostridium symbiosum* WAL-14163		XIVa
5	*Blautia producta*	*Clostridium bacterium* UC5.1-1D4	*Blautia* product ATCC 27340	XIVa
6	*Dorea longicatena*	*Dorea longicatena* CAG: 42		XIVa
7	*Clostridium innocuum*	*Erysipelotrichaceae bacterium* 21_3		XVII

TABLE 3-continued

Bacterial species with highest degree of homology based on whole genome analysis				
8	*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, *Clostridium 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* GPI. 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_50 AFAA.

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.

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: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

>SEQ ID NO: 02|102|
CTAACCGTGGAGGTCATTGGAAACTGGTCAACTTGAGTGCAGAAGAGGGAAGTGGAATTCCATGTGTAGCGGTGAAA

TGCGTAGAGATATGGAGGAACACCAGTGGCGAAGGCGGCTTCCTGGTCTGTAACTGACACTGAGGCGCGAAAGCGTG

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>SEQ ID NO: 07|59|
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>SEQ ID NO: 08|79|
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>SEQ ID NO: 15|VE202-14|
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>SEQ ID NO: 26|YK110|
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>SEQ ID NO: 27|YK149|
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>SEQ ID NO: 28|YK154|
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>SEQ ID NO: 30|YK95|
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>SEQ ID NO: 31|YK32|
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>SEQ ID NO: 32|YK64|
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>SEQ ID NO: 33|YK73|
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>SEQ ID NO: 34|YK87|
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>SEQ ID NO: 35|YK105|
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>SEQ ID NO: 36|YK153|
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>SEQ ID NO: 37|YK163|
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>SEQ ID NO: 38|YK191|
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>SEQ ID NO: 39|YK99|
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>SEQ ID NO: 40|YK55|
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>SEQ ID NO: 41|YK75|
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>SEQ ID NO: 42|YK90|
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>SEQ ID NO: 43|YK30|
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>SEQ ID NO: 44|YK31|
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>SEQ ID NO: 45|YK12|
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>SEQ ID NO: 46|YK27|
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>SEQ ID NO: 50|YK34|70A_009_YK34_A1_A02
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>SEQ ID NO: 62|YK71|
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>SEQ ID NO: 68|YK139|
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>SEQ ID NO: 69|YK141|
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>SEQ ID NO: 70|YK142|
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>SEQ ID NO: 71|YK152|
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>SEQ ID NO: 73|YK157|
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>SEQ ID NO: 79|YK192|
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>SEQ ID NO: 80|VE202-18|
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>SEQ ID NO: 81|PE5|
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>SEQ ID NO: 82|PE9|
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>SEQ ID NO: 83|211-B|
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>SEQ ID NO: 84|NR_119185.1|*Ruminococcus obeum* 16S ribosomal RNA gene, complete sequence
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>SEQ ID NO: 85|NR_118692.1|*Ruminococcus obeum* strain ATCC 29174 16S ribosomal RNA gene, complete sequence
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>SEQ ID NO: 86|NR_026491.1|*Clostridium disporicum* strain DS1 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 87|NR_028785.1|*Clostridium scindens* strain ATCC 35704 16S ribosomal RNA gene, complete sequence
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>SEQ ID NO: 88|NR_028915.1|*Anaerostipes caccae* strain L1-92 16*S* ribosomal RNA gene, partial sequence
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>SEQ ID NO: 89|NR_042152.1|*Marvinbryantia formatexigens* strain I-52 16*S* ribosomal RNA gene, partial sequence >gi|636558750|ref|NR_114807.1|*Marvinbryantia formatexigens* strain I-52 16*S* ribosomal RNA gene, complete sequence
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AGTCAGTGACCCAACCGGAAGGAGGGAGCTGCCGAAGGCGGGGCCGGTAACTGGGGTGAAGTCGTAACAA

>SEQ ID NO: 90|NR_024994.1|*Lactobacillus mucosae* strain S32 16S ribosomal RNA gene, complete sequence
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>SEQ ID NO: 91|NR_028816.1|*Turicibacter sanguinis* strain MOL361 16S ribosomal RNA gene, complete sequence
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TAAAGAGCGCGCAGGTGGTTGATTAAGTCTGATGTGAAAGCCCACGGCTTAACCGTGGAGGGTCATTGGAAACTGGT

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>SEQ ID NO: 92|NR_042832.1|*Roseburia faecis* strain M72/1 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 93|NR_043142.1|*Flavonifractor plautii* strain Prevot S1 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 94|NR_044054.1|*Blautia wexlerae* strain DSM 19850 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 95|NR_027558.1|*Anaerotruncus colihominis* strain WAL 14565 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 96|NR_116747.1|*Ruminococcus faecis* strain Eg2 16S ribosomal RNA gene, partial sequence
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AAGGAGGAGCTGCCGAAG

>SEQ ID NO: 97|NR_028883.1|*Dorea longicatena* strain 111-35 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 98|NR_029164.1|*Clostridium innocuum* strain B-3 16*S* ribosomal RNA gene, partial sequence
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AGGTAGGACCGA

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

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GGAGGAAGGCGGGGACGACGTCAAATCATCATGCCCCTTATGATTTGGGCTACACACGTGCTACAATGGCGTAAACA

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CACGAAGCTGGAATCGCTAGTAATCGCGAATCAGAATGTCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCCC

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>SEQ ID NO: 100|NR_112933.1|*Bacteroides cellulosilyticus* strain JCM 15632
16S ribosomal RNA gene, partial sequence
AGAGTTTGATCCTGGCTCAGGATGAACGCTAGCTACAGGCTTAACACATGCAAGTCGAGGGGCAGCATGACCTAGCA

ATAGGTTGATGGCGACCGGCGCACGGGTGAGTAACACGTATCCAACCTACCGGTTATTCCGGGATAGCCTTTCGAAA

GAAAGATTAATACCGGATAGTATAACGAGAAGGCATCTTTTTGTTATTAAAGAATTTCGATAACCGATGGGGATGCG

TTCCATTAGTTTGTTGGCGGGGTAACGGCCCACCAAGACATCGATGGATAGGGGTTCTGAGAGGAAGGTCCCCCACA

TTGGAACTGAGACACGGTCCAAACTCCTACGGGAGGCAGCAGTGAGGAATATTGGTCAATGGACGAGAGTCTGAACC

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CTTTTTGTATGTACCATACGAATAAGGATCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGATCCGAGCGT

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AGAAGGCAGCTACACAGCGATGTGATGCTAATCCCAAAAGCCTCTCTCAGTTCGGATTGGAGTCTGCAACCCGACTC

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CTAAGTCGTA

>SEQ ID NO: 101|NR_112940.1|*Bacteroides ovatus* strain JCM 5824 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 102|NR_117563.1|*Eubacterium fissicatena* 16S ribosomal RNA gene, partial sequence
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CGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCTGCTCTTGACATCCCACTGACCGGCGTGTAA

TGGCGCCTTCCCTTCGGGGCAGTGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAA

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

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

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

TGAAATTGACTTAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTTACACTGGGGGATAACAGTTAGAAATG

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TGGGACTGAGACACGGCCCAAACTCCTACGGGAGGCAGCAGTGGGGAATATTGGACAATGGGCGAAAGCCTGATCCA

GCGACGCCGCGTGAGTGAAGAAGTATTTCGGTATGTAAAGCTCTATCAGCAGGGAAGAAAATGACGGTACCTGACTA

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AAGGGAGCGTAGACGGTTTAGCAAGTCTGAAGTGAAAGCCCGGGGCTCAACCCCGGTACTGCTTTGGAAACTGTTAG

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AGCGATCTGGAGCAAACCCCAAAAATAACGTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCTGGAAT

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GTTGGTAACGCCCGAAGTCAGTGACCCAACCGAAAGGAGGGAGCT

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

TAACAGTTAGAAATGACTGCTAATACCGCATAAGCGCACAGGACCGCATGGTCTGGTGTGAAAAACTCCGGTGGTAT

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GGTGAACGGCCACATTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGG

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AAAGGGAAGCGAGACAGCGATGTTGAGCGAATCCCAAAAATAACGTCCCAGTTCGGACTGCAGTCTGCAACTCGACT

GCACGAAGCTGGAATCGCTAGTAATCGCGGATCAGAATGCCGCGGTGAATACGTTCCCGGGTCTTGTACACACCGCC

CGTCACACCATGGGAGTCAGTAACGCCCGAAGTCAGTGACCTAACCGAAAGGAAGGAGCTGCCGAAGGCGGGACCGA

TAACTGGGGTGAAGTCGTAACAAGGTAACC

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

TGACGTTTTGTAGACTGAGTGGCGGACGGGTGAGTAACGCGTGGGCAACCTGCCCTGTACAGGGGGATAACAGTCAG

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>SEQ ID NO: 108|NR_117142.1|*Eubacterium fissicatena* strain DSM 3598 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 109|NR_117147.1|*Eubacterium contortum* strain DSM 3982 16S ribosomal RNA gene, partial sequence
TTTGATCCTGGCTCAGGATGAACGCTGGCGACGTGCTTAACACATGCAAGTCGAGCGAAGCACTTTACTTTGATTTC

TTCGGAATGAAAGGTTTTGTGACTGAGCGGCGGACGGGTGAGTAACGCGTGGGTAACCTGCCTCATACAGGGGGATA

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>SEQ ID NO: 110|NR_113410.1|*Clostridium bolteae* strain JCM 12243 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 111|NR_041960.1|*Blautia luti* strain BInIX 16*S* ribosomal RNA gene, complete sequence
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>SEQ ID NO: 112|NR_074306.1|*Acidaminococcus intestini* RyC-MR95 strain RyC-MR95 16*S* ribosomal RNA, complete sequence
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>SEQ ID NO: 113|NR_074399.1|*Ruminococcus albus* strain 7 16S ribosomal RNA gene, complete sequence
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GTAATCGCGGATCAGCATGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGCCATGGGAGTCGG

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CAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCT

>SEQ ID NO: 114|NR_074634.1|*Eubacterium rectale* strain ATCC 33656 16S ribosomal RNA gene, complete sequence
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>SEQ ID NO: 115|NR_074928.1|*Acidaminococcus fermentans* strain DSM 20731 16S ribosomal RNA gene, complete sequence
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CACCT

>SEQ ID NO: 116|NR_114326.1|*Fusicatenibacter saccharivorans* strain HT03-11 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 117|NR_102884.1|*Ruminococcus champanellensis* strain 18P13 16S ribosomal RNA gene, complete sequence
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>SEQ ID NO: 118|NR_102971.1|*Bifidobacterium bifidum* S17 strain S17 16S ribosomal RNA, complete sequence
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>SEQ ID NO: 119|NR_102980.1|*Megasphaera elsdenii* strain DSM 20460 16*S* ribosomal RNA gene, complete sequence
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>SEQ ID NO: 120|NR_044645.2|*Dorea formicigenerans* strain ATCC 27755 16*S* ribosomal RNA gene, complete sequence
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>SEQ ID NO: 121|NR_118643.1|*Eisenbergiella tayi* strain B086562 16S ribosomal RNA gene, partial sequence

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>SEQ ID NO: 122|NR_118730.1|*Clostridium symbiosum* strain ATCC 14940 16S ribosomal RNA gene, partial sequence
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>SEQ ID NO: 123|NR_113243.1|*Erysipelatoclostridium ramosum* strain JCM 1298 16S ribosomal RNA gene, partial sequence
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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: 131 | PROKKA_02671 16S ribosomal RNA gene
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>SEQ ID NO: 132 | PROKKA_00690 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: 135 | PROKKA_02310 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: 137 | PROKKA_00436 16S ribosomal RNA gene
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>SEQ ID NO: 138 | PROKKA_00685 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: 140 | PROKKA_05969 16S ribosomal RNA gene
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>SEQ ID NO: 141 | PROKKA_00279 16S ribosomal RNA gene
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>SEQ ID NO: 142 | PROKKA_01221 16S ribosomal RNA gene
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>SEQ ID NO: 143 | PROKKA_02318 16S ribosomal RNA gene
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>SEQ ID NO: 144 | PROKKA_02336 16S ribosomal RNA gene
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>SEQ ID NO: 145 | PROKKA_04947 16S ribosomal RNA gene
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GACCGATAACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTT

>SEQ ID NO: 146 | PROKKA_00208 16S ribosomal RNA gene
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CCGATAACTGGGGTGAAGTCGTAACAAGGTAGCCGTATCGGAAGGTGCGGCTGGATCACCTCCTTT

>SEQ ID NO: 147 | PROKKA_00340 16S ribosomal RNA gene
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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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GGGATAACAGTTAGAAATGACTGCTAATACCGCATAAGACCACGGTACCGCATGGTACAGTGGTAAAAACTCCGGTG

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>SEQ ID NO: 150 | PROKKA_02944 16S ribosomal RNA gene
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>SEQ ID NO: 151 | PROKKA_04036 16S ribosomal RNA gene
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GGGATAACAGTTAGAAATGACTGCTAATACCGCATAAGACCACGGTACCGCATGGTACAGTGGTAAAAACTCCGGTG

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>SEQ ID NO: 152 | PROKKA_00437 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 (0D600) 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, CA), 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 OD_{600} 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, CA).

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
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

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 login of corresponding determined/estimated CFU for the culture. The results are depicted in Table 6 and Table 7 below.

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 (Tregs)

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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ggagggagct gtcgaaggcg ggacggataa ctggggtgaa gtcgtaacaa ggtagccgta  1500
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SEQ ID NO: 16          moltype = DNA  length = 1527
FEATURE                Location/Qualifiers
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                       note = Synthetic Polynucleotide
source                 1..1527
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 16
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taccgcataa gcgcacagta tcgcatgata cagtgtgaaa aactccggtg gtacaagatg  240
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agaagccccg gctaactacg tgccagcagc cgcggtaata cgtagggggc aagcgttatc  540
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acaccgcccg tcacaccatg ggagtcagta acgcccgaag tcagtgaccc aaccgcaagg  1440
agggagctgc cgaaggcggg accgataact ggggtgaagt cgtaacaagg tagccgtatc  1500
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SEQ ID NO: 17          moltype = DNA  length = 1530
FEATURE                Location/Qualifiers
misc_feature           1..1530
                       note = Synthetic Polynucleotide
source                 1..1530
                       mol_type = other DNA
                       organism = synthetic construct
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tgagtaacgc gtggataacc tgcctcacac tgggggataa cagttagaaa tgactgctaa  180
taccgcataa gcgcacagta ccgcatggta cggtgtgaaa aactccggtg gtgtgagatg  240
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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
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SEQ ID NO: 18           moltype = DNA  length = 1528
FEATURE                 Location/Qualifiers
misc_feature            1..1528
                        note = Synthetic Polynucleotide
source                  1..1528
                        mol_type = other DNA
                        organism = synthetic construct
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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
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cggatttact gggtgtaaag ggagcgtaga cggcacggca agccagatgt gaaagcccgg  600
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cctggtagtc cacgccgtaa acgatgactg ctaggtgtcg ggtggcaaag ccattcggtg  840
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ctggaatcgc tagtaatcgc agatcagaat gctgcggtga atacgttccc gggtcttgta  1380
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gagggagctg ccgaaggtgg gaccgataac tggggtgaag tcgtaacaag gtagccgtat  1500
cggaaggtgc ggctggatca cctccttt                                     1528

SEQ ID NO: 19           moltype = DNA  length = 1531
FEATURE                 Location/Qualifiers
misc_feature            1..1531
                        note = Synthetic Polynucleotide
source                  1..1531
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 19
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tacacaccgc ccgtcacacc atgggagtca gtaacgcccg aagtcagtga cccaacctta  1440
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tatcggaagg tgcggctgga tcacctcctt t                                 1531

SEQ ID NO: 20           moltype = DNA  length = 1528
FEATURE                 Location/Qualifiers
misc_feature            1..1528
                        note = Synthetic Polynucleotide
source                  1..1528
                        mol_type = other DNA
                        organism = synthetic construct
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gacccgcgtc tgattaggta gttggtgggg taacggccta ccaagccgac gatcagtagc  300
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gagggagctg ccgaaggtgg gaccgataac tggggtgaag tcgtaacaag gtagccgtat  1500
cggaaggtgc ggctggatca cctccttt                                     1528

SEQ ID NO: 21          moltype = DNA  length = 1537
FEATURE                Location/Qualifiers
misc_feature           1..1537
                       note = Synthetic Polynucleotide
source                 1..1537
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 21
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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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gaaggtcttc ggatcgtaaa gctctgttgt aagtgaagaa cggctcatag aggaaatgct  480
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SEQ ID NO: 22          moltype = DNA  length = 476
FEATURE                Location/Qualifiers
misc_feature           1..476
                       note = Synthetic Polynucleotide
source                 1..476
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 22
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cccgcgtctg attaggtagt tggtggggta acggcctacc aagccgacga tcagtagccg  180
acctgagagg gtgaccggcc acattgggac tgagacacgg cccagactcc tacgggaggc  240
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gaagtatttc ggtatgtaaa cttctatcag cagggaagaa aatgacggta cctgactaag  360
aagccccggc taactacgtg ccagcagccg cggtaatacg taggggggcaa gcgttatccg  420
gatttactgg gtgtaaaggg agcgtagacg gcacggcaag ccagatgtga aagccc      476
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SEQ ID NO: 23          moltype = DNA  length = 354
FEATURE                Location/Qualifiers
misc_feature           1..354
                       note = Synthetic Polynucleotide
source                 1..354
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 23
caggctggag tgcaggagag gtaagcggaa ttcctagtgt agcggtgaaa tgcgtagata  60
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aagcgtgggg agcaaacagg attagatacc ctggtagtcc acgcggtaaa cgatgattgc  180
taggtgtagg tgggtatgga cccatcggtg ccgcagctaa cgcaataagc aatccacctg  240
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agcatgtggt ttaattcgaa gcaacgcgaa gaaccttacc aagtcttgac atcc        354

SEQ ID NO: 24          moltype = DNA  length = 190
FEATURE                Location/Qualifiers
misc_feature           1..190
                       note = Synthetic Polynucleotide
source                 1..190
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 24
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ggcttgctgg acgatgactg acgttgaggc tcgaaagcgt ggggagcaaa caggattaga  180
taccctggta                                                         190

SEQ ID NO: 25          moltype = DNA  length = 190
FEATURE                Location/Qualifiers
misc_feature           1..190
                       note = Synthetic Polynucleotide
source                 1..190
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 25
agggtcaacc cctggactgc attggaaact gtcaggctgg agtgccggag aggtaagcgg  60
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cttactggac ggtaactgac gttgatgctc gaaagcgtgg ggagcaaaca ggattagata  180
acctggtaaa                                                         190

SEQ ID NO: 26          moltype = DNA  length = 209
FEATURE                Location/Qualifiers
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                       note = Synthetic Polynucleotide
source                 1..209
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 27          moltype = DNA  length = 203
FEATURE                Location/Qualifiers
misc_feature           1..203
                       note = Synthetic Polynucleotide
source                 1..203
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 28          moltype = DNA  length = 207
FEATURE                Location/Qualifiers
misc_feature           1..207
                       note = Synthetic Polynucleotide
source                 1..207
                       mol_type = other DNA
                       organism = synthetic construct
```

```
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

SEQ ID NO: 29          moltype = DNA  length = 424
FEATURE                Location/Qualifiers
misc_feature           1..424
                       note = Synthetic Polynucleotide
source                 1..424
                       mol_type = other DNA
                       organism = synthetic construct
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 cgctcccttt 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

SEQ ID NO: 30          moltype = DNA  length = 441
FEATURE                Location/Qualifiers
misc_feature           1..441
                       note = Synthetic Polynucleotide
source                 1..441
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 31          moltype = DNA  length = 422
FEATURE                Location/Qualifiers
misc_feature           1..422
                       note = Synthetic Polynucleotide
source                 1..422
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 32          moltype = DNA  length = 424
FEATURE                Location/Qualifiers
misc_feature           1..424
                       note = Synthetic Polynucleotide
source                 1..424
                       mol_type = other DNA
                       organism = synthetic construct
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 ggtttcccc attgtgcaat attccccact gctgcctccc gtgggagttt  420
ggaa                                                               424

SEQ ID NO: 33          moltype = DNA  length = 422
FEATURE                Location/Qualifiers
misc_feature           1..422
                       note = Synthetic Polynucleotide
```

```
source                  1..422
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 34           moltype = DNA  length = 419
FEATURE                 Location/Qualifiers
misc_feature            1..419
                        note = Synthetic Polynucleotide
source                  1..419
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 35           moltype = DNA  length = 424
FEATURE                 Location/Qualifiers
misc_feature            1..424
                        note = Synthetic Polynucleotide
source                  1..424
                        mol_type = other DNA
                        organism = synthetic construct
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 atattcccca ctgctgcctc cctgggaagt  420
ttgg                                                               424

SEQ ID NO: 36           moltype = DNA  length = 445
FEATURE                 Location/Qualifiers
misc_feature            1..445
                        note = Synthetic Polynucleotide
source                  1..445
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 37           moltype = DNA  length = 421
FEATURE                 Location/Qualifiers
misc_feature            1..421
                        note = Synthetic Polynucleotide
source                  1..421
                        mol_type = other DNA
                        organism = synthetic construct
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
```

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SEQ ID NO: 38          moltype = DNA  length = 424
FEATURE                Location/Qualifiers
misc_feature           1..424
                       note = Synthetic Polynucleotide
source                 1..424
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 39          moltype = DNA  length = 189
FEATURE                Location/Qualifiers
misc_feature           1..189
                       note = Synthetic Polynucleotide
source                 1..189
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 39
tgggcttacc cataaactgc atttgaaact gtggttcttg agtgaagtag aggtaagcgg  60
aattcctagt gtagcggtga aatgcgtaga tattaggagg aacatcagtg gcgaaggcgg  120
cttactgggc tttaactgac gctgaggctc gaaagcgtgg ggagcaaaca ggattagata  180
cccaagtaa                                                          189

SEQ ID NO: 40          moltype = DNA  length = 414
FEATURE                Location/Qualifiers
misc_feature           1..414
                       note = Synthetic Polynucleotide
source                 1..414
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 41          moltype = DNA  length = 191
FEATURE                Location/Qualifiers
misc_feature           1..191
                       note = Synthetic Polynucleotide
source                 1..191
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 42          moltype = DNA  length = 196
FEATURE                Location/Qualifiers
misc_feature           1..196
                       note = Synthetic Polynucleotide
source                 1..196
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 43          moltype = DNA  length = 192
FEATURE                Location/Qualifiers
misc_feature           1..192
                       note = Synthetic Polynucleotide
```

```
source                  1..192
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 44           moltype = DNA  length = 195
FEATURE                 Location/Qualifiers
misc_feature            1..195
                        note = Synthetic Polynucleotide
source                  1..195
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 45           moltype = DNA  length = 418
FEATURE                 Location/Qualifiers
misc_feature            1..418
                        note = Synthetic Polynucleotide
source                  1..418
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 46           moltype = DNA  length = 416
FEATURE                 Location/Qualifiers
misc_feature            1..416
                        note = Synthetic Polynucleotide
source                  1..416
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 47           moltype = DNA  length = 400
FEATURE                 Location/Qualifiers
misc_feature            1..400
                        note = Synthetic Polynucleotide
source                  1..400
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 48           moltype = DNA  length = 416
FEATURE                 Location/Qualifiers
misc_feature            1..416
                        note = Synthetic Polynucleotide
source                  1..416
                        mol_type = other DNA
                        organism = synthetic construct
```

```
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

SEQ ID NO: 49          moltype = DNA  length = 421
FEATURE                Location/Qualifiers
misc_feature           1..421
                       note = Synthetic Polynucleotide
source                 1..421
                       mol_type = other DNA
                       organism = synthetic construct
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 ttgcccccta  240
cgtattaccg cggctgctgg cacgtagtta gccggggctt cttagtcagg taccgtcatt  300
ttcttccctg ctgatagagc tttacatacc gagatacttc ttcactcacg cggcgtcgct  360
gcatcagggt ttcccccatt gtgcaatatt ccccactgct gcctcccgaa ggaagtttgg  420
a                                                                  421

SEQ ID NO: 50          moltype = DNA  length = 418
FEATURE                Location/Qualifiers
misc_feature           1..418
                       note = Synthetic Polynucleotide
source                 1..418
                       mol_type = other DNA
                       organism = synthetic construct
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 ccccctacgt  240
attaccgcgg ctgctggcac gtagttagcc ggggcttctt agtcaggtac cgtcattttc  300
ttccctgctg atagagcttt acataccgag atacttcttc actcacgcgg cgtcgctgca  360
tcagggtttc ccccattgtg caatattccc cactgctgcc tcccgtaggg agtttgga    418

SEQ ID NO: 51          moltype = DNA  length = 415
FEATURE                Location/Qualifiers
misc_feature           1..415
                       note = Synthetic Polynucleotide
source                 1..415
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 52          moltype = DNA  length = 418
FEATURE                Location/Qualifiers
misc_feature           1..418
                       note = Synthetic Polynucleotide
source                 1..418
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 53          moltype = DNA  length = 416
FEATURE                Location/Qualifiers
misc_feature           1..416
                       note = Synthetic Polynucleotide
```

```
source                  1..416
                        mol_type = other DNA
                        organism = synthetic construct
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
tccctgctga tagagcttta cataccgaaa tacttcttcg ctcacgcggc gtcgctgcat  360
caggctttcg cccattgtgc aatattcccc actgctgcct cccgagggga gtttgg      416

SEQ ID NO: 54           moltype = DNA  length = 435
FEATURE                 Location/Qualifiers
misc_feature            1..435
                        note = Synthetic Polynucleotide
source                  1..435
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 55           moltype = DNA  length = 418
FEATURE                 Location/Qualifiers
misc_feature            1..418
                        note = Synthetic Polynucleotide
source                  1..418
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 56           moltype = DNA  length = 416
FEATURE                 Location/Qualifiers
misc_feature            1..416
                        note = Synthetic Polynucleotide
source                  1..416
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 57           moltype = DNA  length = 417
FEATURE                 Location/Qualifiers
misc_feature            1..417
                        note = Synthetic Polynucleotide
source                  1..417
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 58           moltype = DNA  length = 417
FEATURE                 Location/Qualifiers
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misc_feature            1..417
                        note = Synthetic Polynucleotide
source                  1..417
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 59           moltype = DNA  length = 419
FEATURE                 Location/Qualifiers
misc_feature            1..419
                        note = Synthetic Polynucleotide
source                  1..419
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 60           moltype = DNA  length = 419
FEATURE                 Location/Qualifiers
misc_feature            1..419
                        note = Synthetic Polynucleotide
source                  1..419
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 61           moltype = DNA  length = 421
FEATURE                 Location/Qualifiers
misc_feature            1..421
                        note = Synthetic Polynucleotide
source                  1..421
                        mol_type = other DNA
                        organism = synthetic construct
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

SEQ ID NO: 62           moltype = DNA  length = 420
FEATURE                 Location/Qualifiers
misc_feature            1..420
                        note = Synthetic Polynucleotide
source                  1..420
                        mol_type = other DNA
                        organism = synthetic construct
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
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SEQ ID NO: 63          moltype = DNA  length = 446
FEATURE                Location/Qualifiers
misc_feature           1..446
                       note = Synthetic Polynucleotide
source                 1..446
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 64          moltype = DNA  length = 419
FEATURE                Location/Qualifiers
misc_feature           1..419
                       note = Synthetic Polynucleotide
source                 1..419
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 65          moltype = DNA  length = 418
FEATURE                Location/Qualifiers
misc_feature           1..418
                       note = Synthetic Polynucleotide
source                 1..418
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 66          moltype = DNA  length = 420
FEATURE                Location/Qualifiers
misc_feature           1..420
                       note = Synthetic Polynucleotide
source                 1..420
                       mol_type = other DNA
                       organism = synthetic construct
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
tattaccgcg gctgctggca cgtatttagc cggtgcttct tagtcaggta ccgtcattct  300
tcttccctgc tgatagagct ttacataccg aaatacttct tcgctcacgc ggcgtcgctg  360
catcagggtt tcccccattg tgcaatattc cccactgctg cctcccgaag ggagtttgga  420

SEQ ID NO: 67          moltype = DNA  length = 417
FEATURE                Location/Qualifiers
misc_feature           1..417
                       note = Synthetic Polynucleotide
source                 1..417
                       mol_type = other DNA
                       organism = synthetic construct
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
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tccctgctga tagaagttta cataccgaga tacttcttcc ttcacgcggc gtcgctgcat  360
cagggtttcc cccattgtgc aatattcccc actgctgcct cccgagggaa gtttgga     417

SEQ ID NO: 68          moltype = DNA  length = 416
FEATURE                Location/Qualifiers
misc_feature           1..416
                       note = Synthetic Polynucleotide
source                 1..416
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 69          moltype = DNA  length = 416
FEATURE                Location/Qualifiers
misc_feature           1..416
                       note = Synthetic Polynucleotide
source                 1..416
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 70          moltype = DNA  length = 418
FEATURE                Location/Qualifiers
misc_feature           1..418
                       note = Synthetic Polynucleotide
source                 1..418
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 71          moltype = DNA  length = 420
FEATURE                Location/Qualifiers
misc_feature           1..420
                       note = Synthetic Polynucleotide
source                 1..420
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 72          moltype = DNA  length = 418
FEATURE                Location/Qualifiers
misc_feature           1..418
                       note = Synthetic Polynucleotide
source                 1..418
                       mol_type = other DNA
                       organism = synthetic construct
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
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tattaccgcg gctgctggca cgtagttagc cggggcttct tagtcaggta ccgtcatttt  300
cttccctgct gatagaagtt tacataccga gatacttctt ccttcacgcg gcgtcgctgc  360
atcagggttt cccccattgt gcaatattcc ccactgctgc ctcccgaagg gagtttgg    418

SEQ ID NO: 73          moltype = DNA  length = 421
FEATURE                Location/Qualifiers
misc_feature           1..421
                       note = Synthetic Polynucleotide
source                 1..421
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 74          moltype = DNA  length = 419
FEATURE                Location/Qualifiers
misc_feature           1..419
                       note = Synthetic Polynucleotide
source                 1..419
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 75          moltype = DNA  length = 417
FEATURE                Location/Qualifiers
misc_feature           1..417
                       note = Synthetic Polynucleotide
source                 1..417
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 76          moltype = DNA  length = 419
FEATURE                Location/Qualifiers
misc_feature           1..419
                       note = Synthetic Polynucleotide
source                 1..419
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 76
agctcagctt 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 ctcccgaagg gagtttgga   419

SEQ ID NO: 77          moltype = DNA  length = 418
FEATURE                Location/Qualifiers
misc_feature           1..418
                       note = Synthetic Polynucleotide
source                 1..418
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 77
gtccagcttt cgagcctcag cgtcagttat cgtccagtaa gccgccttcg ccactggtgt  60
tcctcctaat atctacgcat ttcaccgcta cactaggaat tccgcttacc cctccgacac  120
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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

SEQ ID NO: 78          moltype = DNA  length = 193
FEATURE                Location/Qualifiers
misc_feature           1..193
                       note = Synthetic Polynucleotide
source                 1..193
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 79          moltype = DNA  length = 424
FEATURE                Location/Qualifiers
misc_feature           1..424
                       note = Synthetic Polynucleotide
source                 1..424
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 79
cacgatgtca gctttcgagc tcagcgtcag ttatcgtcca gtaagccgcc ttcgccactg  60
gtgttcctcc taatatctac gcatttcacc gctacactag gaattccact taccccctccg  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

SEQ ID NO: 80          moltype = DNA  length = 1524
FEATURE                Location/Qualifiers
misc_feature           1..1524
                       note = Synthetic Polynucleotide
source                 1..1524
                       mol_type = other DNA
                       organism = synthetic construct
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

SEQ ID NO: 81          moltype = DNA  length = 1528
FEATURE                Location/Qualifiers
misc_feature           1..1528
                       note = Synthetic Polynucleotide
source                 1..1528
                       mol_type = other DNA
                       organism = synthetic construct
```

```
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 taggggggcaa 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

SEQ ID NO: 82          moltype = DNA  length = 385
FEATURE                Location/Qualifiers
misc_feature           1..385
                       note = Synthetic Polynucleotide
source                 1..385
                       mol_type = other DNA
                       organism = synthetic construct
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 tagggggttgt  300
catgacctct gtgccgccgc taacgcatta agtattccgc ctggggagta cggtcgcaag  360
attaaaactc aaagaaattg acgga                                        385

SEQ ID NO: 83          moltype = DNA  length = 434
FEATURE                Location/Qualifiers
misc_feature           1..434
                       note = Synthetic Polynucleotide
source                 1..434
                       mol_type = other DNA
                       organism = synthetic construct
SEQUENCE: 83
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

SEQ ID NO: 84          moltype = DNA  length = 1457
FEATURE                Location/Qualifiers
source                 1..1457
                       mol_type = genomic DNA
                       organism = Ruminococcus obeum
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
tgaagtcgta acaaggt                                                 1457
```

SEQ ID NO: 85 moltype = DNA length = 1398
FEATURE Location/Qualifiers
source 1..1398
mol_type = genomic DNA
organism = Ruminococcus obeum
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
```

SEQ ID NO: 86 moltype = DNA length = 1472
FEATURE Location/Qualifiers
source 1..1472
mol_type = genomic DNA
organism = Clostridium disporicum
SEQUENCE: 86

```
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
```

SEQ ID NO: 87 moltype = DNA length = 1529
FEATURE Location/Qualifiers

```
source                  1..1529
                        mol_type = genomic DNA
                        organism = Clostridium scindens
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 cgtagggggc aagcgttatc  540
cggatttact gggtgtaaag ggagcgtaga cggcgatgca agccagatgt gaaagcccgg  600
ggctcaaccc cgggactgca tttggaactg cgtggctgga gtgtcggaga ggcaggcgga  660
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

SEQ ID NO: 88           moltype = DNA  length = 1456
FEATURE                 Location/Qualifiers
source                  1..1456
                        mol_type = genomic DNA
                        organism = Anaerostipes caccae
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 gtttttttct 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
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

SEQ ID NO: 89           moltype = DNA  length = 1456
FEATURE                 Location/Qualifiers
source                  1..1456
                        mol_type = genomic DNA
                        organism = Marvinbryantia formatexigens
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 gagggggagc 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
```

SEQ ID NO: 90 moltype = DNA length = 1568
FEATURE Location/Qualifiers
source 1..1568
mol_type = genomic DNA
organism = Lactobacillus mucosae
SEQUENCE: 90

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agagtttgat cctggctcag gatgaacgcc ggcggtgtgc ctaatacatg caagtcgaac  60
gcgttggccc aactgattga acgtgcttgc acggacttga cgttggttta ccagcgagtg  120
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
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SEQ ID NO: 91 moltype = DNA length = 1508
FEATURE Location/Qualifiers
source 1..1508
mol_type = genomic DNA
organism = Turicibacter sanguinis
SEQUENCE: 91

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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
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
ggaggaaggt ggggatgacg tcaaatcatc atgcccctta tgacctgggc tacacacgtg  1200
ctacaatggt tggtacaaag agaagcgaag cggtgacgtg gagcaaacct cataaagcca  1260
atctcagttc ggattgtagg ctgcaactcg cctacatgaa gttggaatcg ctagtaatcg  1320
cgaatcagca tgtcgcggtg aatacgttcc cgggtcttgt acacaccgcc cgtcacacca  1380
```

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cgagagttta caacacccga agtcagtggc ctaaccgcaa ggagggagct gcctaaggtg  1440
gggtagatga ttggggtgaa gtcgtaacaa ggtatcccta ccggaaggtg gggttggatc  1500
acctcctt                                                           1508

SEQ ID NO: 92          moltype = DNA  length = 1456
FEATURE                Location/Qualifiers
source                 1..1456
                       mol_type = genomic DNA
                       organism = Roseburia faecis
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
caatggggga 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

SEQ ID NO: 93          moltype = DNA  length = 1465
FEATURE                Location/Qualifiers
source                 1..1465
                       mol_type = genomic DNA
                       organism = Flavonifractor plautii
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 tgtgggggt ctgacccct 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

SEQ ID NO: 94          moltype = DNA  length = 1438
FEATURE                Location/Qualifiers
source                 1..1438
                       mol_type = genomic DNA
                       organism = Blautia wexlerae
SEQUENCE: 94
caagtcgaac gggaattant ttattgaaac ttcggtcgat ttaatttaat tctagtggcg  60
gacgggtgag taacgcgtgg gtaacctgcc ttatacaggg ggataacagt cagaaatggc  120
tgctaataccc 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
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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
```

```
SEQ ID NO: 95          moltype = DNA  length = 1365
FEATURE                Location/Qualifiers
source                 1..1365
                       mol_type = genomic DNA
                       organism = Anaerotruncus colihominis
SEQUENCE: 95
aacggagctt acgttttgaa gttttcggat ggatgaatgt aagcttagtg gcggacgggt  60
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
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
```

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SEQ ID NO: 96          moltype = DNA  length = 1404
FEATURE                Location/Qualifiers
source                 1..1404
                       mol_type = genomic DNA
                       organism = Ruminococcus faecis
SEQUENCE: 96
atgcaagtcg aacgaagcac cttgatttga ttcttcggat gaagatcttg gtgactgagt  60
ggcggacggg tgagtaacgc gtgggtaacc tgcctcatac agggggataa 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
aaccgtaagg aggagctgcc gaag                                         1404

SEQ ID NO: 97          moltype = DNA  length = 1316
FEATURE                Location/Qualifiers
source                 1..1316
                       mol_type = genomic DNA
                       organism = Dorea longicatena
SEQUENCE: 97
taacgcgtgg gtaacctgcc tcatacaggg ggataacagt tagaaatgac tgctaatacc  60
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
ttactgggtg taaagggagc gtagacggca cggcaagcca gatgtgaaaa gcccggggct  480
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

SEQ ID NO: 98          moltype = DNA  length = 1475
FEATURE                Location/Qualifiers
source                 1..1475
                       mol_type = genomic DNA
                       organism = Clostridium innocuum
SEQUENCE: 98
atggagagtt tgatcctggc tcaggatgaa cgctggcggc atgcctaata catgcaagtc  60
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
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
gtgacaagaa gcgaatctca taaagatcgt ctcagttcgg attgaagtct gcaactcgac  1320
ttcatgaagt cggaatcgct agtaatcgca gatcagcatg ctgcggtgaa tacgttctcg  1380
ggccttgtac acaccgcccg tcaaaccatg ggagtcagta atacccgaag ccggtggcat  1440
aaccgtaagg agtgagccgt cgaaggtagg accga                             1475

SEQ ID NO: 99          moltype = DNA  length = 1492
FEATURE                Location/Qualifiers
source                 1..1492
                       mol_type = genomic DNA
                       organism = Blautia hansenii
SEQUENCE: 99
agagtttgat cctggctcag gatgaacgct ggcggcgtgc ttaacacatg caagtcgagc  60
gaagcactta tcattgactc ttcggaagat ttgatatttg actgagcggc ggacgggtga  120
gtaacgcgtg ggtaacctgc ctcatacagg ggaataacag ttagaaatgg ctgctaatgc  180
cgcataagcg cacaggaccg catggtctgg tgtgaaaaac tgaggtggta tgagatggac  240
ccgcgtctga ttaggtagtt ggtggggtaa cggcctacca agccgacgat cagtagccgg  300
cctgagaggg tgaacggcca cattgggact gagacacggc ccagactcct acgggaggca  360
gcagtgggga atattgcaca atgggggaaa ccctgatgca gcgacgccgc gtgaaggaag  420
aagtatctcg gtatgtaaac ttctatcagc agggaagaaa atgacggtac ctgactaaga  480
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agccccggct aactacgtgc cagcagccgc ggtaatacgt agggggcaag 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
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
```

SEQ ID NO: 100 moltype = DNA length = 1473
FEATURE Location/Qualifiers
source 1..1473
mol_type = genomic DNA
organism = Bacteroides cellulosilyticus
SEQUENCE: 100

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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 ggagtacgc 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
```

SEQ ID NO: 101 moltype = DNA length = 1459
FEATURE Location/Qualifiers
source 1..1459
mol_type = genomic DNA
organism = Bacteroides ovatus
SEQUENCE: 101

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ggctcaggat gaacgctagc tacaggctta acacatgcaa gtcgaggggc agcattttag  60
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
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gtcaagccat gaaagccggg ggtacctgaa gtacgtaacc gcaaggagcg tcctagggta  1440
aaactggtaa ttggggcta                                               1459

SEQ ID NO: 102          moltype = DNA  length = 1526
FEATURE                 Location/Qualifiers
source                  1..1526
                        mol_type = genomic DNA
                        organism = Eubacterium fissicatena
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
atgaagtatt tcggtatgta aacttctatc agcagggaag aaaatgacgg tacctgacta  480
agaagccccg gctaactacg tgccagcagc cgcggtaata cgtagggggc 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 ctcctt                                       1526

SEQ ID NO: 103          moltype = DNA  length = 1493
FEATURE                 Location/Qualifiers
source                  1..1493
                        mol_type = genomic DNA
                        organism = Blautia coccoides
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
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aagtatctcg gtatgtaaac ttctatcagc agggaagaaa atgacggtac ctgactaaga  480
agccccggct aactacgtgc cagcagccgc ggtaatacgt agggggcaag 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

SEQ ID NO: 104          moltype = DNA  length = 1262
FEATURE                 Location/Qualifiers
source                  1..1262
                        mol_type = other DNA
                        note = Blautia faecis
                        organism = unidentified
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
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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
```

SEQ ID NO: 105 moltype = DNA length = 1431
FEATURE Location/Qualifiers
source 1..1431
mol_type = genomic DNA
organism = Clostridium hathewayi

SEQUENCE: 105

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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
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taaagctcta tcagcaggga agaaaatgac ggtacctgac taagaagccc cggctaacta  480
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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
cttatcctta gtagccagcg agtagagtcg ggcactctgg ggagactgcc agggataacc  1140
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
```

SEQ ID NO: 106 moltype = DNA length = 1493
FEATURE Location/Qualifiers
source 1..1493
mol_type = genomic DNA
organism = Blautia producta

SEQUENCE: 106

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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
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gcagtgggga atattgcaca atgggggaaa ccctgatgca gcgacgccgc gtgaaggaag  420
aagtatctcg gtatgtaaac ttctatcagc agggaagaaa atgacggtac ctgactaaga  480
agccccggct aactacgtgc cagcagccgc ggtaatacgt agggggcaag 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
```

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accgcccgtc acaccatggg agtcagtaac gcccgaagtc agtgacctaa ccgaaaggaa  1440
ggagctgccg aaggcgggac cgataactgg ggtgaagtcg taacaaggta acc         1493

SEQ ID NO: 107          moltype = DNA  length = 1515
FEATURE                 Location/Qualifiers
source                  1..1515
                        mol_type = other DNA
                        note = Anaerostipes hadrus
                        organism = unidentified
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 agggggcaag 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

SEQ ID NO: 108          moltype = DNA  length = 1523
FEATURE                 Location/Qualifiers
source                  1..1523
                        mol_type = genomic DNA
                        organism = Eubacterium fissicatena
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
cagtggggaa tattgcacaa tgggggaaac cctgatgcag cgacgccgcg tgaaggatga  420
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gccccggcta actacgtgcc agcagccgcg gtaatacgta gggggcaagc gttatccgga  540
tttactgggt gtaaagggag cgtagacggt tatgtaagtc tgatgtgaaa acccggggct  600
caaccccggg actgcattgg aaactatgta actagagtgt cggagaggta agtggaattc  660
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
agctgccgaa ggcgggatcg ataactgggg tgaagtcgta acaaggtagc cgtatcggaa  1500
ggtgcggctg gatcacctcc ttt                                          1523

SEQ ID NO: 109          moltype = DNA  length = 1524
FEATURE                 Location/Qualifiers
source                  1..1524
                        mol_type = genomic DNA
                        organism = Eubacterium contortum
SEQUENCE: 109
tttgatcctg gctcaggatg aacgctggcg acgtgcttaa cacatgcaag tcgagcgaag  60
cactttactt tgatttcttc ggaatgaaag gttttgtgac tgagcggcgg acgggtgagt  120
aacgcgtggg taacctgcct catacagggg gataacagtt agaaatgact gctaataccg  180
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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
ccccggctaa ctacgtgcca gcagccgcgg taatacgtag ggggcaagcg ttatccggat  540
ttactgggtg taaagggagc gtagacggtt atgtaagtct gatgtgaaaa cccggggctc  600
aaccccggga ctgcattgga aactatgtaa ctagagtgtc ggagaggtaa gtggaattcc  660
tagtgtagcg gtgaaatgcg tagatattag gaggaacacc agtggcgaag gcggcttact  720
ggacgatgac tgacgttgag gctcgaaagc gtggggagca aacaggatta gataccctgg  780
tagtccacgc cgtaaacgat gaatactagg tgtcgggtgg caaagccatt cggtgccgca  840
gcaaacgcaa taagtattcc acctggggag tacgttcgca agaatgaaac tcaaaggaat  900
tgacggggac ccgcacaagc ggtggagcat gtggtttaat tcgaagcaac gcgaagaacc  960
ttacctgctc ttgacatccc cctgaccggc gtgtaatggt gcctttcctt cgggacaggg  1020
gagacaggtg gtgcatggtt gtcgtcagct cgtgtcgtga gatgttgggt taagtcccgc  1080
aacgagcgca acccttatct ttagtagcca gcggtttggc cgggcactct agagagactg  1140
ccagggataa cctggaggaa ggtggggatg acgtcaaatc atcatgcccc ttatgagcag  1200
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
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SEQ ID NO: 110 moltype = DNA length = 1390
FEATURE Location/Qualifiers
source 1..1390
mol_type = genomic DNA
organism = Clostridium bolteae
SEQUENCE: 110

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ggataacagt tagaaatgac tgctaatacc gcataagcgc acagtaccgc atggtacagt  120
gtgaaaaact ccggtggtgt gagatggatc cgcgtctgat tagccagttg gcggggtaac  180
ggcccaccaa agcgacgatc agtagccgac ctgagagggt gaccggccac attgggactg  240
agacacggcc caaactccta cgggaggcag cagtggggaa tattgcacaa tgggcgaaag  300
cctgatgcag cgacgccgcg tgagtgaaga agtatttcgg tatgtaaagc tctatcagca  360
gggaagaaaa tgacggtacc tgactaagaa gccccggcta actacgtgcc agcagccgcg  420
gtaatacgta gggggcaagc gttatccgga tttactgggt gtaaagggag cgtagacggc  480
gaagcaagtc tgaagtgaaa acccagggct caaccctggg actgctttgg aaactgtttt  540
gctagagtgt cggagaggta agtggaattc ctagtgtagc ggtgaaatgc gtagatatta  600
ggaggaacac cagtggcgaa ggcggcttac tggacgataa ctgacgttga ggctcgaaag  660
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
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SEQ ID NO: 111 moltype = DNA length = 1308
FEATURE Location/Qualifiers
source 1..1308
mol_type = genomic DNA
organism = Blautia luti
SEQUENCE: 111

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gtgggtaacc tgccttatac agggggataa cagtcagaaa tgactgctaa taccgcataa  60
gcgcacagag ctgcatggct ccggtgtgaa aaactccggt ggtataagat ggacccgcgt  120
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
tgtagcggtg aaatgcgtag atattaggag gaacaccagt ggcgaaggcg gcttactgga  600
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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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

SEQ ID NO: 112          moltype = DNA  length = 1489
FEATURE                 Location/Qualifiers
source                  1..1489
                        mol_type = genomic DNA
                        organism = Acidaminococcus intestini
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

SEQ ID NO: 113          moltype = DNA  length = 1500
FEATURE                 Location/Qualifiers
source                  1..1500
                        mol_type = genomic DNA
                        organism = Ruminococcus albus
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
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gcacaatggg cgaaagcctg atgcagcgat gccgcgtgag ggaagaaggt tttaggattg  420
taaacctctg tctttgggga cgataatgac ggtacccaag gaggaagctc cggctaacta  480
cgtgccagca gccgcggtaa tacgtaggga gcgagcgttg tccggaatta ctgggtgtaa  540
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cgctgaggct cgaaagcgtg gggagcaaac aggattagat accctggtag tccacgccgt  780
aaacgatgat tactaggtgt ggggggactg 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

SEQ ID NO: 114          moltype = DNA  length = 1521
FEATURE                 Location/Qualifiers
source                  1..1521
                        mol_type = genomic DNA
                        organism = Eubacterium rectale
SEQUENCE: 114
agagtttgat cctggctcag gatgaacgct ggcggcgtgc ttaacacatg caagtcgaac  60
gaagcacttt atttgatttc cttcgggact gattattttg tgactgagtg gcggacgggt  120
gagtaacgcg tgggtaacct gccttgtaca gggggataac agttggaaac ggctgctaat  180
accgcataag cgcacggcat cgcatgatgc agtgtgaaaa actccggtgg tataagatgg  240
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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
ggaatcgcta gtaatcgcag atcagaatgc tgcggtgaat acgttcccgg gtcttgtaca  1380
caccgcccgt cacaccatgg gagttgggaa tgcccgaagc cagtgaccta accgaaagga  1440
aggagctgtc gaaggcaggc tcgataactg gggtgaagtc gtaacaaggt agccgtatcg  1500
gaaggtgcgg ctggatcacc t                                            1521
```

SEQ ID NO: 115 moltype = DNA length = 1545
FEATURE Location/Qualifiers
source 1..1545
mol_type = genomic DNA
organism = Acidaminococcus fermentans

SEQUENCE: 115

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ggagaacttt cttcggaatg ttcttagtgg cgaacgggtg agtaacgcgt aggcaacctg  120
ccctctggtt ggggacaaca ttccgaaagg gatgctaata ccgaatgaga tcctctttcc  180
gcatggagag aggatgaaag atggcctcta cttgtaagct atcgccagaa gatgggcctg  240
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
cgtgagatgt tgggttaagt cccgcaacga gcgcaaccct tatcctatgt taccagcacg  1140
taatggtggg gactcatagg agactgccag ggataacctg gaggaaggcg gggatgacgt  1200
caagtcatca tgccccttat gtcttgggct acacacgtac tacaatggtc ggcaacaaag  1260
ggcagcgaag ccgcgaggcg gagccaatcc cagaaacccg accccagttc ggatcgcagg  1320
ctgcaacccg cctgcgtgaa gttggaatcg ctagtaatcg caggtcagca tactgcggtg  1380
aatacgttcc cgggccttgt acacaccgcc cgtcacacca cgaaagttgg taacacccga  1440
agccggtgag ataacctttt aggagtcagc tgtctaaggt ggggccgatg attggggtga  1500
agtcgtaaca aggtagccgt tcgagaacga gcggctggat cacct                  1545
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SEQ ID NO: 116 moltype = DNA length = 1423
FEATURE Location/Qualifiers
source 1..1423
mol_type = genomic DNA
note = Fusicatenibacter saccharivorans
organism = unidentified

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
gcattggaaa ctgtctggct cgagtgccgg agaggtaagc ggaattccta gtgtagcggt  660
gaaatgcgta gatattagga agaacaccag tggcgaaggc ggcttactgg acggtaactg  720
acgttgaggc tcgaaagcgt ggggagcaaa caggattaga taccctggta gtccacgccg  780
taaacgatga atgctaggtg ttggggagca aagctcttcg gtgccgccgc aaacgcatta  840
agcattccac ctggggagta cgttcgcaag aatgaaactc aaaggaattg acggggaccc  900
gcacaagcgg tggagcatgt ggtttaattc gaagcaacgc gaagaacctt accaggtctt  960
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```
gacatcccga tgaccggccc gtaacggggc cttctcttcg gagcattgga gacaggtggt  1020
gcatggttgt cgtcagctcg tgtcgtgaga tgttgggtta agtcccgcaa cgagcgcaac  1080
ccttatcctc agtagccagc aggtaaagct gggcactctg tggagactgc cagggataac  1140
ctggaggaag gtggggatga cgtcaaatca tcatgcccct tatgatctgg gctacacacg  1200
tgctacaatg gcgtaaacaa agggaggcaa agccgcgagg tggagcaaat cccaaaaata  1260
acgtctcagt tcggactgca gtctgcaact cgactgcacg aagctggaat cgctagtaat  1320
cgcgaatcag aatgtcgcgg tgaatacgtt cccgggtctt gtacacaccg cccgtcacac  1380
catgggagtt ggtaacgccc gaagtcagtg acccaacctt tta                    1423
```

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SEQ ID NO: 117          moltype = DNA  length = 1494
FEATURE                 Location/Qualifiers
source                  1..1494
                        mol_type = genomic DNA
                        organism = Ruminococcus champanellensis
SEQUENCE: 117
agagtttgat cctggctcag gacgaacgct ggcggcacgc ctaacacatg caagtcgaac  60
ggagataaag acttcggttt ttatcttagt ggcggacggg tgagtaacac gtgagcaacc  120
tgcctctgag agagggatag cttctggaaa cggatggtaa tacctcataa catagcggta  180
ccgcatgata ctgctatcaa agatttatcg ctcagagatg ggctcgcgtc tgattagcta  240
gatggtgagg taacggctca ccatggcgac gatcagtagc cggactgaga ggttgaacgg  300
ccacattggg actgagacac ggcccagact cctacgggag gcagcagtgg ggaatattgc  360
acaatgggcg caagcctgat gcagcgatgc cgcgtggagg aagaaggttt tcggattgta  420
aactcctgtc ttaagggacg ataatgacgg taccttagga ggaagctccg gctaactacg  480
tgccagcagc cgcggtaata cgtagggagc gagcgttgtc cggaattact gggtgtaaag  540
ggagcgtagg cgggattgca agtcagatgt gaaaactatg ggcttaaccc atagactgca  600
tttgaaactg tagttcttga gtgaagtaga ggtaagcgga attcctagtg tagcggtgaa  660
atgcgtagat attaggagga acatcggtgg cgaaggcggc ttactgggct tttactgacg  720
ctgaggctcg aaagcgtggg gagcaaacag gattagatac cctggtagtc cacgctgtaa  780
acgatgatta ctaggtgtgg ggggactgac cccttccgtg ccgcagttaa cacaataagt  840
aatccacctg gggagtacgg ccgcaaggtt gaaactcaaa ggaattgacg ggggcccgca  900
caagcagtgg agtatgtggt ttaattcgaa gcaacgcgaa aaaccttacc aggtcttgac  960
atcgagtgaa tgatctagag atagatcagt ccttcgggac acaaagacag gtggtgcatg  1020
gttgtcgtca gctcgtgtcg tgagatgttg ggttaagtcc cgcaacgagc gcaaccctta  1080
cctttagttg ctacgcaaga gcactctaga gggactgccg ttgacaaaac ggaggaaggt  1140
ggggatgacg tcaaatcatc atgcccctta tgacctgggc tacacacgta ctacaatggc  1200
aatgaacaga gggaagcaat acagtgatgt ggagcaaatc cccaaaaatt gtcccagttc  1260
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
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SEQ ID NO: 118          moltype = DNA  length = 1533
FEATURE                 Location/Qualifiers
source                  1..1533
                        mol_type = genomic DNA
                        organism = Bifidobacterium bifidum
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
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ttcgggttgt aaacctcttt tgtttgggag caagccttcg ggtgagtgta cctttcgaat  480
aagcgccggc taactacgtg ccagcagccg cggtaatacg tagggcgcaa gcgttatccg  540
gatttattgg gcgtaaaggg ctcgtaggcg gctcgtcgcg tccggtgtga aagtccatcg  600
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 gccccttacg  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 taaccccttg  1440
tgggatggag ccgtctaagg tgaggctcgt gattgggact aagtcgtaac aaggtagccg  1500
taccggaagg tgcggctgga tcacctcctt tct                               1533
```

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SEQ ID NO: 119          moltype = DNA  length = 1552
FEATURE                 Location/Qualifiers
source                  1..1552
                        mol_type = genomic DNA
                        organism = Megasphaera elsdenii
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SEQUENCE: 119
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aagcaacctg cccttcagat ggggacaaca gctggaaacg gctgctaata ccgaatacgt  180
tctttttgtc gcatggcaga gggaagaaag ggaggctctt cggagctttc gctgaaggag  240
gggcttgcgt ctgattagct agttggaggg gtaacggccc accaaggcga cgatcagtag  300
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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
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 aaccttttgg agccagccgt cgaaggtggg ggcgatgatt  1500
ggggtgaagt cgtaacaagg tagccgtatc ggaaggtgcg gctggatcac ct          1552

SEQ ID NO: 120          moltype = DNA  length = 1479
FEATURE                 Location/Qualifiers
source                  1..1479
                        mol_type = genomic DNA
                        organism = Dorea formicigenerans
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
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
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ataccctggt agtccacgcc gtaaacgatg actgctaggt gtcgggtagc aaagctattc  840
ggtgccgcag ctaacgcaat aagcagtcca cctggggagt acgttcgcaa gaatgaaact  900
caaaggaatt gacgggggncc 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

SEQ ID NO: 121          moltype = DNA  length = 1390
FEATURE                 Location/Qualifiers
source                  1..1390
                        mol_type = genomic DNA
                        note = Eisenbergiella tayi
                        organism = unidentified
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
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taggtgggta tggacccatc ggtgccgcag ctaacgcaat aagcaatcca cctggggagt  780
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tggtttaatt cgaagcaacg cgaagaacct taccaagtct tgacatccca atgacgcacc  900
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caggtaaagc tgggcactct aaggagactg ccggggataa cccggaggaa ggcggggatg  1080
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
```

```
SEQ ID NO: 122          moltype = DNA  length = 1478
FEATURE                 Location/Qualifiers
source                  1..1478
                        mol_type = genomic DNA
                        organism = Clostridium symbiosum
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
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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
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aaggagggag ctgccgaagg cgggaccgan aacnnggg                          1478
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SEQ ID NO: 123          moltype = DNA  length = 1488
FEATURE                 Location/Qualifiers
source                  1..1488
                        mol_type = genomic DNA
                        note = Erysipelatoclostridium ramosum
                        organism = unidentified
SEQUENCE: 123
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gcgagcactt gtgctcgagt ggcgaacggg tgagtaatac ataagtaacc tgccctagac  120
agggggataa ctattggaaa cgatagctaa gaccgcatag gtacggacac tgcatggtga  180
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ggcggggtaa cggcccacca aggcgacgat gcgtagccga cctgagaggg tgaccggcca  300
cactgggact gagacacggc ccagactcct acgggaggca gcagtaggga attttcggca  360
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tccggaatta ttgggcgtaa agagggagca ggcggcagca agggtctgtg gtgaaagcct  600
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ccctagtagt ccacgccgta aacgatgagt actaagtgtt ggatgtcaaa gttcagtgct  840
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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
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SEQ ID NO: 124          moltype = DNA  length = 1528
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FEATURE                 Location/Qualifiers
misc_feature            1..1528
                        note = Synthetic Polynucleotide
source                  1..1528
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 124
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agtaacgcgt ggataacctg cctcacactg ggggataaca gttagaaatg actgctaata  180
ccgcataagc gcacagtacc gcatggtacg gtgtgaaaaa ctccggtggt gtgagatgga  240
tccgcgtctg attagccagt tggcggggta acggcccacc aaagcgacga tcagtagccg  300
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gaagtatttc ggtatgtaaa gctctatcag cagggaagaa aatgacggta cctgactaag  480
aagccccggc taactacgtg ccagcagccg cggtaatacg taggggggcaa gcgttatccg  540
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ctcaaccctg ggactgcttt ggaaactgtt ttgctagagt gtcggagagg taagtggaat  660
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aattgacggg gacccgcaca agcggtggag catgtggttt aattcgaagc aacgcgaaga  960
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caccgcccgt cacaccatgg gagtcagcaa cgcccgaagt cagtgaccca actcgcaaga  1440
gagggagctg ccgaaggcgg ggcaggtaac tggggtgaag tcgtaacaag gtagccgtat  1500
cggaaggtgc ggctggatca cctccttt                                     1528

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misc_feature            1..1530
                        note = Synthetic Polynucleotide
source                  1..1530
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 125
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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
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agaagccccg gctaactacg tgccagcagc cgcggtaata cgtagggggc aagcgttatc  540
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caagagagac aggtggtgca tggttgtcgt cagctcgtgt cgtgagatgt tgggttaagt  1080
cccgcaacga gcgcaaccct tatccttagt agccagcagg taaagctggg cactctaggg  1140
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gatttgggct acacacgtgc tacaatggcg taaacaaagg gaagcaagac agtgatgtgg  1260
agcaaatccc aaaaataacg tcccagttcg gactgtagtc tgcaacccga ctacacgaag  1320
ctggaatcgc tagtaatcgc gaatcagaat gtcgcggtga atacgttccc gggtcttgta  1380
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gagagggagc tgccgaaggc ggggcaggta actggggtga agtcgtaaca aggtagccgt  1500
atcggaaggt gcggctggat cacctccttt                                   1530

SEQ ID NO: 126          moltype = DNA  length = 1528
FEATURE                 Location/Qualifiers
misc_feature            1..1528
                        note = Synthetic Polynucleotide
source                  1..1528
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 126
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aacgaagcaa ttaaaatgaa gttttcggat ggatttttga ttgactgagt ggcggacggg  120
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gaagccccgg ctaactacgt gccagcagcc gcggtaatac gtagggggca agcgttatcc  540
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gctcaaccct gggactgctt tggaaactgt tttgctagag tgtcggagag gtaagtggaa  660
ttcctagtgt agcggtgaaa tgcgtagata ttaggaggaa caccagtggc gaaggcggct  720
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ctggtagtcc acgccgtaaa cgatgaatgc taggtgttgg gggcaaagcc cttcggtgcc  840
gtcgcaaacg cagtaagcat tccacctggg gagtacgttc gcaagaatga aactcaaagg  900
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caccgcccgt cacaccatgg gagtcagcaa cgcccgaagt cagtgaccca actcgcaaga  1440
gagggagctg ccgaaggcgg ggcaggtaac tggggtgaag tcgtaacaag gtagccgtat  1500
cggaaggtgc ggctggatca cctccttt                                     1528
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SEQ ID NO: 127          moltype = DNA  length = 1528
FEATURE                 Location/Qualifiers
misc_feature            1..1528
                        note = Synthetic Polynucleotide
source                  1..1528
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 127
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SEQ ID NO: 128          moltype = DNA  length = 1528
FEATURE                 Location/Qualifiers
misc_feature            1..1528
                        note = Synthetic Polynucleotide
source                  1..1528
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 128
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aacgaagcaa ttaaaatgaa gttttcggat ggattttaat tgactgagtg gcggacgggt  120
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accgcataag cgcacagtac cgcatggtac ggtgtgaaaa actccggtgg tgtgagatgg  240
atccgcgtct gattagccag ttggcggggt aacggcccac caaagcgacg atcagtagcc  300
gacctgagag ggtgaccggc cacattggga ctgagacacg gcccaaactc ctacgggagg  360
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gaagccccgg ctaactacgt gccagcagcc gcggtaatac gtagggggca agcgttatcc  540
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cggaaggtgc ggctggatca cctccttt                                     1528
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FEATURE                 Location/Qualifiers
misc_feature            1..1522
                        note = Synthetic Polynucleotide
source                  1..1522
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 129
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SEQ ID NO: 130          moltype = DNA  length = 1521
FEATURE                 Location/Qualifiers
misc_feature            1..1521
                        note = Synthetic Polynucleotide
source                  1..1521
                        mol_type = other DNA
                        organism = synthetic construct
SEQUENCE: 130
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attcctagtg tagcggtgaa atgcgtagat attaggagga acaccagtgg cgaaggcggc  720
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cccgtcacac catgggagtc ggtaacaccc gaagccagta gcctaaccgc aagggggcg   1440
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source                  1..1522
                        mol_type = other DNA
                        organism = synthetic construct
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source                  1..1529
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                        note = Synthetic Polynucleotide
source                  1..1529
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                        organism = synthetic construct
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source                  1..1529
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                        note = Synthetic Polynucleotide
source                  1..1529
                        mol_type = other DNA
                        organism = synthetic construct
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                        organism = synthetic construct
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SEQ ID NO: 147 moltype = DNA length = 1528
FEATURE Location/Qualifiers
misc_feature 1..1528
note = Synthetic Polynucleotide
source 1..1528
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 147

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SEQ ID NO: 148 moltype = DNA length = 1529
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note = Synthetic Polynucleotide
source 1..1529
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 148

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SEQ ID NO: 149          moltype = DNA  length = 1529
FEATURE                 Location/Qualifiers
misc_feature            1..1529
                        note = Synthetic Polynucleotide
source                  1..1529
                        mol_type = other DNA
                        organism = synthetic construct
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                        note = Synthetic Polynucleotide
source                  1..1528
                        mol_type = other DNA
                        organism = synthetic construct
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                        note = Synthetic Polynucleotide
source                  1..1529
                        mol_type = other DNA
                        organism = synthetic construct
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source                  1..1537
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                        organism = synthetic construct
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source                  1..1537
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SEQ ID NO: 154 moltype = DNA length = 1537
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misc_feature 1..1537
note = Synthetic Polynucleotide
source 1..1537
mol_type = other DNA
organism = synthetic construct
SEQUENCE: 154

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organism = synthetic construct
SEQUENCE: 157

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source                  1..1529
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                        organism = synthetic construct
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What is claimed is:

1. A pharmaceutical composition comprising a purified bacterial mixture, wherein the purified bacterial mixture consists of 7 to 10 bacterial strains, wherein the purified bacterial mixture comprises at least 7 of:

(i) a bacterial strain comprising a 16S rDNA sequence having at least 97% sequence identity to the nucleotide sequence of SEQ ID NO: 157;

(ii) a bacterial strain comprising a 16S rDNA sequence having at least 97% sequence identity to the nucleotide sequence of SEQ ID NO: 129;

(iii) a bacterial strain comprising a 16S rDNA sequence having at least 97% sequence identity to the nucleotide sequence of SEQ ID NO: 132;

(iv) a bacterial strain comprising a 16S rDNA sequence having at least 97% sequence identity to the nucleotide sequence of SEQ ID NO: 137;

(v) a bacterial strain comprising a 16S rDNA sequence having at least 97% sequence identity to the nucleotide sequence of SEQ ID NO: 124;

(vi) a bacterial strain comprising a 16S rDNA sequence having at least 97% sequence identity to the nucleotide sequence of SEQ ID NO: 141;

(vii) a bacterial strain comprising a 16S rDNA sequence having at least 97% sequence identity to the nucleotide sequence of SEQ ID NO: 146; and

(viii) a bacterial strain comprising a 16S rDNA sequence having at least 97% sequence identity to the nucleotide sequence of SEQ ID NO: 152,

wherein the bacterial strains are lyophilized.

2. The pharmaceutical composition of claim 1, wherein the purified bacterial mixture comprises:

(i) a bacterial strain comprising a 16S rDNA sequence having at least 99% sequence identity to the nucleotide sequence of SEQ ID NO: 157;

(ii) a bacterial strain comprising a 16S rDNA sequence having at least 99% sequence identity to the nucleotide sequence of SEQ ID NO: 129;

(iii) a bacterial strain comprising a 16S rDNA sequence having at least 99% sequence identity to the nucleotide sequence of SEQ ID NO: 132;

(iv) a bacterial strain comprising a 16S rDNA sequence having at least 99% sequence identity to the nucleotide sequence of SEQ ID NO: 137;

(v) a bacterial strain comprising a 16S rDNA sequence having at least 99% sequence identity to the nucleotide sequence of SEQ ID NO: 124;

(vi) a bacterial strain comprising a 16S rDNA sequence having at least 99% sequence identity to the nucleotide sequence of SEQ ID NO: 141;

(vii) a bacterial strain comprising a 16S rDNA sequence having at least 99% sequence identity to the nucleotide sequence of SEQ ID NO: 146; and

(viii) a bacterial strain comprising a 16S rDNA sequence having at least 99% sequence identity to the nucleotide sequence of SEQ ID NO: 152.

3. The pharmaceutical composition of claim 1, wherein the pharmaceutical composition comprises a pH-sensitive composition comprising one or more enteric polymers.

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

5. The pharmaceutical composition of claim 1, wherein the pharmaceutical composition comprises between 1×10^7 and 1×10^{10} colony forming units (CFUs) per bacterial strain.

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

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

8. The pharmaceutical composition of claim 1, wherein the pharmaceutical composition is formulated for rectal administration.

9. The pharmaceutical composition of claim 1, wherein the pharmaceutical composition is formulated for delivery to the intestine.

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

11. A method of reducing the likelihood of a *Clostridium difficile* infection in a subject, the method comprising administering the pharmaceutical composition of claim 1 to the subject in a therapeutically effective amount to reduce the likelihood of the *Clostridium difficile* infection.

12. The method of claim 11, wherein the *Clostridium difficile* infection is a first occurrence of a *Clostridium difficile* infection.

13. The method of claim 11, wherein the *Clostridium difficile* infection is a recurrence of *Clostridium difficile* infection.

14. The method of claim 11, wherein the subject is administered one or more doses of an antibiotic prior to the pharmaceutical composition.

15. The method of claim 14, wherein the antibiotic is vancomycin, kanamycin, gentamicin, colistin, metronidazole, clindamycin, fidaxomicin, or cefoperazone.

16. The method of claim 14, wherein the antibiotic is vancomycin.

17. A method to suppress an abnormal or excessive immune response in a subject comprising administering the pharmaceutical composition of claim 1 to the subject in a therapeutically effective amount to suppress the abnormal or excessive immune response.

18. The method of claim 17, wherein the abnormal or excessive immune response is suppressed by inducing proliferation and/or accumulation of regulatory T cells.

19. The method of claim 17, wherein the subject is administered one or more doses of an antibiotic prior to the pharmaceutical composition.

20. The method of claim 19, wherein the antibiotic is vancomycin, kanamycin, gentamicin, colistin, metronidazole, clindamycin, fidaxomicin, or cefoperazone.

* * * * *