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(54) **PROBIOTIC AND PREBIOTIC COMPOSITIONS, AND METHODS OF USE THEREOF FOR TREATMENT AND PREVENTION OF GRAFT VERSUS HOST DISEASE**

(71) Applicant: **Epiva Biosciences, Inc.**, Cambridge, MA (US)

(72) Inventors: **David Berry**, Waban, MA (US); **Noubar B. Afeyan**, Lexington, MA (US); **Johanne Kaplan**, Sherborn, MA (US); **Neal Gordon**, Brookline, MA (US); **Shaila Rahman**, Cambridge, MA (US)

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(60) Provisional application No. 62/257,714, filed on Nov. 19, 2015, provisional application No. 62/162,562, filed on May 15, 2015, provisional application No. 62/117,632, filed on Feb. 18, 2015, provisional application No. 62/117,637, filed on Feb. 18, 2015, provisional application No. 62/117,639, filed on Feb. 18, 2015, provisional application No. 62/084,536, filed on Nov. 25, 2014, provisional application No. 62/084,537, filed on Nov. 25, 2014, provisional application No. 62/084,540, filed on Nov. 25, 2014.

Publication Classification

(51) **Int. Cl.**

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A61K 35/744	(2006.01)
A61K 35/745	(2006.01)
A61K 35/742	(2006.01)

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

CPC ***A61K 35/747*** (2013.01); ***A61K 35/742*** (2013.01); ***A61K 35/744*** (2013.01); ***A61K 35/745*** (2013.01); *A61K 2035/115* (2013.01)

(57) **ABSTRACT**

Probiotic compositions containing non-pathogenic microbial entities, e.g., bacterial or fungal entities, are described herein. The probiotic compositions may optionally contain or be used in conjunction with one or more prebiotics. Uses of the probiotic compositions to treat or prevent transplant disorders, e.g., graft-versus-host disease (GVHD), in a subject are also provided.

FIG. 1

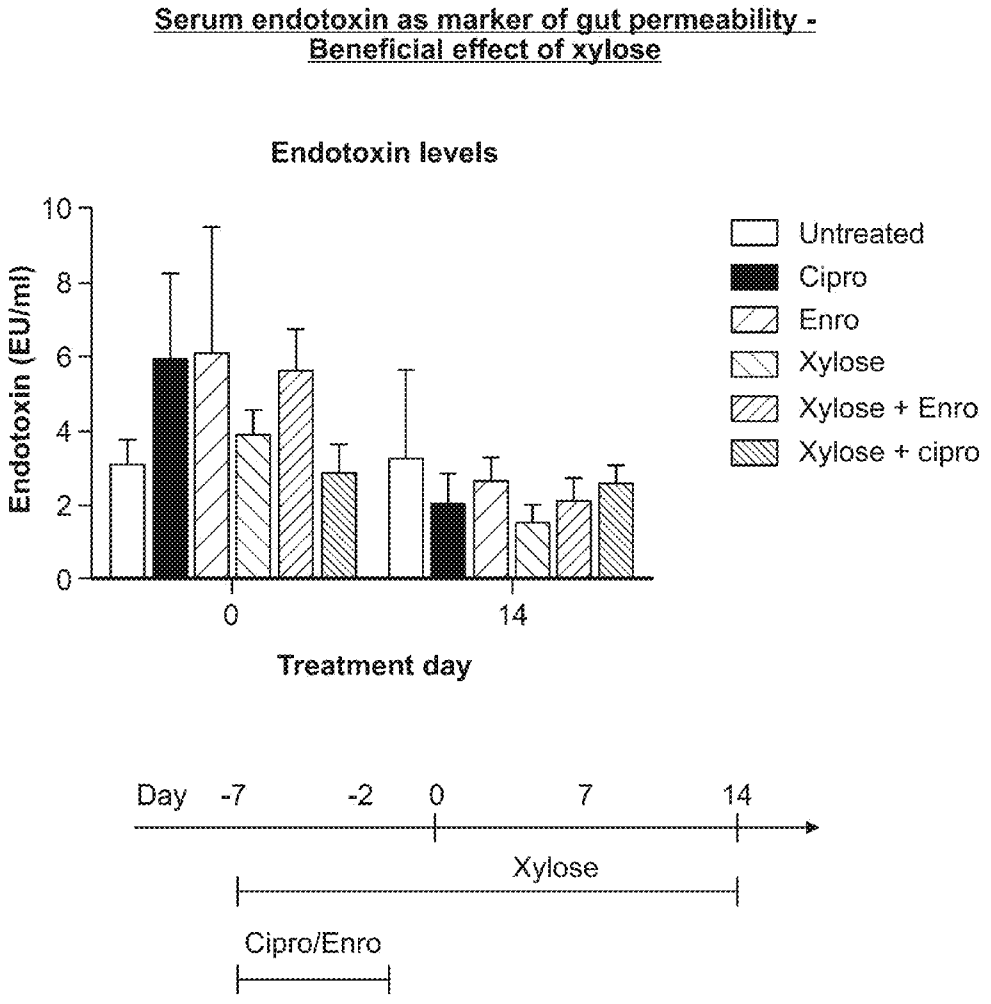

Serum endotoxin as marker of gut permeability -
Beneficial effect of xylose
Endotoxin levels
Endotoxin (EU/ml)
10
8
6
4
2
0
0
14
Treatment day
Untreated
Cipro
Enro
Xylose
Xylose + Enro
Xylose + cipro
Day -7 -2 0 7 14
Xylose
Cipro/Enro

FIG. 2A

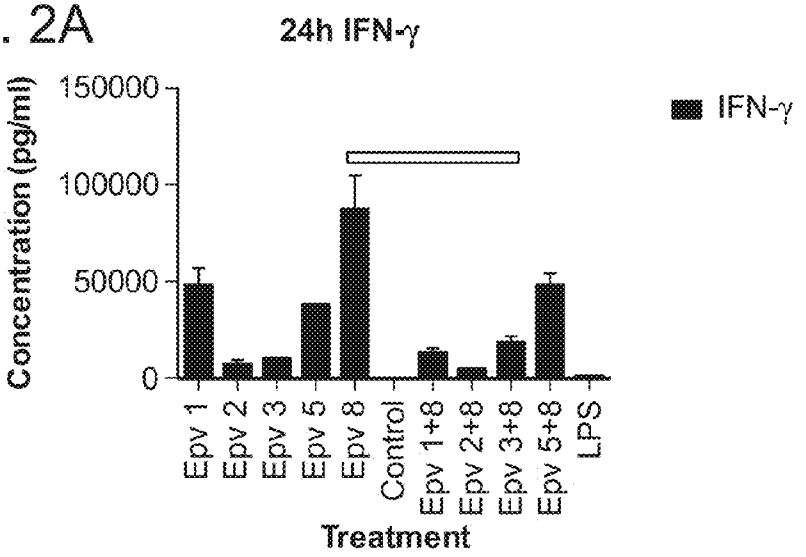


FIG. 2B

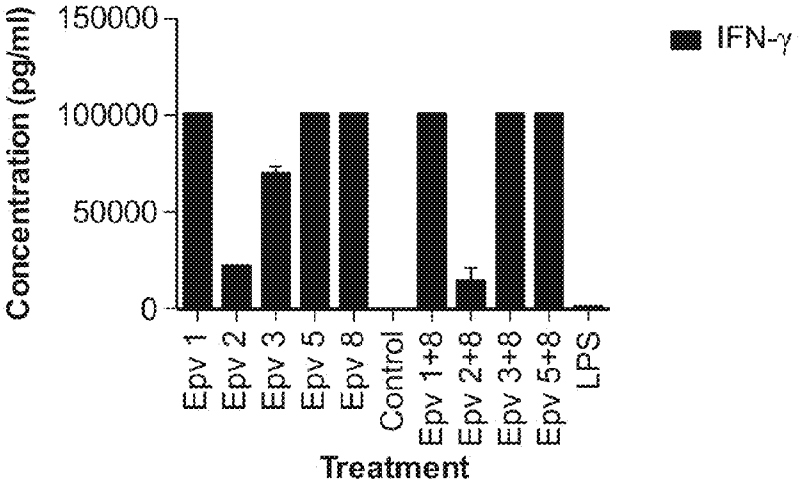


FIG. 2C

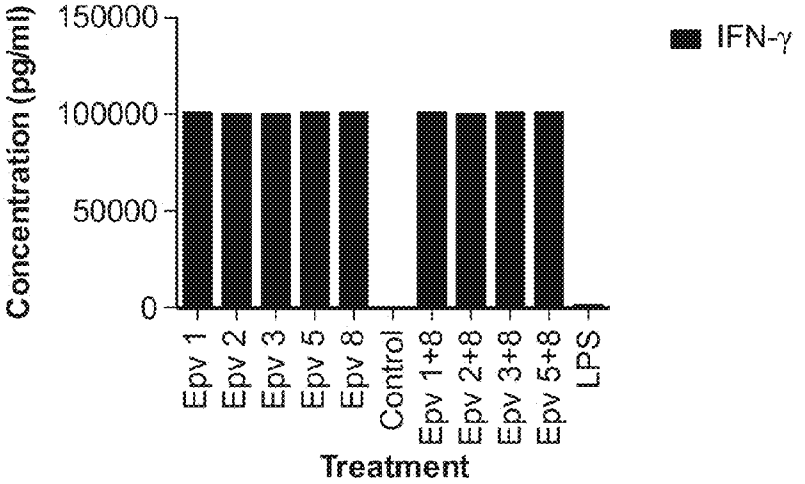


FIG. 2D

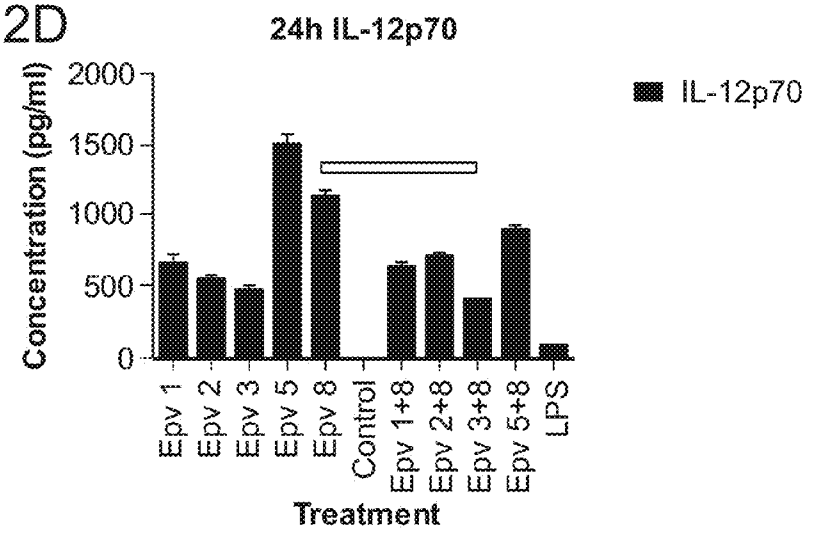


FIG. 2E

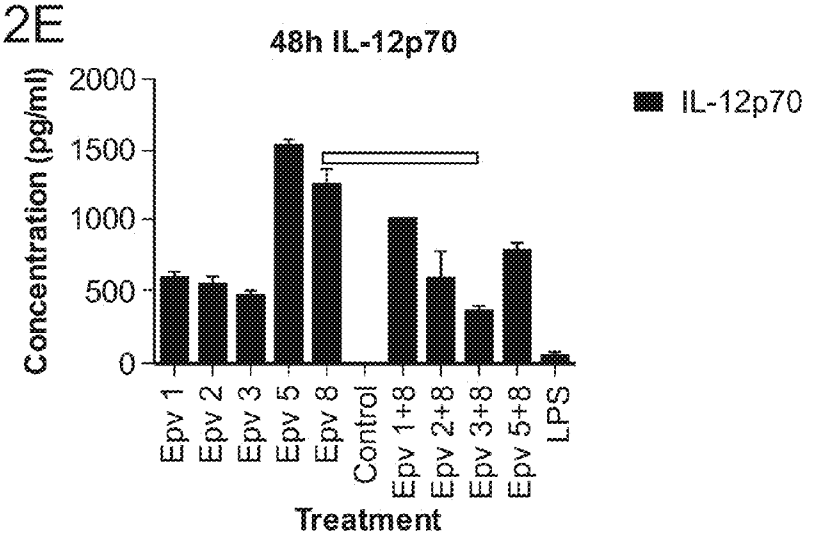


FIG. 2F

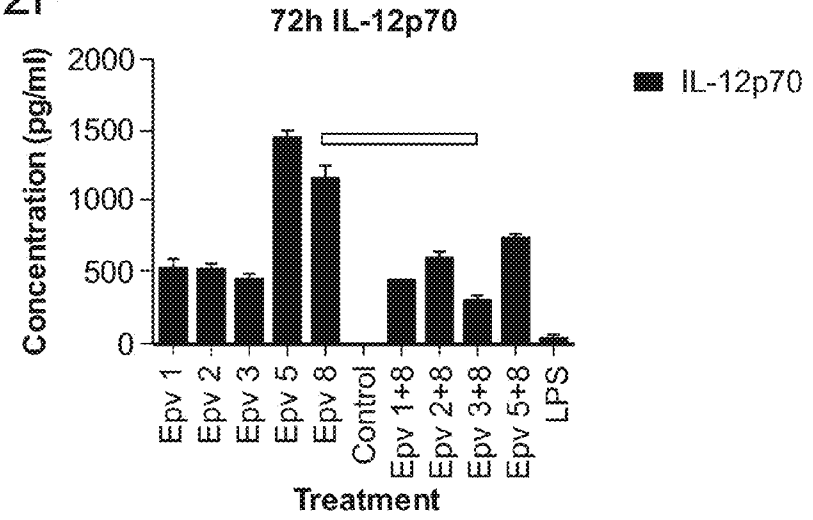


FIG. 2G

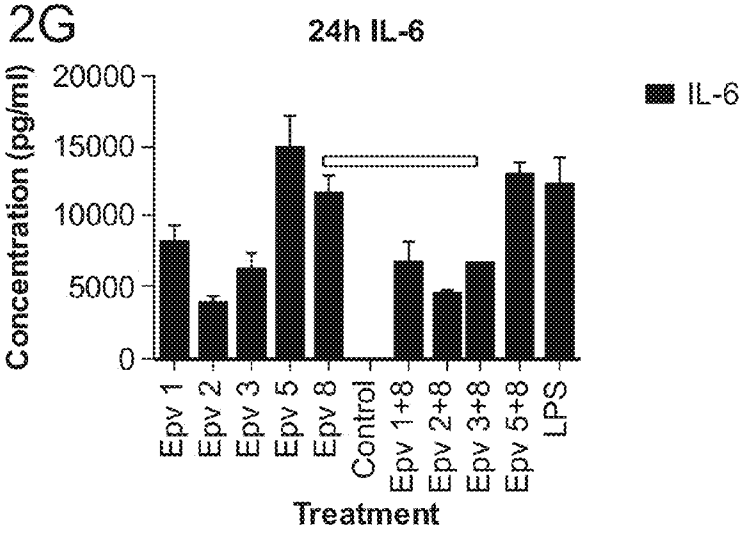


FIG. 2H

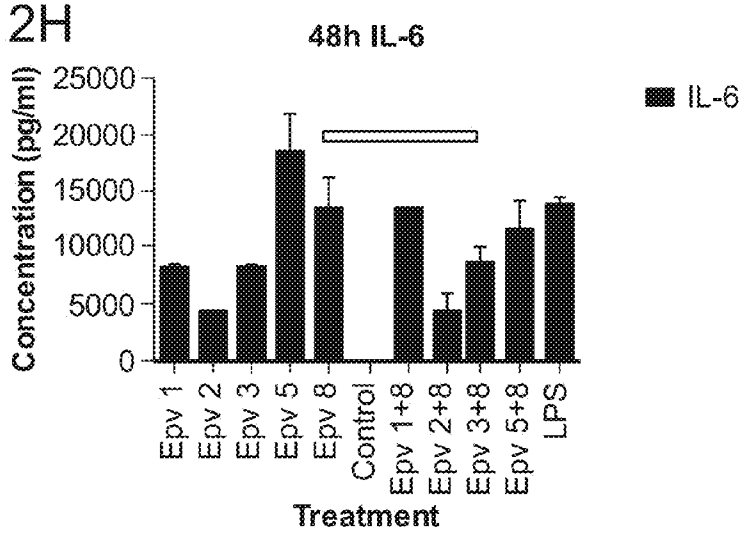


FIG. 2I

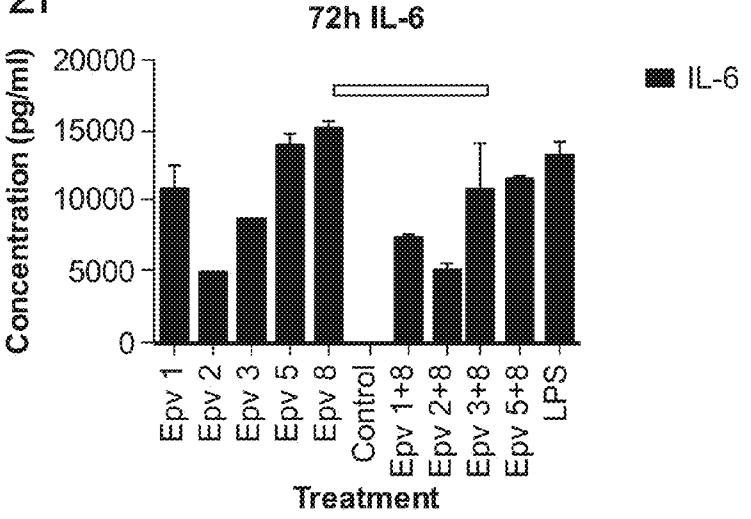


FIG. 2J

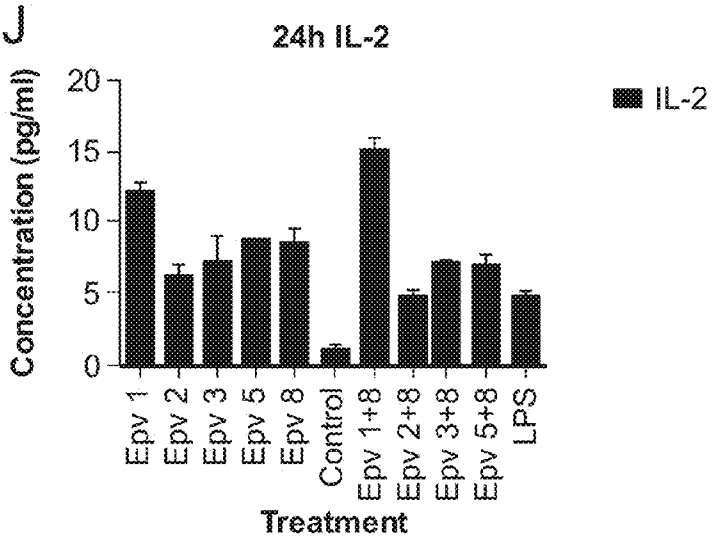


FIG. 2K

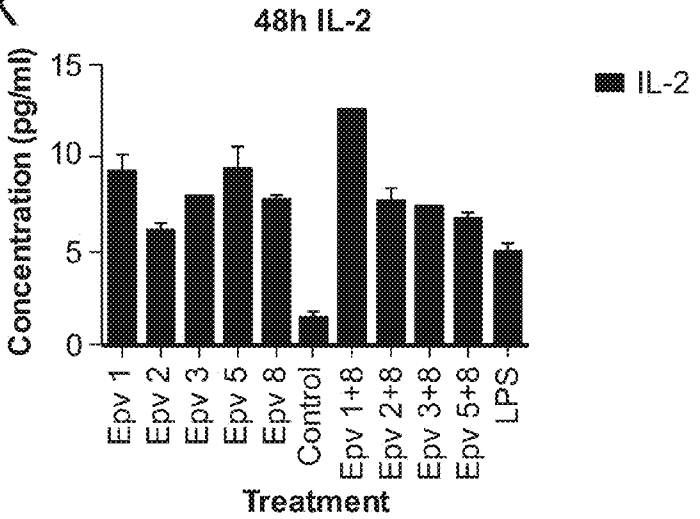


FIG. 2L

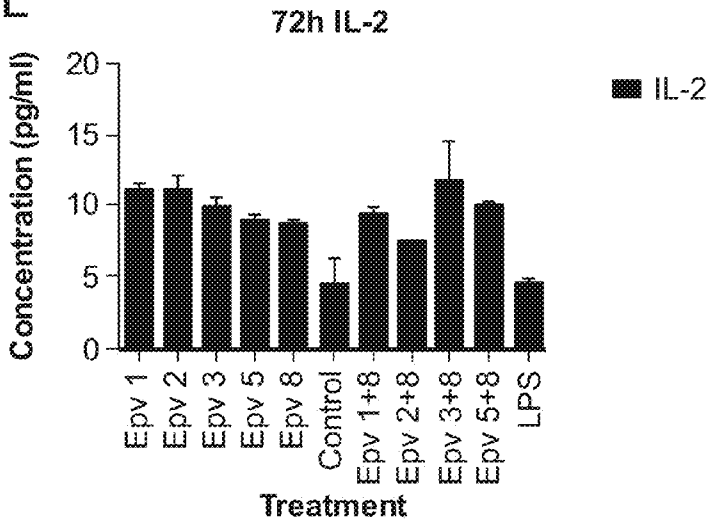


FIG. 2M

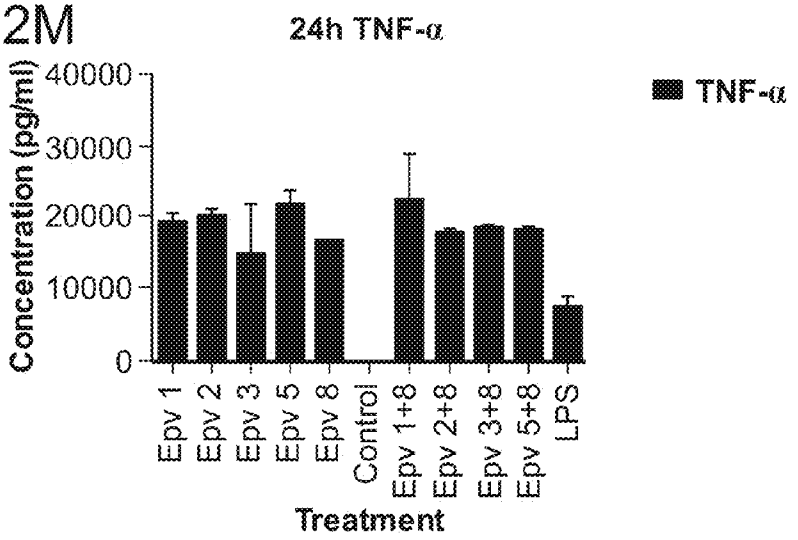


FIG. 2N

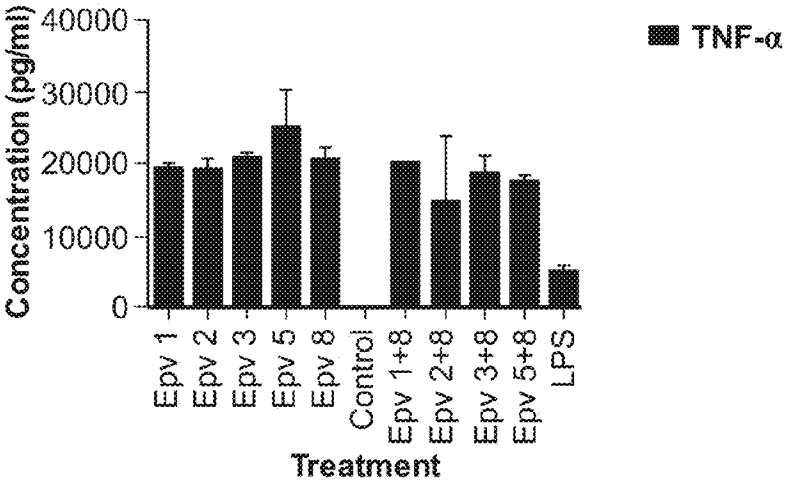


FIG. 2O

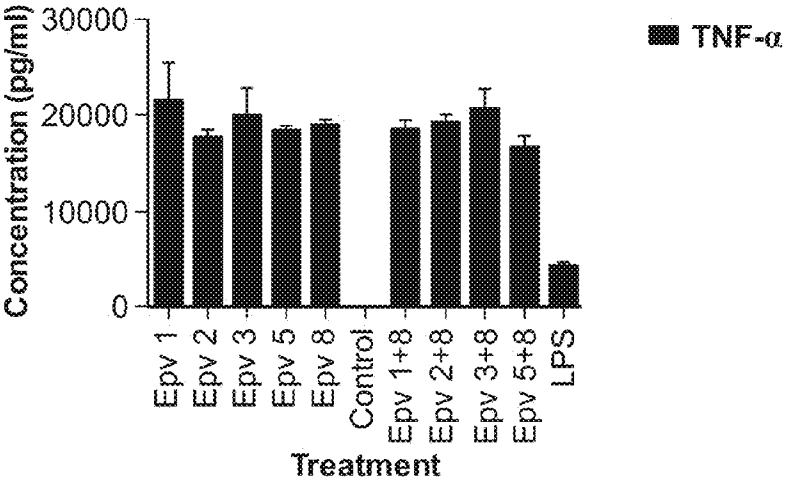


FIG. 3A

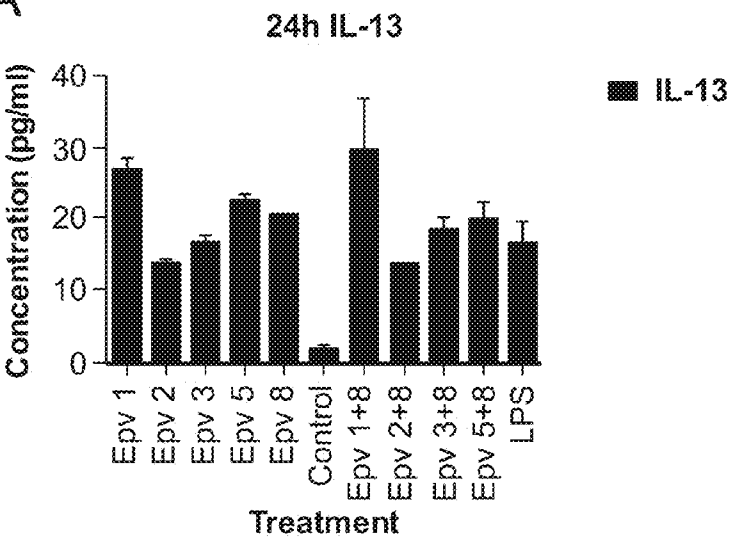


FIG. 3B

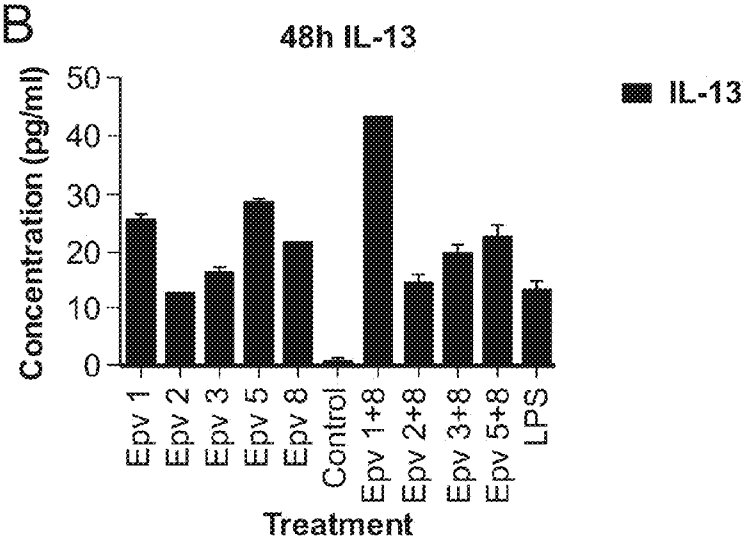


FIG. 3C

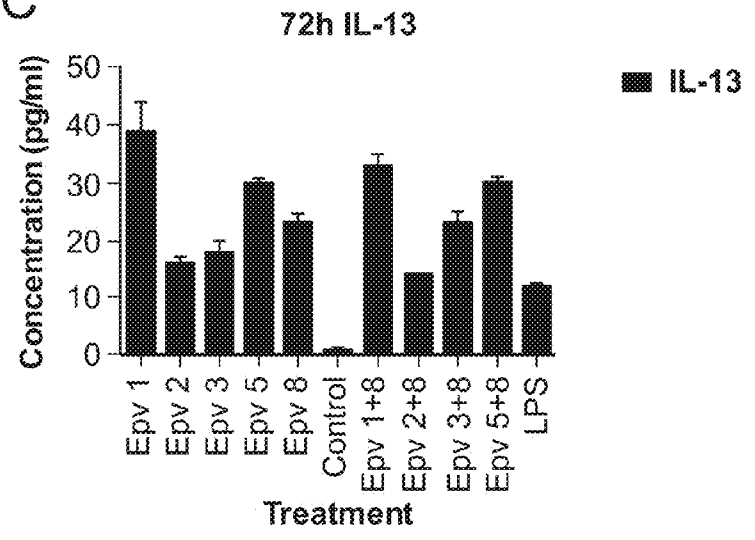


FIG. 3D

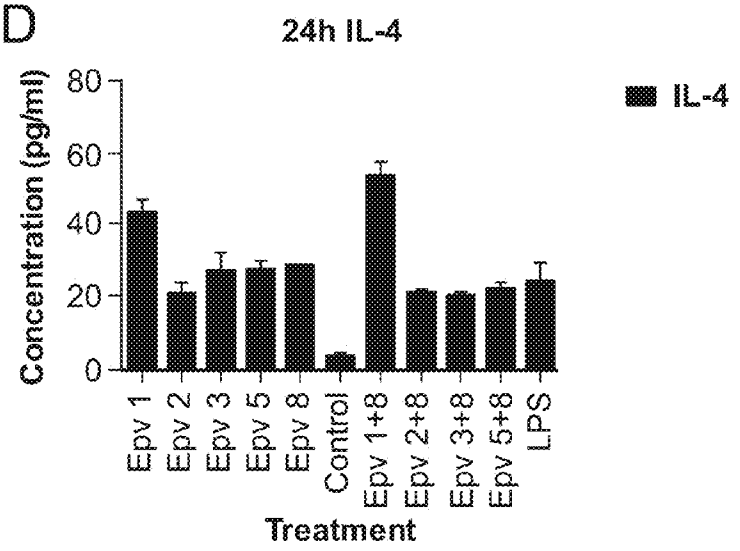
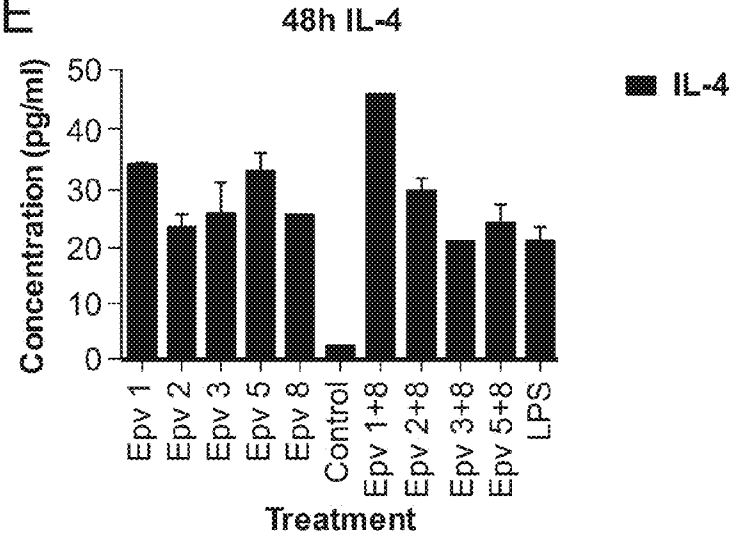


FIG. 3E



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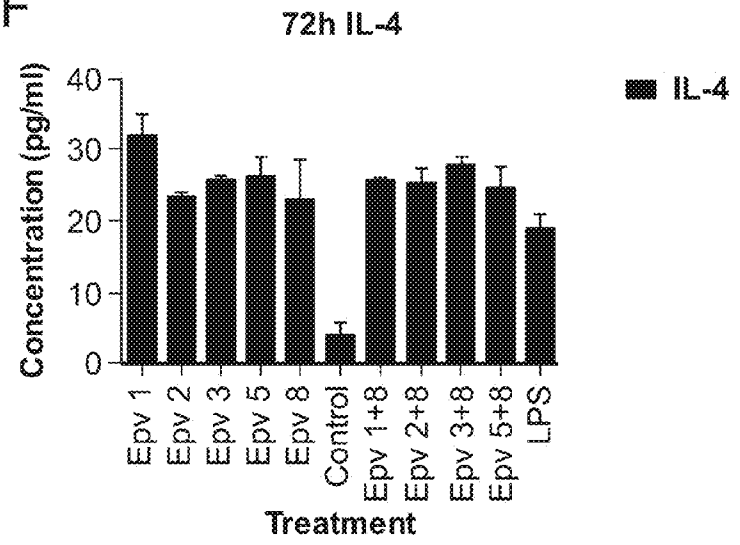

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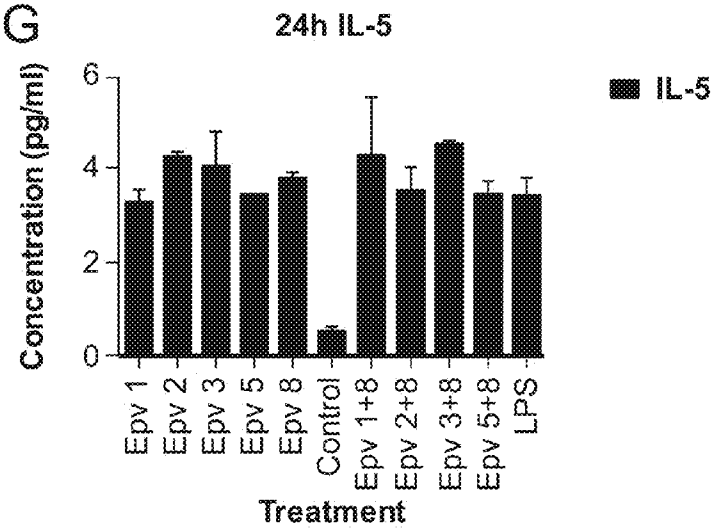

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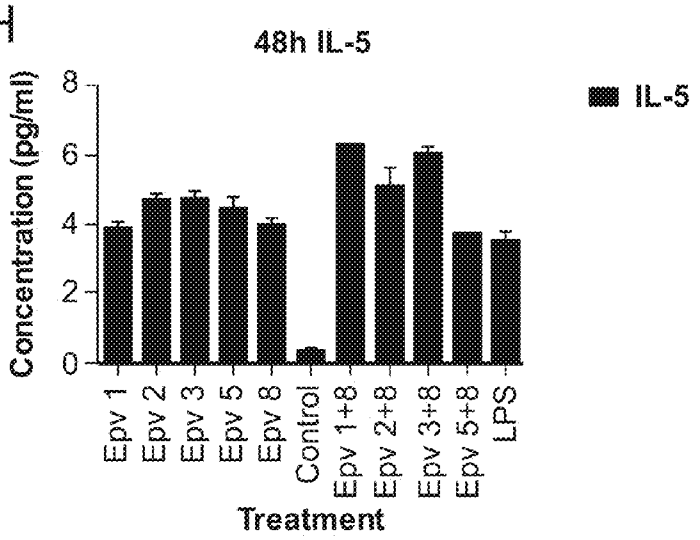


FIG. 3I

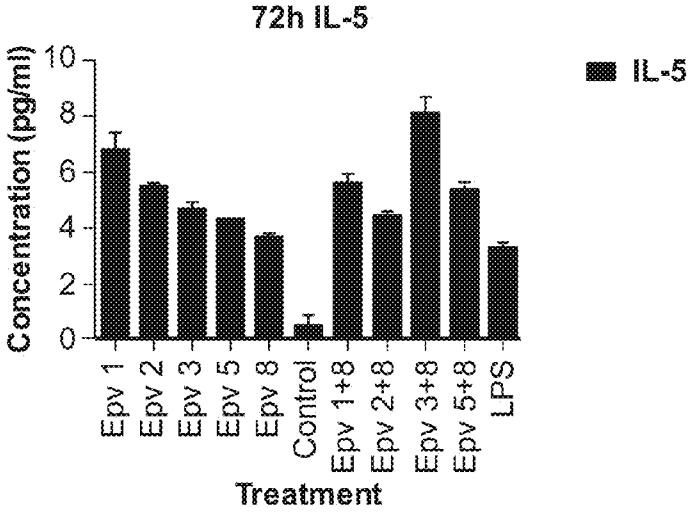


FIG. 4A

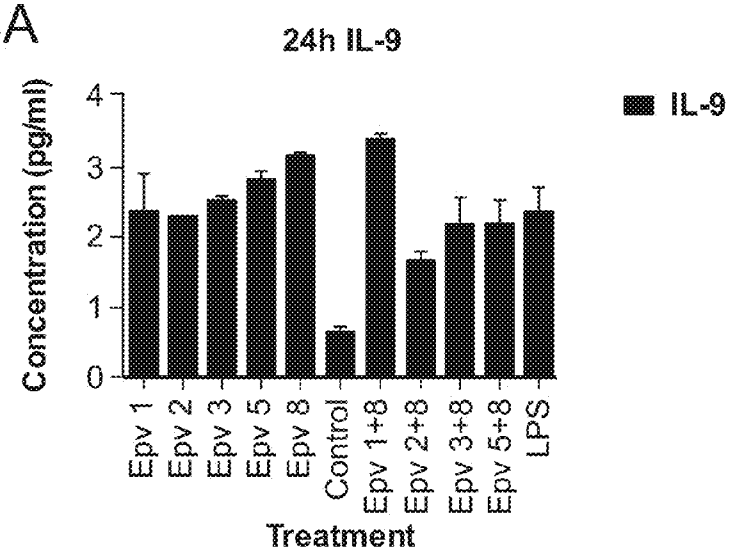


FIG. 4B

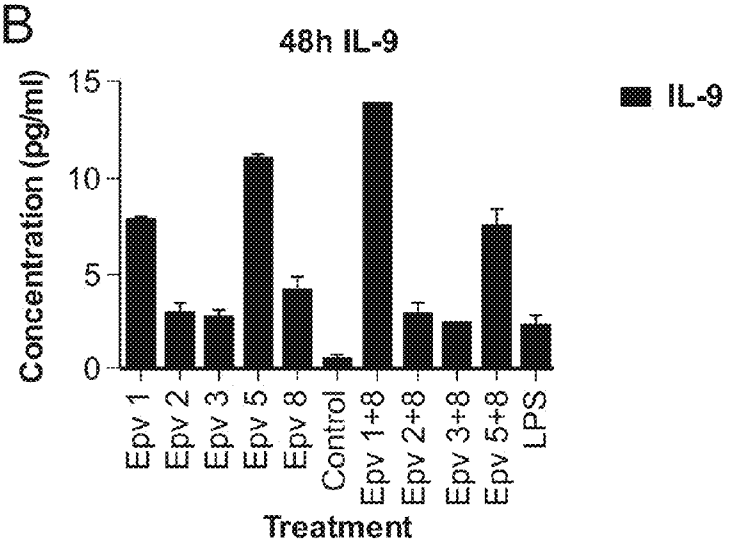


FIG. 4C

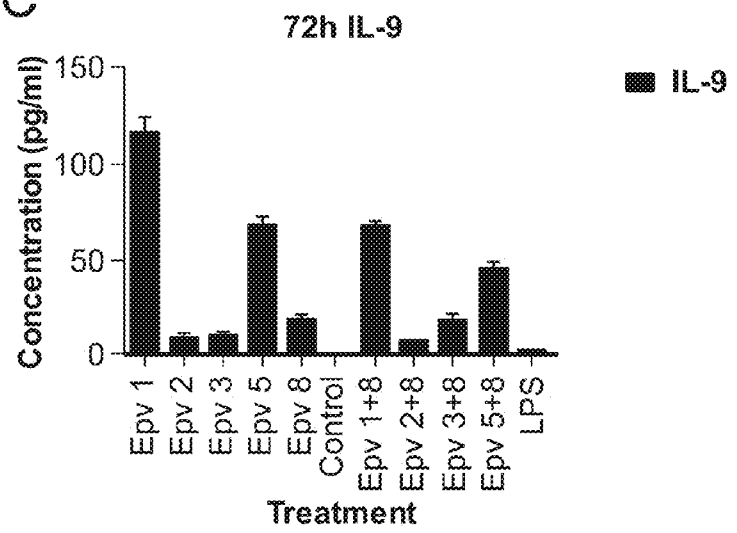
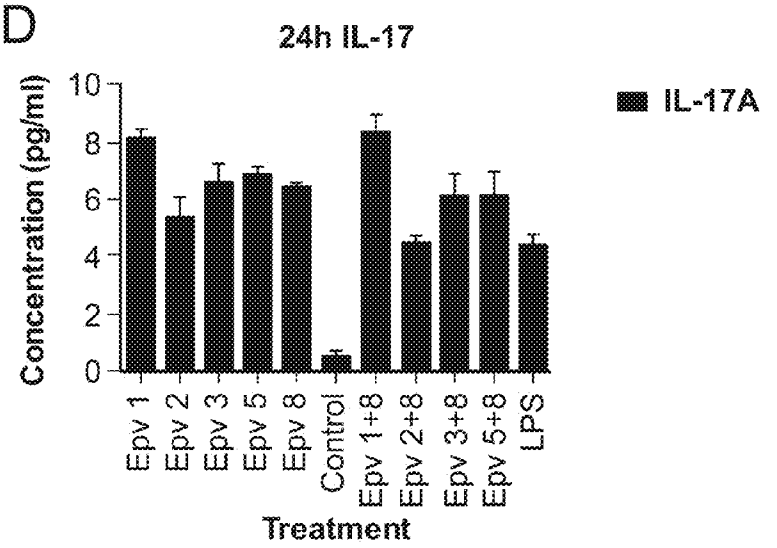


FIG. 4D



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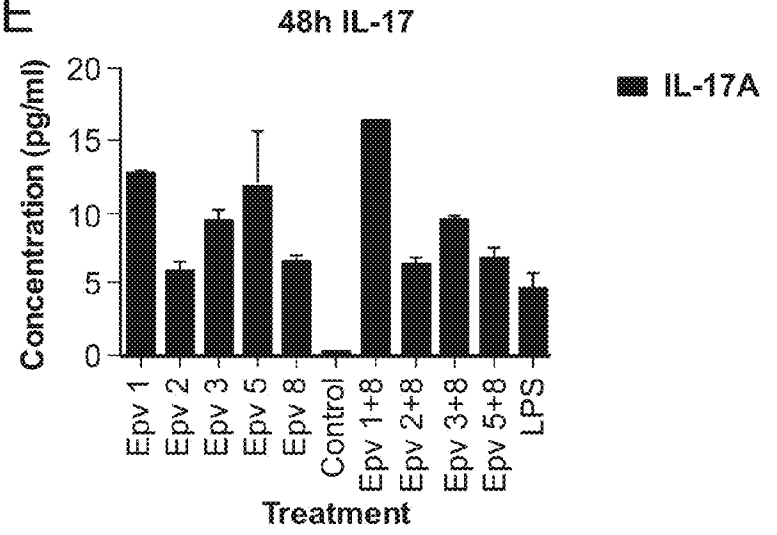

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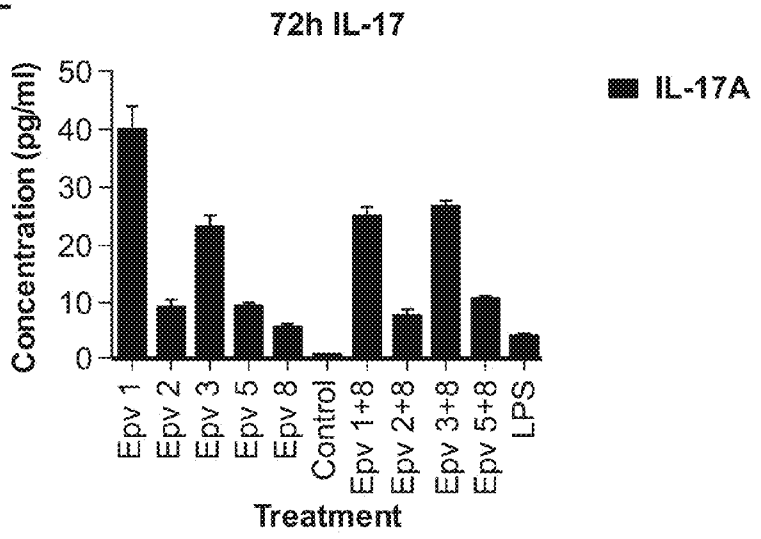

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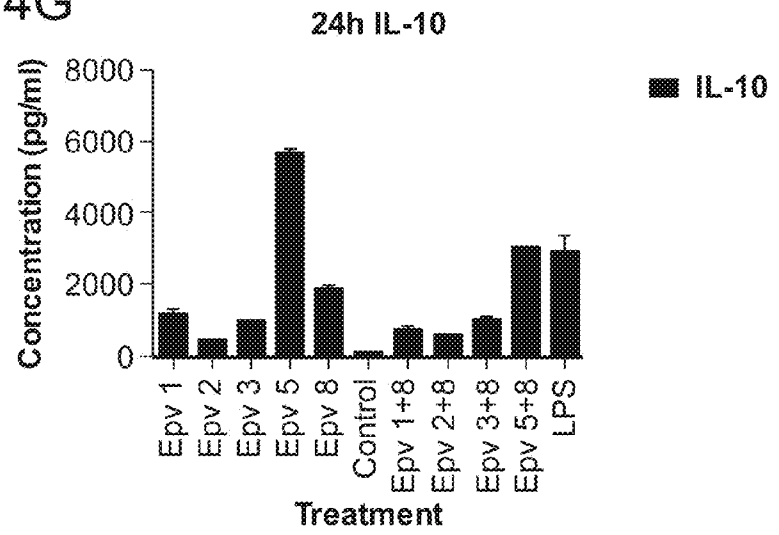

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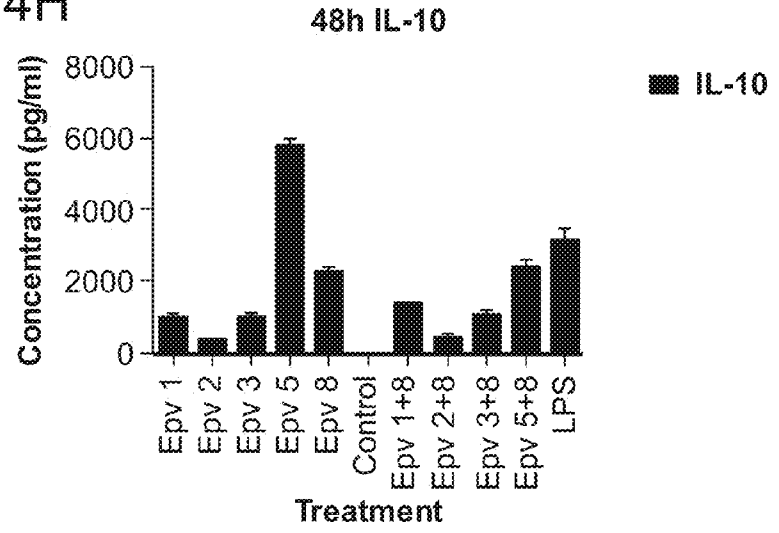


FIG. 4I

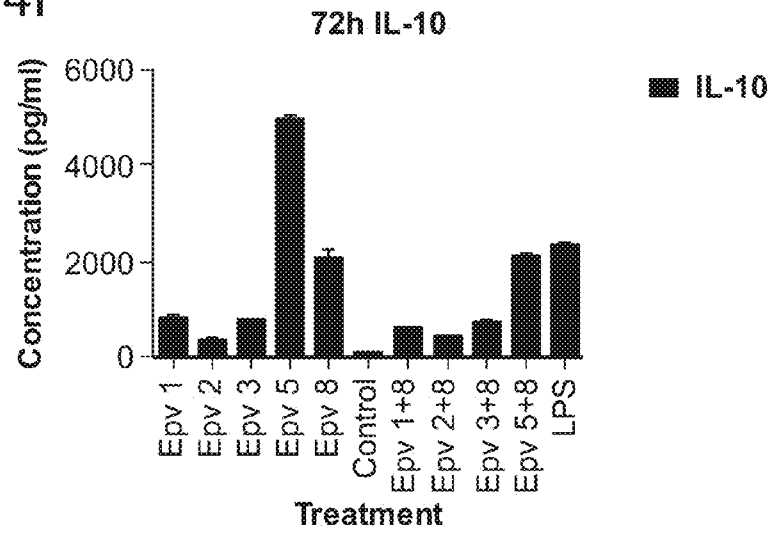


FIG. 5A

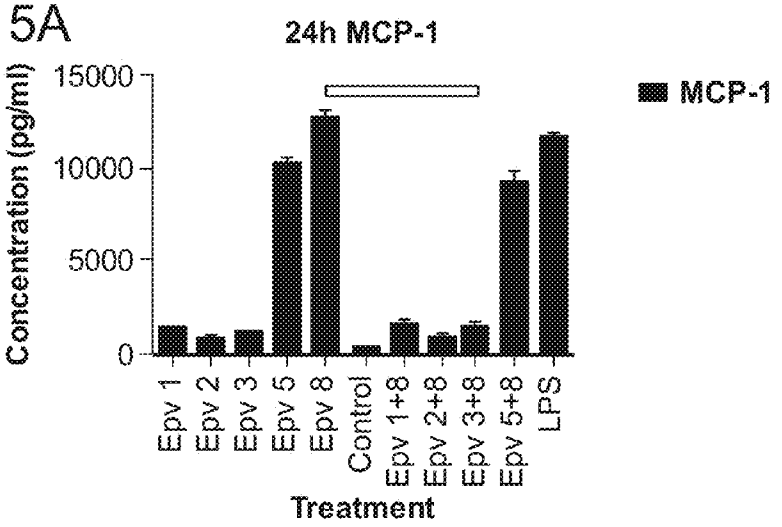


FIG. 5B

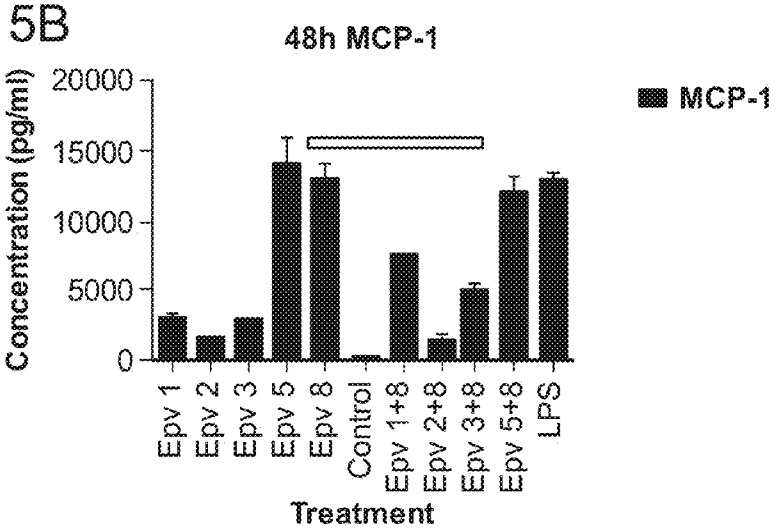
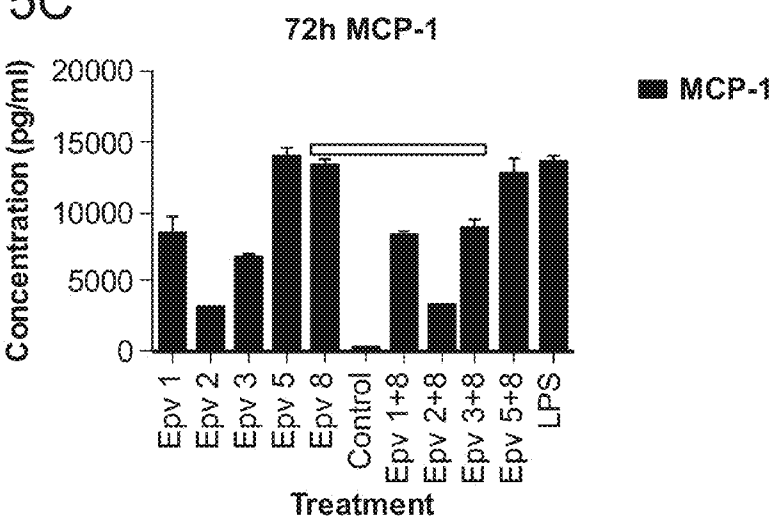


FIG. 5C



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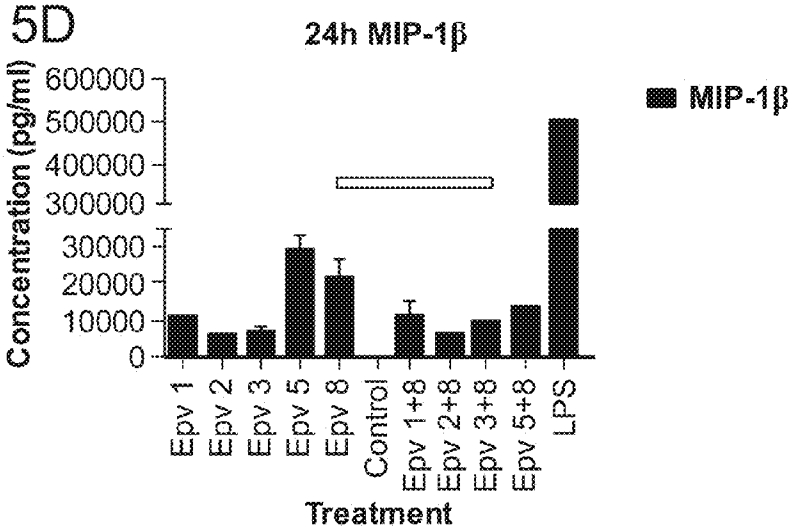
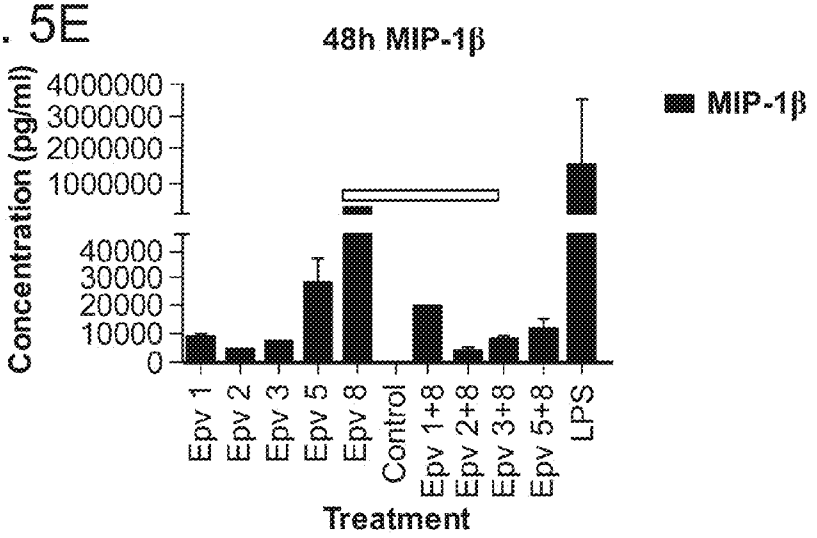


FIG. 5E



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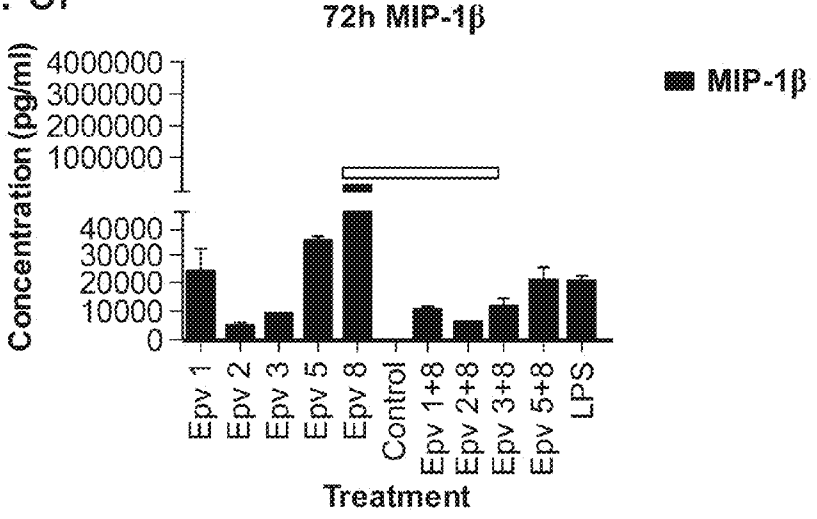

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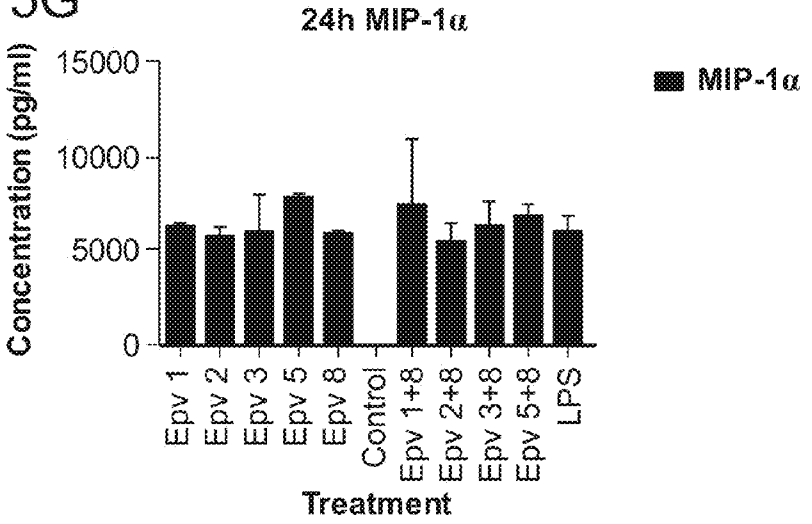

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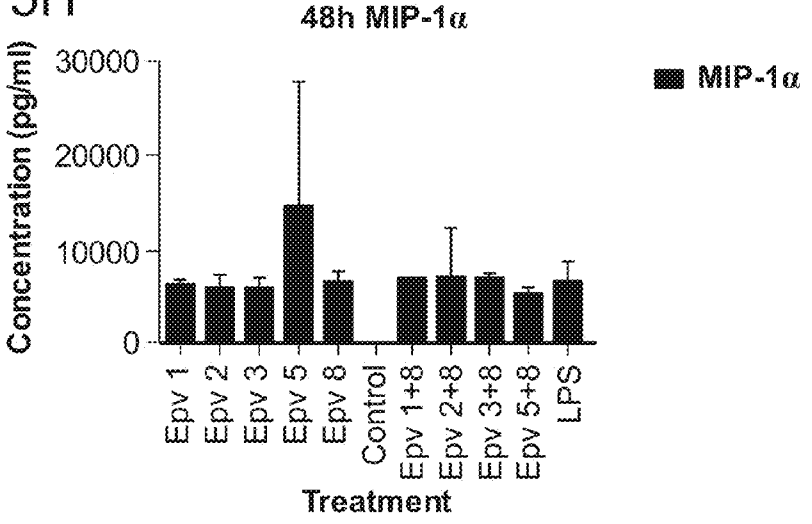


FIG. 5I

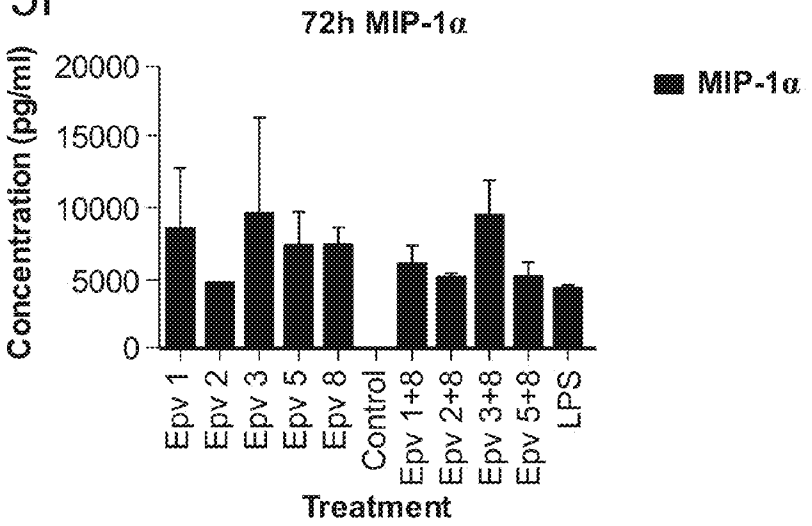


FIG. 5J

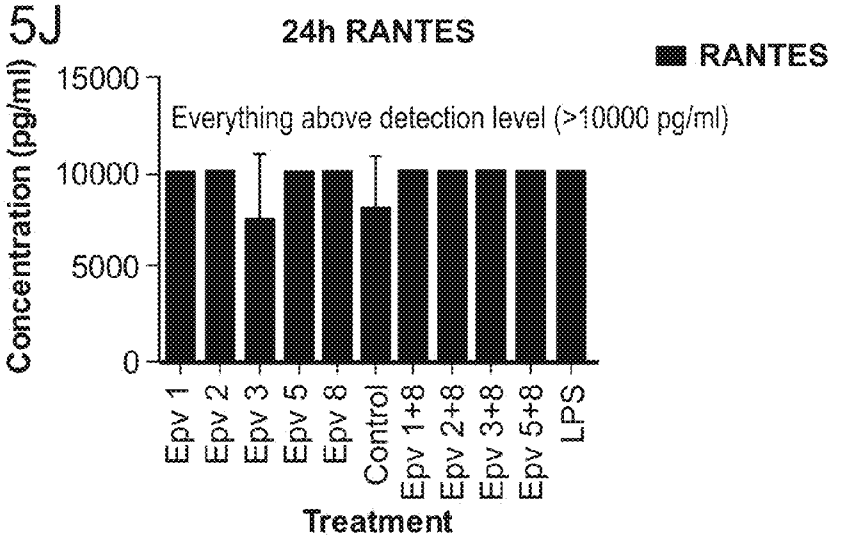


FIG. 5K

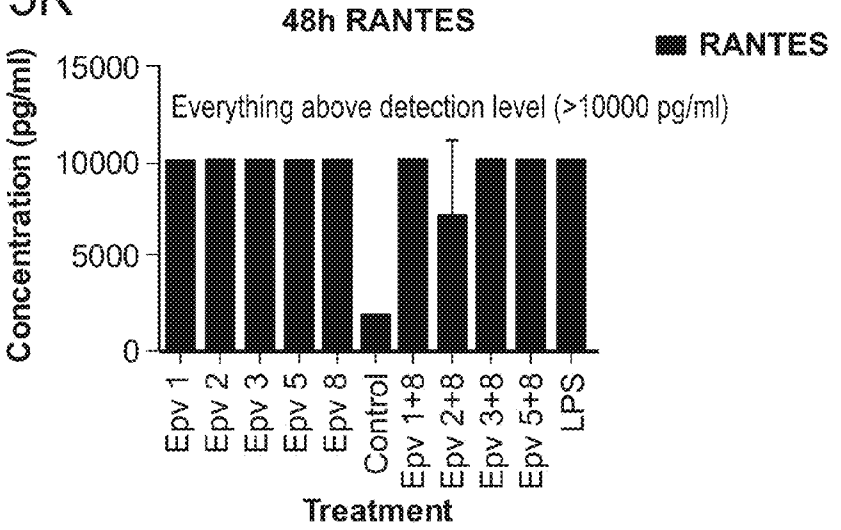


FIG. 5L

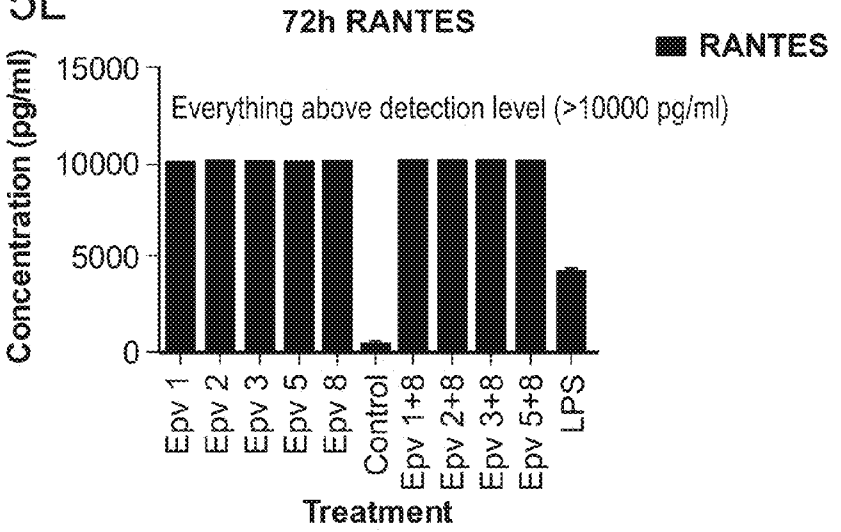


FIG. 5M

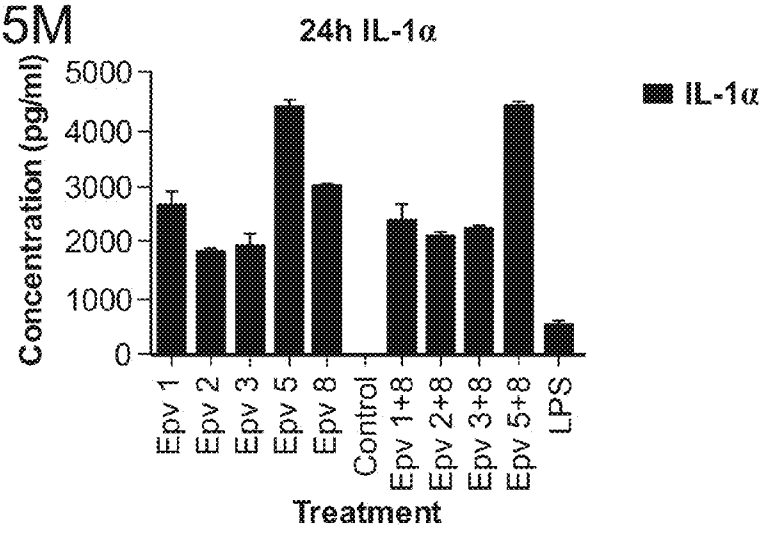


FIG. 5N

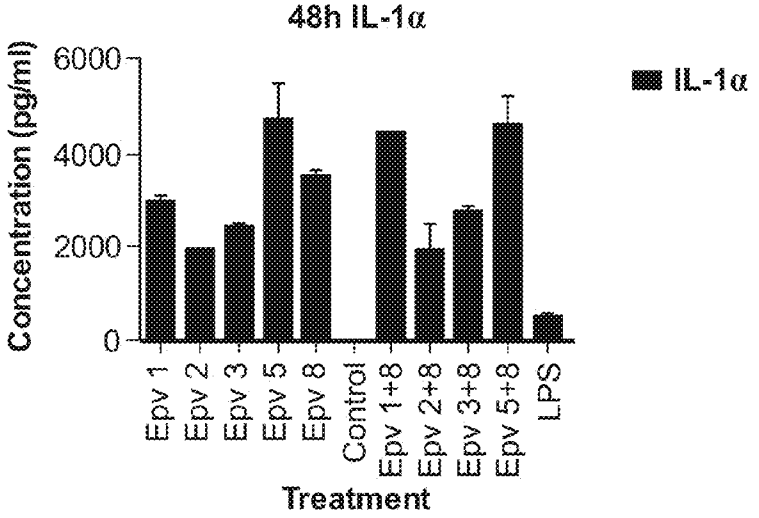


FIG. 5O

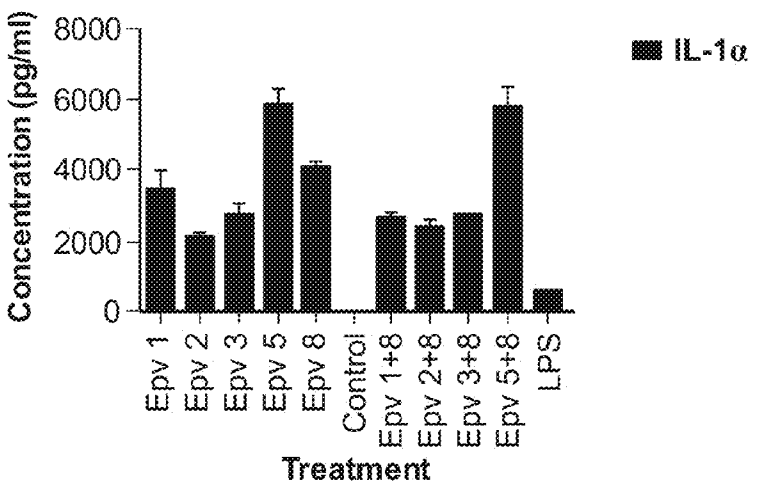


FIG. 5P

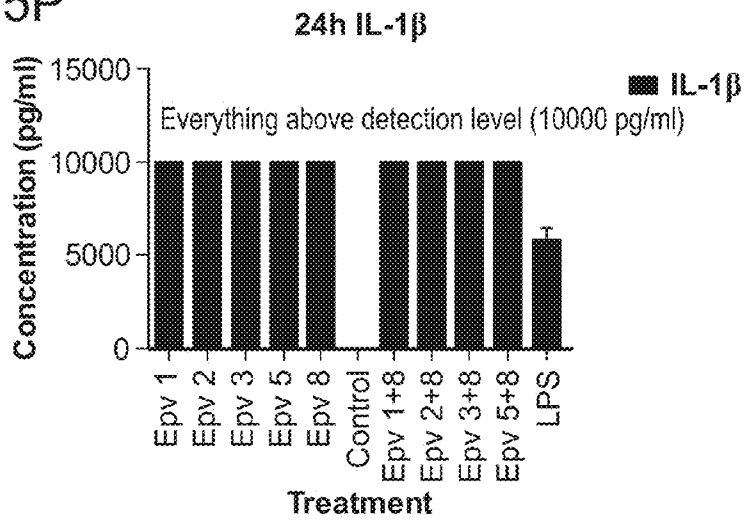


FIG. 5Q

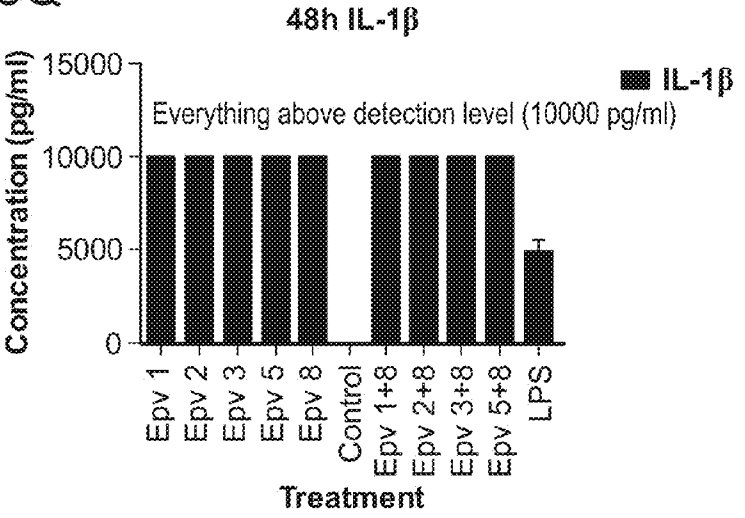


FIG. 5R

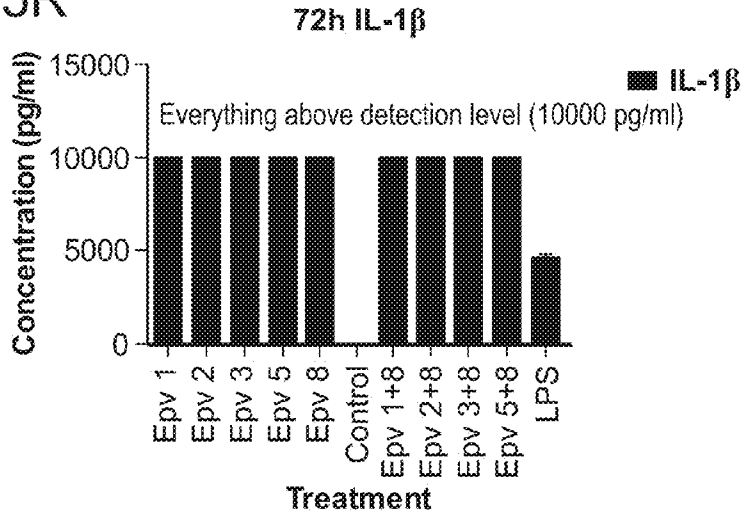


FIG. 5S

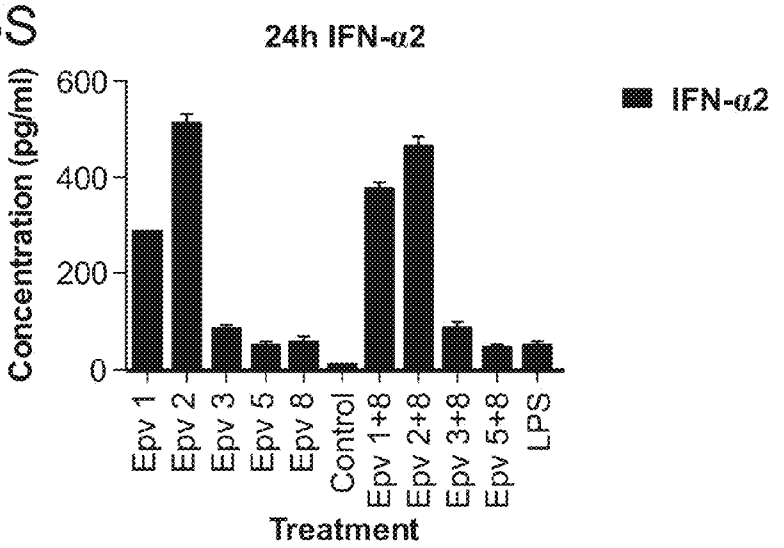


FIG. 5T

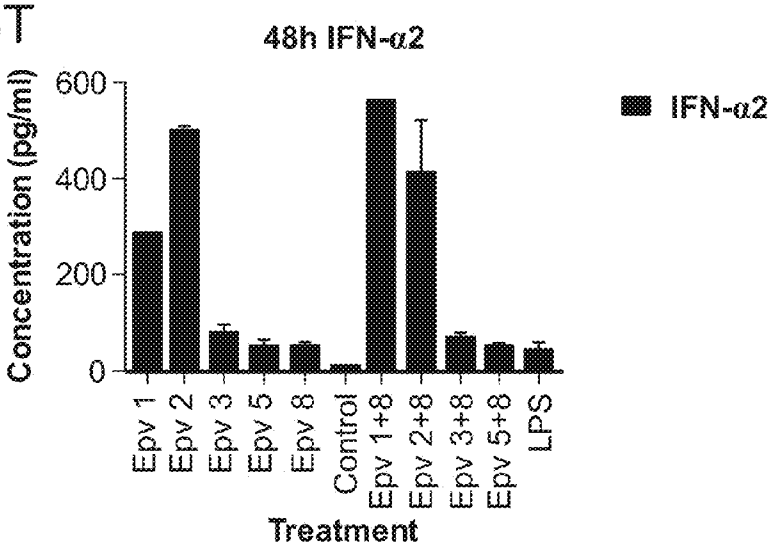


FIG. 5U

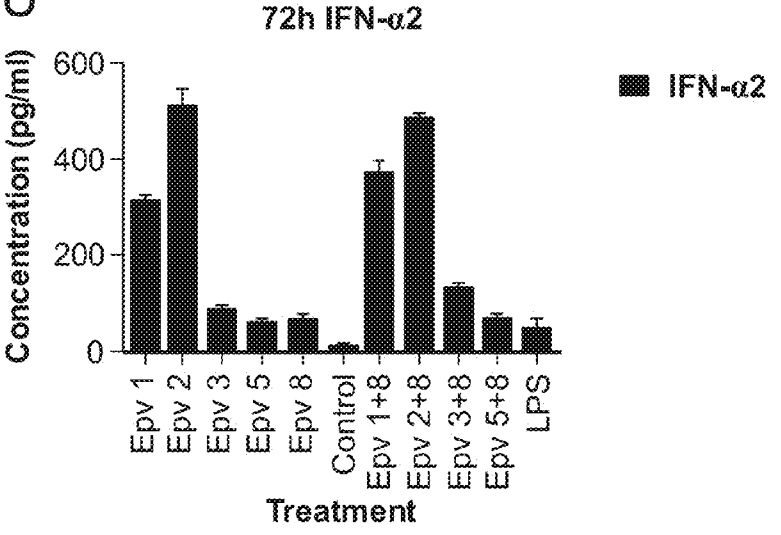


FIG. 5V

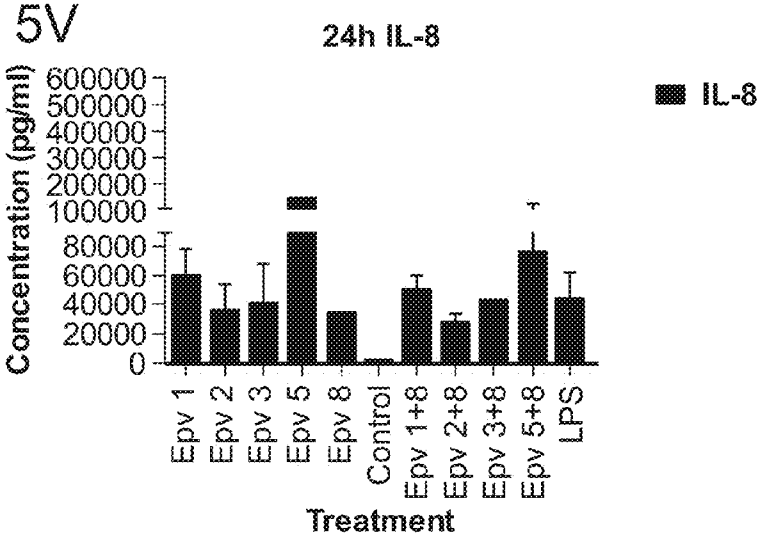


FIG. 5W

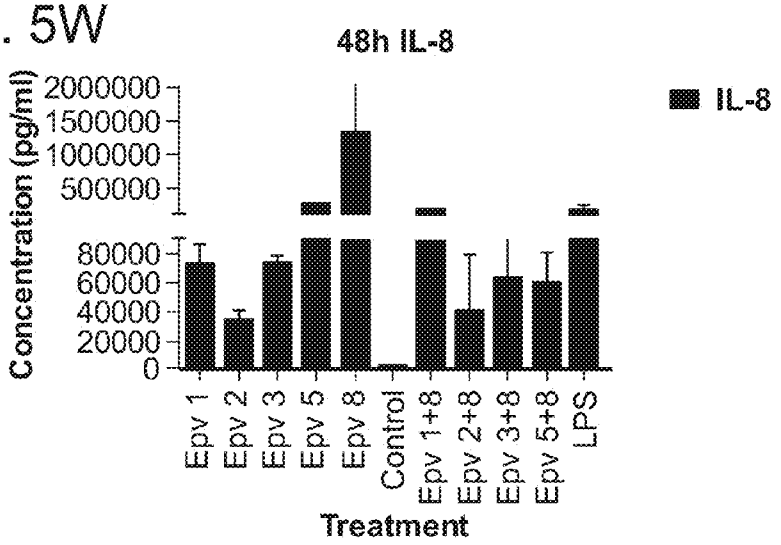
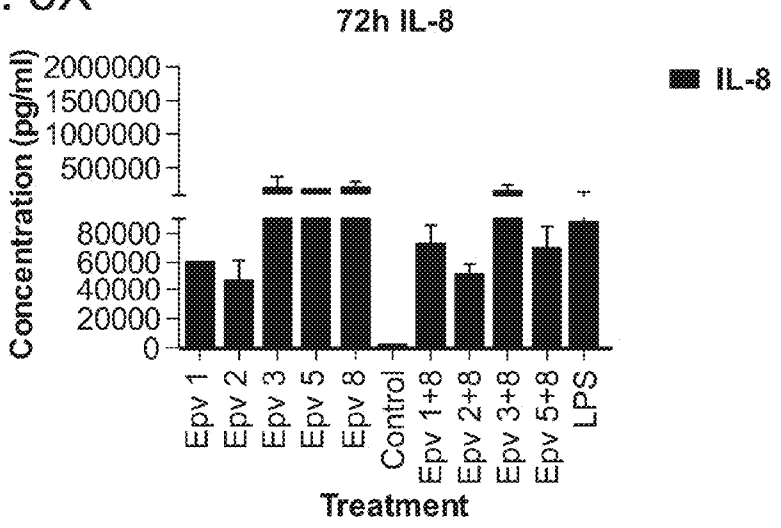


FIG. 5X



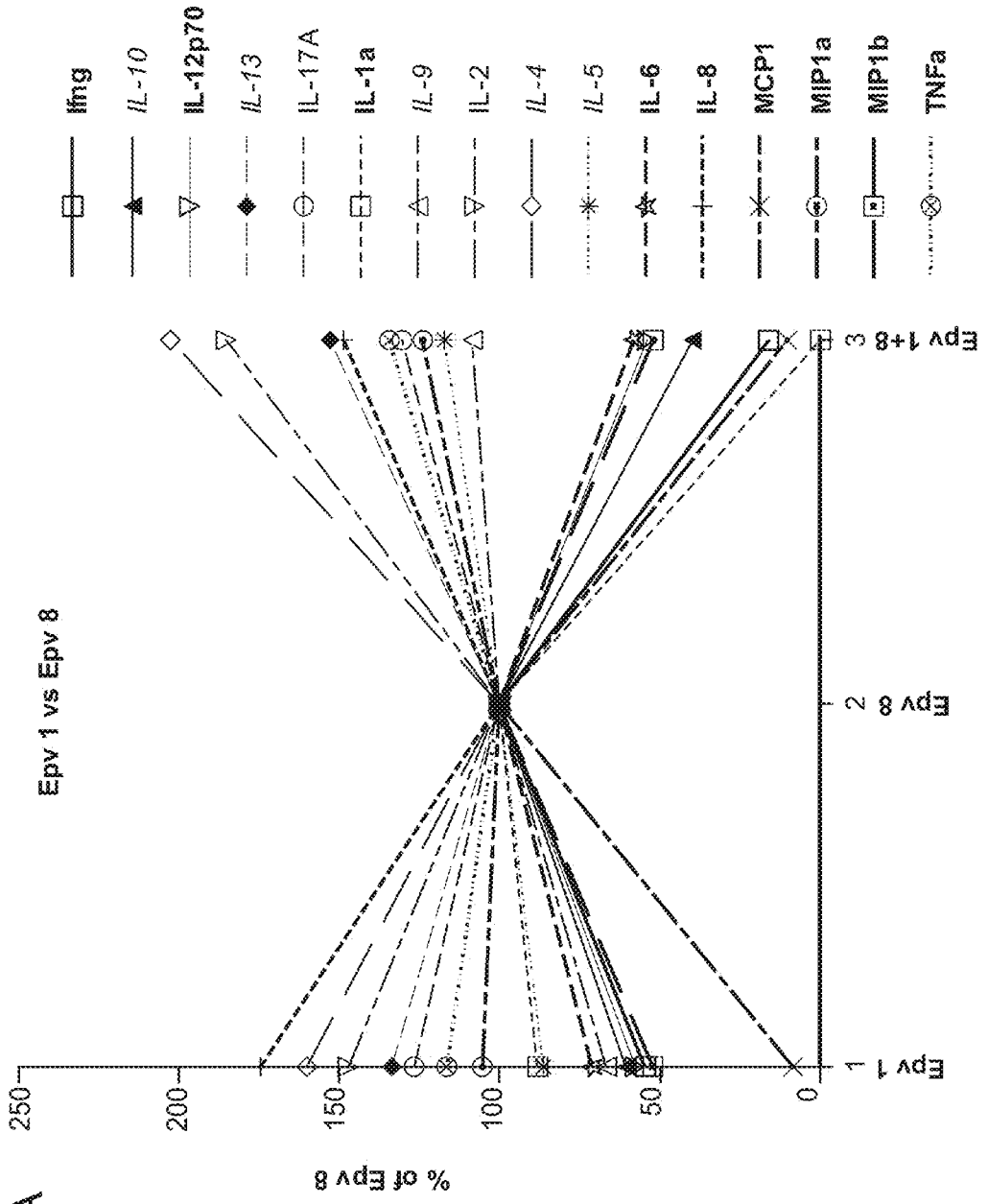

Ifng
IL-10
IL-12p70
IL-13
IL-17A
IL-1a
IL-9
IL-2
IL-4
IL-5
IL-6
IL-8
MCP1
MIP1a
MIP1b
TNFa
Epv 1 vs Epv 8
% of Epv 8
250
200
150
100
50
0
Epv 1
Epv 8
Epv 1+8
1
2
3

FIG. 6A

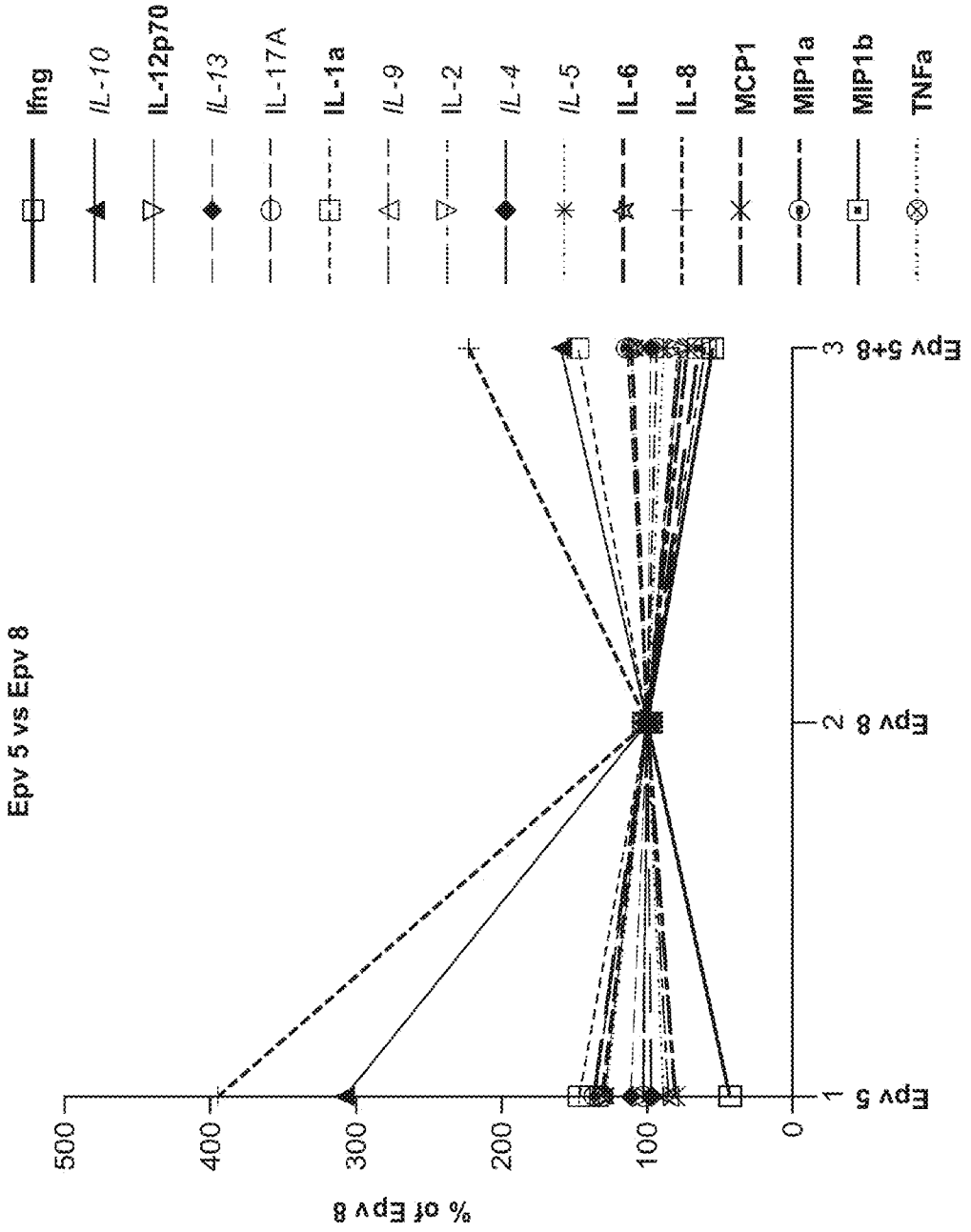

Ifng
IL-10
IL-12p70
IL-13
IL-17A
IL-1a
IL-9
IL-2
IL-4
IL-5
IL-6
IL-8
MCP1
MIP1a
MIP1b
TNFa
Epv 5 vs Epv 8
% of Epv 8
500
400
300
200
100
0
Epv 5
Epv 8
Epv 5+8
1
2
3

FIG. 6B

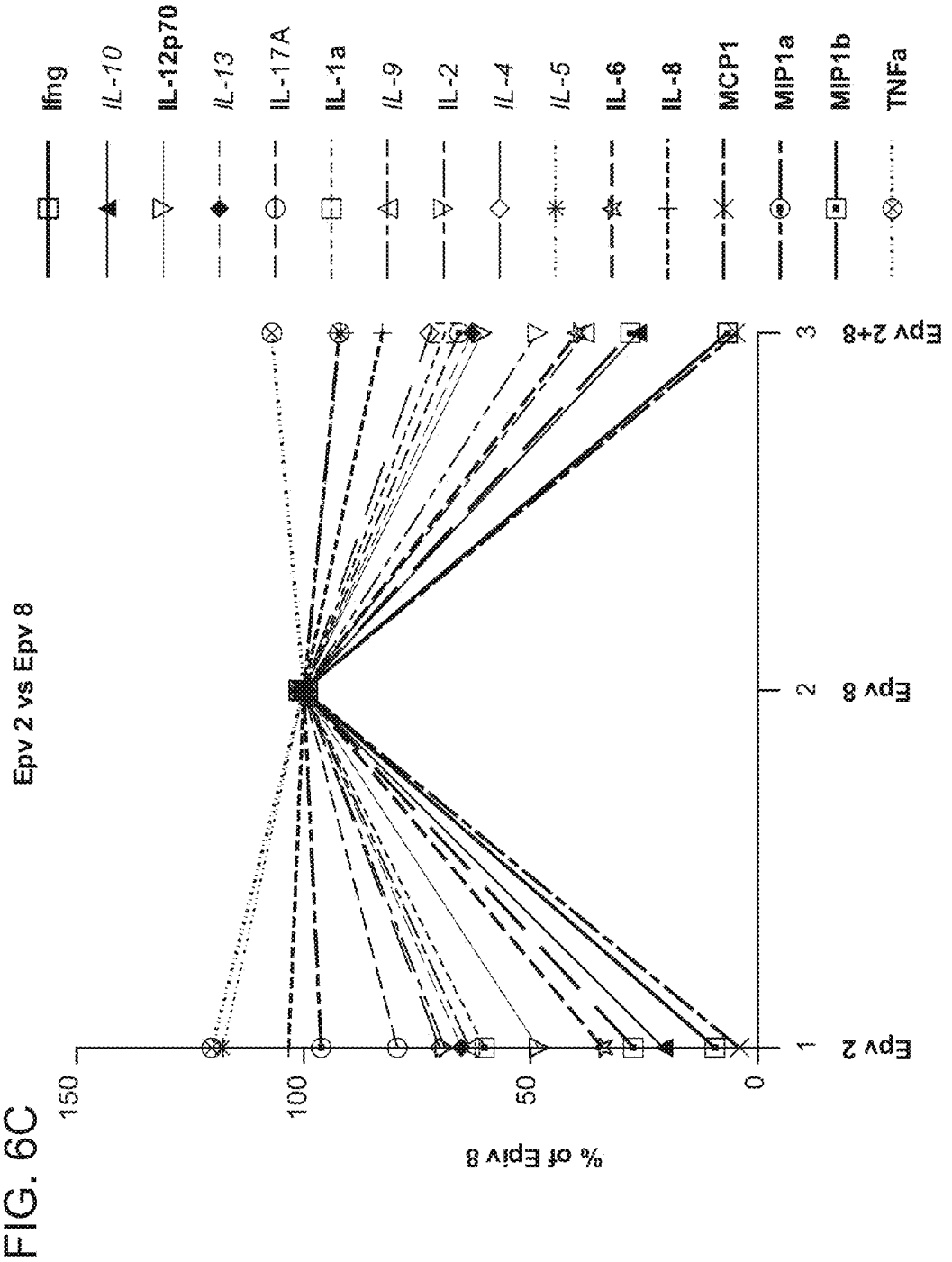

Epv 2 vs Epv 8
% of Epiv 8
150
100
50
0
1
2
3
Epv 2
Epv 8
Epv 2+8
Ifng
IL-10
IL-12p70
IL-13
IL-17A
IL-1a
IL-9
IL-2
IL-4
IL-5
IL-6
IL-8
MCP1
MIP1a
MIP1b
TNFa

FIG. 6C

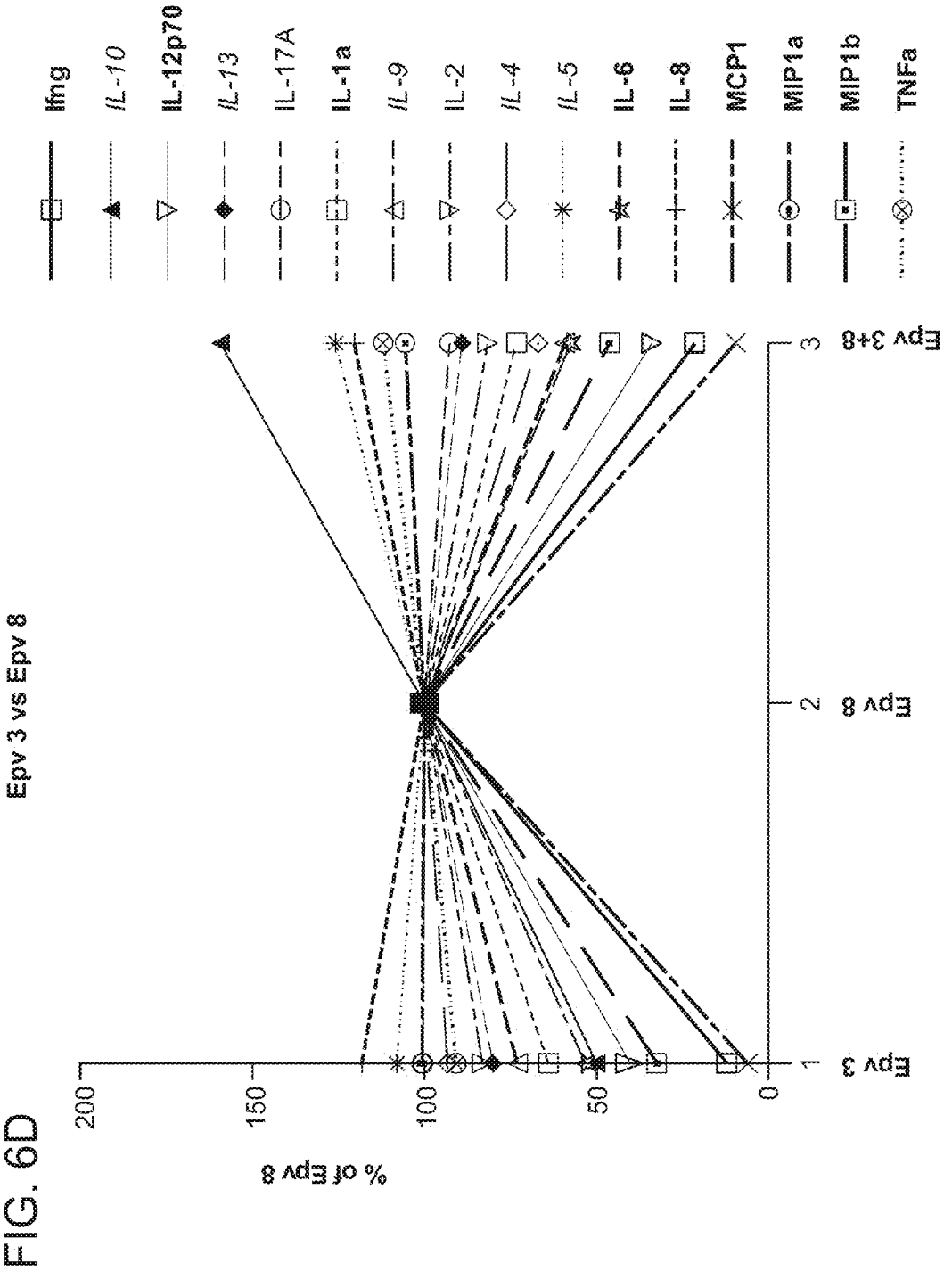

Epv 3 vs Epv 8
% of Epv 8
200
150
100
50
0
Epv 3
Epv 8
Epv 3+8
1
2
3
Ifng
IL-10
IL-12p70
IL-13
IL-17A
IL-1a
IL-9
IL-2
IL-4
IL-5
IL-6
IL-8
MCP1
MIP1a
MIP1b
TNFa

FIG. 6D

FIG. 7A

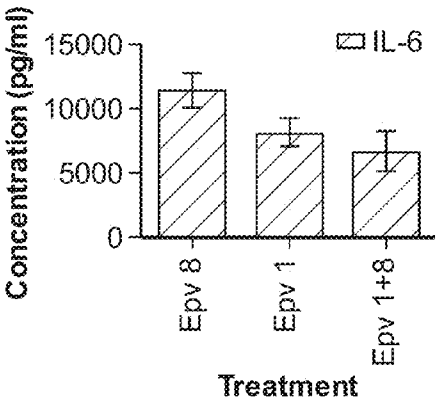


FIG. 7B

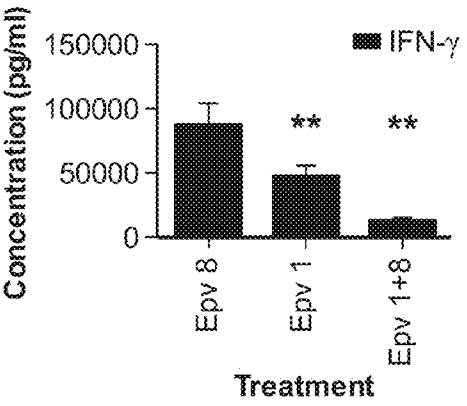


FIG. 7C

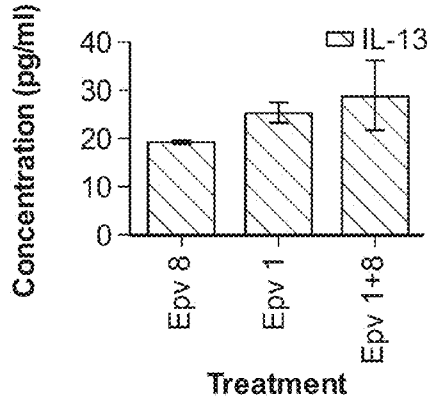


FIG. 7D

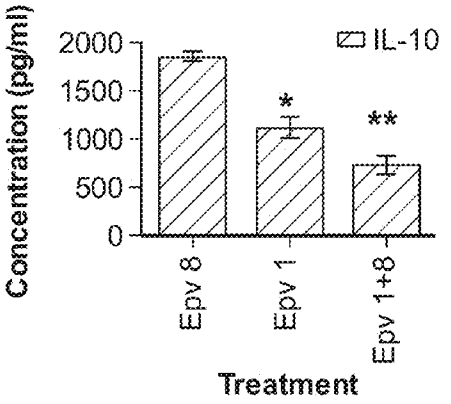


FIG. 7E

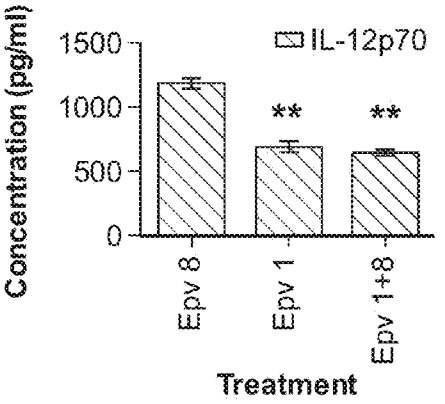


FIG. 7F

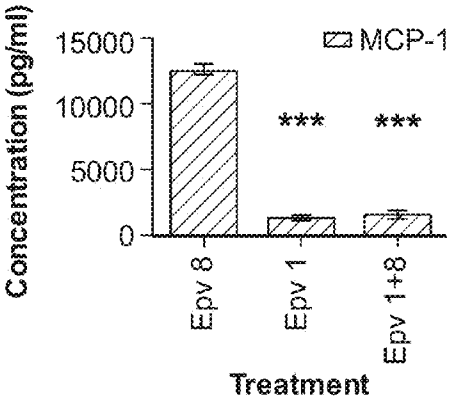


FIG. 7G

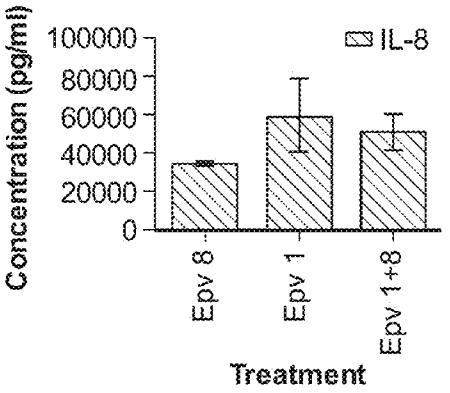


FIG. 7H

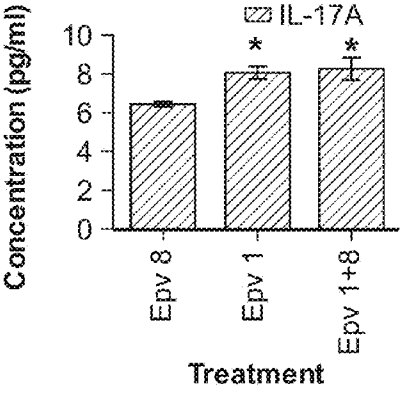


FIG. 7I

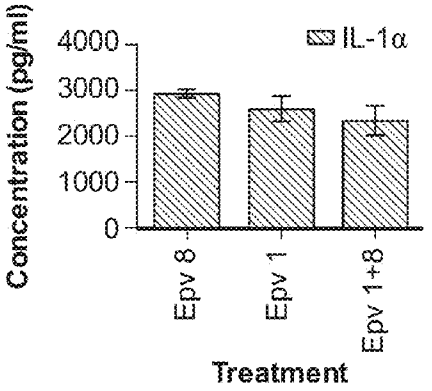


FIG. 7J

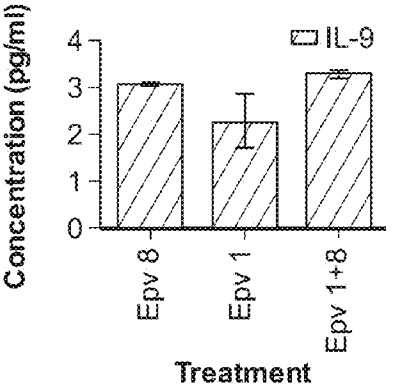


FIG. 7K

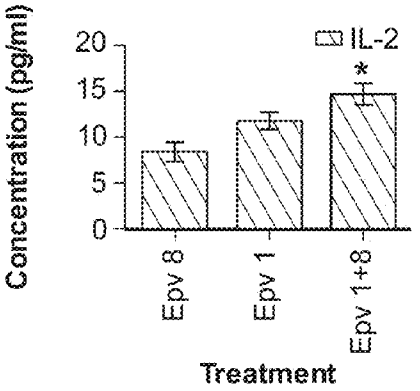


FIG. 7L

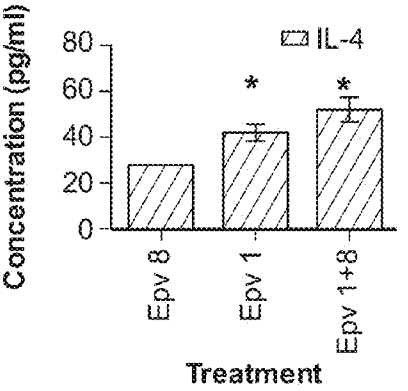


FIG. 7M

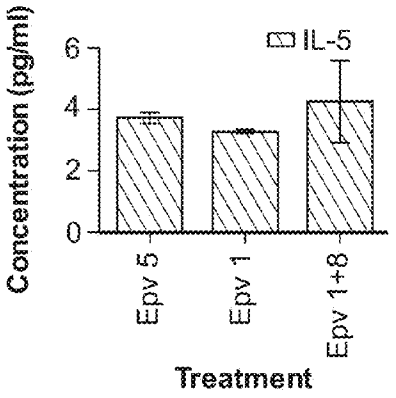


FIG. 7N

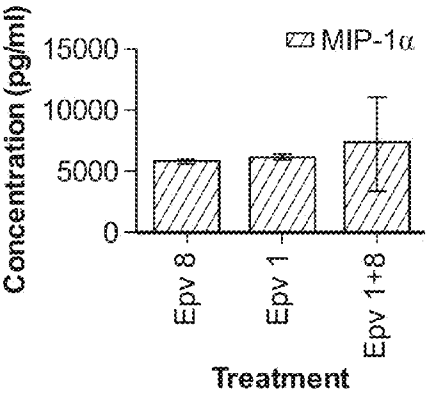


FIG. 7O

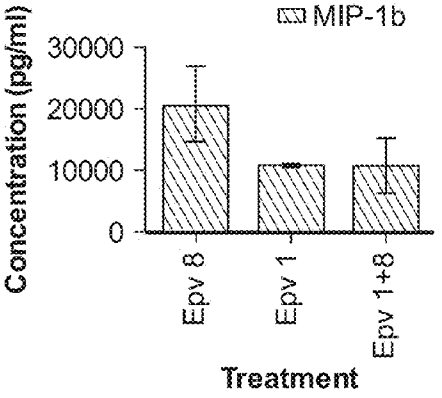


FIG. 7P

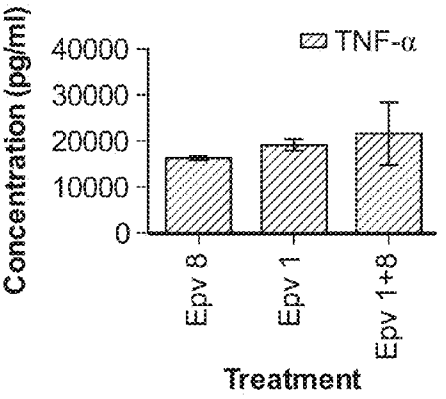


FIG. 8A

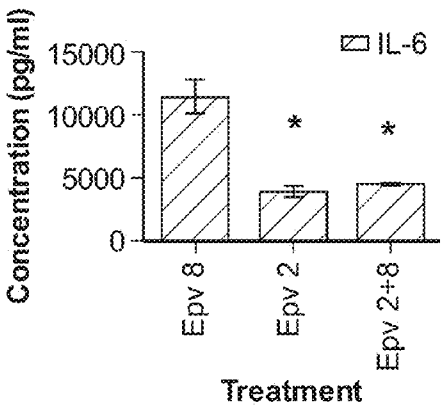


FIG. 8B

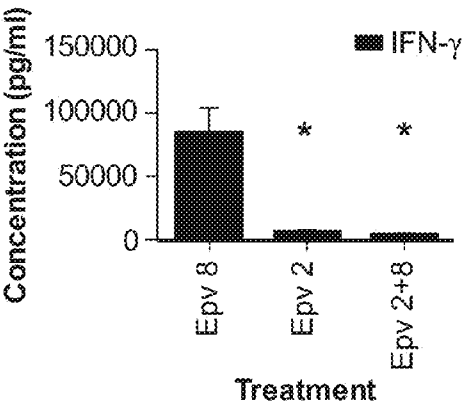


FIG. 8C

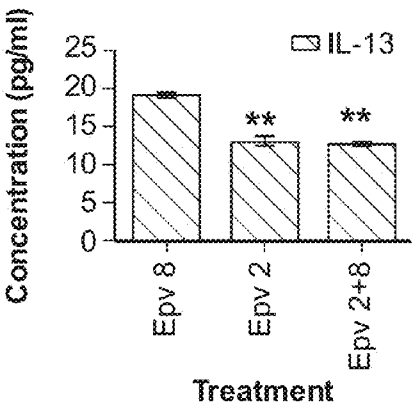


FIG. 8D

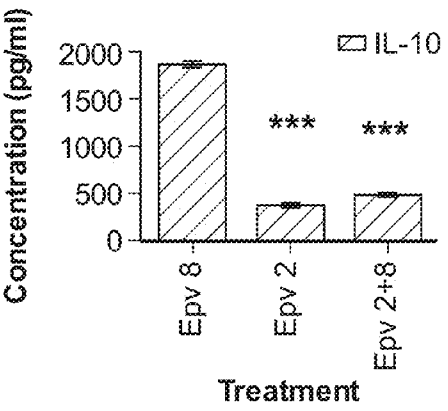


FIG. 8E

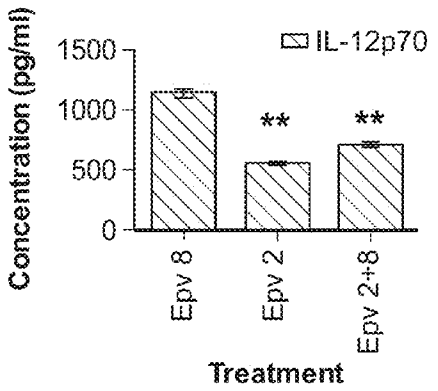


FIG. 8F

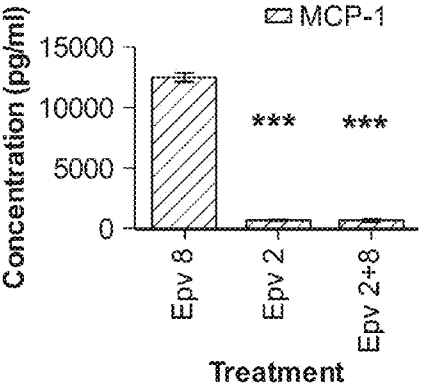


FIG. 8G

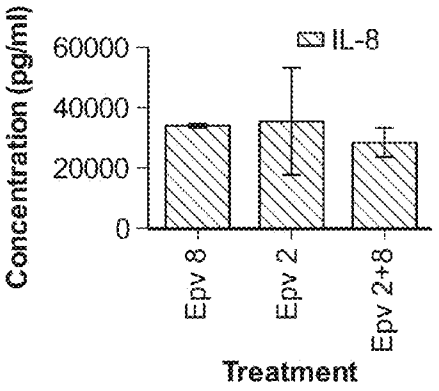


FIG. 8H

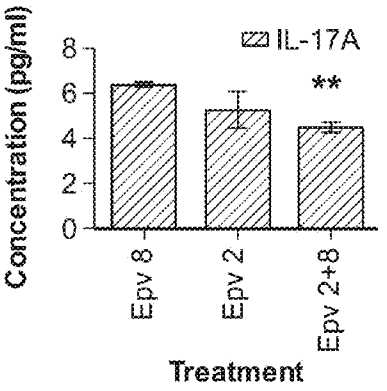


FIG. 8I

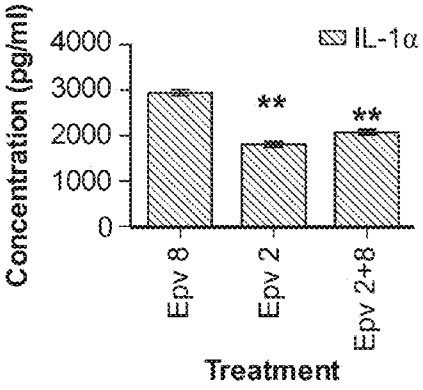


FIG. 8J

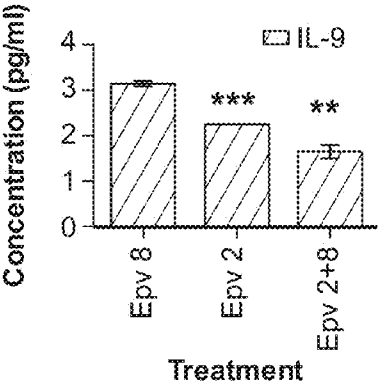


FIG. 8K

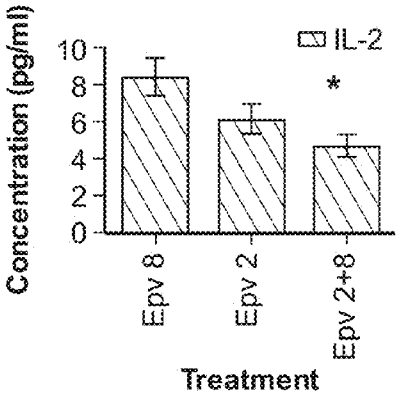


FIG. 8L

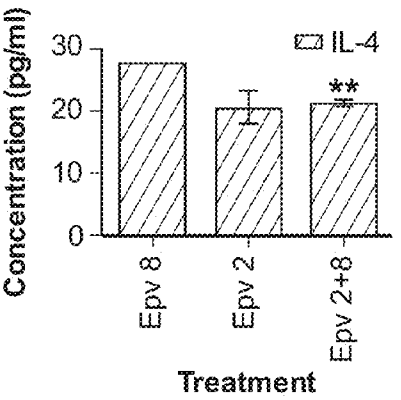


FIG. 8M

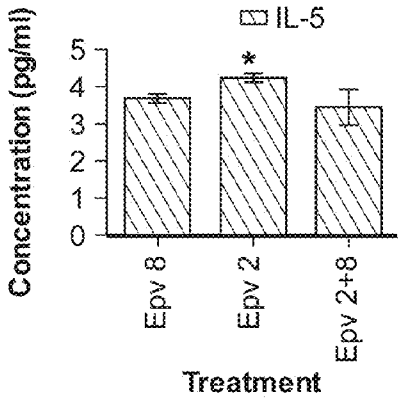


FIG. 8N

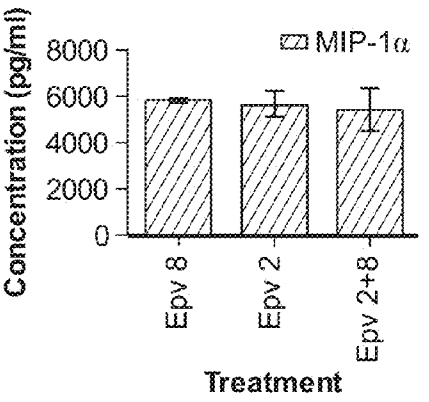


FIG. 8O

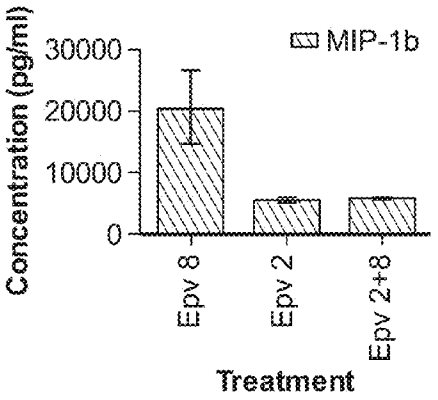


FIG. 8P

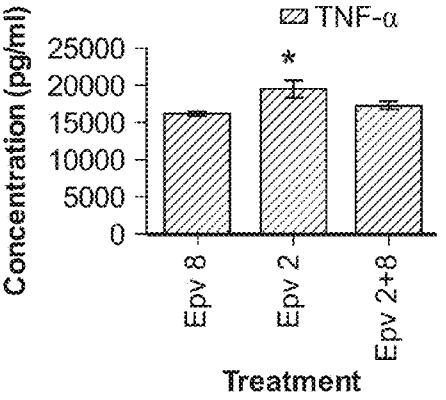


FIG. 9A

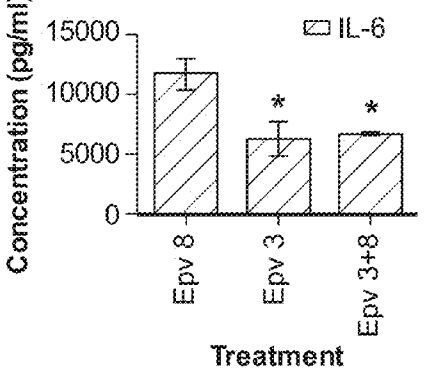


FIG. 9B

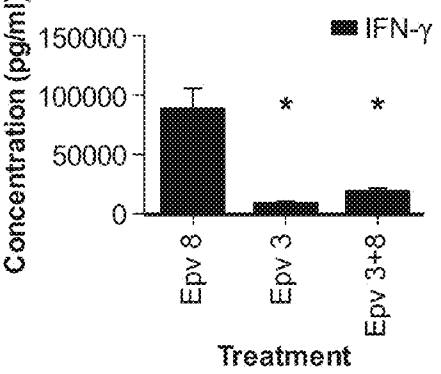


FIG. 9C

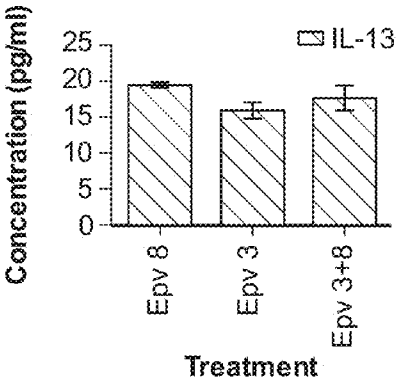


FIG. 9D

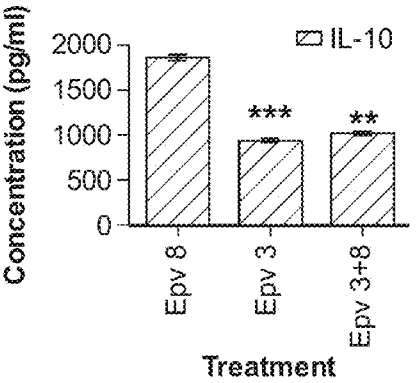


FIG. 9E

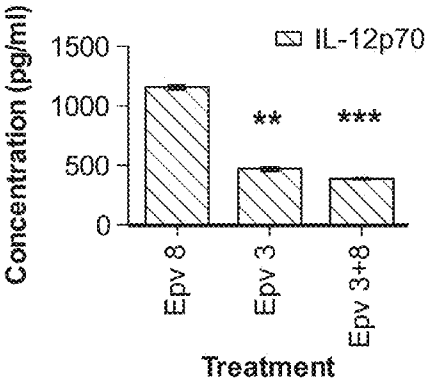


FIG. 9F

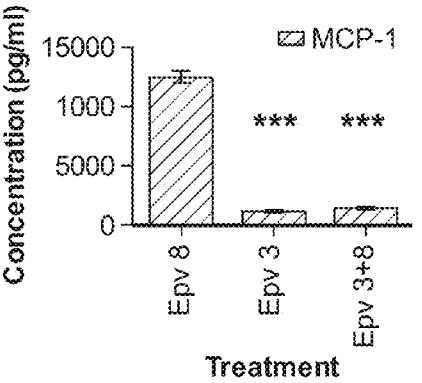


FIG. 9G

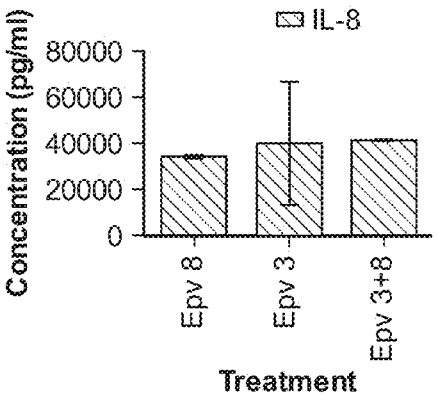


FIG. 9H

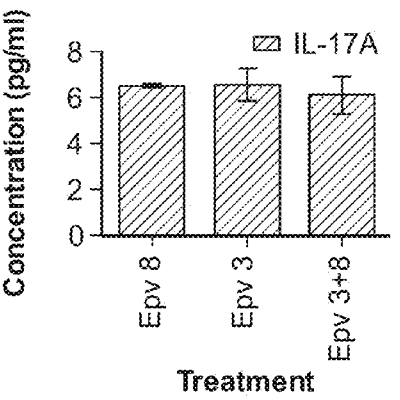


FIG. 9I

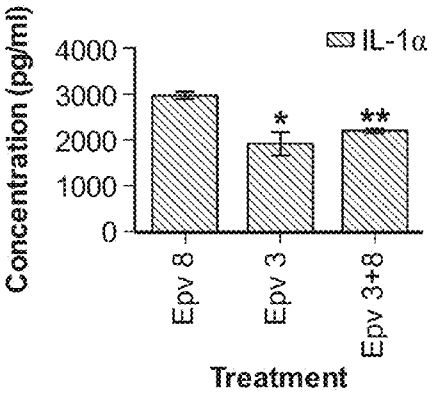


FIG. 9J

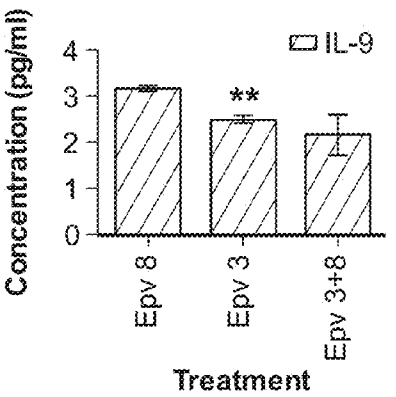


FIG. 9K

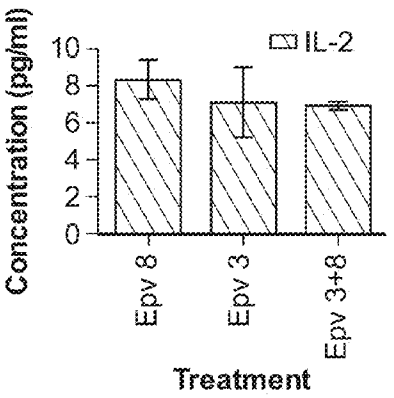


FIG. 9L

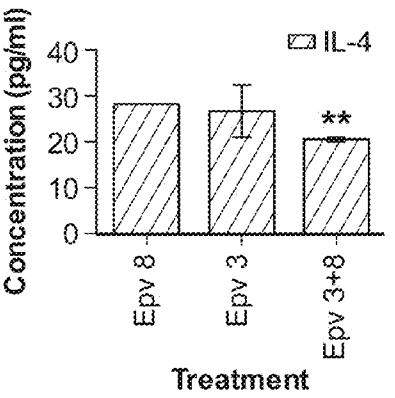


FIG. 9M

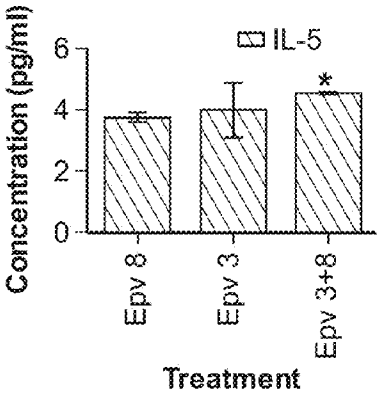


FIG. 9N

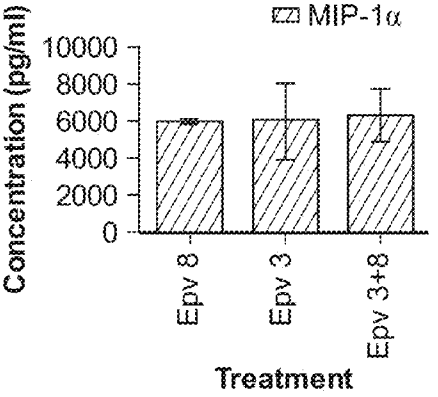


FIG. 9O

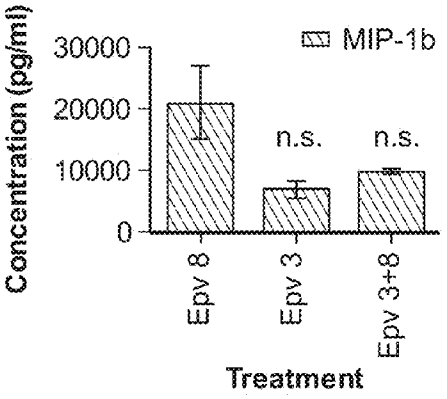


FIG. 9P

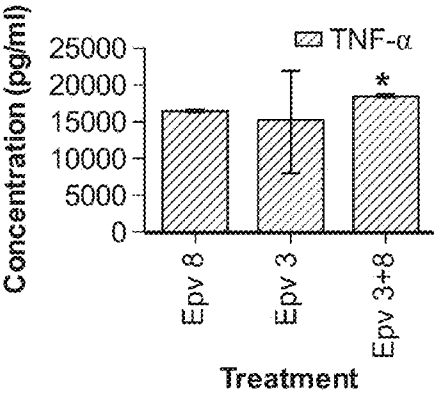


FIG. 10A

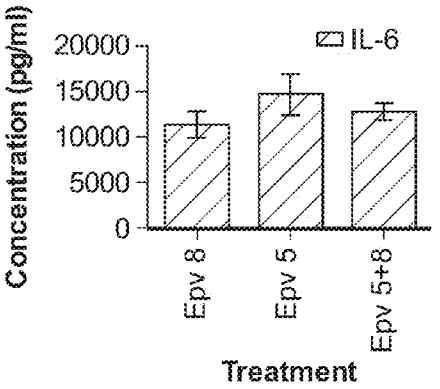


FIG. 10B

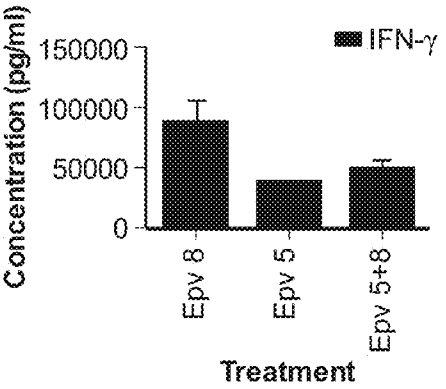


FIG. 10C

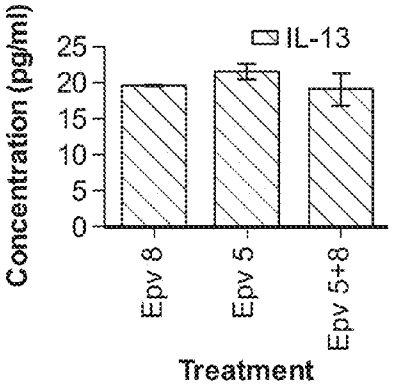


FIG. 10D

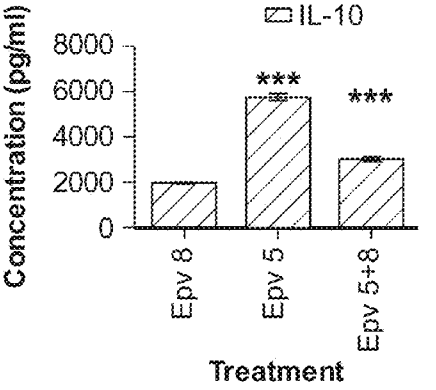


FIG. 10E

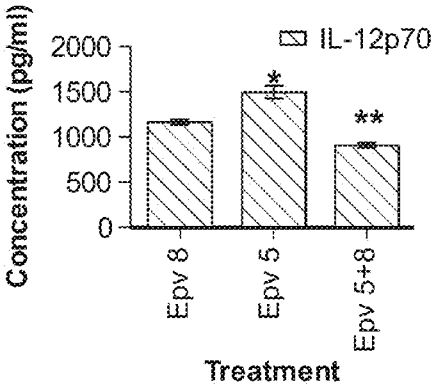


FIG. 10F

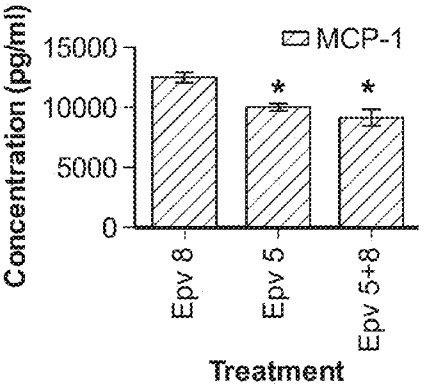


FIG. 10G

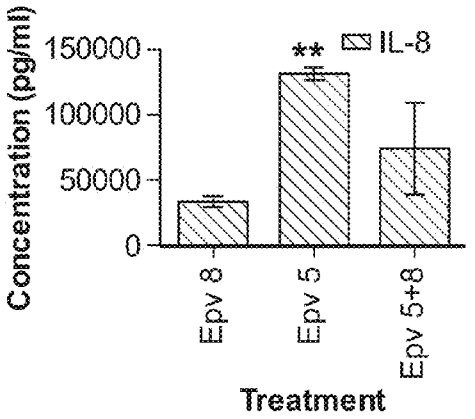


FIG. 10H

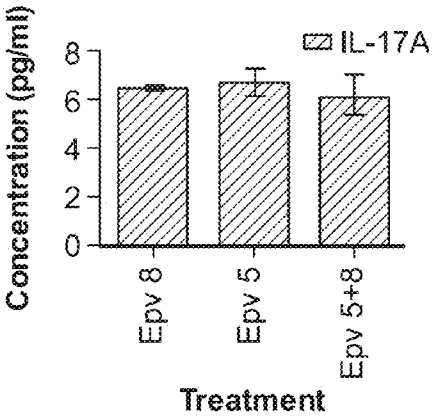


FIG. 10I

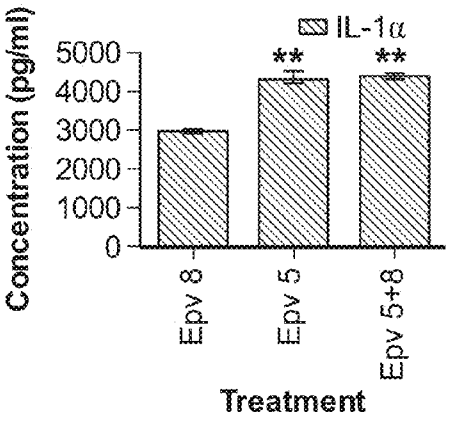


FIG. 10J

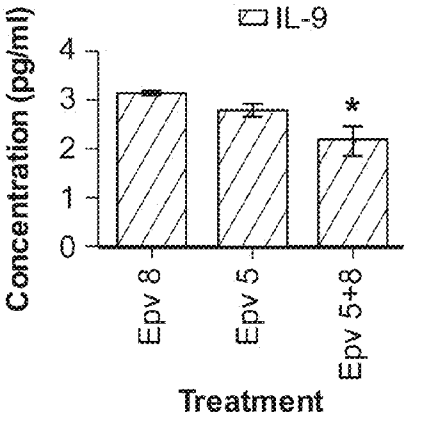


FIG. 10K

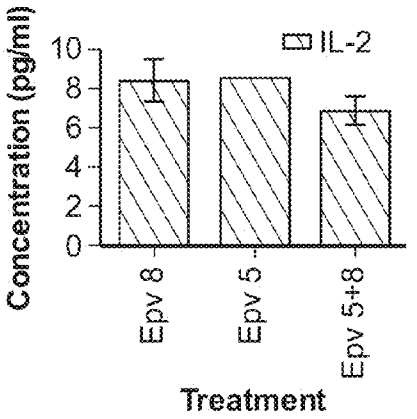


FIG. 10L

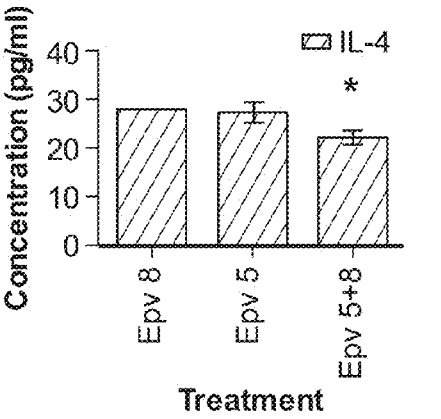


FIG. 10M

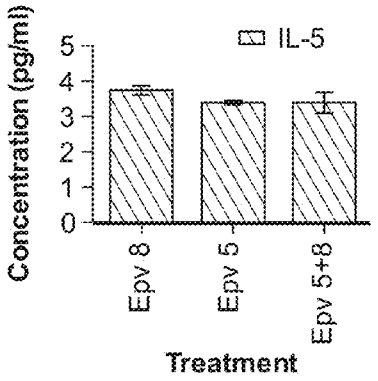


FIG. 10N

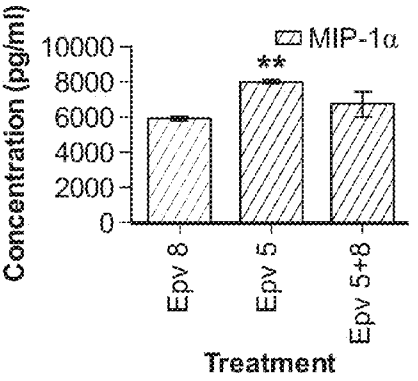


FIG. 10O

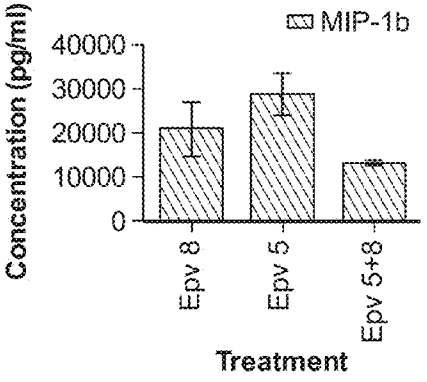


FIG. 10P

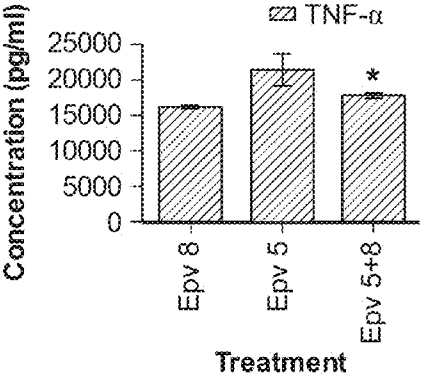
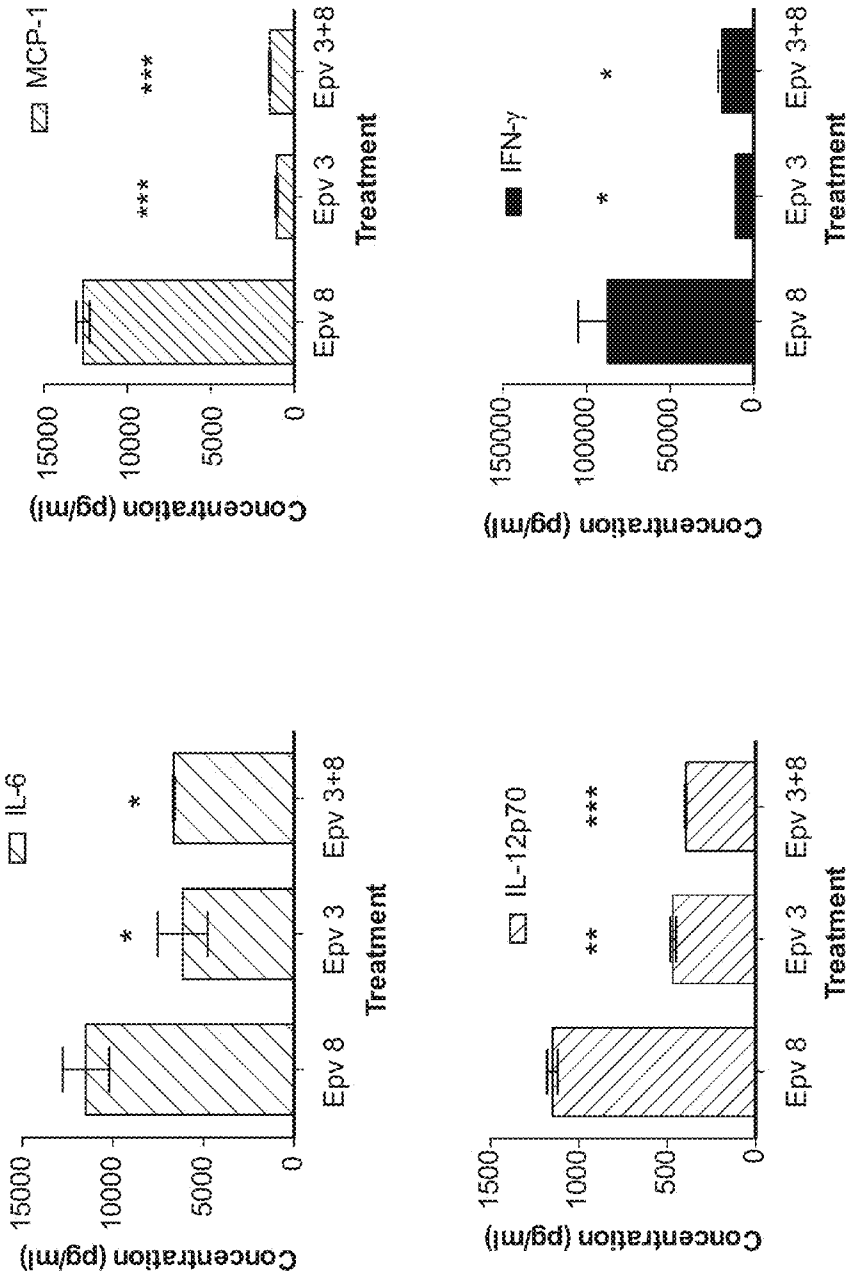


FIG. 11A


EPV3 – Desirable anti-inflammatory profile for GVHD
IL-6
MCP-1
IL-12p70
IFN-γ
Concentration (pg/ml)
Treatment
Epv 8
Epv 3
Epv 3+8
15000
10000
5000
0
1500
1000
500
150000
100000
50000
*
**
***

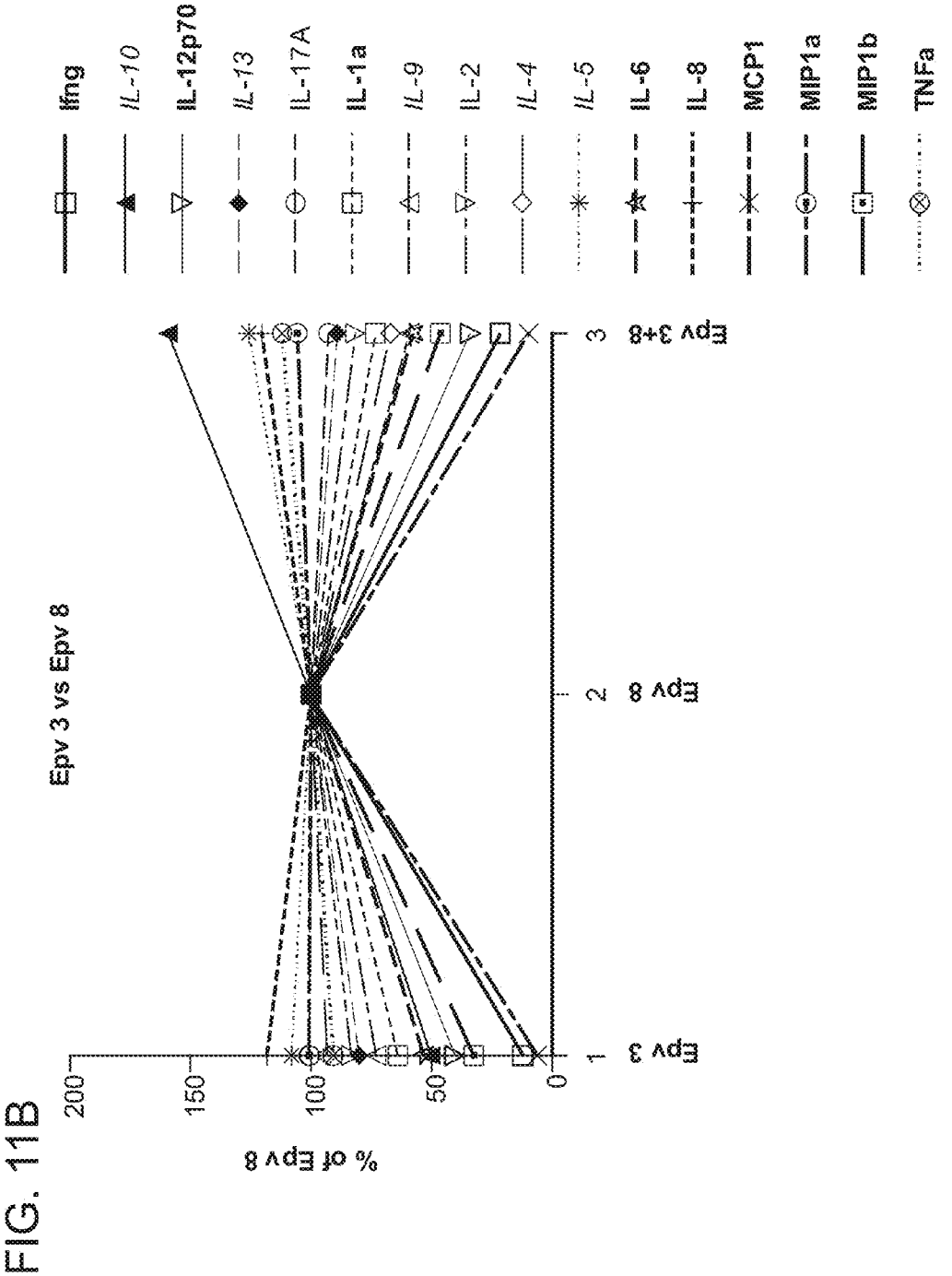
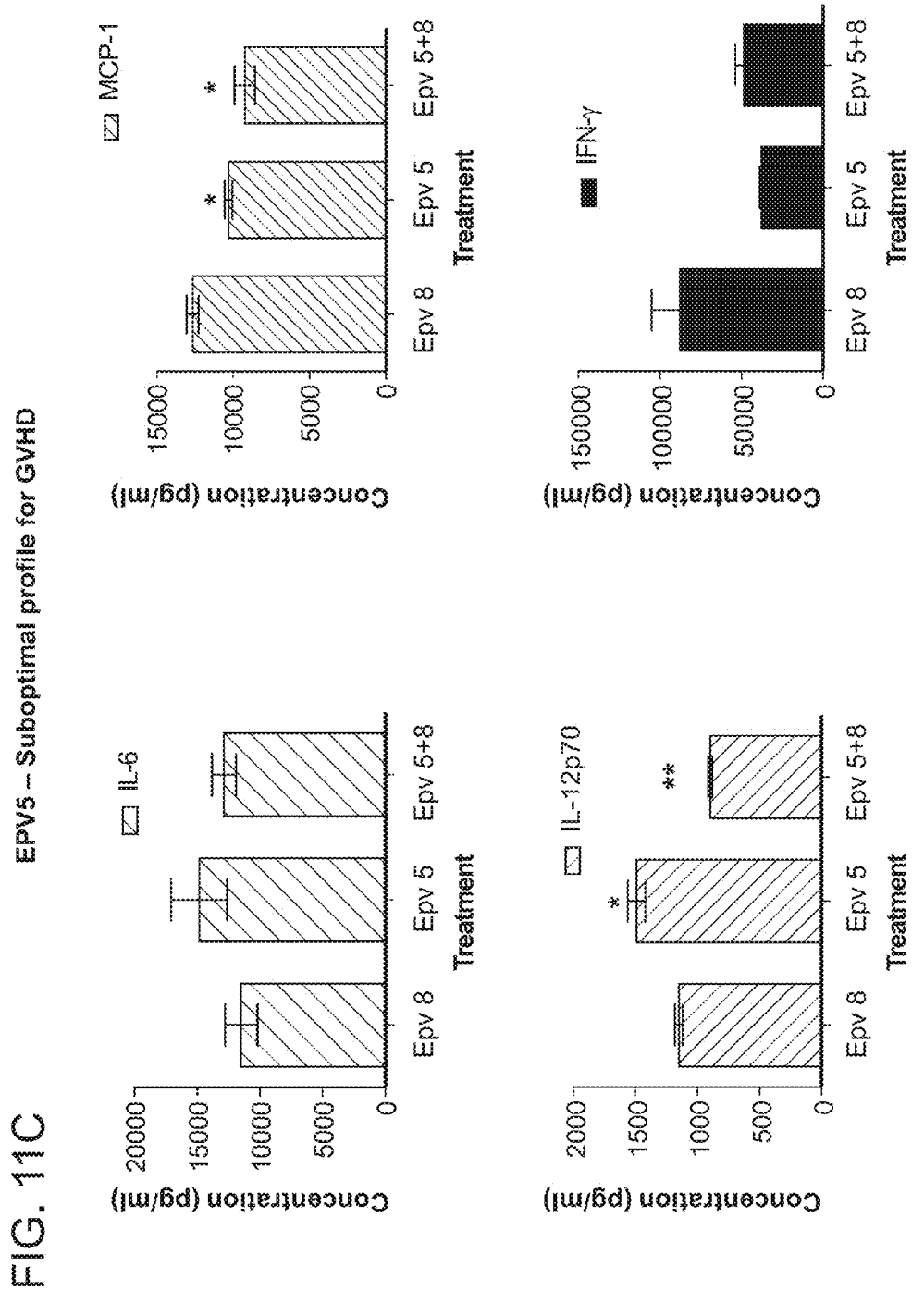

Epv 3 vs Epv 8
% of Epv 8
200
150
100
50
0
1
2
3
Epv 3
Epv 8
Epv 3+8
Ifng
IL-10
IL-12p70
IL-13
IL-17A
IL-1a
IL-9
IL-2
IL-4
IL-5
IL-6
IL-8
MCP1
MIP1a
MIP1b
TNFa

FIG. 11B

FIG. 11C


EPV5 – Suboptimal profile for GVHD
MCP-1
IFN-γ
IL-6
IL-12p70
Concentration (pg/ml)
Treatment
Epv 8
Epv 5
Epv 5+8
*
**

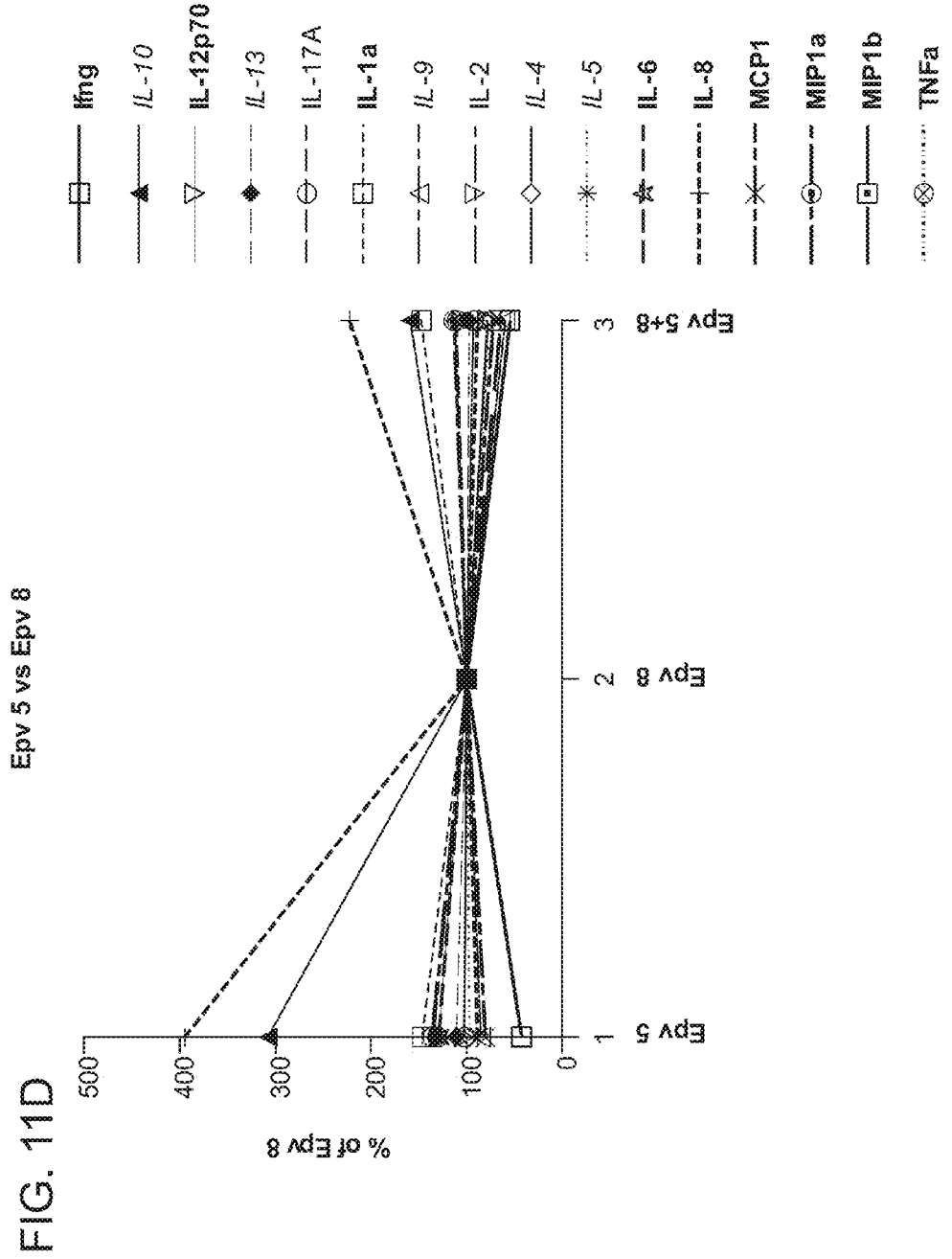
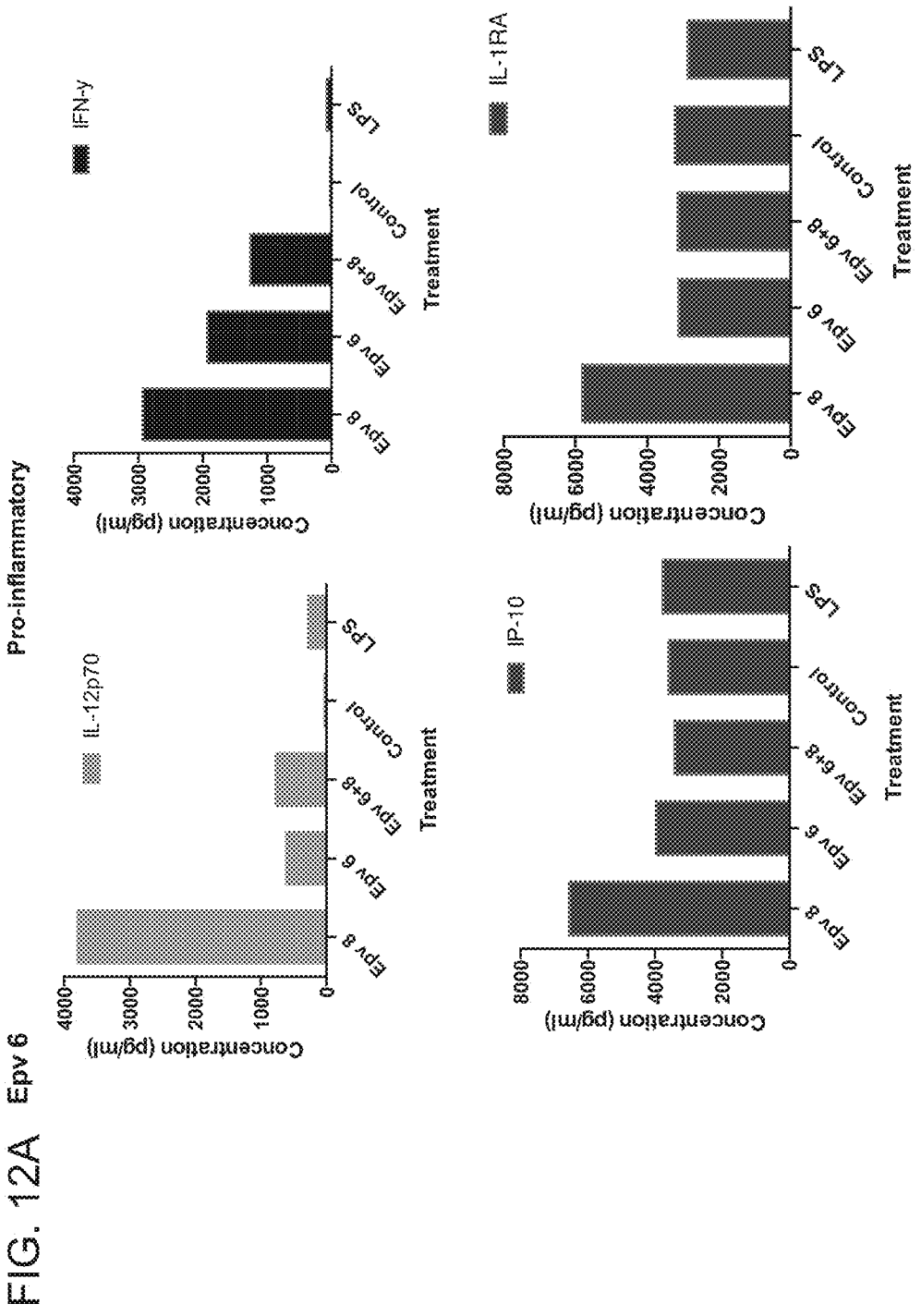

Epv 5 vs Epv 8
% of Epv 8
500
400
300
200
100
0
1
2
3
Epv 5
Epv 8
Epv 5+8
Ifng
IL-10
IL-12p70
IL-13
IL-17A
IL-1a
IL-9
IL-2
IL-4
IL-5
IL-6
IL-8
MCP1
MIP1a
MIP1b
TNFa

FIG. 11D

FIG. 12A Epv 6


Pro-inflammatory
IFN-γ
IL-12p70
IL-1RA
IP-10
Concentration (pg/ml)
Treatment
Epv 8
Epv 6
Epv 6+8
Control
LPS
0
1000
2000
3000
4000
6000
8000

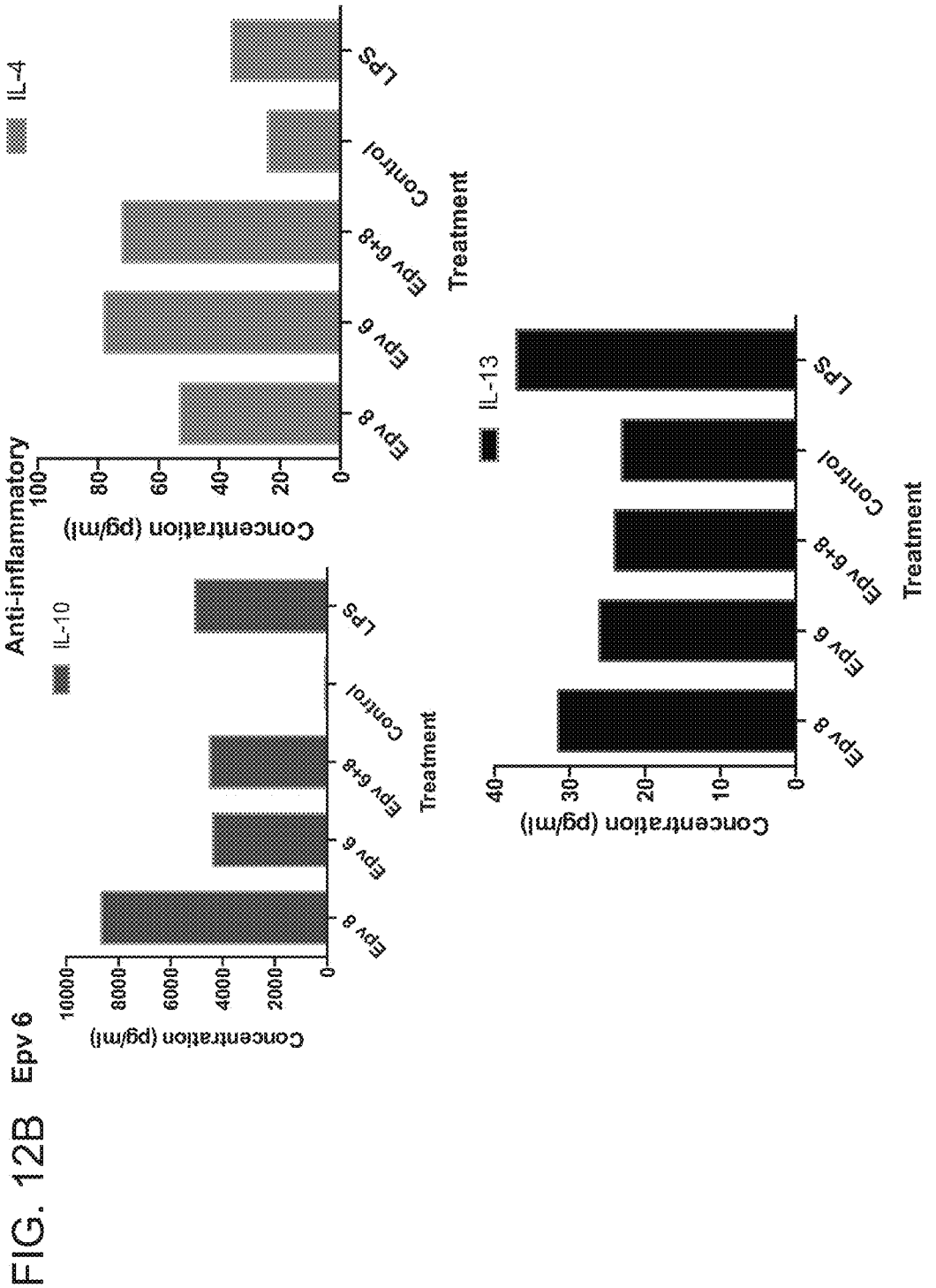

Epv 6
Anti-inflammatory
IL-10
Concentration (pg/ml)
10000
8000
6000
4000
2000
0
Epv 8
Epv 6
Epv 6+8
Control
LPS
Treatment
IL-4
Concentration (pg/ml)
100
80
60
40
20
0
Epv 8
Epv 6
Epv 6+8
Control
LPS
Treatment
IL-13
Concentration (pg/ml)
40
30
20
10
0
Epv 8
Epv 6
Epv 6+8
Control
LPS
Treatment

FIG. 12B

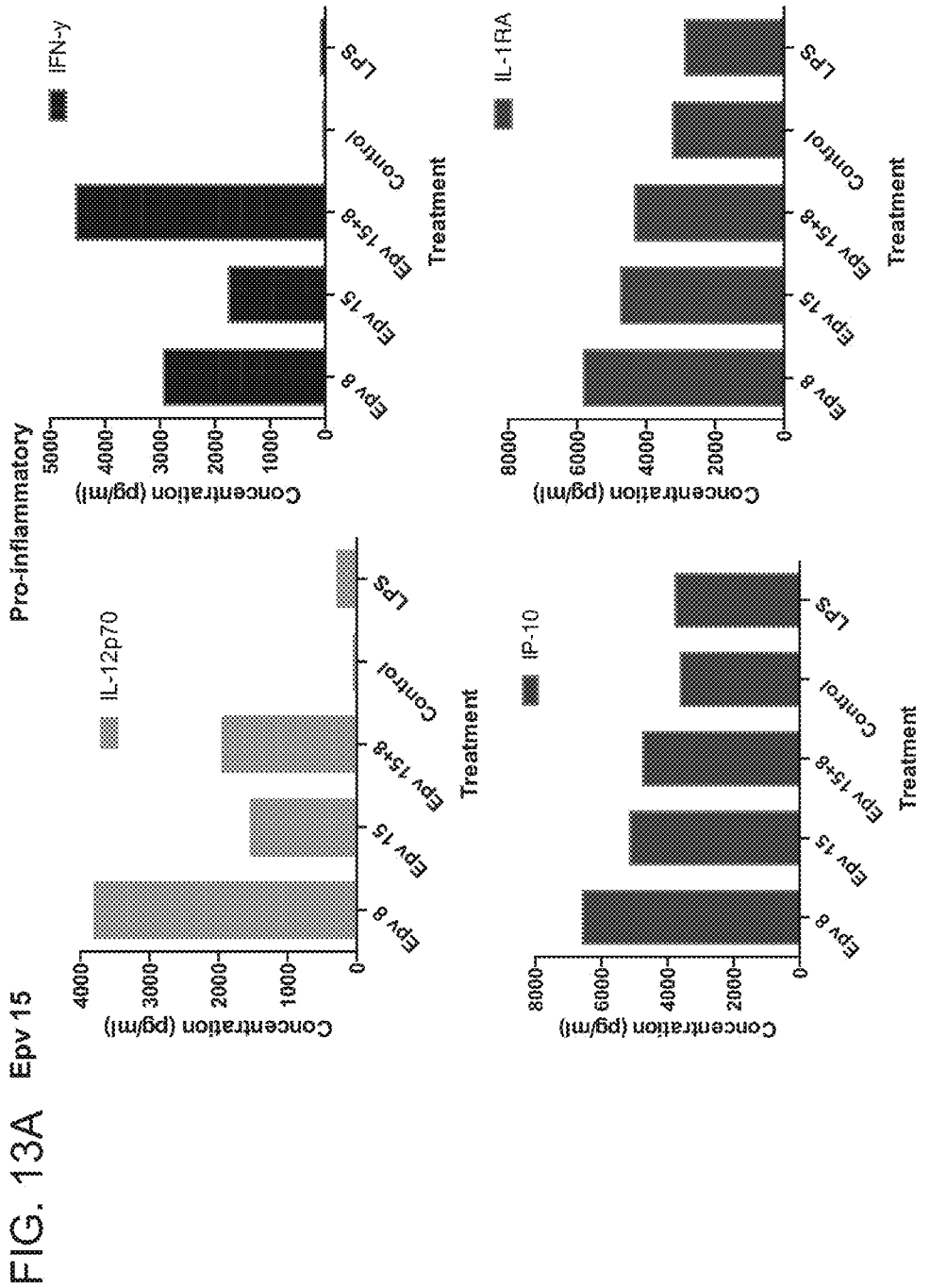


FIG. 13A Epv 15

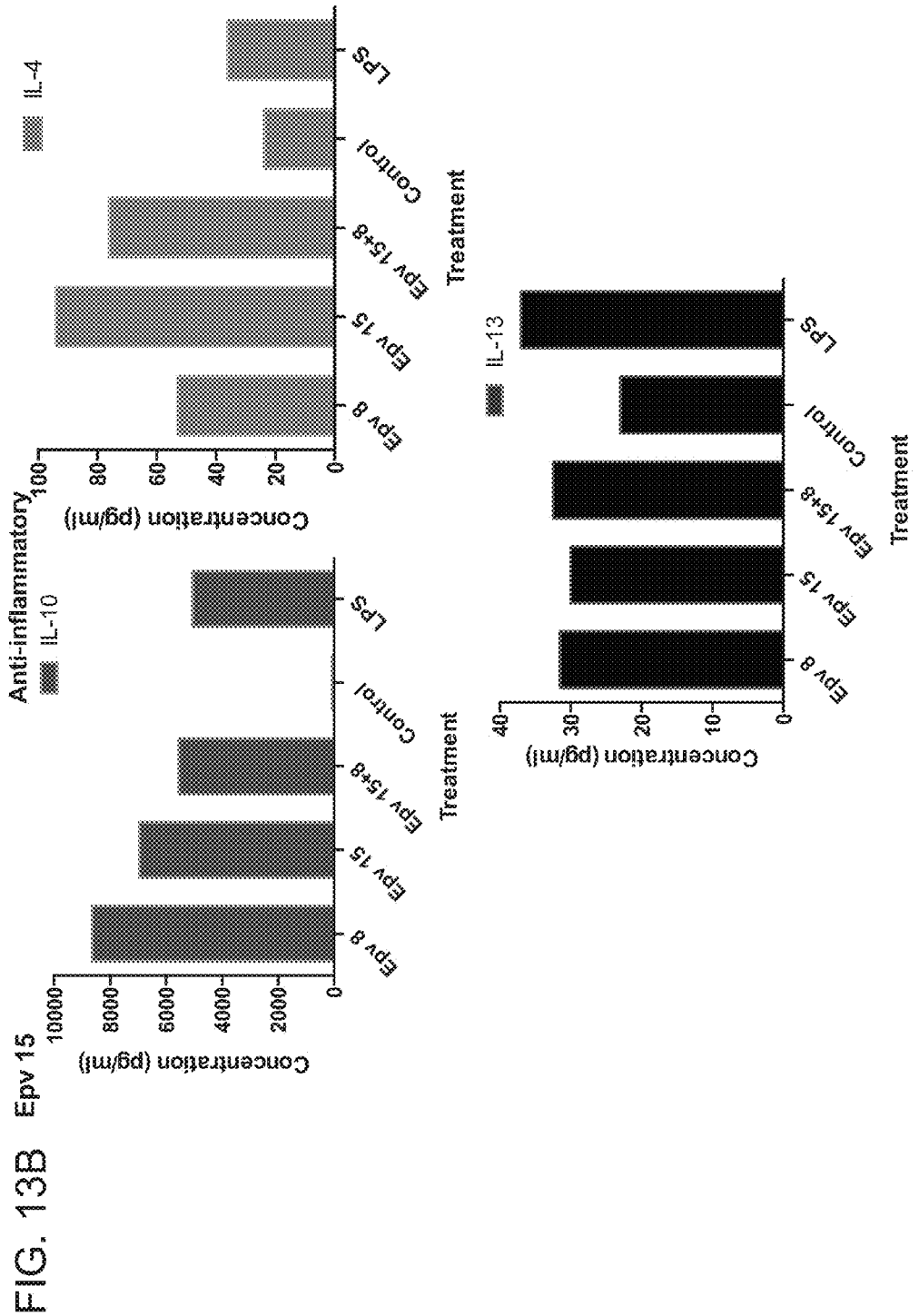
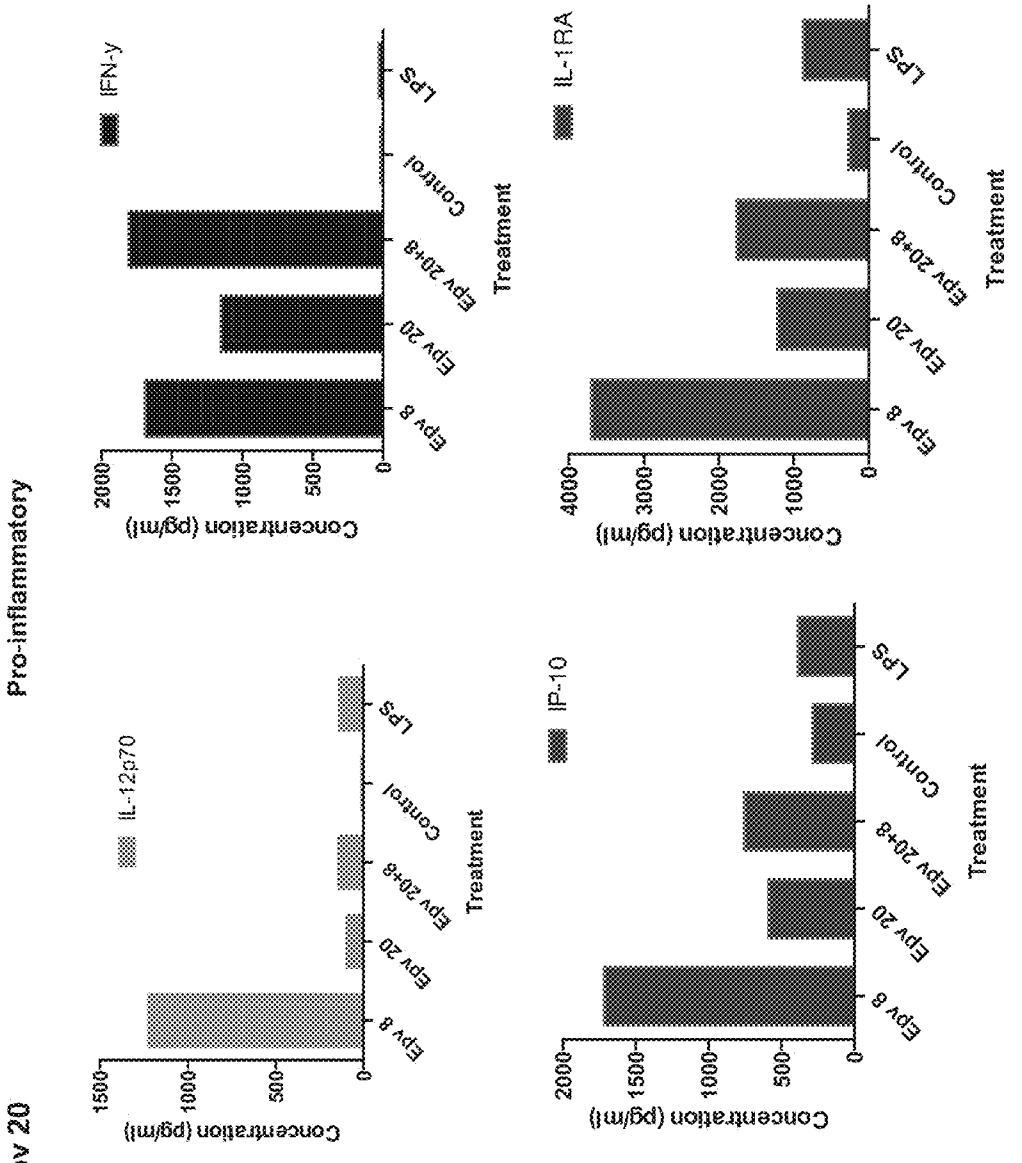

Epv 15
Anti-inflammatory
IL-10
Concentration (pg/ml)
10000
8000
6000
4000
2000
0
Epv 8
Epv 15
Epv 15+8
Control
LPS
Treatment
IL-4
Concentration (pg/ml)
100
80
60
40
20
0
Epv 8
Epv 15
Epv 15+8
Control
LPS
Treatment
IL-13
Concentration (pg/ml)
40
30
20
10
0
Epv 8
Epv 15
Epv 15+8
Control
LPS
Treatment

FIG. 13B

FIG. 14A Epv 20



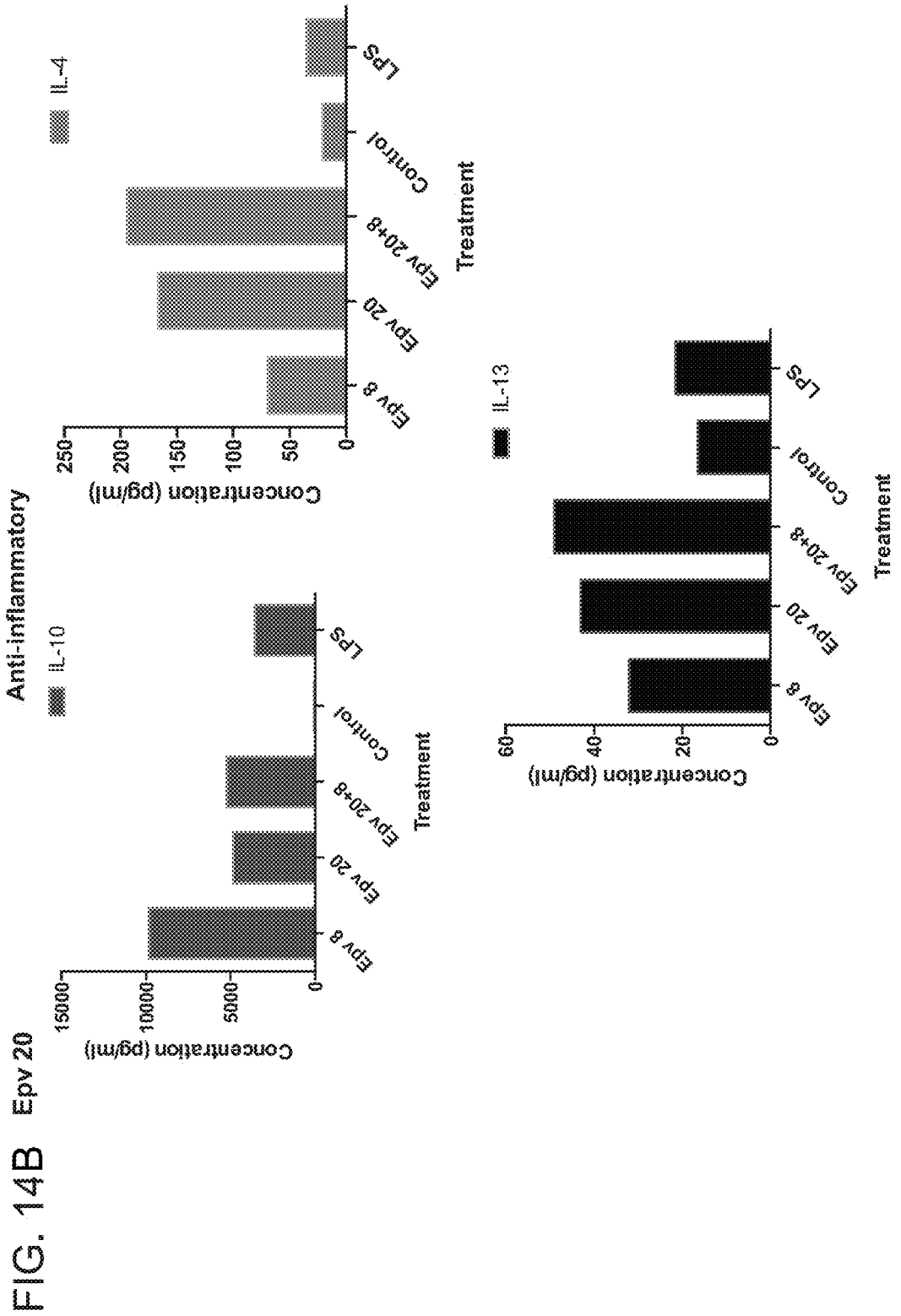


FIG. 14B Epv 20

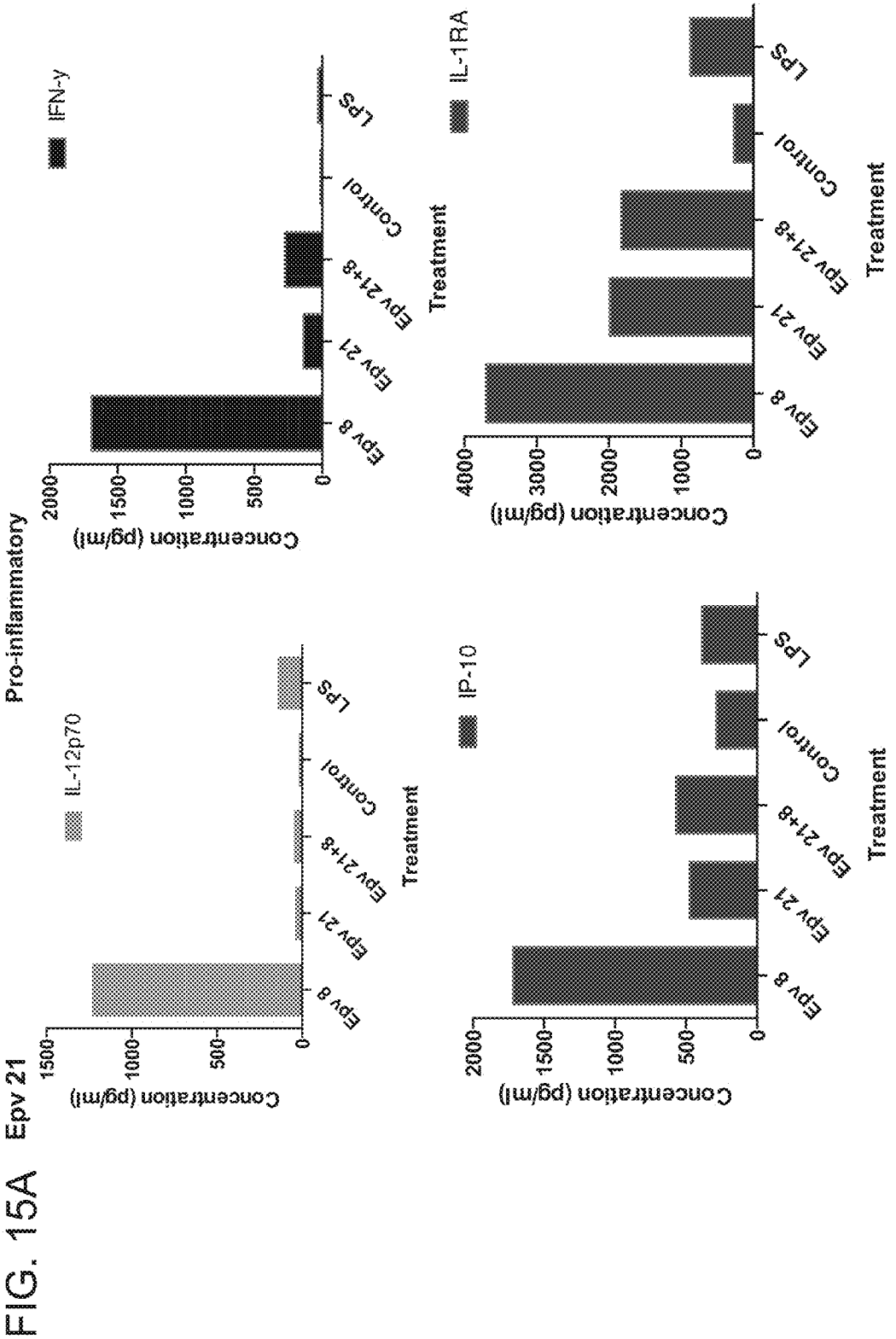


FIG. 15A Epv 21

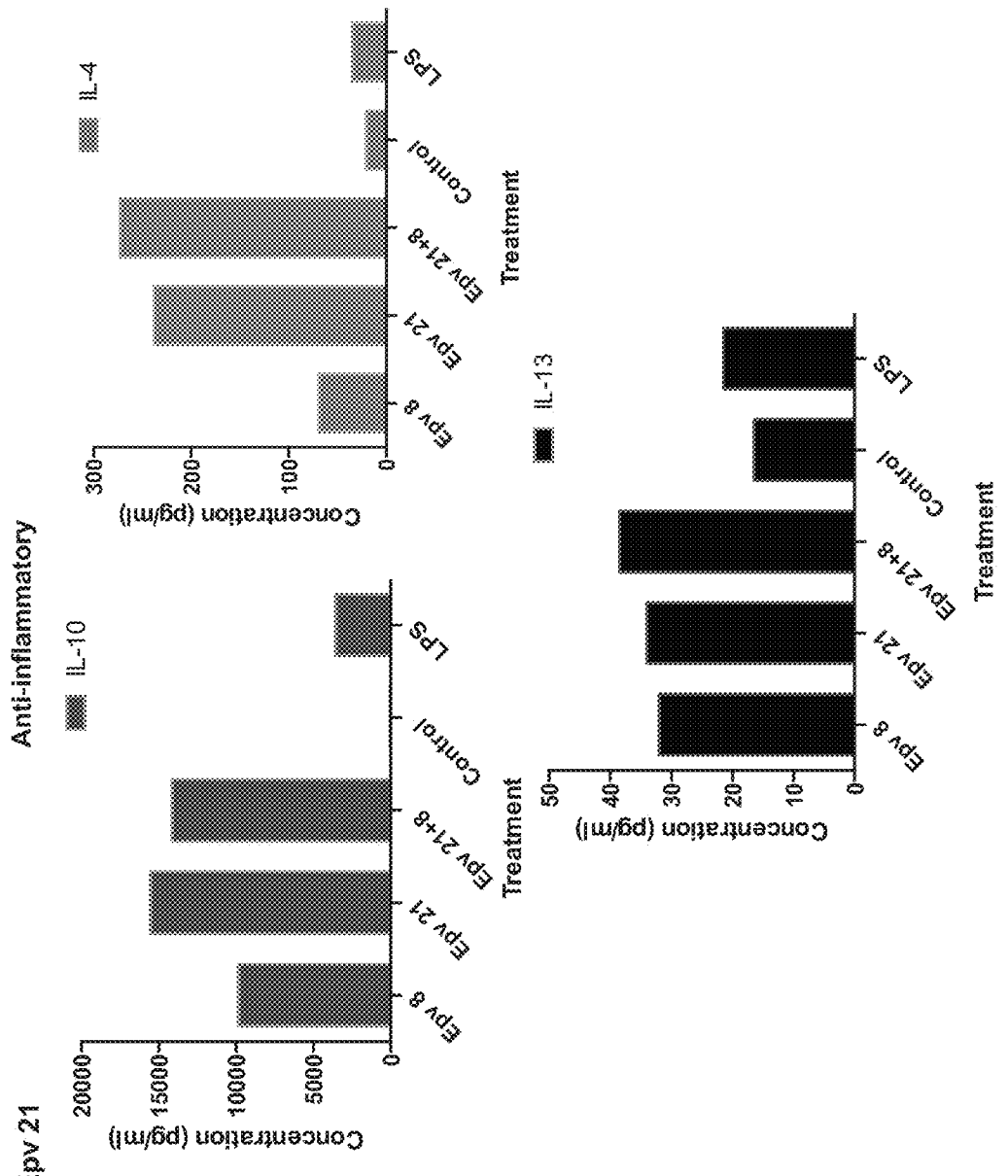
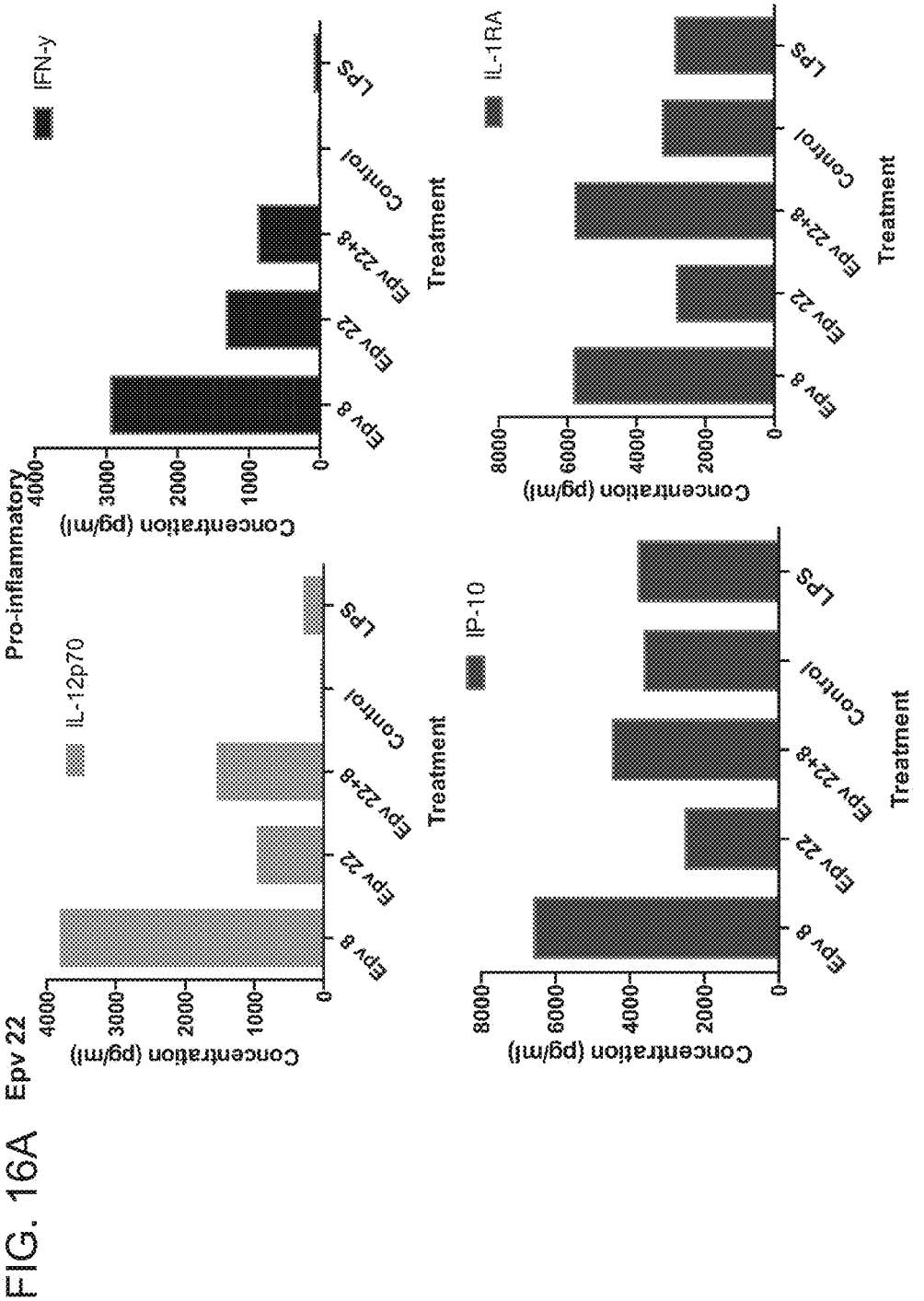


FIG. 15B Epv 21

FIG. 16A


Epv 22
Pro-inflammatory
IFN-γ
IL-12p70
IL-1RA
IP-10
Concentration (pg/ml)
Treatment
Epv 8
Epv 22
Epv 22+8
Control
LPS
0
1000
2000
3000
4000
6000
8000

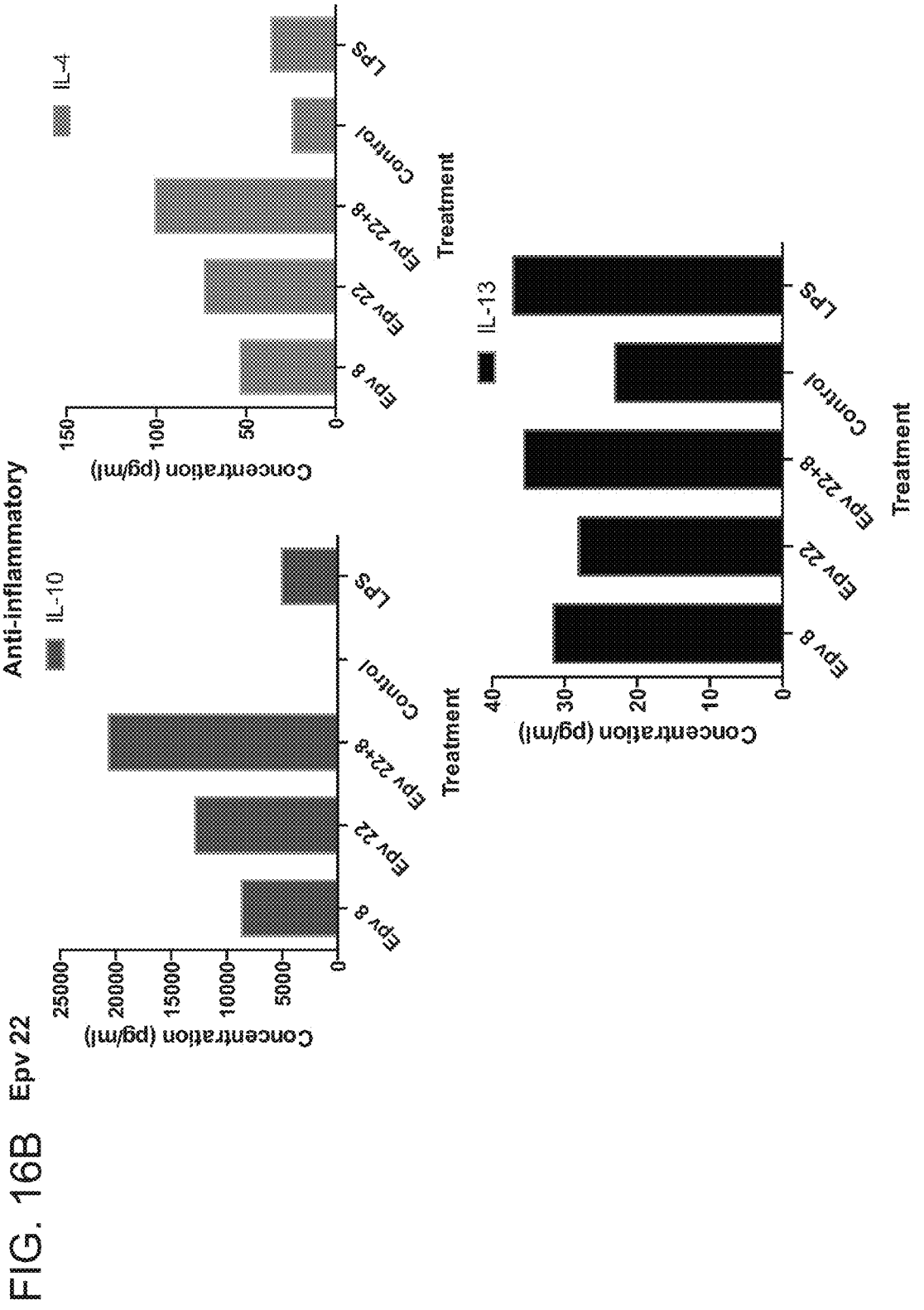


FIG. 16B Epv 22

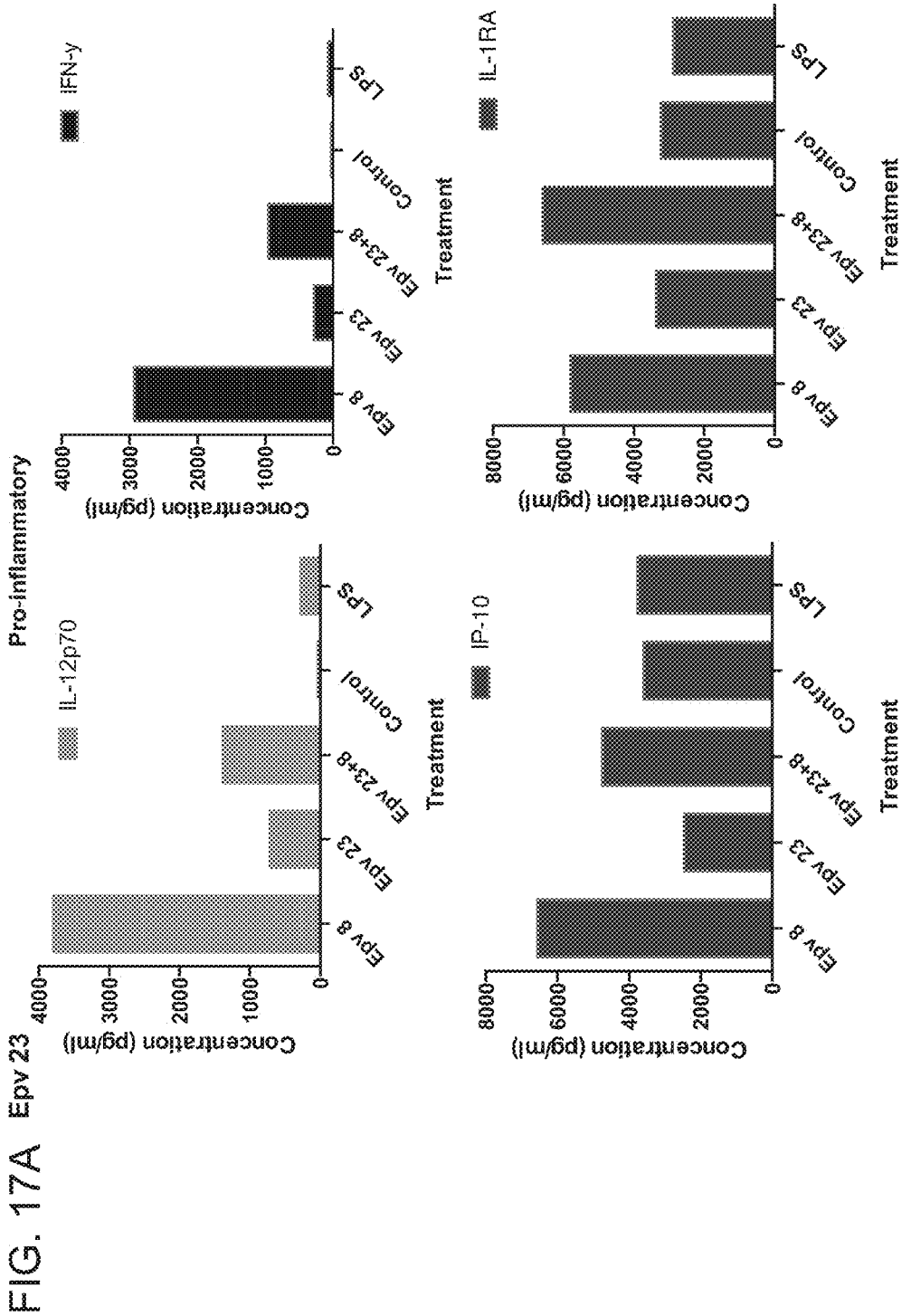


FIG. 17A Epv 23

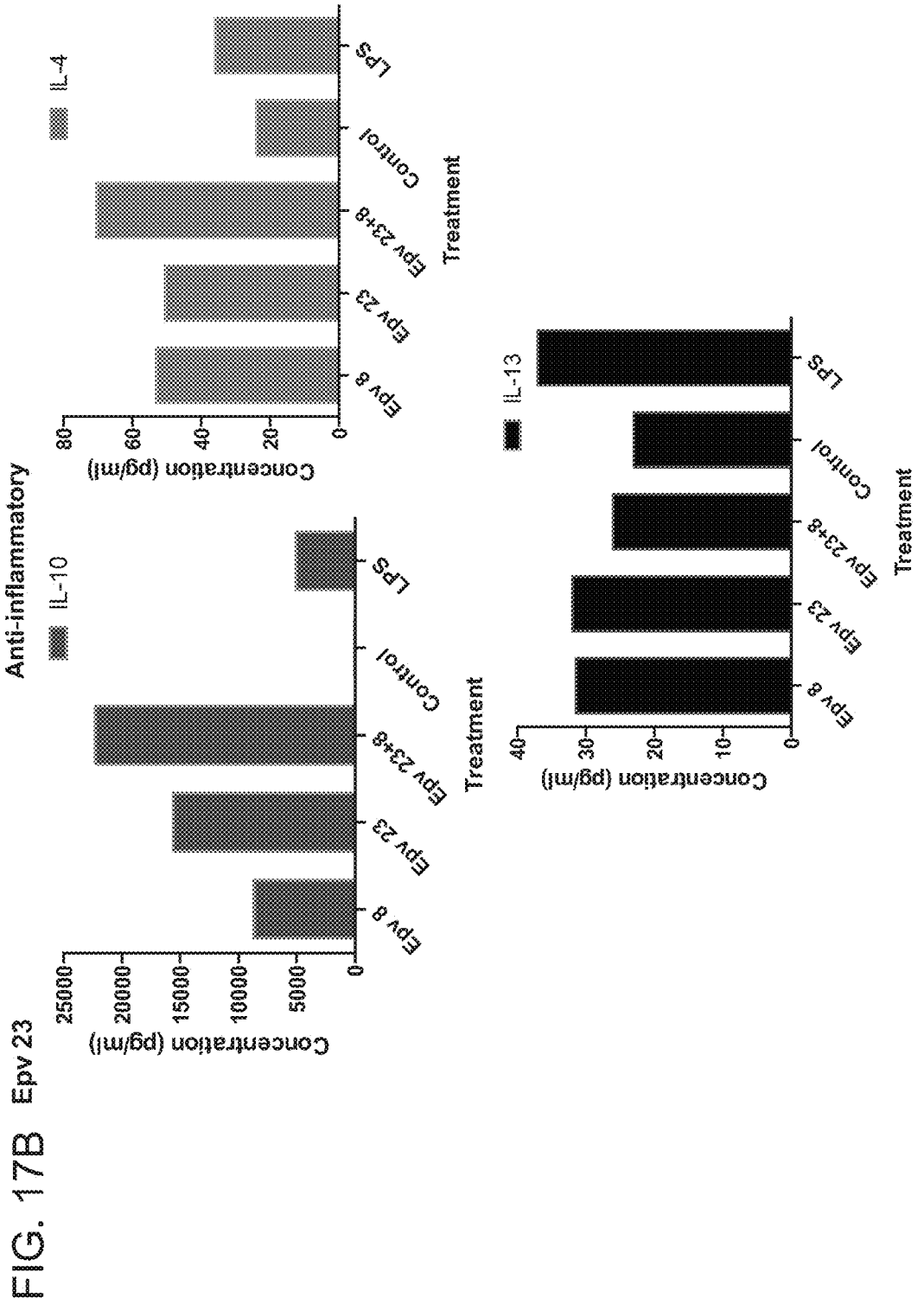
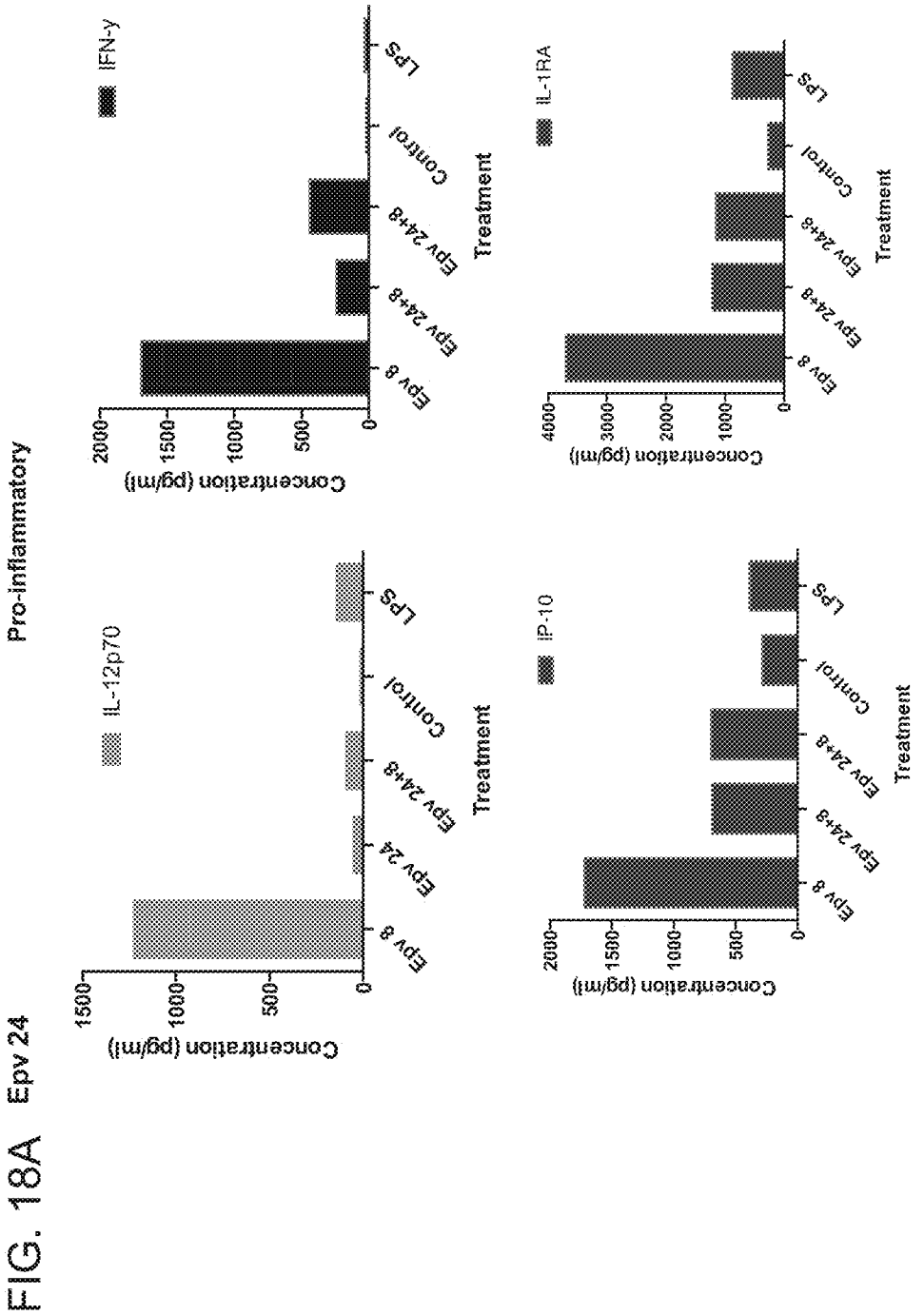


FIG. 17B Epv 23

FIG. 18A Epv 24



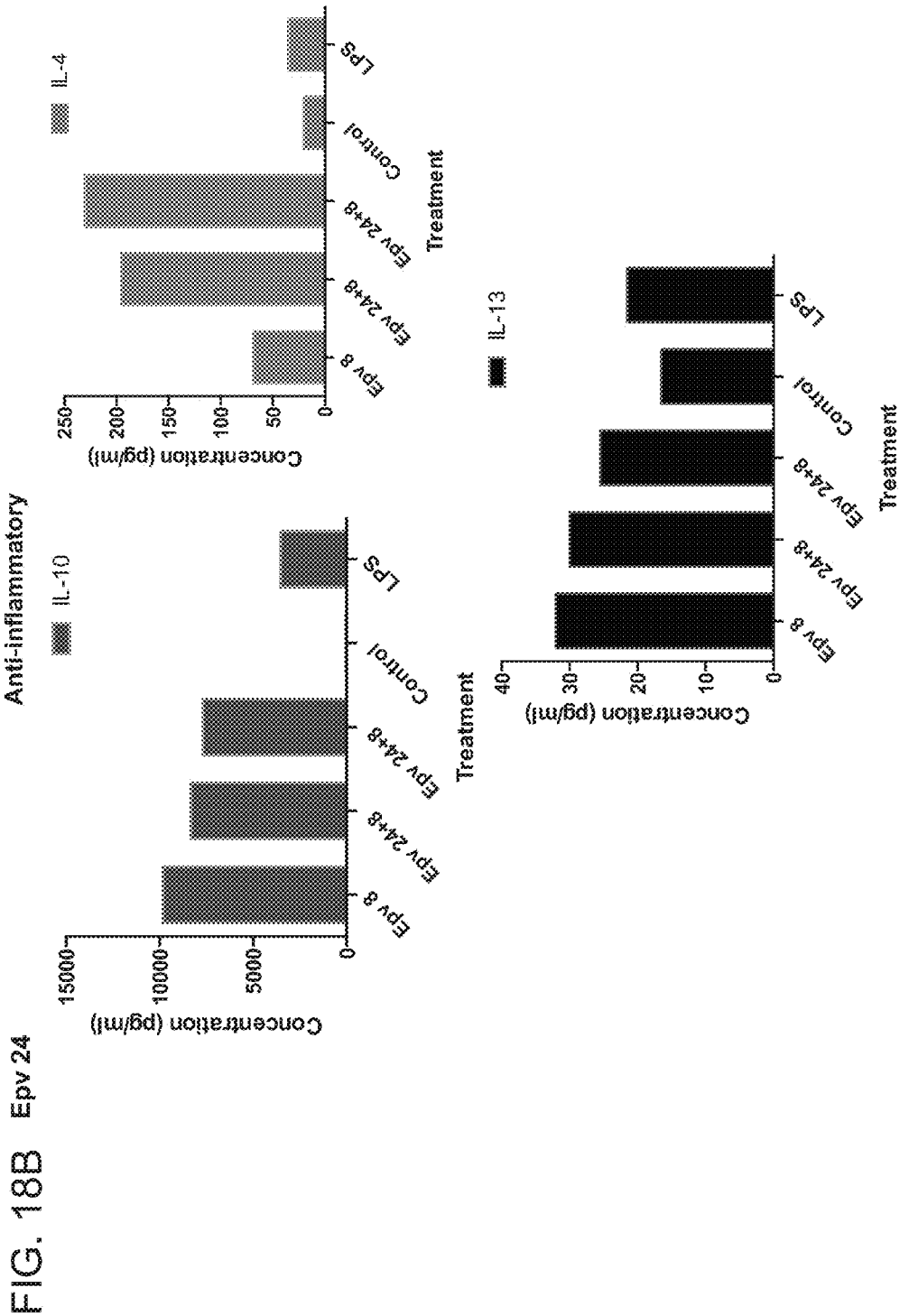


FIG. 18B Epv 24

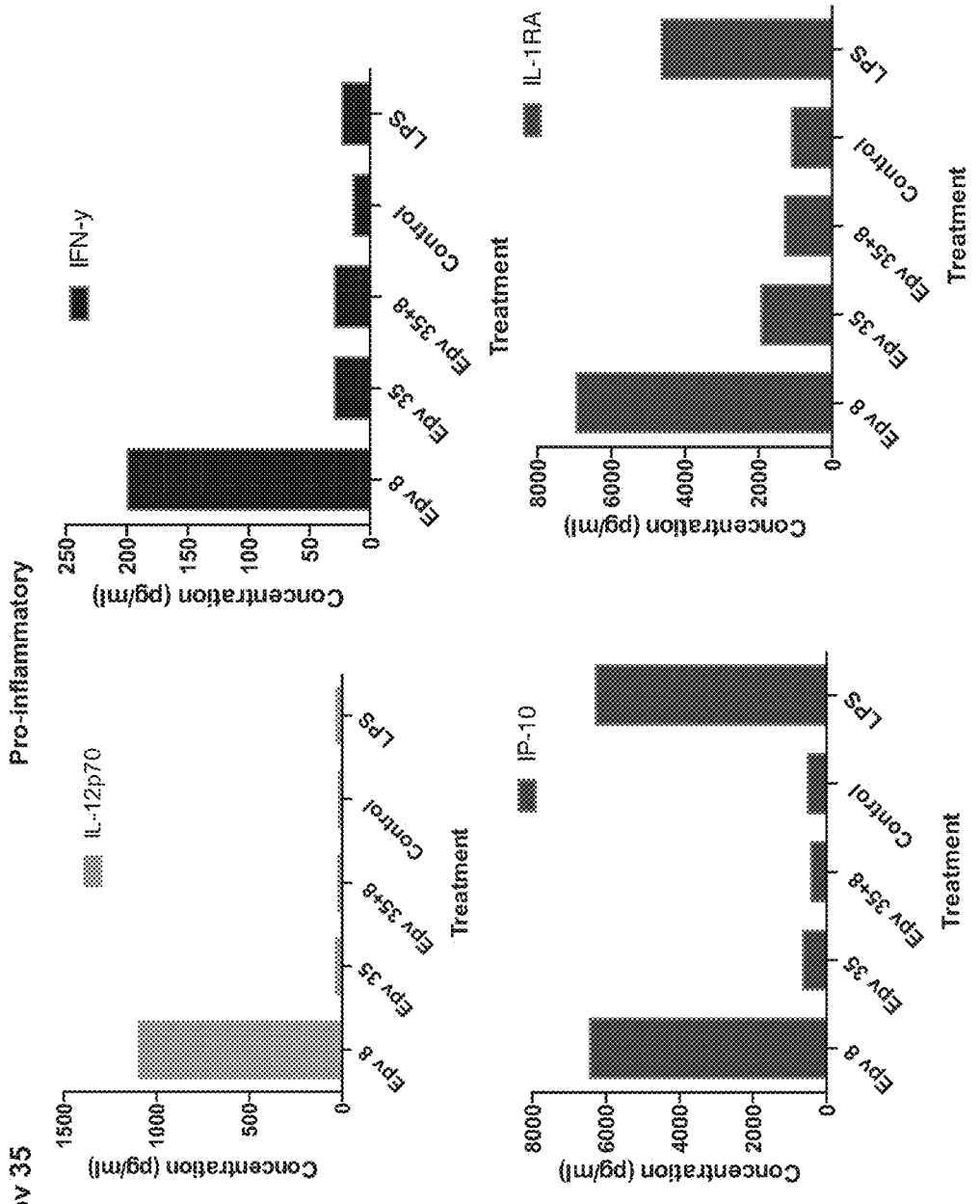


FIG. 19A Epv 35

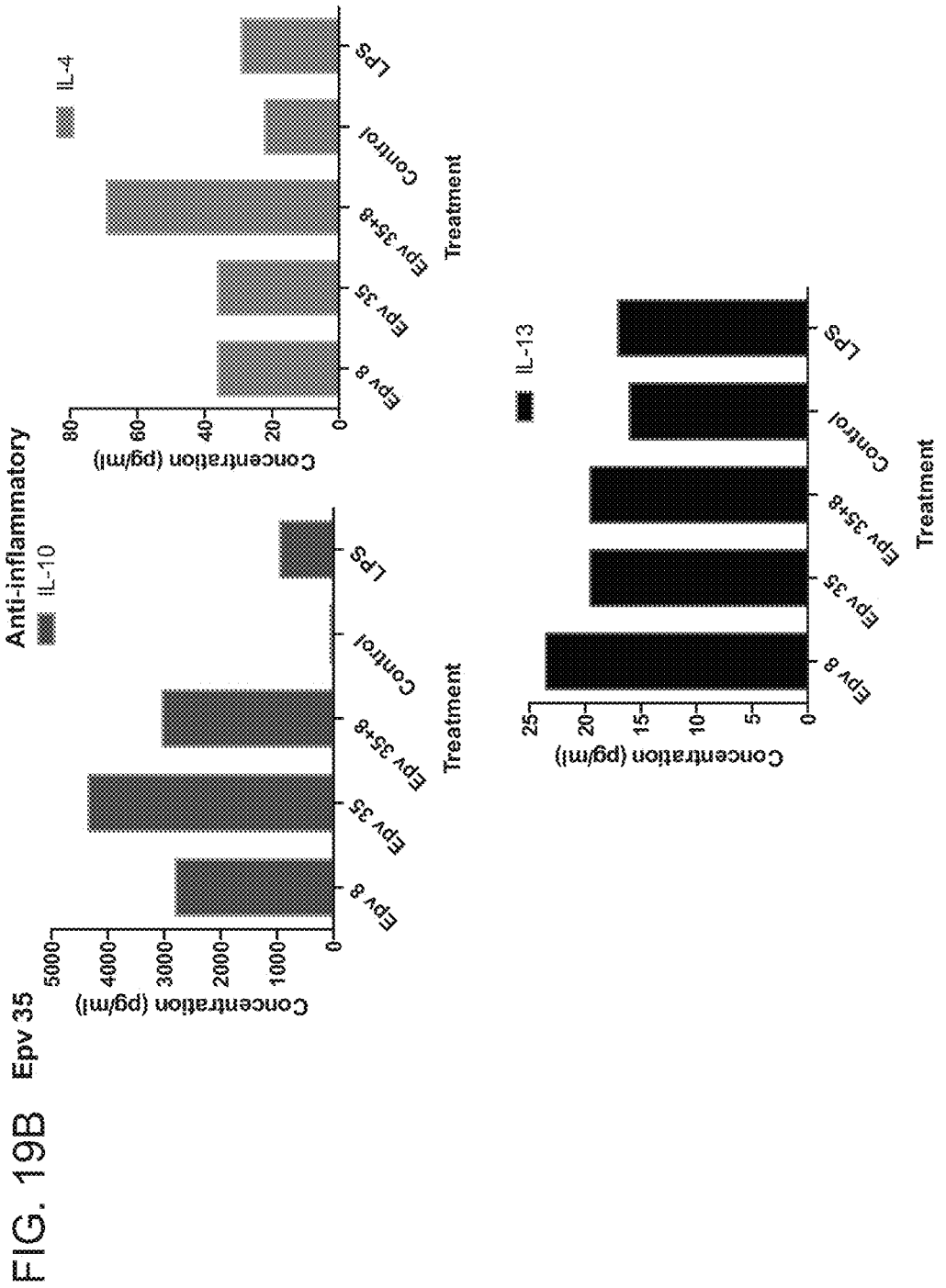
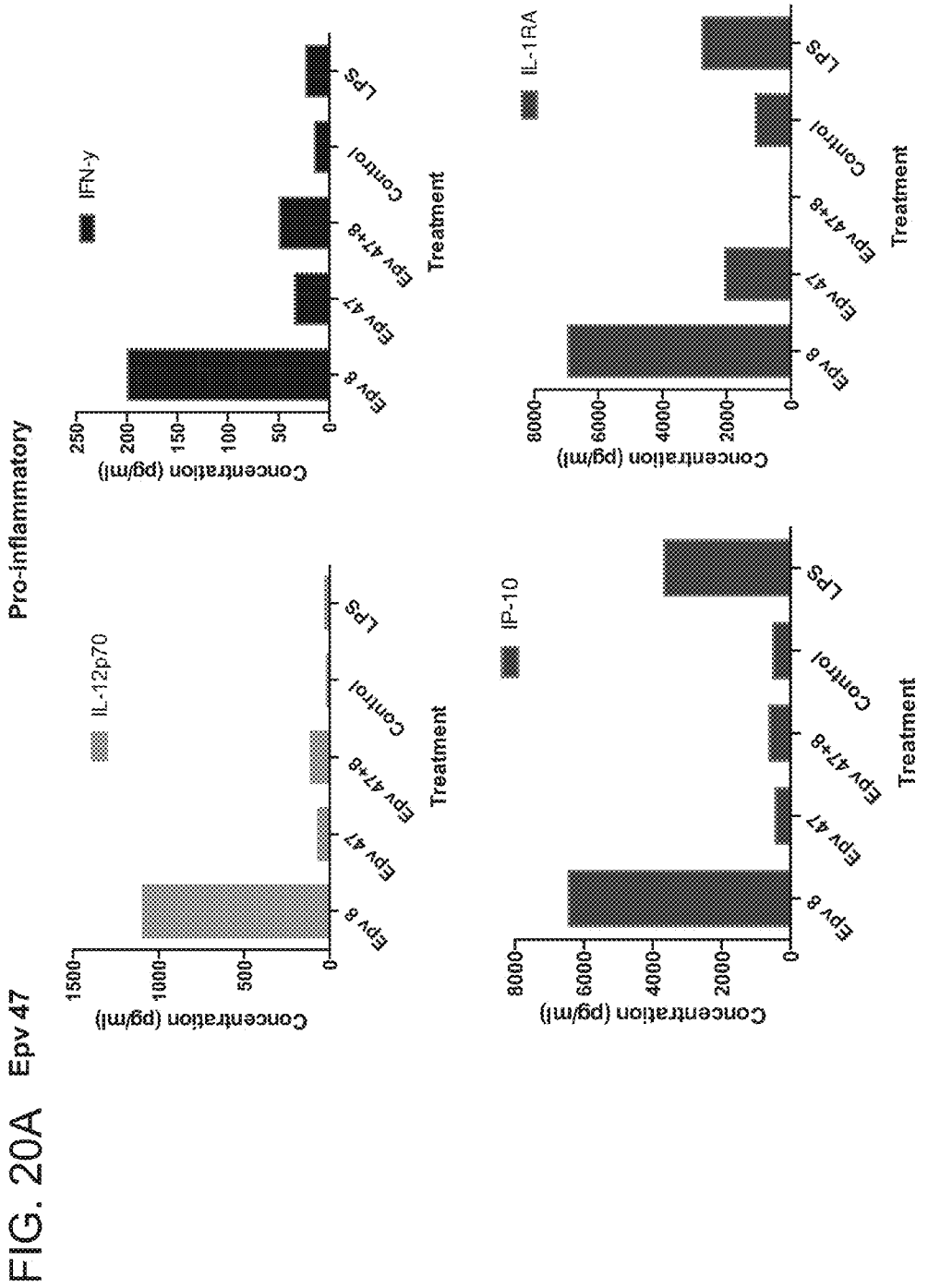


FIG. 19B Epv 35

FIG. 20A Epv 47



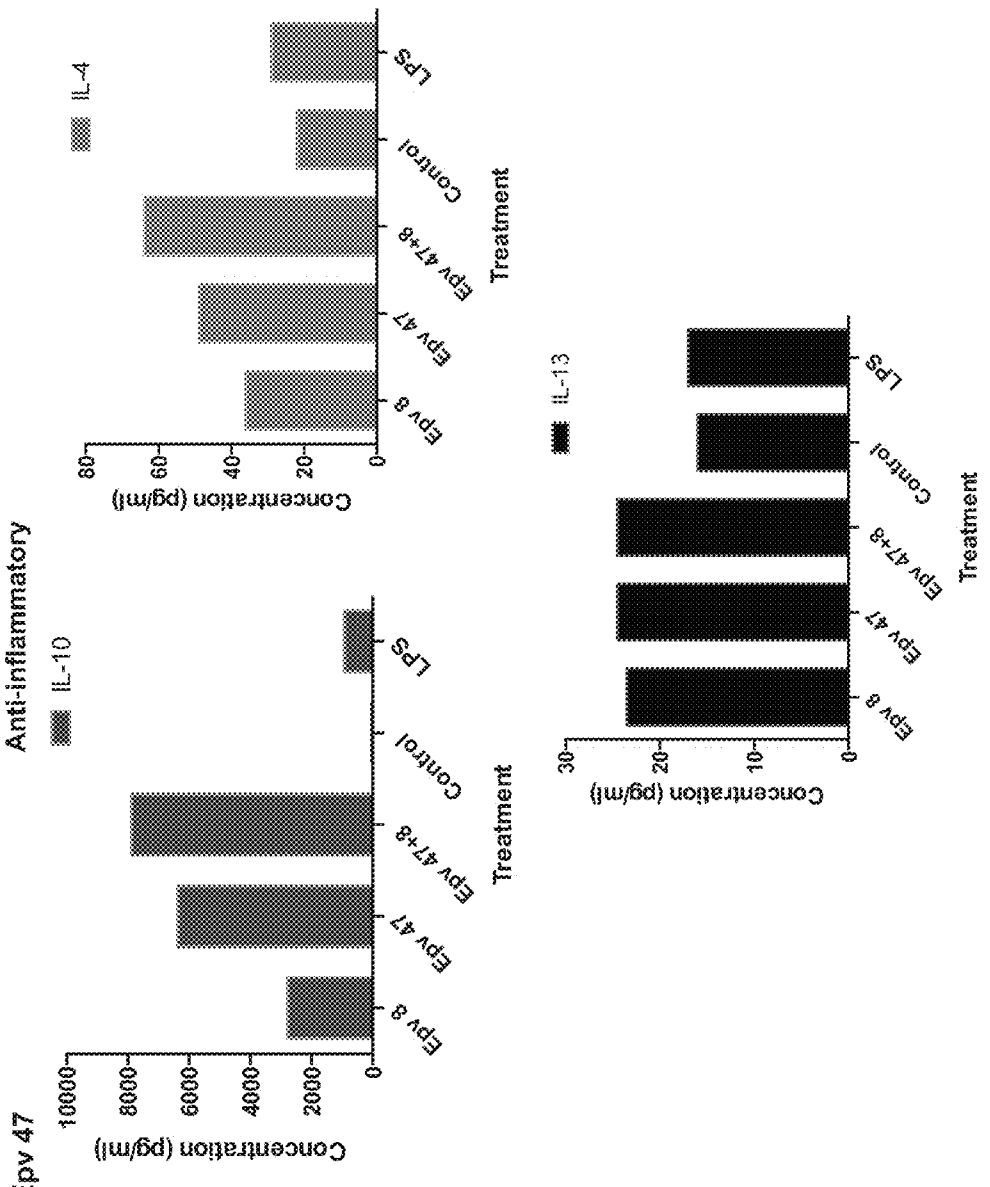
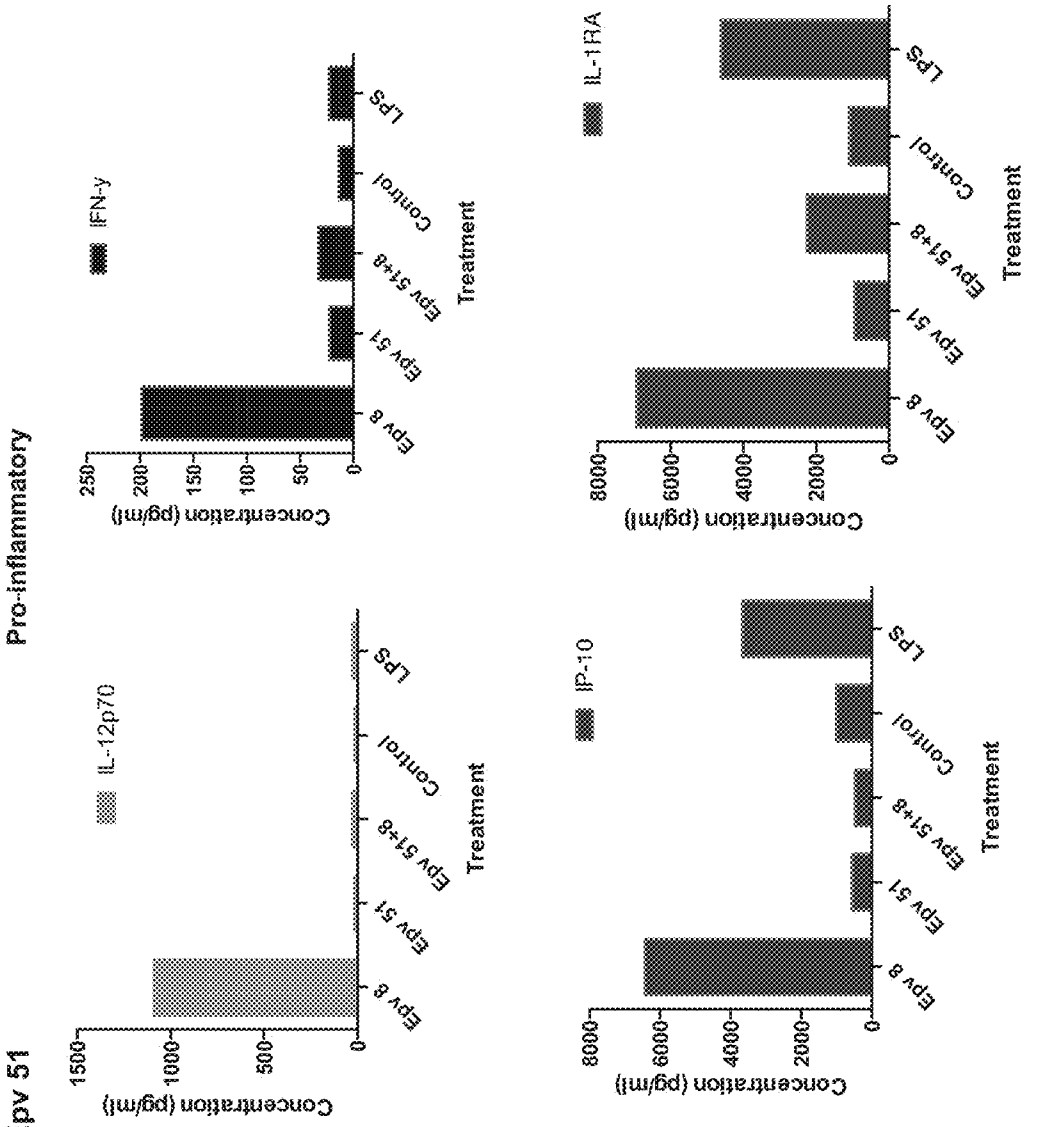


FIG. 20B Epv 47

FIG. 21A Epv 51



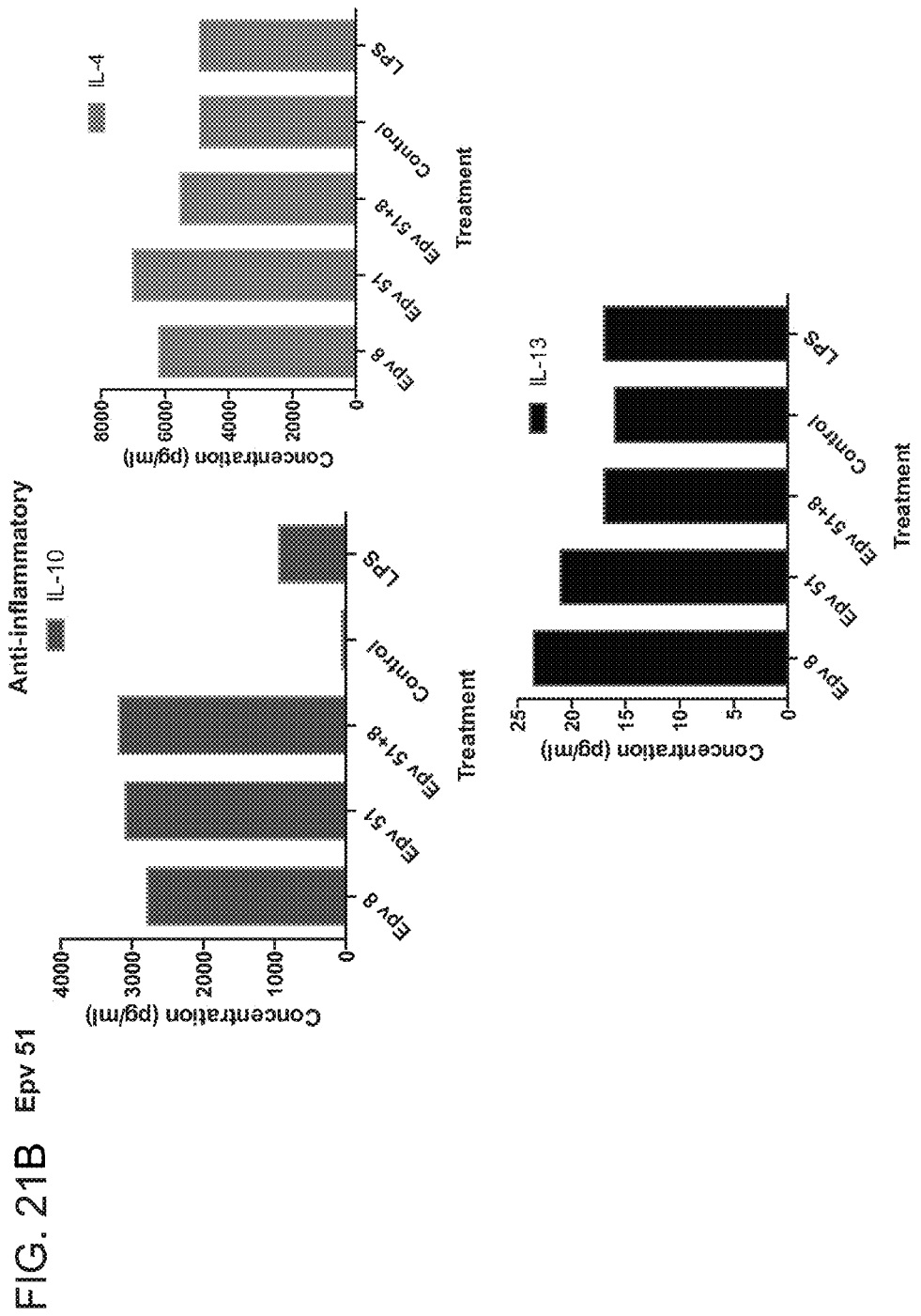


FIG. 21B Epv 51

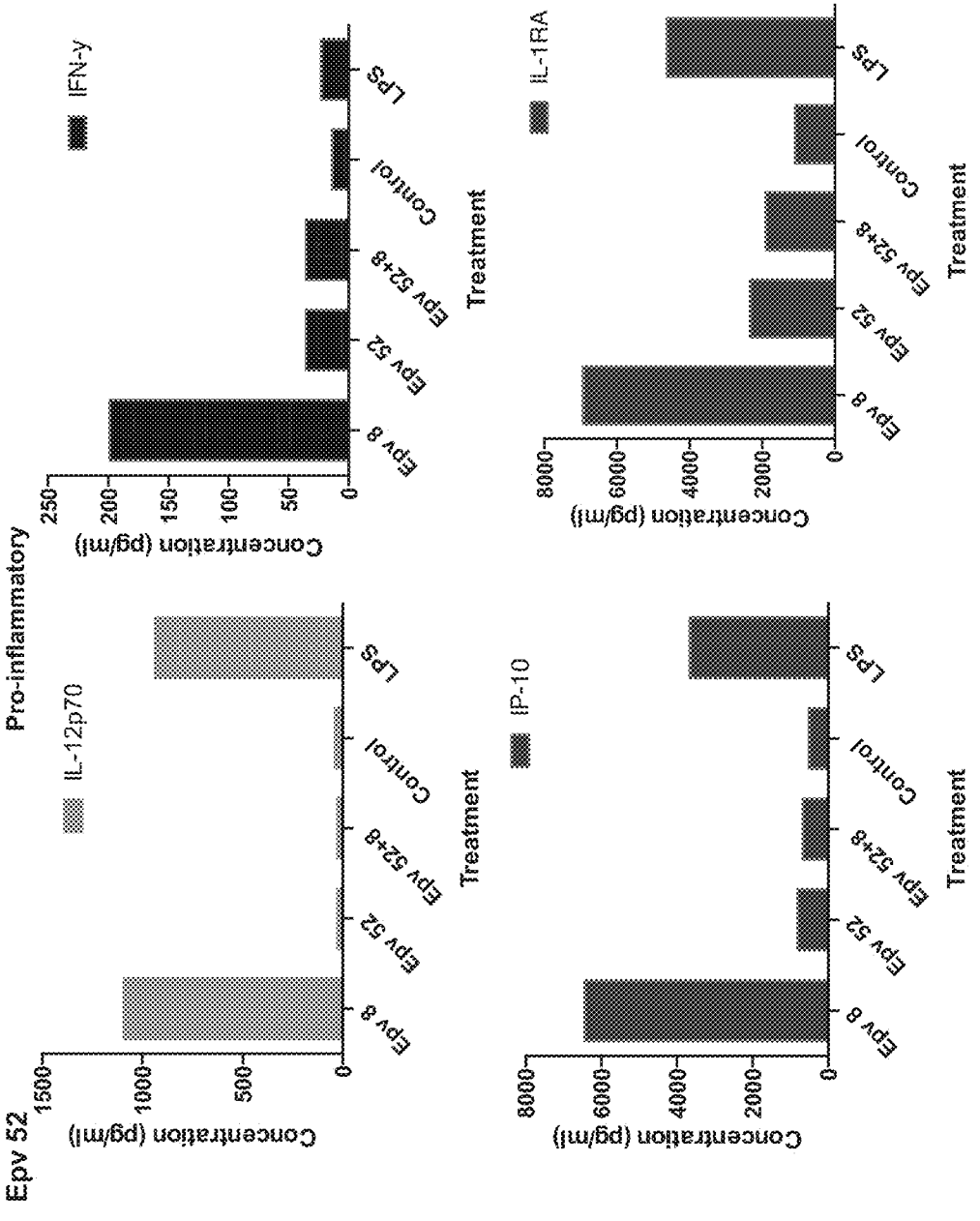

Pro-inflammatory
Epv 52
IFN-γ
IL-12p70
IL-1RA
IP-10
Concentration (pg/ml)
Treatment
Epv 8
Epv 52
Epv 52+8
Control
LPS

FIG. 22A

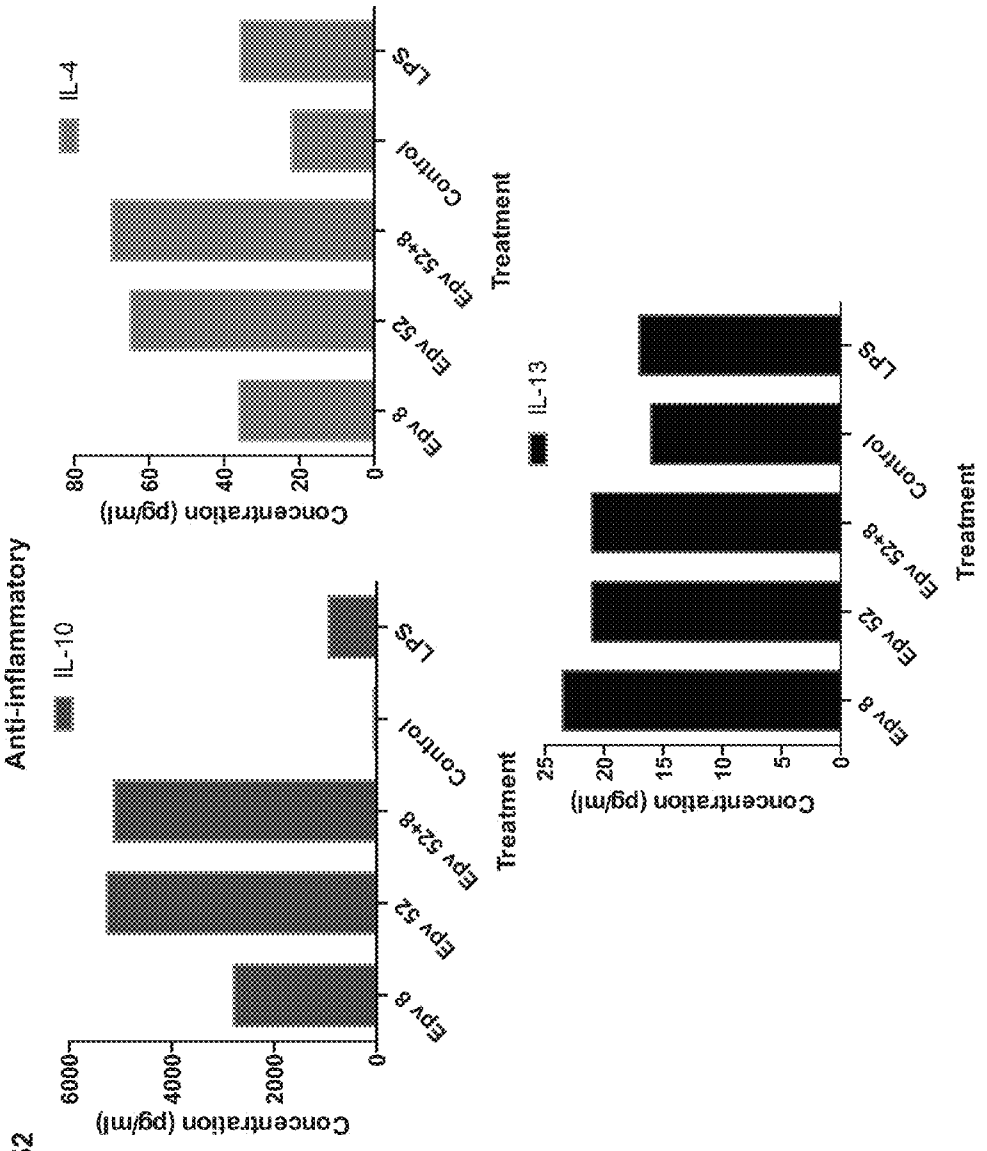


FIG. 22B Epv 52

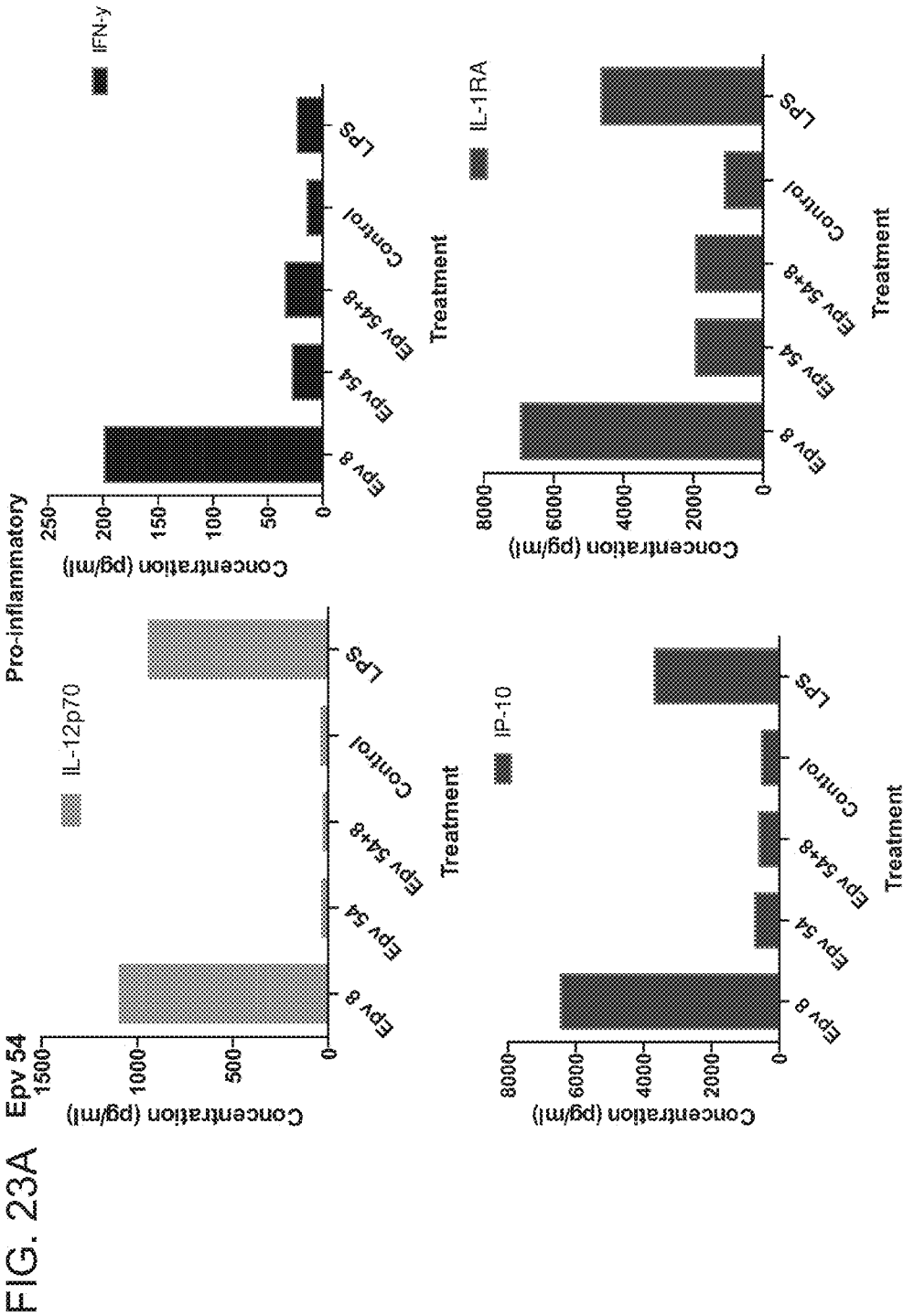

Epv 54
Pro-inflammatory
IFN-γ
IL-12p70
IL-1RA
IP-10
Concentration (pg/ml)
Treatment
Epv 8
Epv 54
Epv 54+8
Control
LPS

FIG. 23A

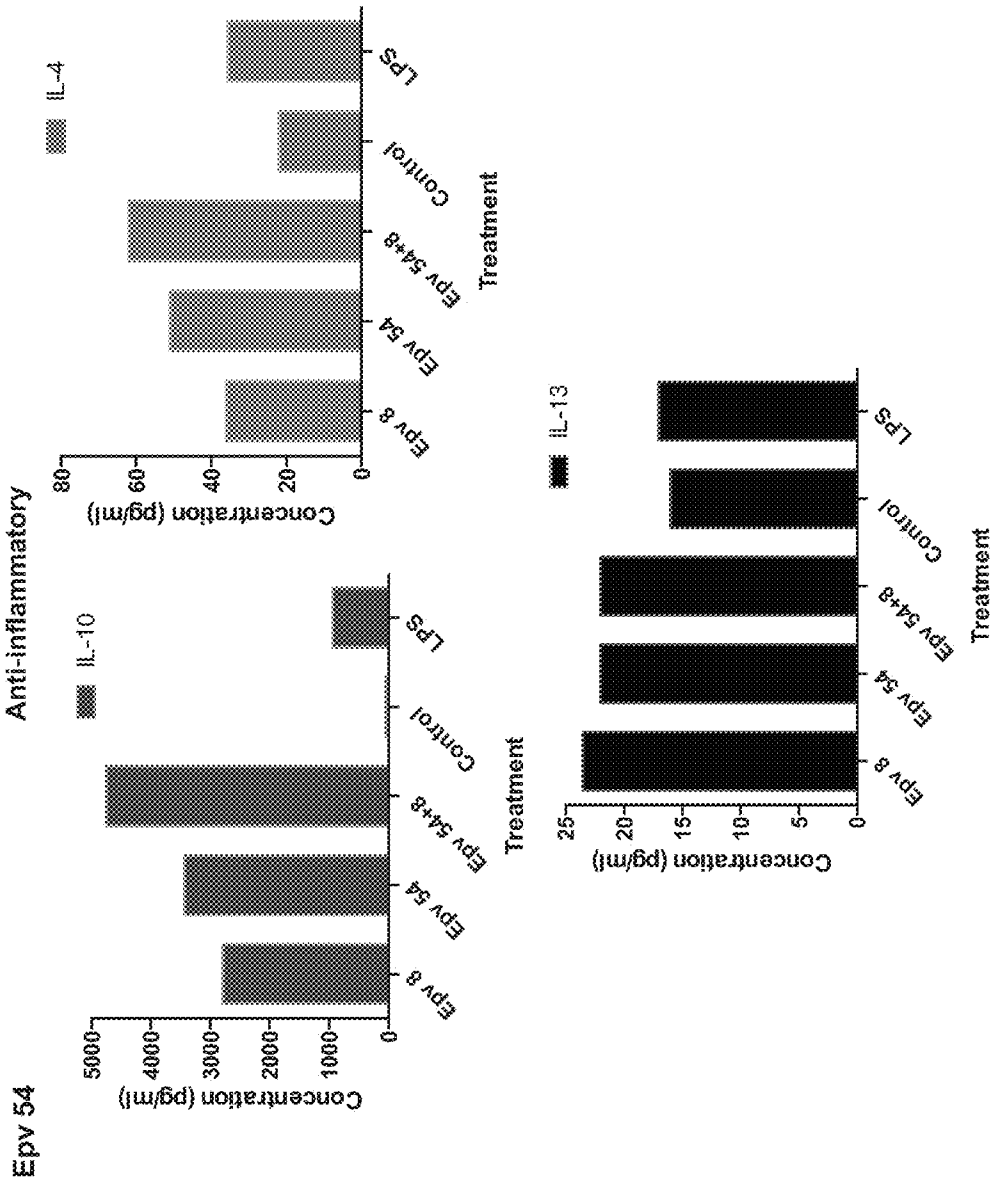


FIG. 23B Epv 54

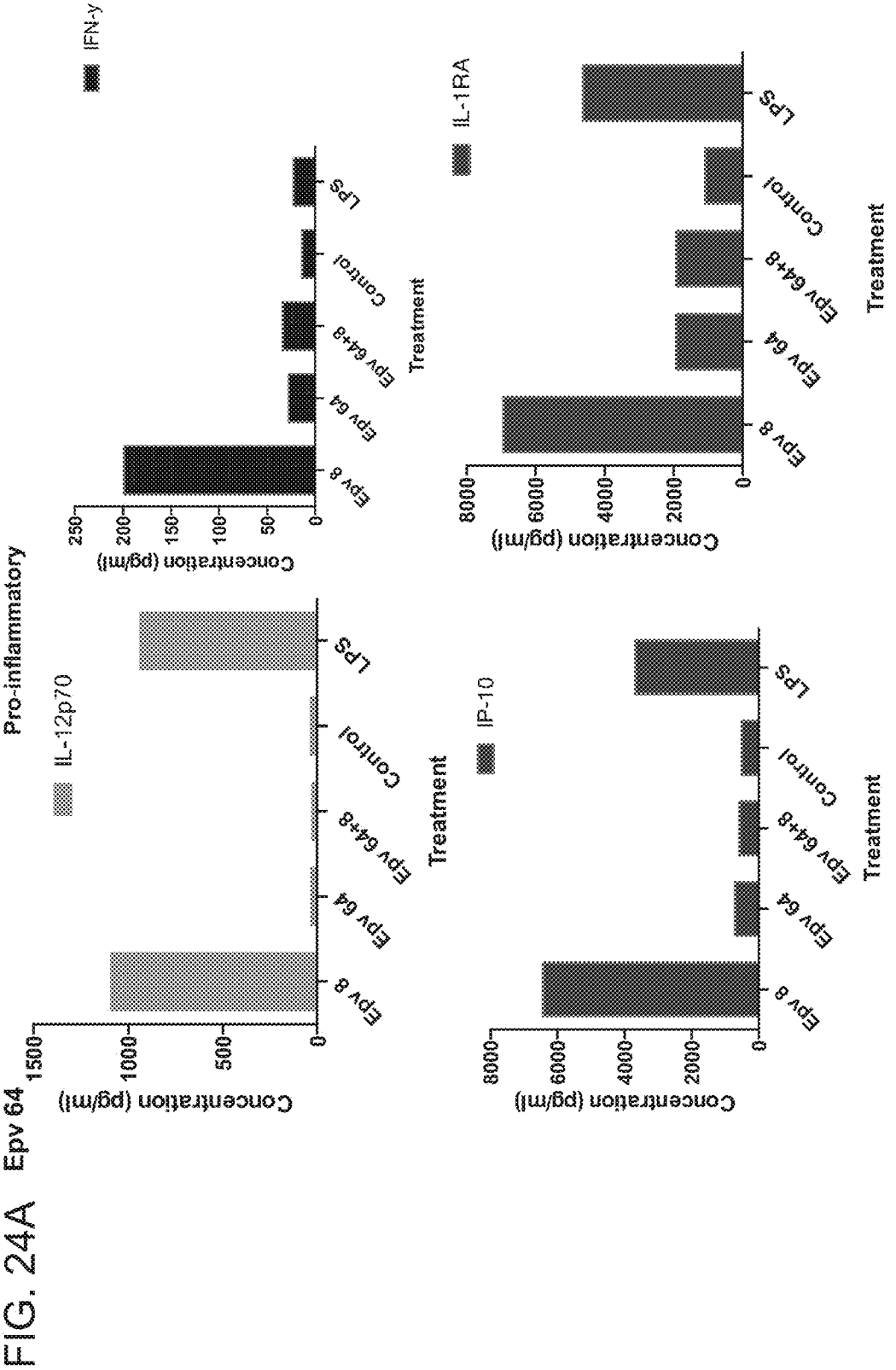

Epv 64
Pro-inflammatory
IL-12p70
IFN-γ
IP-10
IL-1RA
Concentration (pg/ml)
Treatment
Epv 8
Epv 64
Epv 64+8
Control
LPS

FIG. 24A

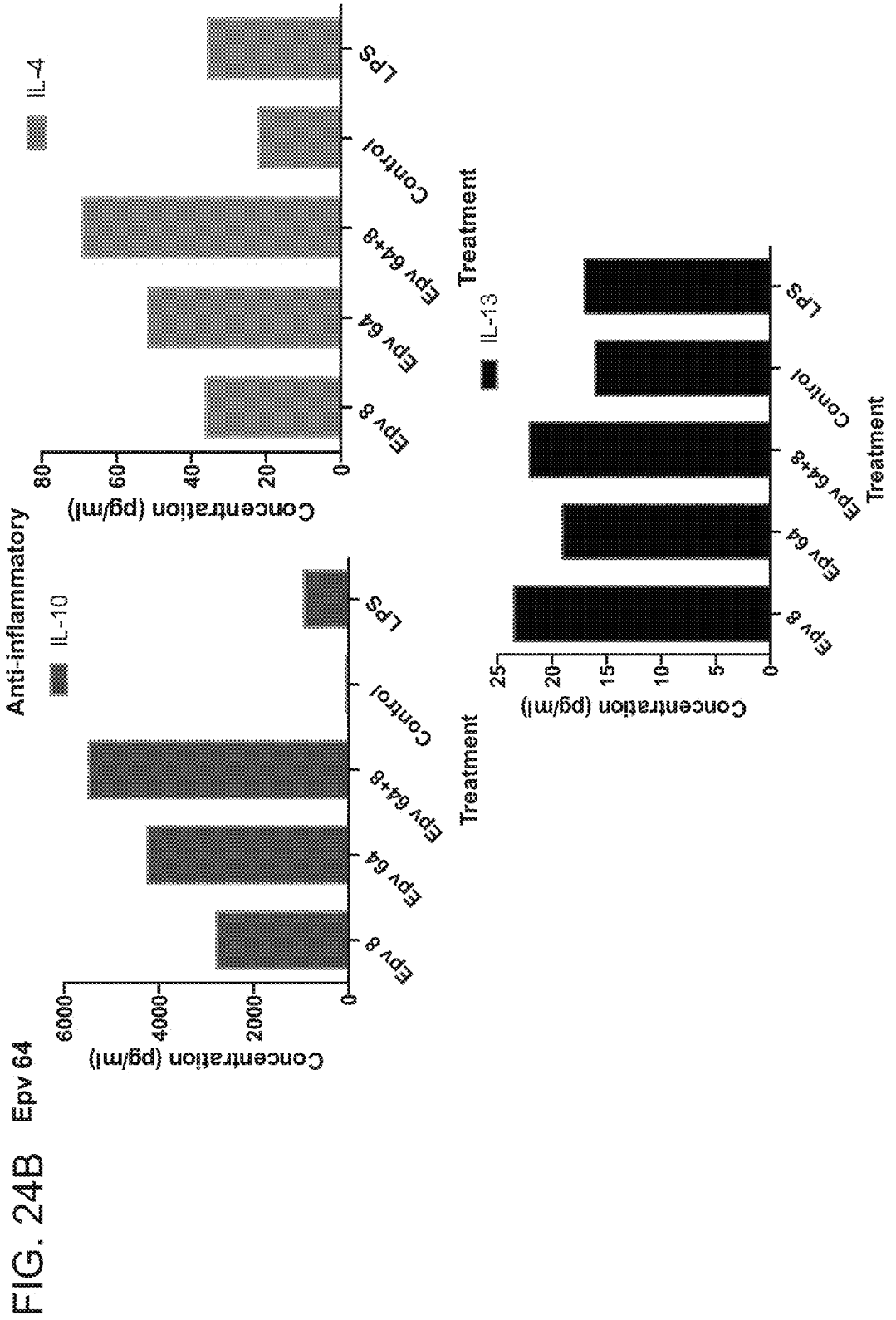
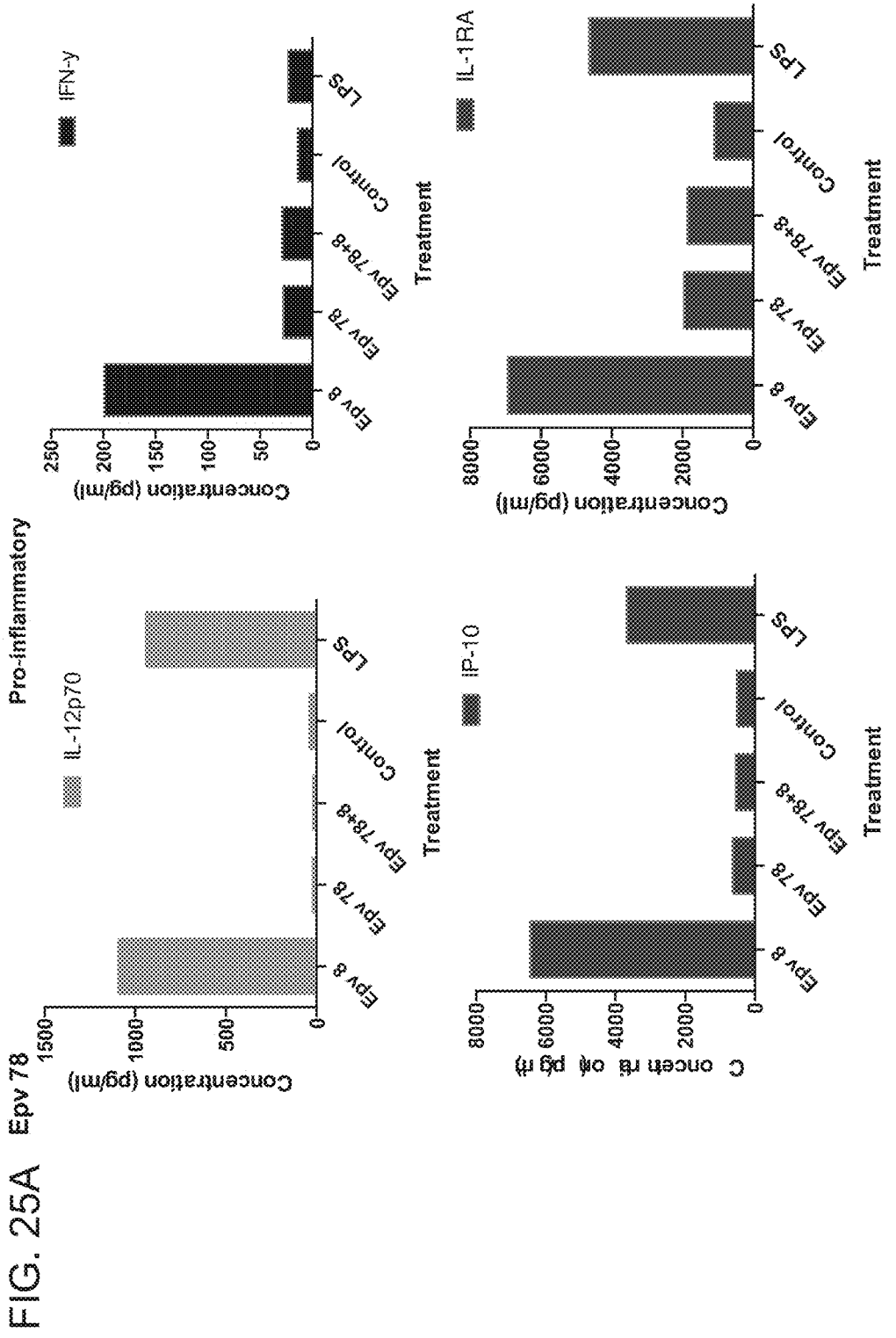

Epv 64
Anti-inflammatory
IL-10
Concentration (pg/ml)
6000
4000
2000
0
Epv 8
Epv 64
Epv 64+8
Control
LPS
Treatment
IL-4
Concentration (pg/ml)
80
60
40
20
0
Epv 8
Epv 64
Epv 64+8
Control
LPS
Treatment
IL-13
Concentration (pg/ml)
25
20
15
10
5
0
Epv 8
Epv 64
Epv 64+8
Control
LPS
Treatment

FIG. 24B

FIG. 25A Epv 78



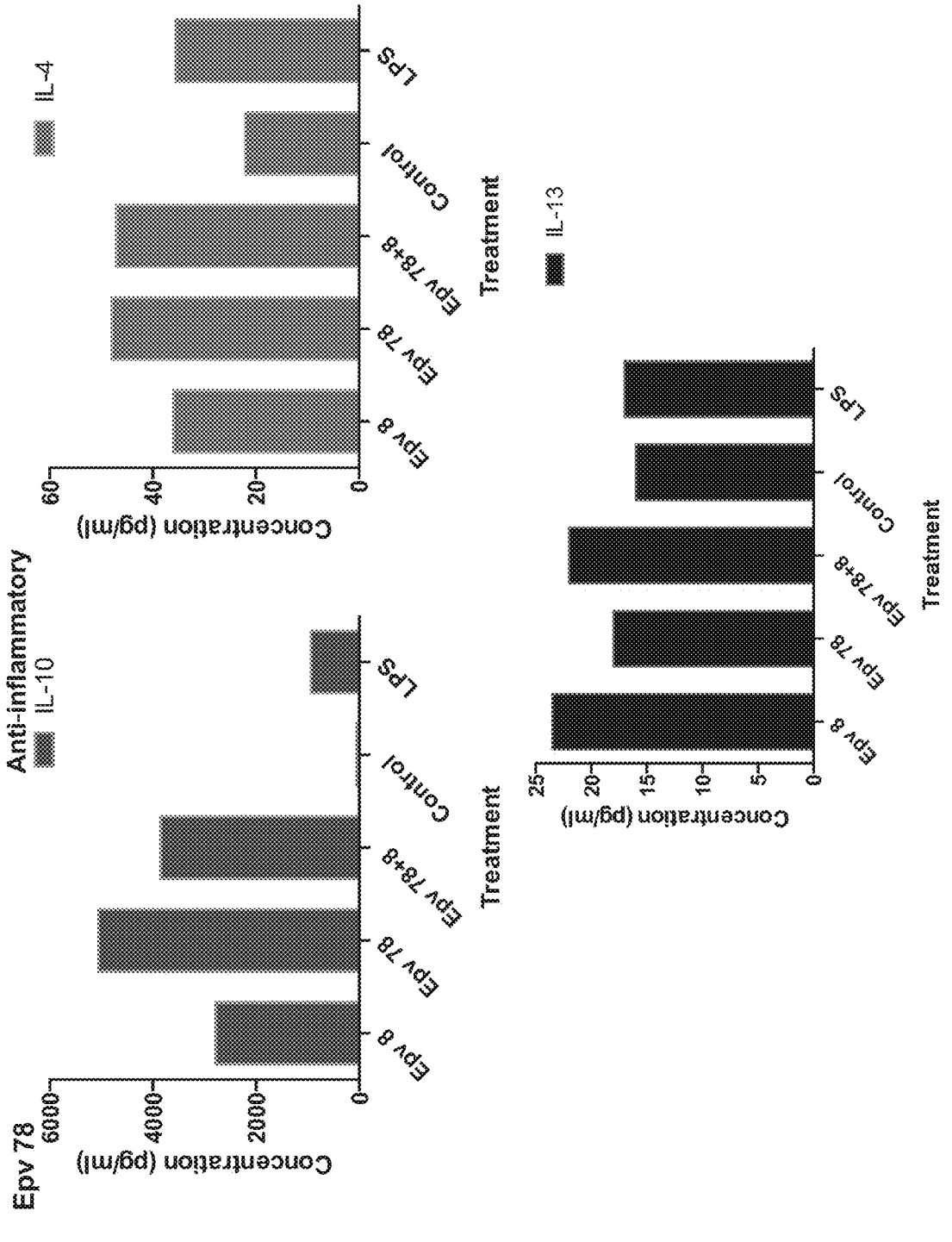

Epv 78
Anti-inflammatory
IL-10
Concentration (pg/ml)
6000
4000
2000
0
Epv 8
Epv 78
Epv 78+8
Control
LPS
Treatment
IL-4
Concentration (pg/ml)
60
40
20
0
Epv 8
Epv 78
Epv 78+8
Control
LPS
Treatment
IL-13
Concentration (pg/ml)
25
20
15
10
5
0
Epv 8
Epv 78
Epv 78+8
Control
LPS
Treatment

FIG. 25B

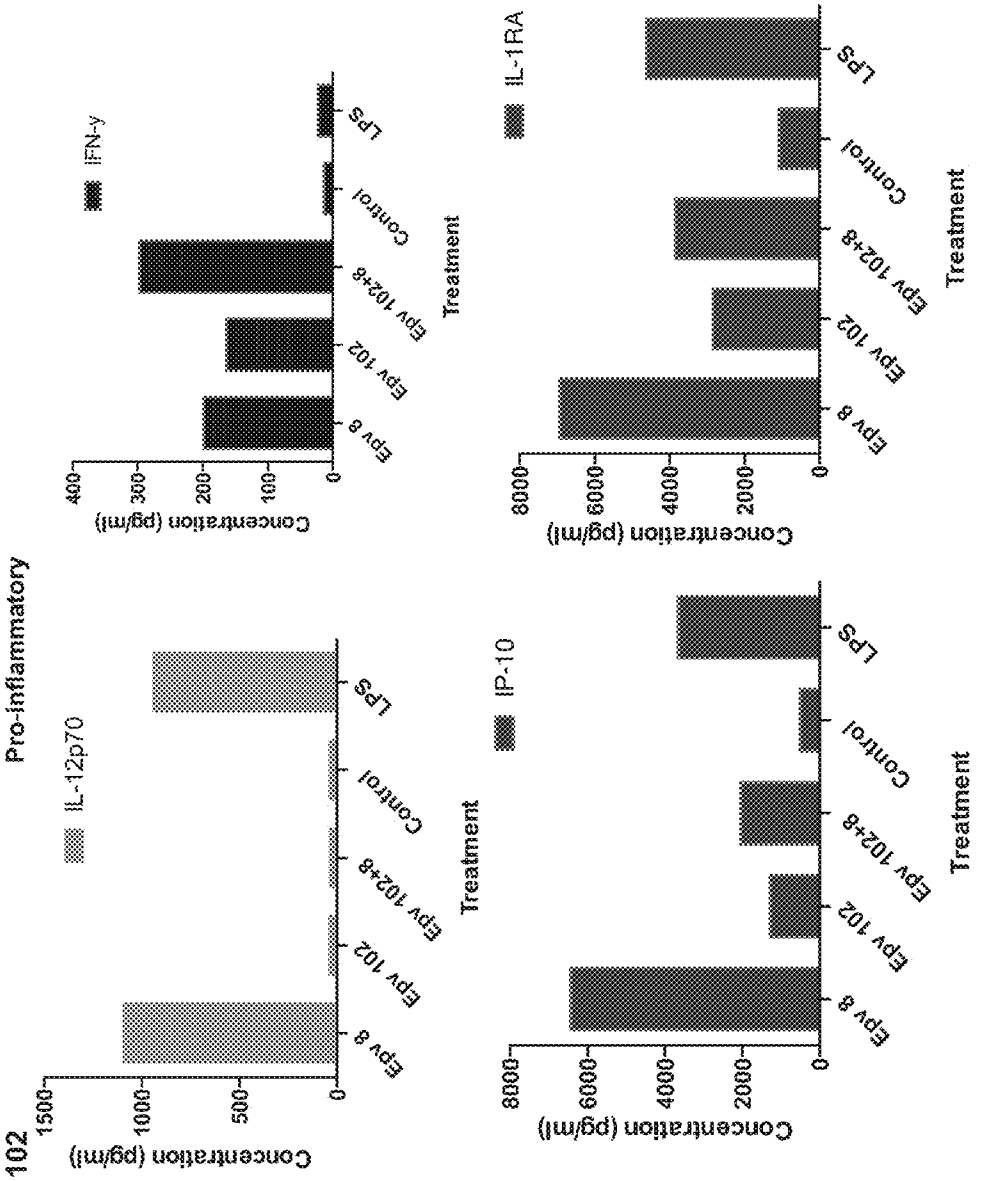


FIG. 26A Epv 102

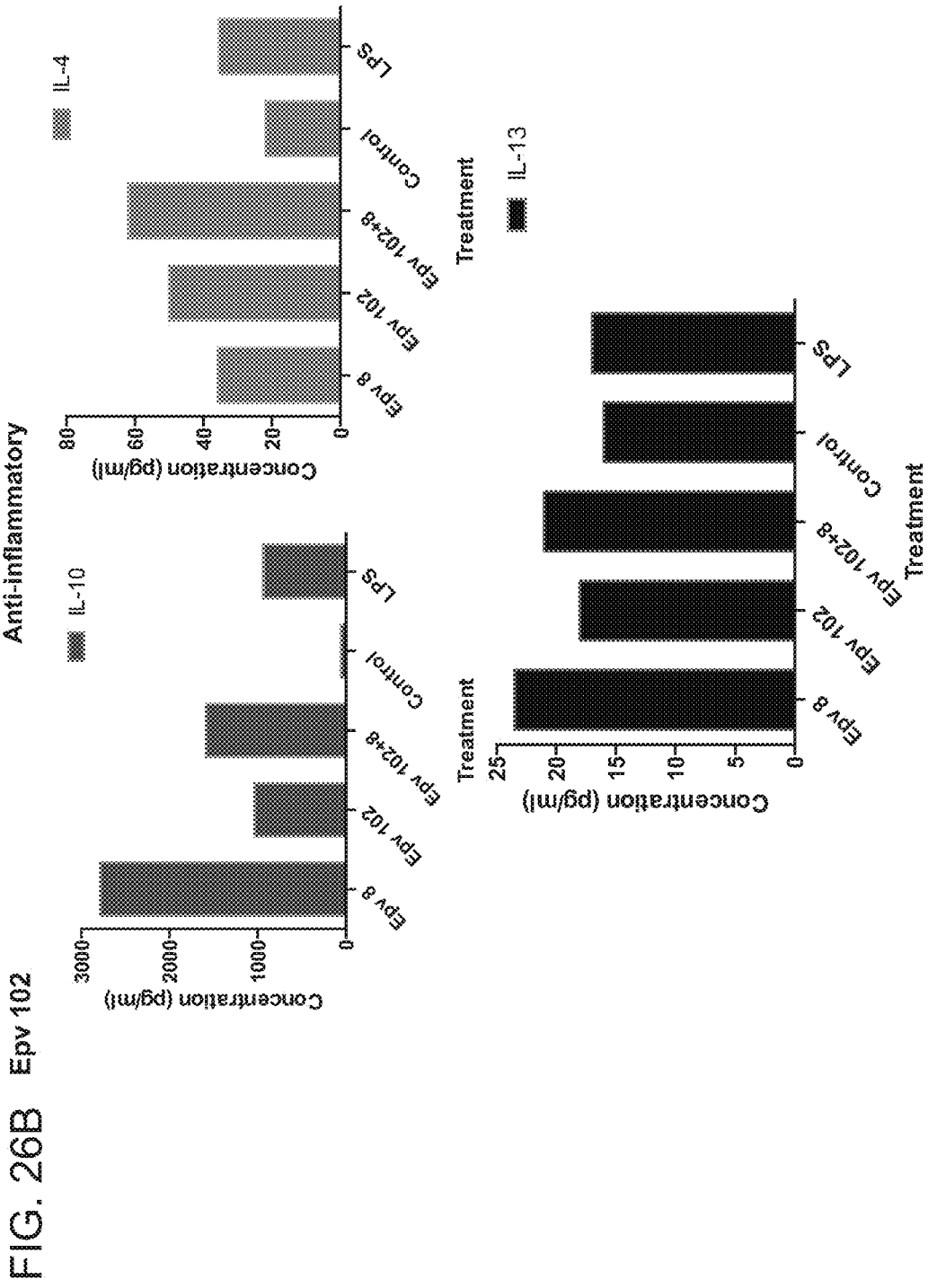


FIG. 26B Epv 102

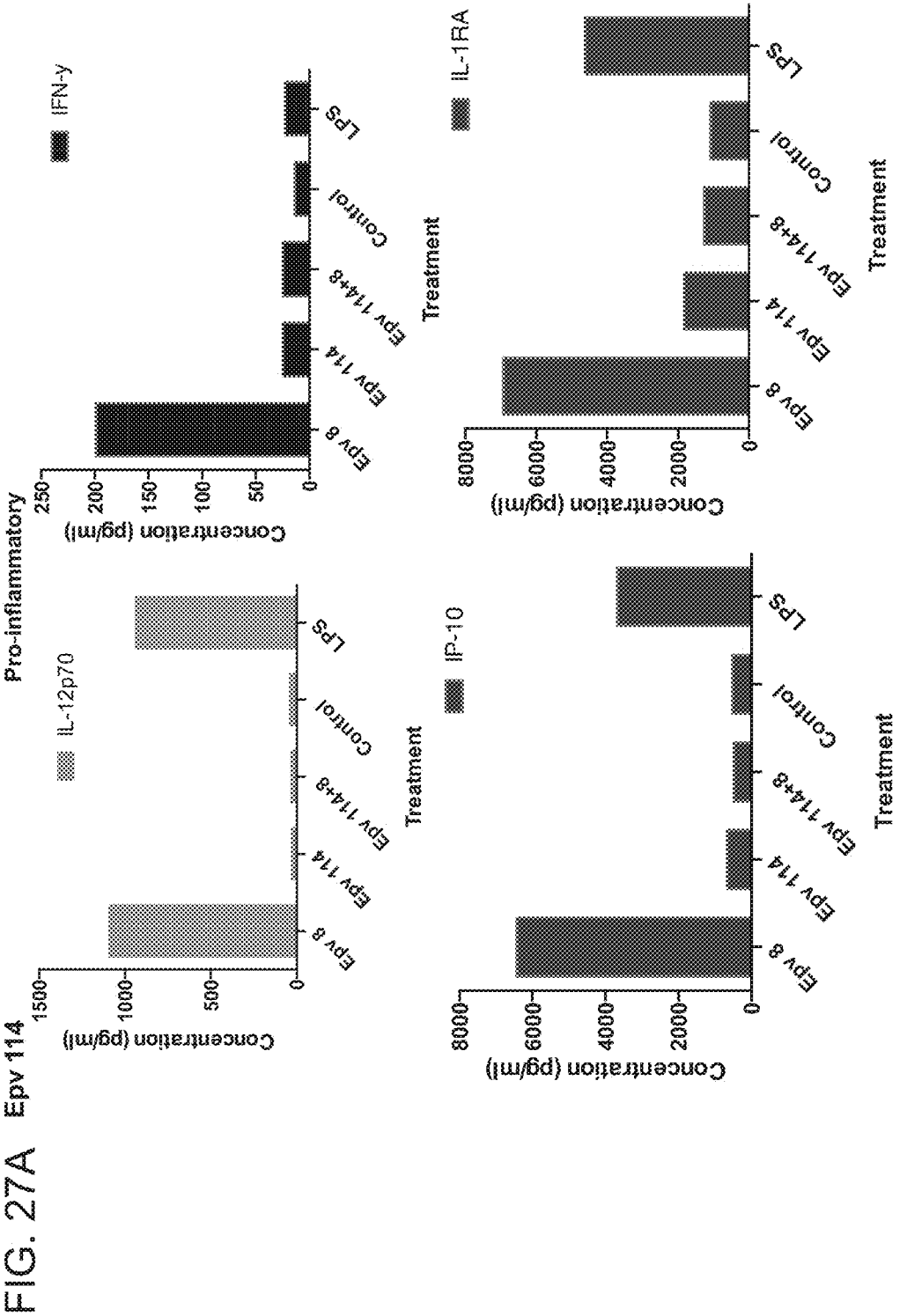

Epv 114
Pro-inflammatory
IL-12p70
IFN-γ
IP-10
IL-1RA
Concentration (pg/ml)
Treatment
Epv 8
Epv 114
Epv 114+8
Control
LPS

FIG. 27A

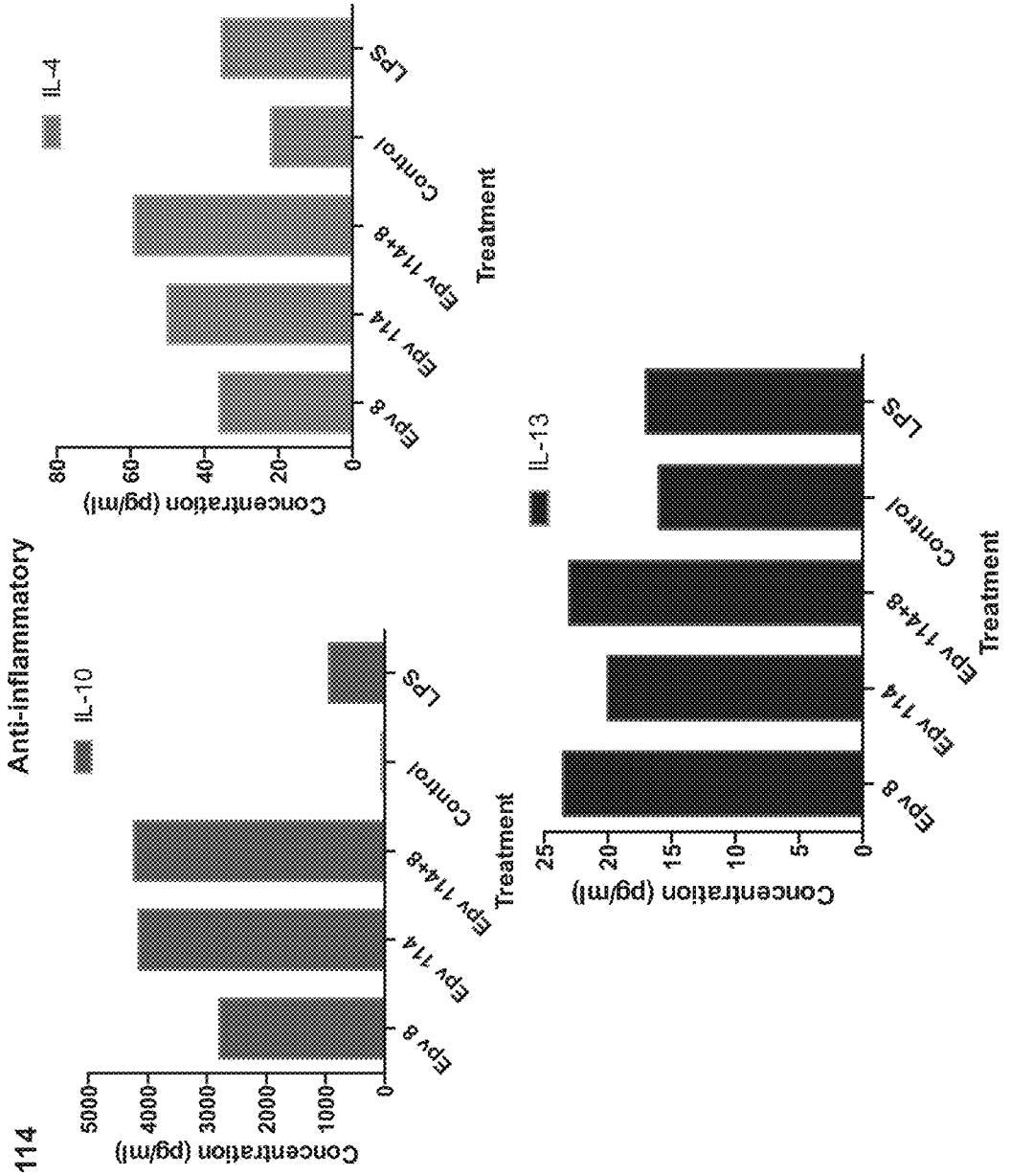


FIG. 27B Epv 114

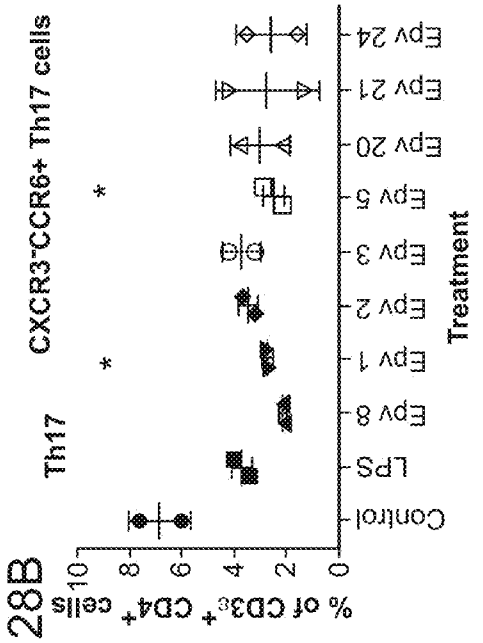


FIG. 28B

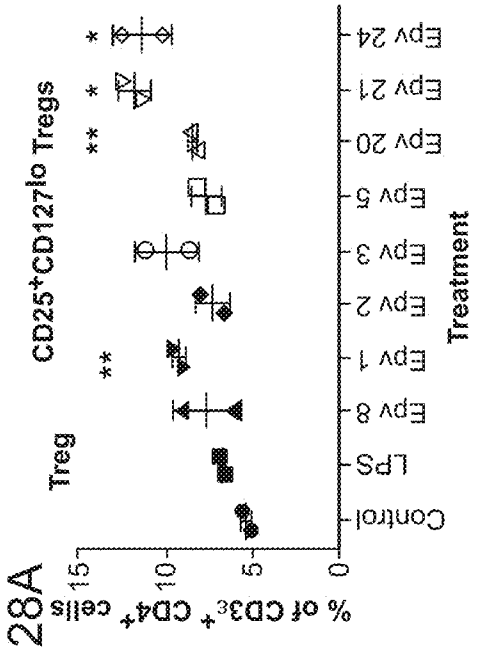


FIG. 28A

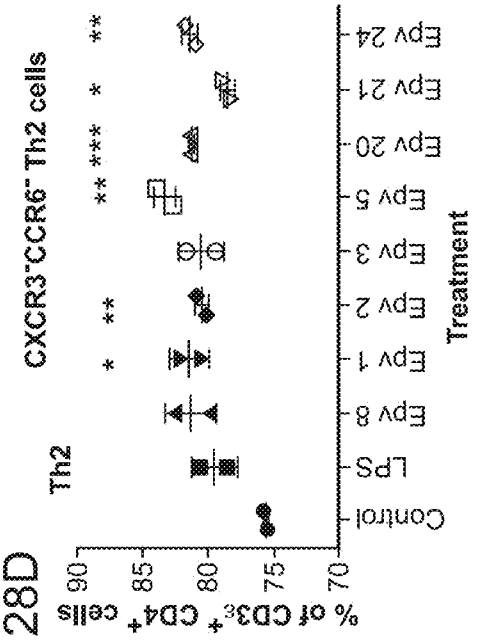


FIG. 28D

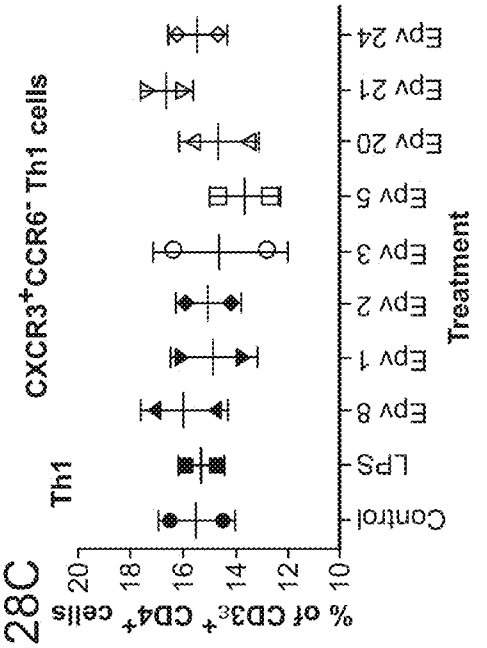


FIG. 28C

FIG. 29A

Preferred carbon sources out of 192 different carbon sources tested

R. gnavus (EPV1)	OD750
Arbutin	0.525
a-D-Lactose	0.522
b-Methyl-D-Glucoside	0.498
Maltose	0.49
N-Acetyl-D-Glucosamine	0.49
Maltotriose	0.478
Gentiobiose	0.465
Salicin	0.449
a-D-Glucose	0.445
D-Fructose	0.428
L-Fucose	0.36
D-Galactose	0.345
L-Arabinose	0.334
D-Gluconic acid	0.304
D-Ribose	0.3
D-Glucosamine	0.273
D-Arabinose	0.269
Sucrose	0.234
D-Xylose	0.215
Lactulose	0.143
L-Tartaric acid	0.141
3-O-b-D-Galactopyranosyl-D-Arabinose	0.133
b-Methyl-D-Glucuronic acid	0.131
D-Mannose	0.124
L-Rhamnose	0.101
Uridine	0.101

FIG. 29B

Preferred carbon sources out of 192 different carbon sources tested

E. rectale (EPV2)	OD750
N-Acetyl-D-Glucosamine	0.174
D-Raffinose	0.173
Palatinose	0.157
a-D-Lactose	0.155
Stachyose	0.154
g-Cyclodextrin	0.148
Dextrin	0.14
Gentiobiose	0.136
D-Galactose	0.123
D-Glucosamine	0.117
D-Melibiose	0.112
3-O-b-D-Galactopyranosyl-D-Arabinose	0.105
b-Methyl-D-Galactoside	0.103

FIG. 29C

C. leptum (EPV6)	OD750
D-Fructose-6-Phosphate	0.11
D-Trehalose	0.109

FIG. 29D

Preferred carbon sources out of 192 different carbon sources tested

B. luti (EPV3)	OD750
a-D-Glucose	0.628
Maltotriose	0.625
Sucrose	0.592
Palatinose	0.588
L-Fucose	0.576
Stachyose	0.554
a-D-Lactose	0.549
D-Fructose	0.544
D-Melibiose	0.527
Maltose	0.523
Salicin	0.493
D-Raffinose	0.486
Arbutin	0.435
D-Mannitol	0.423
Lactulose	0.381
D-Lactitol	0.36
D-Gluconic acid	0.344
m-Inositol	0.32
Melibionic acid	0.29
D-Sorbitol	0.239
D-Arabinose	0.183
L-Tartaric acid	0.178
L-Arabinose	0.133
Bromosuccinic acid	0.114
D-Ribose	0.107

FIG. 29E

B. wexlerae (EPV5)	OD750
a-D-Glucose	0.988
D-Fructose	0.964
Stachyose	0.96
a-D-Lactose	0.912
Sucrose	0.84
D-Lactitol	0.671
L-Fucose	0.647
Lactulose	0.566
D-Melibiose	0.561
D-Raffinose	0.522
D-Galactose	0.428
D-Glucosamine	0.239
b-Methyl-D-Galactoside	0.206
D-Cellobiose	0.163
Pectin	0.109
Inulin	0.105

FIG. 29F

Preferred carbon sources out of 192 different carbon sources tested

B. faecis (EPV15)	OD750
Arbutin	0.525
Gentiobiose	0.465
Salicin	0.449
D-Glucosamine	0.273
D-Arabinose	0.269
D-Sorbitol	0.227
D-Fructose	0.213
D-Cellobiose	0.212
Sucrose	0.183
Maltose	0.183
Lactulose	0.168
a-D-Lactose	0.164
a-D-Glucose	0.164
D-Melibiose	0.163
D-Mannose	0.143
L-Tartaric acid	0.141
Bromosuccinic acid	0.141
3-O-b-D-Galactopyranosyl-D-Arabinose	0.133
b-Methyl-D-Glucuronic acid	0.131
Maltotriose	0.127
D-Galactose	0.125
L-Fucose	0.123
D-Gluconic acid	0.121
D-Mannitol	0.117
Thymidine	0.105
Inosine	0.102

FIG. 29G

Preferred carbon sources out of 192 different carbon sources tested

B. obeum (EPV20)	OD750
D-Melibiose	0.588
D-Sorbitol	0.545
Lactulose	0.543
D-Lactitol	0.48
Sucrose	0.463
L-Arabinose	0.442
a-D-Glucose	0.438
D-Galactose	0.427
D-Mannose	0.419
D-Fructose	0.414
Stachyose	0.405
b-Methyl-D-Galactoside	0.402
D-Arabinose	0.395
D-Xylose	0.377
D-Ribose	0.376
D-Raffinose	0.376
D-Fucose	0.373
Maltose	0.362
a-D-Lactose	0.361
Maltotriose	0.36
3-O-b-D-Galactopyranosyl-D-Arabinose	0.352
L-Rhamnose	0.338
L-Fucose	0.299

FIG. 29H

Preferred carbon sources out of 192 different carbon sources tested

***B. producta* (EPV21)**	**OD750**
Maltose	0.199
D-Fructose	0.193
D-Trehalose	0.182
a-Methyl-D-Galactoside	0.179
Stachyose	0.177
b-Methyl-D-Xyloside	0.175
Turanose	0.175
a-D-Glucose	0.174
Maltotriose	0.174
D-Galactose	0.173
b-Methyl-D-Glucoside	0.17
Maltitol	0.17
Palatinose	0.17
D-Arabitol	0.168
D-Raffinose	0.167
b-Methyl-D-Galactoside	0.163
a-D-Lactose	0.161
Lactulose	0.156
D-Melibiose	0.155
Sucrose	0.153
D-Cellobiose	0.152
D-Arabinose	0.148
m-Inositol	0.146

FIG. 29H (cont.)

Preferred carbon sources out of 192 different carbon sources tested

3-O-b-D-Galactopyranosyl-D-Arabinose	0.146
D-Mannitol	0.144
a-Methyl-D-Mannoside	0.142
D-Lactitol	0.14
Gentiobiose	0.137
D-Mannose	0.135
N-Acetyl-Neuraminic acid	0.134
D-Sorbitol	0.132
a-Methyl-D-Glucoside	0.131
L-Rhamnose	0.129
L-Sorbose	0.129
L-Arabinose	0.125
Pyruvic acid	0.124
Arbutin	0.118
Salicin	0.116
Bromosuccinic acid	0.114
D-Melezitose	0.113
b-Methyl-D-Glucuronic acid	0.113
Glucuronamide	0.107
Amygdalin	0.107
Pectin	0.105

FIG. 29I

***B. coccoides* (EPV22)**	**OD750**
D-Sorbitol	0.468
Lactulose	0.442
a-D-Lactose	0.438
D-Raffinose	0.423
D-Arabitol	0.417
Stachyose	0.407
D-Melibiose	0.403
Maltotriose	0.401

FIG. 29I (cont.)

Preferred carbon sources out of 192 different carbon sources tested

Sucrose	0.398
D-Trehalose	0.394
Palatinose	0.392
D-Melezitose	0.388
Turanose	0.387
Amygdalin	0.386
b-Methyl-D-Glucoside	0.384
D-Galactose	0.381
Maltose	0.367
D-Lactitol	0.363
a-D-Glucose	0.354
D-Fructose	0.352
b-Methyl-D-Galactoside	0.345
3-O-b-D-Galactopyranosyl-D-Arabinose	0.335
b-Methyl-D-Glucuronic acid	0.33
Maltitol	0.326
D-Cellobiose	0.324
m-Inositol	0.323
b-Methyl-D-Xyloside	0.318
N-Acetyl-Neuraminic acid	0.315
a-Methyl-D-Galactoside	0.306
D-Mannitol	0.286
Gentiobiose	0.256
Salicin	0.255
Uridine	0.215
D-Gluconic acid	0.213
D-Galacturonic acid	0.2

Preferred carbon sources out of 192 different carbon sources tested

FIG. 29J

B. hydrogenotrophica (EPV23)	OD750
D-Trehalose	0.445
Palatinose	0.418
Salicin	0.412
D-Fructose	0.377
Arbutin	0.35
D-Tagatose	0.341
L-Arabinose	0.329
Xylitol	0.301
Maltotriose	0.287
a-D-Glucose	0.282
Maltose	0.248
D-Ribose	0.218
a-Keto-Valeric acid	0.208
D-Aspartic acid	0.182
a-Ketobutyric acid	0.16
Dextrin	0.155
L-Leucine	0.137

FIG. 29K

Blautia hansenii (EPV24)	OD 750
a-D-Glucose	0.34
Maltose	0.317
Maltotriose	0.311
a-D-Lactose	0.273
Stachyose	0.258
D-Galactose	0.254
N-Acetyl-D-Glucosamine	0.243
D-Raffinose	0.232
D-Melibiose	0.216
Chondroitin Sulfate C	0.214
Inosine	0.21
Adenosine	0.161
2`-Deoxyadenosine	0.132

FIG. 29L

Preferred carbon sources out of 192 different carbon sources tested

EPV114 (B. luti BlnlX)	OD750
D-Galactose	0.195
L-Fucose	0.221
D-Xylose	0.252
D-Mannitol	0.169
L-Rhamnose	0.205
D-Fructose	0.253
a-D-Glucose	0.306
Maltose	0.338
D-Melibiose	0.288
a-D-Lactose	0.296
Lactulose	0.217
Sucrose	0.295
Maltotriose	0.352
m-Inositol	0.18
D-Cellobiose	0.143
D-Arabinose	0.181
Arbutin	0.256
D-Lactitol	0.252
b-Methyl-D-Galactoside	0.214
Palatinose	0.249
D-Raffinose	0.314
Salicin	0.292
Stachyose	0.658
L-Tartaric acid	0.14

FIG. 29M

Preferred carbon sources out of 192 different carbon sources tested

EPV54 (B. luti ELU)	OD750
D-Galactose	0.193
L-Fucose	0.193
D-Xylose	0.273
D-Mannitol	0.168
L-Rhamnose	0.245
D-Fructose	0.289
a-D-Glucose	0.431
Maltose	0.246
D-Melibiose	0.193
a-D-Lactose	0.363
Lactulose	0.177
Sucrose	0.305
m-Inositol	0.263
D-Arabinose	0.196
Arbutin	0.195
D-Lactitol	0.204
b-Methyl-D-Galactoside	0.198
Palatinose	0.28
D-Raffinose	0.399
Salicin	0.257
Stachyose	0.88
D-Glucosamine	0.176

FIG. 29N

EPV102 (R. gnavus)	**OD750**
L-Arabinose	0.151
N-Acetyl-D-Glucosamine	0.205
D-Galactose	0.212
D-Mannose	0.134
L-Fucose	0.324
D-Gluconic acid	0.203
D-Xylose	0.14
D-Ribose	0.13
D-Fructose	0.194
a-D-Glucose	0.274
Maltose	0.263
D-Melibiose	0.194
Sucrose	0.298
b-Methyl-D-Glucoside	0.244
Maltotriose	0.337
b-Cyclodextrin	0.192
g-Cyclodextrin	0.14
D-Arabinose	0.277
Arbutin	0.307
Gentiobiose	0.271
D-Raffinose	0.265
Salicin	0.266
Stachyose	0.318
D-Glucosamine	0.19

FIG. 29O

Preferred carbon sources out of 192 different carbon sources tested

EPV78 (B. faecis)	OD750
L-Fucose	0.142
D-Xylose	0.185
D-Ribose	0.338
L-Rhamnose	0.227
a-D-Glucose	0.138
D-Arabinose	0.132
D-Raffinose	0.132
Stachyose	0.146

FIG. 29P

EPV76 (R. torques)	OD750
D-Galactose	0.223
D-Gluconic acid	0.166
D-Fructose	0.244
a-D-Glucose	0.257
a-D-Lactose	0.22
Turanose	0.129

FIG. 29Q

Preferred carbon sources out of 192 different carbon sources tested

EPV64 (B. wexlerae WAL14507)	OD750
L-Arabinose	0.47
D-Galactose	0.536
D-Trehalose	0.472
D-Sorbitol	0.148
L-Fucose	0.679
D-Gluconic acid	0.436
D-Xylose	0.478
D-Ribose	0.133
D-Fructose	0.679
a-D-Glucose	0.503
Maltose	0.719
D-Melibiose	0.747
a-D-Lactose	0.732
Lactulose	0.404
Sucrose	0.572
Maltotriose	0.617
D-Cellobiose	0.163
Dextrin	0.147
Inulin	0.127
Mannan	0.127
Pectin	0.136
D-Arabinose	0.591
Gentiobiose	0.566
D-Lactitol	0.568
D-Melezitose	0.691
Maltitol	0.573
b-Methyl-D-Galactoside	0.281
Palatinose	0.648
D-Raffinose	0.783
Stachyose	0.537
Turanose	0.57
D-Glucosamine	0.204
Oxalic acid	0.125
Oxalomalic acid	0.126
Quinic acid	0.148
L-Tartaric acid	0.146

FIG. 29R

Preferred carbon sources out of 192 different carbon sources tested

EPV52 (B. wexlerae SJTU)	OD750
L-Arabinose	0.642
D-Galactose	0.671
D-Trehalose	0.69
D-Sorbitol	0.339
L-Fucose	0.611
D-Xylose	0.636
D-Mannitol	0.127
L-Rhamnose	0.167
D-Fructose	0.74
a-D-Glucose	0.524
Maltose	0.66
D-Melibiose	0.704
a-D-Lactose	0.815
Lactulose	0.701
Sucrose	0.739
Maltotriose	0.676
D-Cellobiose	0.361
Dextrin	0.116
Inulin	0.137
Mannan	0.123
Pectin	0.123
N-Acetyl-Neuraminic acid	0.467
D-Arabinose	0.534
Arbutin	0.487
Gentiobiose	0.506
D-Lactitol	0.71
D-Melezitose	0.695
Maltitol	0.658
b-Methyl-D-Galactoside	0.321
b-Methyl-D-Xyloside	0.333
Palatinose	0.666
D-Raffinose	0.575
Salicin	0.591
Stachyose	0.74
Turanose	0.581
Oxalic acid	0.123
L-Tartaric acid	0.259

FIG. 29S

Preferred carbon sources out of 192 different carbon sources tested

EPV51 (SJTU1416)	OD750
D-Trehalose	0.136
a-D-Glucose	0.104
Maltose	0.165
D-Melibiose	0.115
a-D-Lactose	0.171
Lactulose	0.17
Sucrose	0.18
b-Methyl-D-Glucoside	0.113
Maltotriose	0.207
Amygdalin	0.12
D-Lactitol	0.137
D-Melezitose	0.222
b-Methyl-D-Galactoside	0.142
D-Raffinose	0.186
Stachyose	0.199
Turanose	0.239

FIG. 29T

Preferred carbon sources out of 192 different carbon sources tested

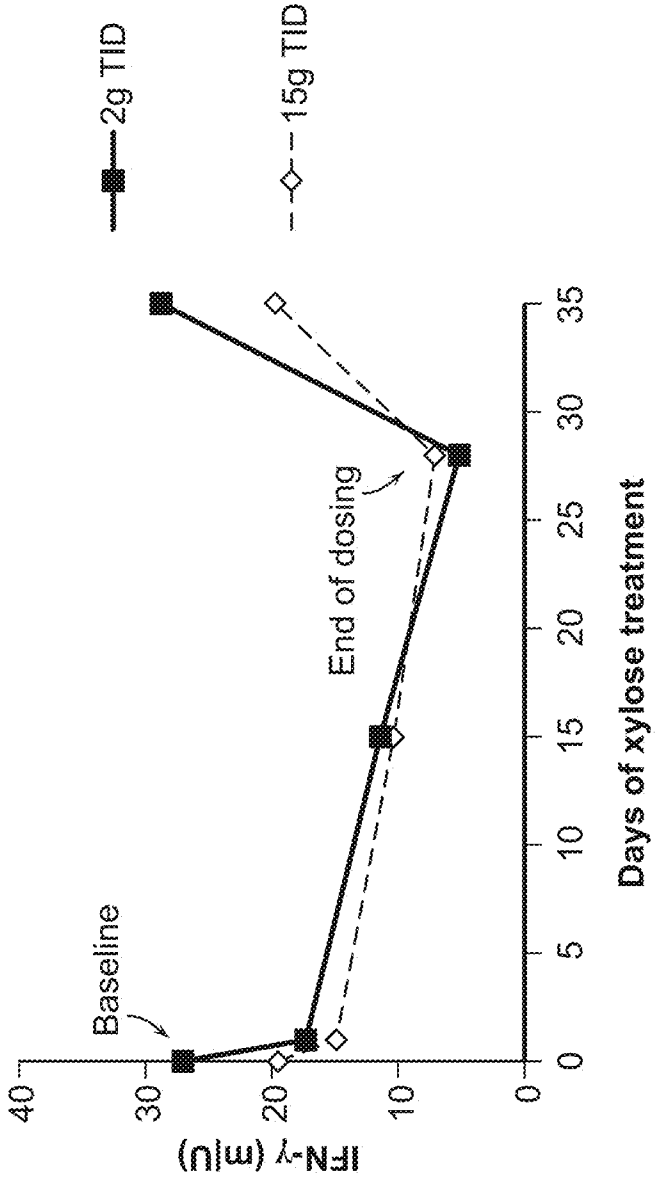
EPV47 (GQ8980099)	OD750
L-Arabinose	0.336
N-Acetyl-D-Glucosamine	0.328
D-Saccharic acid	0.128
D-Galactose	0.365
L-Fucose	0.255
D-Xylose	0.131
L-Rhamnose	0.286
D-Fructose	0.466
a-D-Glucose	0.421
D-Melibiose	0.428
a-D-Lactose	0.468
Lactulose	0.551
Sucrose	0.475
Mucic acid	0.153
D-Arabinose	0.307
Arbutin	0.389
3-O-b-D-Galactopyranosyl-D-Arabinose	0.16
D-Raffinose	0.408
Salicin	0.342
Sedoheptulosan	0.442
Stachyose	0.516
D-Glucosamine	0.247

FIG. 29U

Preferred carbon sources out of 192 different carbon sources tested

EPV35 (E rectale)	OD750
L-Arabinose	0.216
D-Galactose	0.208
D-Xylose	0.14
D-Fructose	0.178
a-D-Glucose	0.185
Maltose	0.113
D-Melibiose	0.173
a-Methyl-D-Galactoside	0.14
a-D-Lactose	0.188
Lactulose	0.112
b-Methyl-D-Glucoside	0.171
Maltotriose	0.151
Dextrin	0.172
Glycogen	0.144
Gentiobiose	0.169
a-Methyl-D-Glucoside	0.165
b-Methyl-D-Galactoside	0.119
Stachyose	0.196
Turanose	0.22
D-Glucosamine	0.144

FIG. 30


Serum IFN-γ levels
2g TID
15g TID
Baseline
End of dosing
IFN-γ (mIU)
Days of xylose treatment
0
10
20
30
40
0
5
10
15
20
25
30
35

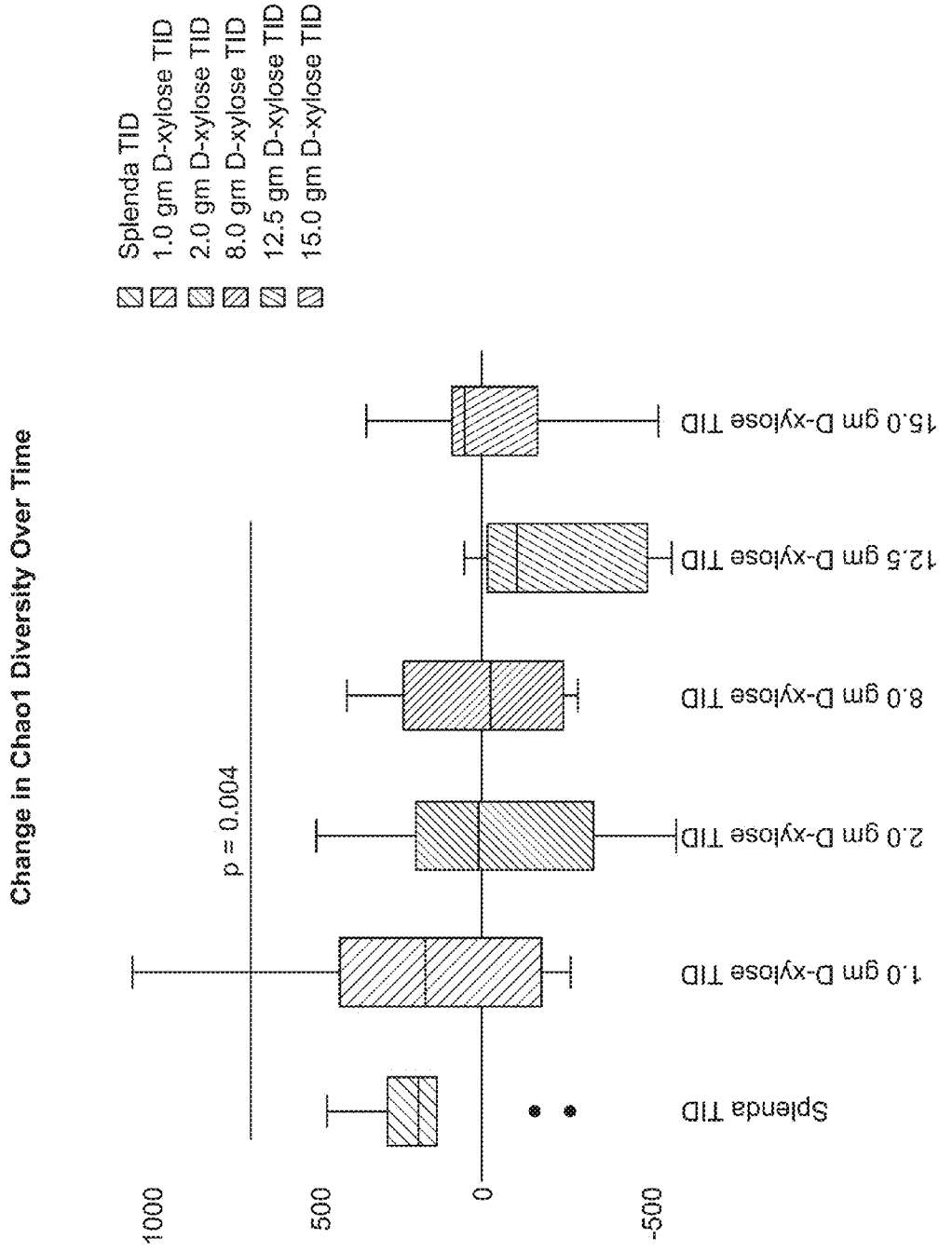
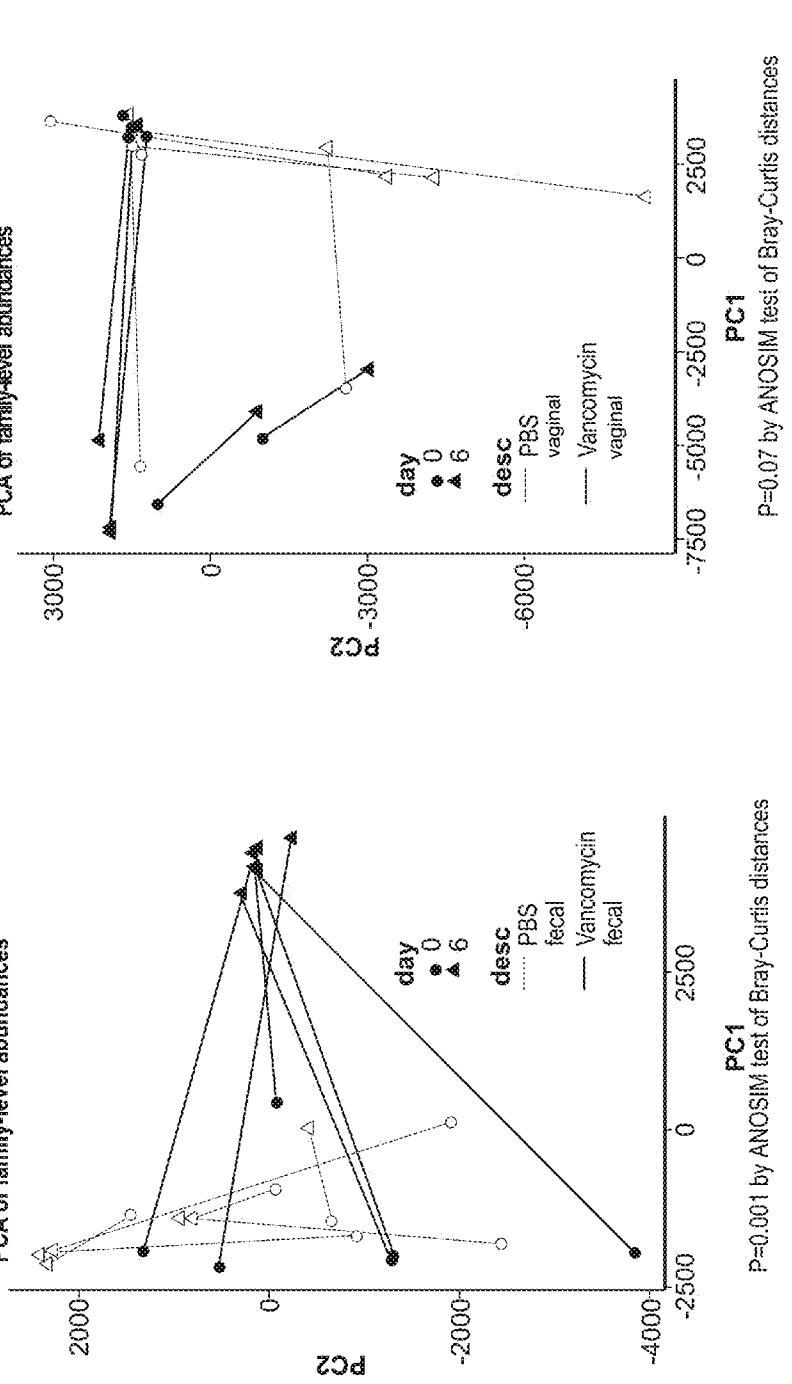

Change in Chao1 Diversity Over Time
Splenda TID
1.0 gm D-xylose TID
2.0 gm D-xylose TID
8.0 gm D-xylose TID
12.5 gm D-xylose TID
15.0 gm D-xylose TID
p = 0.004
1000
500
0
-500
Splenda TID
1.0 gm D-xylose TID
2.0 gm D-xylose TID
8.0 gm D-xylose TID
12.5 gm D-xylose TID
15.0 gm D-xylose TID

FIG. 31

FIG. 32 Shifts in the microbiome of the gut and vagina following treatment with oral vancomycin



PROBIOTIC AND PREBIOTIC COMPOSITIONS, AND METHODS OF USE THEREOF FOR TREATMENT AND PREVENTION OF GRAFT VERSUS HOST DISEASE

RELATED APPLICATIONS

[0001] This application claims priority to U.S. Provisional Patent Application No. 62/084,536, filed Nov. 25, 2014; U.S. Provisional Patent Application No. 62/084,537, filed Nov. 25, 2014; U.S. Provisional Patent Application No. 62/084,540, filed Nov. 25, 2014; U.S. Provisional Patent Application No. 62/117,632, filed Feb. 18, 2015; U.S. Provisional Patent Application No. 62/117,637, filed Feb. 18, 2015; U.S. Provisional Patent Application No. 62/117,639, filed Feb. 18, 2015; U.S. Provisional Patent Application No. 62/162,562, filed May 15, 2015; and U.S. Provisional Patent Application No. 62/257,714, filed Nov. 19, 2015. The entire contents of each of the foregoing applications are incorporated herein by reference.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Nov. 25, 2015, is named 126383_01903_SL.txt and is 4,147,472 bytes in size.

BACKGROUND

[0003] Graft versus host disease (GVHD) is a common and devastating complication following a hematopoietic or tissue transplant and occurs in approximately 50% of transplant recipients. Acute GVHD is a major source of morbidity and mortality following allogeneic hematopoietic cell transplantation. Approximately 25,000 allogeneic hematopoietic cell transplants (e.g., bone marrow, peripheral blood stem cell [PBSC], or cord blood transplants) are performed annually worldwide. Over time, the number of transplants from unrelated donors, and in the number of allogeneic transplants for AML, ALL, MDS, and lymphomas, continues to rise. There is also an increase in the number of allogeneic transplantants for non-malignant diseases, and an increase in the number of transplant patients over 50 years of age. The global incidence of acute GVHD ranges from 26%-34% in recipients of fully matched, sibling donor grafts to 42%-52% in recipients of matched, unrelated donor grafts. Evidence from the US suggests that incidence ranges from 30% in recipients of fully histocompatible transplants to 60%-70% in recipients of mismatched hematopoietic cells or hematopoietic cells from an unrelated donor. There is no FDA approved treatment for either acute or chronic GVHD. Treatment strategies for acute GVHD aim to reduce the immune reaction of the donor T cells against host tissues and therefore includes immunosuppressive treatment like cyclosporine, high dose steroids, and methotrexate. The standard therapy for de novo acute GVHD is high dose methylprednisolone, with expected response rates of 18%-50%. For patients who develop steroid-refractory acute GVHD, there is no standard of care therapy, and expected survival is less than 30%. Therefore, novel therapies are urgently needed for the treatment and prevention of GVHD.

SUMMARY OF THE INVENTION

[0004] Disclosed herein are therapeutic compositions containing probiotic, non-pathogenic bacterial populations and networks thereof, for the prevention, control, and treatment of transplant disorders and conditions, in particular diseases associated with graft versus host disease (GVHD). In some embodiments, the therapeutic compositions contain prebiotics, e.g., carbohydrates, in conjunction with microbial populations and/or networks thereof. These compositions are advantageous in being suitable for safe administration to humans and other mammalian subjects and are efficacious in numerous dysbiotic diseases, disorders and conditions and in general nutritional health.

[0005] In one aspect, the instant invention provides a method of increasing the duration of survival of a subject receiving a transplant, e.g., a bone marrow transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population, such that the duration of survival of the subject is increased.

[0006] In one embodiment of the foregoing aspect, the bacterial population is a human-derived bacterial population.

[0007] In one embodiment of the foregoing aspect, administration of the probiotic composition reduces the likelihood that the subject will develop sepsis following the bone marrow transplant. In one embodiment of the foregoing aspect, administration of the probiotic composition reduces the likelihood that the subject will develop graft versus host disease (GVHD) following the bone marrow transplant.

[0008] In one embodiment of the foregoing aspect, the probiotic composition is administered to the subject prior to receiving the bone marrow transplant. In one embodiment of the foregoing aspect, the probiotic composition is administered to the subject after receiving the bone marrow transplant. In one embodiment of the foregoing aspect, the probiotic composition is administered to the subject concurrently with the bone marrow transplant.

[0009] In one embodiment of the foregoing aspect, the probiotic composition reduces intestinal permeability in the subject.

[0010] In one embodiment of the foregoing aspect, the probiotic composition comprises a bacterial population that produces short chain fatty acids. In one embodiment of the foregoing aspect, the bacterial population produces a short chain fatty acid selected from the group consisting of butyrate, acetate, propionate, valerate, and combinations thereof.

[0011] In one embodiment of the foregoing aspect, the probiotic composition reduces inflammation in the gastrointestinal tract of the subject. In one embodiment of the foregoing aspect, the probiotic composition comprises an anti-inflammatory bacterial population. In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population decreases secretion of pro-inflammatory cytokines and/or increases secretion of anti-inflammatory cytokines by human peripheral blood mononuclear cells (PBMCs). In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population decreases secretion of a pro-inflammatory cytokine selected from the group consisting of IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population increases secretion of an anti-inflammatory cytokine selected from the group consisting of IL-10, IL-13, IL-4, IL-5, TGFβ

and combinations thereof. In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population produces short chain fatty acids.

[0012] In one embodiment of the foregoing aspect, the isolated bacterial population comprises one or more bacterial species of the order *Clostridiales*. In one embodiment of the foregoing aspect, the bacterial species is from the genus *Blautia, Clostridium*, or *Ruminococcus*. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F. In one embodiment, the bacterial population comprises a single bacterial species set forth in Table 5. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F. In another embodiment, the bacterial population comprises two or more bacterial species set forth in Table 5.

[0013] In one embodiment of the foregoing aspect, the subject has a disorder selected from the group consisting of a hematopoietic neoplastic disorder, leukemia, lymphoma, and multiple myeloma. In one embodiment of the foregoing aspect, the probiotic composition does not significantly reduce or eliminate the graft versus tumor (GVT) effect of the bone marrow transplant. In one embodiment of the foregoing aspect, the subject has an autoimmune disorder. In one embodiment of the foregoing aspect, the autoimmune disorder is selected from the group consisting of lupus, multiple sclerosis, systemic sclerosis, Crohn's disease, type I diabetes, and juvenile idiopathic arthritis. In one embodiment of the foregoing aspect, the subject has sickle cell disease or sickle cell anemia.

[0014] In embodiments of the foregoing aspects, the methods further comprise administering a prebiotic to the subject. In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of arabinoxylan, xylose, soluble fiber dextran, soluble corn fiber, polydextrose, lactose, N-acetyl-lactosamine, glucose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of galactose, fructose, rhamnose, mannose, uronic acids, 3'-fucosyllactose, 3' sialylactose, 6'-sialyllactose, lacto-N-neotetraose, 2'-2'-fucosyllactose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a monosaccharide selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a disaccharide selected from the group consisting of xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a polysaccharide, wherein the polysaccharide is xylooligosaccharide. In one embodiment of the foregoing aspect, the prebiotic comprises a sugar selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, xylooligosaccharide, and combinations thereof.

[0015] In another aspect, the instant invention provides a method of increasing the duration of survival of a subject receiving a bone marrow transplant, comprising administering to the subject a probiotic composition comprising an isolated population of anti-inflammatory bacteria capable of decreasing secretion of pro-inflammatory cytokines and/or increasing secretion of anti-inflammatory cytokines by human peripheral blood mononuclear cells (PBMCs), and a pharmaceutically acceptable excipient, in an amount effective to reduce inflammation in the gastrointestinal tract of the subject, such that the duration of survival of the subject is increased.

[0016] In one embodiment of the foregoing aspect, the anti-inflammatory bacteria decrease secretion of pro-inflammatory cytokines and/or increase secretion of anti-inflammatory cytokines by human peripheral blood mononuclear cells (PBMCs) in vitro.

[0017] In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F.

[0018] In another aspect, the instant invention provides a method of increasing the duration of survival of a subject receiving a bone marrow transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population, wherein the probiotic composition reduces intestinal permeability in the subject; and administering to the subject a prebiotic that enhances the activity of the bacterial population, such that the duration of survival of the subject is increased.

[0019] In one embodiment of the foregoing aspect, the isolated bacterial population produces short chain fatty acids. In one embodiment of the foregoing aspect, the bacterial population produces a short chain fatty acid selected from the group consisting of butyrate, acetate, propionate, valerate, and combinations thereof.

[0020] In one embodiment of the foregoing aspect, the isolated bacterial population comprises one or more bacterial species of the order *Clostridiales*. In one embodiment of the foregoing aspect, the bacterial species is from the genus *Blautia, Clostridium*, or *Ruminococcus*. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F.

[0021] In one embodiment of the foregoing aspect, the subject has a disorder selected from the group consisting of a hematopoietic neoplastic disorder, leukemia, lymphoma, and multiple myeloma. In one embodiment of the foregoing

aspect, the probiotic composition does not significantly reduce or eliminate the graft versus tumor (GVT) effect of the bone marrow transplant.

[0022] In one embodiment of the foregoing aspect, the subject has an autoimmune disorder. In one embodiment of the foregoing aspect, the autoimmune disorder is selected from the group consisting of lupus, multiple sclerosis, systemic sclerosis, Crohn's disease, type I diabetes, and juvenile idiopathic arthritis.

[0023] In one embodiment of the foregoing aspect, the subject has sickle cell disease. In one embodiment of the foregoing aspect, the subject has sickle cell anemia.

[0024] In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of arabinoxylan, xylose, soluble fiber dextran, soluble corn fiber, polydextrose, lactose, N-acetyl-lactosamine, glucose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of galactose, fructose, rhamnose, mannose, uronic acids, 3'-fucosyllactose, 3'sialylactose, 6'-sialyllactose, lacto-N-neotetraose, 2'-2'-fucosyllactose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a monosaccharide selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a disaccharide selected from the group consisting of xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a polysaccharide, wherein the polysaccharide is xylooligosaccharide. In one embodiment of the foregoing aspect, the prebiotic comprises a sugar selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, xylooligosaccharide, and combinations thereof.

[0025] In another aspect, the instant invention provides a method of preventing or treating graft versus host disease (GVHD) in a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population, such that GVHD is prevented or treated.

[0026] In one embodiment of the foregoing aspect, the bacterial population is a human-derived bacterial population.

[0027] In one embodiment of the foregoing aspect, the subject is receiving a hematopoietic stem cell transplant. In one embodiment of the foregoing aspect, the subject is receiving a bone marrow transplant. In one embodiment of the foregoing aspect, the subject is receiving a solid organ transplant. In one embodiment of the foregoing aspect, the solid organ transplant is selected from the group consisting of a kidney transplant, a heart transplant, a lung transplant, a skin transplant, a liver transplant, a pancreas transplant, an intestinal transplant, an endocrine gland transplant, a bladder transplant, and a skeletal muscle transplant.

[0028] In one embodiment of the foregoing aspect, the subject has a disorder selected from the group consisting of a hematopoietic neoplastic disorder, leukemia, lymphoma, and multiple myeloma. In one embodiment of the foregoing aspect, the probiotic composition does not significantly reduce or eliminate the graft versus tumor (GVT) effect of the bone marrow transplant.

[0029] In one embodiment of the foregoing aspect, the subject has an autoimmune disorder. In one embodiment of the foregoing aspect, the autoimmune disorder is selected from the group consisting of lupus, multiple sclerosis, systemic sclerosis, Crohn's disease, type I diabetes, and juvenile idiopathic arthritis.

[0030] In one embodiment of the foregoing aspect, the subject has sickle cell disease or sickle cell anemia.

[0031] In one embodiment of the foregoing aspect, the probiotic composition reduces intestinal permeability in the subject. In one embodiment of the foregoing aspect, the probiotic composition comprises a bacterial population that produces short chain fatty acids. In one embodiment of the foregoing aspect, the bacterial population produces a short chain fatty acid selected from the group consisting of butyrate, acetate, propionate, valerate, and combinations thereof.

[0032] In one embodiment of the foregoing aspect, the probiotic composition reduces inflammation in the gastrointestinal tract of the subject. In one embodiment of the foregoing aspect, the probiotic composition comprises an anti-inflammatory bacterial population. In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population decreases secretion of pro-inflammatory cytokines and/or increases secretion of anti-inflammatory cytokines by human peripheral blood mononuclear cells (PBMCs). In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population decreases secretion of a pro-inflammatory cytokine selected from the group consisting of IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population increases secretion of an anti-inflammatory cytokine selected from the group consisting of IL-10, IL-13, IL-4, IL-5, and combinations thereof. In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population produces short chain fatty acids.

[0033] In one embodiment of the foregoing aspect, the isolated bacterial population comprises one or more bacterial species of the order *Clostridiales*. In one embodiment of the foregoing aspect, the bacterial species is from the genus *Blautia, Clostridium*, or *Ruminococcus*. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F.

[0034] In embodiments of the foregoing aspects, the methods further comprise administering a prebiotic to the subject. In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of arabinoxylan, xylose, soluble fiber dextran, soluble corn fiber, polydextrose, lactose, N-acetyl-lactosamine, glucose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of galactose, fructose, rhamnose, mannose, uronic acids, 3'-fucosyllactose, 3' sialylactose, 6'-sialyllactose, lacto-N-neotetraose, 2'-2'-fucosyllactose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises

a monosaccharide selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a disaccharide selected from the group consisting of xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a polysaccharide, wherein the polysaccharide is xylooligosaccharide. In one embodiment of the foregoing aspect, the prebiotic comprises a sugar selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, xylooligosaccharide, and combinations thereof.

[0035] In another aspect, the instant invention provides a method of reducing inflammation in the gastrointestinal tract of a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated, anti-inflammatory bacterial population and a pharmaceutically acceptable excipient, such that inflammation in the gastrointestinal tract of the subject receiving the transplant is reduced.

[0036] In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population decreases secretion of pro-inflammatory cytokines and/or increases secretion of anti-inflammatory cytokines by human peripheral blood mononuclear cells (PBMCs). In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population decreases secretion of a pro-inflammatory cytokine selected from the group consisting of IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population increases secretion of an anti-inflammatory cytokine selected from the group consisting of IL-10, IL-13, IL-4, IL-5, TGFβ, and combinations thereof. In one embodiment of the foregoing aspect, the anti-inflammatory bacterial population produces short chain fatty acids.

[0037] In one embodiment of the foregoing aspect, the isolated bacterial population comprises one or more bacterial species of the order *Clostridiales*. In one embodiment of the foregoing aspect, the bacterial species is from the genus *Blautia, Clostridium*, or *Ruminococcus*. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1. In one embodiment of the foregoing aspect, the bacterial population comprises a single bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F. In one embodiment of the foregoing aspect, the bacterial population comprises two or more bacterial species set forth in Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, or Table 1F.

[0038] In embodiments of the foregoing aspects, the methods further comprising administering a prebiotic to the subject. In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of arabinoxylan, xylose, soluble fiber dextran, soluble corn fiber, polydextrose, lactose, N-acetyl-lactosamine, glucose, and combinations thereof. In one embodiment of the foregoing aspect, wherein the prebiotic comprises a monomer or polymer selected from the group consisting of galactose, fructose, rhamnose, mannose, uronic acids, 3'-fucosyllactose, 3' sialylactose, 6'-sialyllactose, lacto-N-neotetraose, 2'-2'-fucosyllactose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a monosaccharide selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a disaccharide selected from the group consisting of xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a polysaccharide, wherein the polysaccharide is xylooligosaccharide. In one embodiment of the foregoing aspect, the prebiotic comprises a sugar selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, xylooligosaccharide, and combinations thereof.

[0039] In another aspect, the instant invention provides a method of reducing intestinal permeability in a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population and a pharmaceutically acceptable excipient, such that the intestinal permeability of the subject of the subject receiving the transplant is reduced.

[0040] In one embodiment of the foregoing aspect, the isolated bacterial population produces short chain fatty acids. In one embodiment of the foregoing aspect, the bacterial population produces a short chain fatty acid selected from the group consisting of butyrate, acetate, propionate, valerate, and combinations thereof. In one embodiment of the foregoing aspect, the bacterial population produces butyrate.

[0041] In one embodiment of the foregoing aspect, the method further comprises administering a prebiotic to the subject. In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of arabinoxylan, xylose, soluble fiber dextran, soluble corn fiber, polydextrose, lactose, N-acetyl-lactosamine, glucose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a monomer or polymer selected from the group consisting of galactose, fructose, rhamnose, mannose, uronic acids, 3'-fucosyllactose, 3' sialylactose, 6'-sialyllactose, lacto-N-neotetraose, 2'-2'-fucosyllactose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a monosaccharide selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a disaccharide selected from the group consisting of xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, and combinations thereof. In one embodiment of the foregoing aspect, the prebiotic comprises a polysaccharide, wherein the polysaccharide is xylooligosaccharide. In one embodiment of the foregoing aspect, the prebiotic comprises a sugar selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, xylooligosaccharide, and combinations thereof.

[0042] In one aspect, the instant invention provides a method of increasing the duration of survival of a subject receiving a bone marrow transplant, comprising administering to the subject a probiotic composition comprising an

isolated, human-derived bacterial population, such that the duration of survival of the subject is increased.

[0043] In one embodiment of the foregoing aspect, administration of the probiotic composition reduces the likelihood that the subject will develop sepsis following the bone marrow transplant. In one embodiment of the foregoing aspect, administration of the probiotic composition reduces the likelihood that the subject will develop graft versus host disease (GVHD) following the bone marrow transplant.

[0044] In another aspect, the instant invention provides a method of increasing the duration of survival of a subject receiving a bone marrow transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population and a pharmaceutically acceptable excipient, wherein the probiotic composition reduces intestinal permeability in the subject; and administering to the subject a prebiotic that enhances the activity of the bacterial population, such that the duration of survival of the subject is increased.

[0045] In another aspect, the instant invention provides a method of preventing graft versus host disease (GVHD) in a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated, human-derived bacterial population, such that GVHD is prevented.

[0046] In some embodiments of the foregoing aspects, the subject is receiving a hematopoietic stem cell transplant. In some embodiments of the foregoing aspects, the subject is receiving a bone marrow transplant. In some embodiments of the foregoing aspects, the subject is receiving a solid organ transplant. In some embodiments of the foregoing aspects, the solid organ transplant is selected from the group consisting of a kidney transplant, a heart transplant, a lung transplant, a skin transplant, a liver transplant, a pancreas transplant, an intestinal transplant, an endocrine gland transplant, a bladder transplant, and a skeletal muscle transplant.

[0047] In another aspect, the instant invention provides a method of reducing inflammation in the gastrointestinal tract of a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated, anti-inflammatory bacterial population, such that inflammation in the gastrointestinal tract of the subject receiving the transplant is reduced.

[0048] In another aspect, the instant invention provides a method of reducing intestinal permeability in a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population, such that the intestinal permeability of the subject receiving the transplant is reduced.

[0049] In another aspect, the instant invention provides a pharmaceutical composition comprising an isolated anti-inflammatory bacterial population capable of decreasing secretion of a pro-inflammatory cytokine and/or increasing secretion of an anti-inflammatory cytokine by human peripheral blood mononuclear cells (PBMCs), and a pharmaceutically acceptable excipient.

[0050] In one embodiment of the foregoing aspect, the composition further comprising a prebiotic.

[0051] In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Acidaminococcus intestine*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Acinetobacter baumannii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Acinetobacter lwoffii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Akkermansia muciniphila*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Alistipes putredinis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Alistipes shahii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Anaerostipes hadrus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Anaerotruncus colihominis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides caccae*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides cellulosilyticus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides dorei*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides eggerthii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides finegoldii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides fragilis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides massiliensis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides ovatus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides salanitronis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides salyersiae*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides* sp. 1_1_6. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides* sp. 3_1_23. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides* sp. D20. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides thetaiotaomicron*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides uniformis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bacteroides vulgatus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bifidobacterium adolescentis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bifidobacterium bifidum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bifidobacterium breve*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bifidobacterium faecale*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bifidobacterium kashiwanohense*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bifidobacterium longum* subsp. *longum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bifidobacterium pseudocatenulatum*. In

some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Bifidobacterium stercoris*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* (*Ruminococcus*) *coccoides*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia faecis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia glucerasea*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* (*Ruminococcus*) *hansenii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* (*Ruminococcus*) *luti*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* (*Ruminococcus*) *obeum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia producta* (*Ruminococcus productus*). In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* (*Ruminococcus*) *schinkii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia stercoris*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Blautia wexlerae*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Candidatus Arthromitus* sp. SFB-mouse-Yit. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Catenibacterium mitsuokai*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridiales* bacterium 1_7_47FAA. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium asparagiforme*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium bolteae*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium clostridioforme*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium glycyrrhizinilyticum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium* (*Hungatella*) *hathewayi*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium histolyticum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium indolis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium leptum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium* (*Tyzzerella*) *nexile*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium perfringens*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium scindens*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium* sp. 14774. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium* sp. 7_3_54FAA. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium* sp. HGF2. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Clostridium symbiosum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Collinsella aerofaciens*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Collinsella intestinalis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Coprobacillus* sp. D7. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Coprococcus catus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Coprococcus comes*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Dorea formicigenerans*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Dorea longicatena*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Enterococcus faecalis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Enterococcus faecium*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Erysipelotrichaceae* bacterium 3_1_53. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Escherichia coli*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Escherichia coli* S88. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Eubacterium eligens*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Eubacterium fissicatena*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Eubacterium ramulus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Eubacterium rectale*. In some

embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Faecalibacterium prausnitzii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Flavonifractor plautii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Fusobacterium mortiferum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Fusobacterium nucleatum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Holdemania filiformis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Hydrogenoanaerobacterium saccharovorans*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Klebsiella oxytoca*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Lachnospiraceae* bacterium 7_1_58FAA. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Lachnospiraceae* bacterium 5_1_57FAA. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Lactobacillus casei*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Lactobacillus rhamnosus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Lactobacillus ruminis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Lactococcus casei*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Odoribacter splanchnicus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Oscillibacter valericigenes*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Parabacteroides gordonii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Parabacteroides johnsonii*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Parabacteroides merdae*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Pediococcus acidilactici*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Peptostreptococcus asaccharolyticus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Propionibacterium granulosum*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Roseburia intestinalis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Roseburia inulinivorans*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Ruminococcus faecis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Ruminococcus gnavus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Ruminococcus* sp. ID8. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Ruminococcus torques*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Slackia piriformis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Staphylococcus epidermidis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Staphylococcus saprophyticus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Streptococcus cristatus*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Streptococcus dysgalactiae* subsp. *equisimilis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Streptococcus infantis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Streptococcus oralis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Streptococcus sanguinis*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Streptococcus viridans*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Streptococcus thermophiles*. In some embodiments of the foregoing aspects, the bacterial population comprises an isolated population of *Veillonella dispar.*

BRIEF DESCRIPTION OF THE TABLES

[0052] Table 1 provides a list of Operational Taxonomic Units (OTU) with taxonomic assignments made to Genus, Species, and Phylogenetic Clade. Clade membership of bacterial OTUs is based on 16S sequence data. Clades are defined based on the topology of a phylogenetic tree that is constructed from full-length 16S sequences using maximum likelihood methods familiar to individuals with ordinary skill in the art of phylogenetics. Clades are constructed to ensure that all OTUs in a given Glade are: (i) within a specified number of bootstrap supported nodes from one another, and (ii) within 5% genetic similarity. OTUs that are within the same Glade can be distinguished as genetically and phylogenetically distinct from OTUs in a different Glade based on 16S-V4 sequence data, while OTUs falling within the same Glade are closely related. OTUs falling within the same Glade are evolutionarily closely related and may or may not be distinguishable from one another using 16S-V4 sequence data. Members of the same Glade, due to their evolutionary relatedness, play similar functional roles in a microbial ecology such as that found in the human gut. Compositions substituting one species with another from the same Glade are likely to have conserved ecological function and therefore are useful in the present invention. All OTUs are denoted as to their putative capacity to form spores and whether they are a Pathogen or Pathobiont (see Definitions for description of "Pathobiont"). NIAID Priority Pathogens are denoted as 'Category-A', 'Category-13', or 'Category-C', and Opportunistic Pathogens are denoted as 'OP'. OTUs that are not pathogenic or for which their ability to exist as a pathogen is unknown are denoted as 'N'. The 'SEQ ID Number' denotes the identifier of the OTU in the Sequence Listing File and 'Public DB Accession' denotes the identifier of the OTU in a public sequence repository. See, e.g., WO2014/121304.

[0053] Table 1A provides a list of exemplary bacteria useful in the present invention.

[0054] Table 1B provides a list of exemplary bacteria useful in the present invention.

[0055] Table 1C provides a list of exemplary bacteria useful in the present invention.

[0056] Table 1D provides a list of exemplary bacteria useful in the present invention.

[0057] Table 1E provides a list of exemplary bacteria useful in the present invention. These bacteria are preferably down-modulated in a subject.

[0058] Table 1F provides a list of exemplary bacteria that may be used in the invention. These bacteria are preferably up-modulated in a subject.

[0059] Table 2A lists species identified as "germinable" and "sporulatable" by colony picking approach.

[0060] Table 2B lists species identified as "germinable" using 16S colony picking approach.

[0061] Table 2C lists species identified as "sporulatable" using 16s-V4 NGS approach. See, e.g., WO2014/121304.

[0062] Table 3 provides criteria for stages of acute GVHD.

[0063] Table 4 provides representative examples of microbial enzymes that allow utilization of prebiotics.

[0064] Table 5 provides a list of species enriched in alive GVHD patients.

[0065] Table 6 lists anaerobic bacterial species tested for carbon source usage.

[0066] Table 7 provides exemplary prebiotics/carbon sources for use in the compositions and methods of the invention.

[0067] Table 8 provides bacterial species detected at low frequency in vaginal samples from vancomycin-treated mice (day 6) that were not present in untreated mice (day 0).

BRIEF DESCRIPTION OF THE DRAWINGS

[0068] FIG. **1** is a graph depicting serum endotoxin levels (EU/ml) over time following treatment with xylose. Treatment of mice with xylose alone reduces basal levels of serum endotoxin (day 14 vs day 0). Antibiotic treatment (Ciprofloxacin (cipro) or enrofloxacin (enro)) leads to an increase in serum endotoxin levels (measured 2 days after a 5 day course, at day 0) with a return to baseline by day 14. Xylose counteracts the endotoxin increase caused by cipro but not enro antibiotic treatment.

[0069] FIG. **2***a*-FIG. **2***o* is a panel of graphs showing the time course of Th1 related cytokines that were released by human peripheral mononuclear cells (PBMCs) incubated with *Ruminococcus gnavus* (Epv 1), *Eubacterium rectale* (Epv 2), *Blautia luti* (Epv 3), *Blautia wexlerae* (Epv 5) and *Enterococcus faecalis* (Epv 8), or combinations of each bacterium with *E. faecalis*. Amounts of interferon gamma (IFN-γ), IL-12p70, IL-6, IL-2 and TNFα that were released in culture supernatants by PBMCs were measured after 24, 48 and 72 hours. a) IFN-γ concentration (pg/ml) after 24 hours. b) IFN-γ concentration (pg/ml) after 48 hours. c) IFN-γ concentration (pg/ml) after 72 hours. d) IL-12p70 concentration (pg/ml) after 24 hours. e) IL-12p70 concentration (pg/ml) after 48 hours. f) IL-12p70 concentration (pg/ml) after 72 hours. g) IL-6 concentration (pg/ml) after 24 hours. h) IL-6 concentration (pg/ml) after 48 hours. i) IL-6 concentration (pg/ml) after 72 hours. j) IL-2 concentration (pg/ml) after 24 hours. k) IL-2 concentration (pg/ml) after 48 hours. 1) IL-2 concentration (pg/ml) after 72 hours. m) TNFα concentration (pg/ml) after 24 hours. n) TNFα concentration (pg/ml) after 48 hours. o) TNFα concentration (pg/ml) after 72 hours.

[0070] FIG. **3***a*-FIG. **3***i* is a panel of graphs showing the time course of Th2 related cytokines that were released by human PBMCs incubated with *R. gnavus* (Epv 1), *E. rectale* (Epv 2), *B. luti* (Epv 3), *B. wexlerae* (Epv 5) and *E. faecalis* (Epv 8), or combinations of each bacterium with *E. faecalis*. Amounts of IL-13, IL-4 and IL-5 that were released in culture supernatants by PBMCs were measured after 24, 48 and 72 hours. a) IL-13 concentration (pg/ml) after 24 hours. b) IL-13 concentration (pg/ml) after 48 hours. c) IL-13 concentration (pg/ml) after 72 hours. d) IL-4 concentration (pg/ml) after 24 hours. e) IL-4 concentration (pg/ml) after 48 hours. f) IL-4 concentration (pg/ml) after 72 hours. g) IL-5 concentration (pg/ml) after 24 hours. h) IL-5 concentration (pg/ml) after 48 hours. i) IL-5 concentration (pg/ml) after 72 hours.

[0071] FIG. **4***a*-FIG. **4***i* is a panel of graphs showing the time course of Th9, Th17 and Treg cytokines that were released by human PBMCs incubated with *R. gnavus* (Epv 1), *E. rectale* (Epv 2), *B. luti* (Epv 3), *B. wexlerae* (Epv 5) and *E. faecalis* (Epv 8), or combinations of each bacterium with *E. faecalis*. Amounts of IL-9, IL-17 and IL-10 that were released in culture supernatants by PBMCs were measured after 24, 48 and 72 hours. a) IL-9 concentration (pg/ml) after 24 hours. b) IL-9 concentration (pg/ml) after 48 hours. c) IL-9 concentration (pg/ml) after 72 hours. d) IL-17 concentration (pg/ml) after 24 hours. e) IL-17 concentration (pg/ml) after 48 hours. f) IL-17 concentration (pg/ml) after 72 hours. g) IL-10 concentration (pg/ml) after 24 hours. h) IL-10 concentration (pg/ml) after 48 hours. i) IL-10 concentration (pg/ml) after 72 hours.

[0072] FIG. **5***a*-FIG. **5***x* is a panel of graphs showing the time course of monocyte, macrophage and neutrophil-derived inflammatory cytokines that were released by human PBMCs incubated with *R. gnavus* (Epv 1), *E. rectale* (Epv 2), *B. luti* (Epv 3), *B. wexlerae* (Epv 5) and *E. faecalis* (Epv 8), or combinations of each bacterium with *E. faecalis*. Amounts of monocyte chemotactic protein 1 (MCP-1), macrophage inflammatory protein 1β (MIP1β), macrophage inflammatory protein 1α (MIP1α), regulated on activation, normal T expressed and secreted protein (RANTES), interleukin-1α (IL-1α), interleukin-1β (IL1β), interferon α2 (IFN-α2) and interleukin-8 (IL-8) that were released in culture supernatants by PBMCs were measured after 24, 48 and 72 hours. a) MCP-1 concentration (pg/ml) after 24 hours. b) MCP-1 concentration (pg/ml) after 48 hours. c) MCP-1 concentration (pg/ml) after 72 hours. d) MIP1β concentration (pg/ml) after 24 hours. e) MIP1β concentration (pg/ml) after 48 hours. f) M1β concentration (pg/ml) after 72 hours. g) MIP1α concentration (pg/ml) after 24 hours. h) MIP1α concentration (pg/ml) after 48 hours. i) MIP1α concentration (pg/ml) after 72 hours. j) RANTES concentration (pg/ml) after 24 hours. k) RANTES concentration (pg/ml) after 48 hours. 1) RANTES concentration (pg/ml) after 72 hours. m) IL-1α concentration (pg/ml) after 24 hours. n) IL-1α concentration (pg/ml) after 48 hours. o) IL-1α concentration (pg/ml) after 72 hours. p) IL1β concentration (pg/ml) after 24 hours. q) IL1β concentration (pg/ml) after 48 hours. r) IL1β concentration (pg/ml) after 72 hours. s) IFN-α2 concentration (pg/ml) after 24 hours. t) IFN-α2 concentration (pg/ml) after 48 hours. u) IFN-α2 concentration (pg/ml) after 72 hours. v) IL-8 concentration (pg/ml) after 24 hours. w) IL-8 concentration (pg/ml) after 48 hours. x) IL-8 concentration (pg/ml) after 72 hours.

[0073] FIG. **6***a*-FIG. **6***d* is a panel of graphs showing the secreted levels of cytokines IFNγ (Ifng), IL-12p70, IL-1α (IL-1α), IL-6, IL-8, MCP1, MIP1α (MIP1α), MIP1β

(MIP1b), TNFα (TNFa), IL-10, IL-13, IL-9, IL-4, IL-5, IL-17α (IL-17A) and IL-2 produced by PBMCs in the presence of a) *R. gnavus*, b) *B. wexlerae*, c) *E. rectale* and d) *B. luti*, alone or in combination with *E. faecalis* (Epv 8), relative to levels secreted following treatment with *E. faecalis* alone for 24 hours (*E. faecalis*=100%).

[0074] FIG. **7***a*-FIG. **7***p* is a panel of graphs that show the effect of *R. gnavus* (Epv1) on cytokine concentration (pg/ml) either alone or in combination with Epv 8 (*E. faecalis*) on cytokine production by human PBMCs (pg/ml). a) IL-6, b) IFN-γ, c) IL-13, d) IL-10, e) IL-12p70, f) MCP-1, g) IL-8, h) IL17A, i) IL-α, j) IL-9, k) IL-2, 1) IL-4, m) IL-5, n) MIP-1α, o) MIP-1β, p) TNF-α.

[0075] FIG. **8***a*-FIG. **8***p* is a panel of graphs that show the effect of *E. rectale* (Epv2) on cytokine concentration (pg/ml) either alone or in combination with Epv 8 (*E. faecalis*) on cytokine production by human PBMCs (pg/ml). a) IL-6, b) IFN-γ, c) IL-13, d) IL-10, e) IL-12p70, f) MCP-1, g) IL-8, h) IL17A, i) IL-α, j) IL-9, k) IL-2, 1) IL-4, m) IL-5, n) MIP-1α, o) MIP-1β, p) TNF-α.

[0076] FIG. **9***a*-FIG. **9***p* is a panel of graphs that show the effect of *B. luti* (Epv3) on cytokine concentration (pg/ml) either alone or in combination with Epv 8 (*E. faecalis*) on cytokine production by human PBMCs (pg/ml). a) IL-6, b) IFN-γ, c) IL-13, d) IL-10, e) IL-12p70, f) MCP-1, g) IL-8, h) IL17α, i) IL-α, j) IL-9, k) IL-2, 1) IL-4, m) IL-5, n) MIP-1α, o) MIP-1β, p) TNF-α.

[0077] FIG. **10***a*-FIG. **10***p* is a panel of graphs that show the effect of *B. wexlarae*) on cytokine concentration (pg/ml) either alone or in combination with Epv 8 (*E. faecalis*) on cytokine production by human PBMCs (pg/ml). a) IL-6, b) IFN-γ, c) IL-13, d) IL-10, e) IL-12p70, f) MCP-1, g) IL-8, h) IL17α, i) IL-α, j) IL-9, k) IL-2, 1) IL-4, m) IL-5, n) MIP-1α, o) MIP-1β, p) TNF-α.

[0078] FIG. **11***a*-FIG. **11***d* is a panel of graphs showing that (a-b) EPV3 is capable of inducing a desirable anti-inflammatory cytokine profile for treating or preventing GVHD and (c-d) EPV5 induces a suboptimal profile for GVHD.

[0079] FIG. **12***a*-FIG. **12***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv6 (*Clostridium leptum*).

[0080] FIG. **13***a*-FIG. **13***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv15 (*Blautia faecis*).

[0081] FIG. **14***a*-FIG. **14***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv20 (*Blautia/Ruminococcus obeum* ATCC 29174).

[0082] FIG. **15***a*-FIG. **15***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv21 (*Blautia producta* ATCC 27340).

[0083] FIG. **16***a*-FIG. **16***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv22 (*Blautia coccoides* ATCC 29236).

[0084] FIG. **17***a*-FIG. **17***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv23 (*Blautia hydrogenotrophica* ATCC BAA-2371).

[0085] FIG. **18***a*-FIG. **18***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv24 (*Blautia Hansenii* ATCC27752).

[0086] FIG. **19***a*-FIG. **19***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv35 (*Eubacterium rectale*).

[0087] FIG. **20***a*-FIG. **20***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv47 (previously uncultured *Blautia*, similar to GQ898099_s S1-5).

[0088] FIG. **21***a*-FIG. **21***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv51 (previously uncultured *Blautia*, similar to SJTU_C_14_16).

[0089] FIG. **22***a*-FIG. **22***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv52 (*Blautia wexlerae* (SJTU_B_09_77)).

[0090] FIG. **23***a*-FIG. **23***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv54 (*Blautia luti* ELU0087-T13-S-NI_000247).

[0091] FIG. **24***a*-FIG. **24***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv64 (*Blautia wexlerae* WAL 14507).

[0092] FIG. **25***a*-FIG. **25***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv78 (*Blautia obeum*).

[0093] FIG. **26***a*-FIG. **26***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv102 (*Ruminococcus gnavus*).

[0094] FIG. **27***a*-FIG. **27***b* depicts the production of (a) pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and (b) anti-inflammatory (IL-10, IL-4, IL-13) cytokines by human PBMCs following treatment with Epv114 (*Blautia luti* (BlnIX)).

[0095] FIG. **28***a*-FIG. **28***d* presents results from flow cytometry analysis of T cell populations in human PBMCs incubated in the presence of various commensal bacteria, determined using flow cytometry. A) Proportion of Treg cells) ($CD25^{+}CD127^{lo}$); B) Proportion of Th17 cells ($CXCR3^{-}CCR6^{+}$); C) Proportion of Th1 cells ($CXCR3^{+}CCR6^{-}$); D) Proportion of Th2 cells ($CXCR3^{-}CCR6^{-}$). Bacterial strains are as follows: Epv 1*: R. gnavus*; Epv 3*: B. luti*; Epv 2*: E. rectale*; Epv 5*: B. wexlerae*; Epv. 8: *E. faecalis*; Epv 20*: B. obeum*; Epv 21*: B. producta*; Epv 24*: B. hansenii*. The results are shown as percent (%) of $CD3\epsilon^{+}CD4^{+}$ cells.

[0096] FIG. **29***a*-FIG. **29***u* presents the preferred carbon sources utilized by various commensal bacteria. (a) *R. gnavus*; (b) *E. rectale*; (c) *C. leptum*; (d) *B. luti*; (e) *B. wexlerae*; (f) *B. faecis*; (g) *B. obeum*; (h) *B. producta*; (i) *B. coccoides*; (j) *B. hydrogenotrophica*; (k) *B. hansenii*; (1) *B. luti* Blnl X; (m) *B. luti* ELU; (n) *R. gnavus*; (o) *B. faecis*; (p) *R. torques*; (q) *B. wexlerae* WAL14507; (r) *B. wexlerae* SJTU; (s) SJTU1416; (t) GQ8980099; (u) *E. rectale.*

[0097] FIG. **30** graphically depicts levels of serum IFNγ before, during, and after treatment with a prebiotic formulation containing xylose.

[0098] FIG. **31** is a graph that shows the change in Chaol diversity (indicator of community richness) over time in subjects administered xylose three times per day (TID) at 1, 2, 8, 12.5 or 15 grams.

[0099] FIG. **32** depicts the impact of oral vancomycin on the microbiome of the gut and the vagina, by principal component analysis (PCA).

DETAILED DESCRIPTION

I. Overview

[0100] Disclosed herein are therapeutic compositions containing bacterial entities (e.g., non-pathogenic germination-competent bacterial entities), fungal entities, and/or prebiotics for the prevention, control, and treatment of immune and inflammatory diseases, disorders and conditions, and for general nutritional health. These compositions are advantageous in being suitable for safe administration to humans and other mammalian subjects and are efficacious in treating or preventing numerous immune and inflammatory diseases and gastrointestinal diseases, disorders and conditions associated with a dysbiosis.

[0101] While spore-based compositions are known, these are generally prepared according to various techniques such as lyophilization or spray-drying of liquid bacterial cultures, resulting in poor efficacy, instability, substantial variability and lack of adequate safety and efficacy.

[0102] It has now been found that populations of bacterial entities can be obtained from biological materials obtained from mammalian subjects, including humans. These populations are formulated into compositions as provided herein, and can be administered to mammalian subjects in accordance with the methods described herein.

[0103] The microbes that inhabit the human gastrointestinal tract, skin, lungs, vagina, and other niches are starting to be understood and appreciated for their roles in human health and disease (e.g. see Human Microbiome Project Consortium 2012, Structure, function, and diversity of the healthy human microbiome. Nature 486(7402):207-14). Aspects of the invention are based, in part, on the realization that, although autoimmune and inflammatory diseases are often attributed to genetic mutations, these conditions are also influenced by microbes. It is also appreciated that, because microbes not only interact with the host but with one another, the immunomodulatory behavior of microbes can depend on relationships between microbes. For example, a microbial network in a given niche may comprise diverse microbes that all accomplish one or more of the same functions, or may instead comprise diverse microbes that all individually contribute to accomplish one or more functions. In another example, microbes in a given niche may compete with one another for nutrients or space.

[0104] Microbes may influence the risk, progression, or treatment efficacy of an autoimmune or inflammatory disease. In certain aspects, microbes play a role in the prevention of an autoimmune or inflammatory disease or in the suppression of an innate or adaptive immune response. Conversely, in certain aspects, microbes may stimulate an inflammatory immune response and thereby contribute to, increase the risk of, or worsen the symptoms of an autoimmune or inflammatory disease. In certain aspects, some microbes may be associated with lower disease severity or mortality.

[0105] Accordingly, disclosed herein are compositions and methods for the prevention and/or treatment of disorders associated with disruptions of the systemic microbiome, e.g., autoimmune and inflammatory diseases, in human subjects.

II. Definitions

[0106] As used in the specification and the appended claims, the singular forms "a," "an," and "the" include plural referents unless the context clearly dictates otherwise. Thus, for example, "a compound" includes mixtures of compounds.

[0107] The term "about" or "approximately" means within an acceptable error range for the particular value as determined by one of ordinary skill in the art, which will depend in part on how the value is measured or determined, i.e., the limitations of the measurement system. For example, "about" can mean within 3 or more than 3 standard deviations, jper the practice in the art. Alternatively, "about" can mean a range of up to 20%, or up to 10%, or up to 5%, or up to 1% of a given value. Alternatively, particularly with respect to biological systems or processes, the term can mean within an order of magnitude, or within 5-fold, or within 2-fold, of a value.

[0108] As used herein, the term "purified bacterial preparation" refers to a preparation that includes "isolated" bacteria or bacteria that have been separated from at least one associated substance found in a source material or any material associated with the bacteria in any process used to produce the preparation.

[0109] A "bacterial entity" includes one or more bacteria. Generally, a first bacterial entity is distinguishable from a second bacterial entity.

[0110] As used herein, the term "formulation" refers to synthesis or production.

[0111] As used herein, the term "inducing" means increasing the amount or activity a given material as dictated by context.

[0112] As used herein, the term "depletion" refers to reduction in amount of.

[0113] As used herein, a "prebiotic" refers to an ingredient that allows specific changes, both in the composition and/or activity in the gastrointestinal microbiota that may (or may not) confer benefits upon the host. In some embodiments, a prebiotic can be a comestible food or beverage or ingredient thereof. In some embodiments, a prebiotic may be a selectively fermented ingredient. Prebiotics may include complex carbohydrates, amino acids, peptides, minerals, or other essential nutritional components for the survival of the bacterial composition. Prebiotics include, but are not limited to, amino acids, biotin, fructooligosaccharide, galactooligosaccharides, hemicelluloses (e.g., arabinoxylan, xylan, xyloglucan, and glucomannan), inulin, chitin, lactulose, mannan oligosaccharides, oligofructose-enriched inulin, gums (e.g., guar gum, gum arabic and carregenaan), oligofructose, oligodextrose, tagatose, resistant maltodextrins (e.g., resistant starch), trans-galactooligosaccharide, pectins (e.g., xyloga-

lactouronan, citrus pectin, apple pectin, and rhamnogalacturonan-I), dietary fibers (e.g., soy fiber, sugarbeet fiber, pea fiber, corn bran, and oat fiber) and xylooligosaccharides.

[0114] As used herein, "predetermined ratios" refer to ratios determined or selected in advance.

[0115] As used herein, "germinable bacterial spores" are spores capable of forming vegetative cells in response to a particular cue (e.g., an environmental condition or a small molecule).

[0116] As used herein, "detectably present" refers to presence in an amount that can be detected using assays provided herein or otherwise known in the art that exist as of the filing date.

[0117] As used herein, "augmented" refers to an increase in amount and/or localization within to a point where it becomes detectably present.

[0118] As used herein. "fecal material" refers to a solid waste product of digested food and includes feces or bowel washes.

[0119] As used herein, the phrase "host cell response" refers to a response produced by a cell of a host organism.

[0120] As used herein, a "mammalian subject protein" refers to a protein produced by a mammalian subject and encoded by the mammalian subject genome. The term mammalian subject protein includes proteins that have been post-translationally processed and/or modified.

[0121] As used herein, the term "food-derived" refers to a protein or carbohydrate found in a consumed food.

[0122] As used herein, the term "biological material" refers to a material produced by a biological organism.

[0123] As used herein, the term "detection moiety" refers to an assay component that functions to detect an analyte.

[0124] As used herein, the term "incomplete network" refers to a partial network that lacks at least one of the entire set of components needed to carry out one or more network functions.

[0125] As used herein, the term "supplemental" refers to something that is additional and non-identical.

[0126] As used herein, a composition is "substantially free" of microbes when microbes are absent or undetectable as determined by the use of standard genomic and microbiological techniques. A composition is "substantially free" of a prebiotic or immunostimulatory carbohydrate when non-microbial carbohydrates are absent or undetectable as determined by the use of standard biochemical techniques, e.g., dye-based assays.

[0127] Microbial agents (individual or populations of microbes, microbial networks or parts of networks, or microbial metabolites) are considered to be "exogenous" to a subject (e.g., a human or non-human animal), a cell, tissue, organ or other environment of a human or non-human animal, if said subject, or said cell, tissue, organ or other environment of the subject, does not contain detectable levels of the microbial agent.

[0128] A microbial agent or population thereof is "heterologous" or "heterologously contained" on or in a host environment when, e.g., the microbial agent or population is administered or disposed on or in the host or host environment in a number, concentration, form or other modality that is not found in the host prior to administration of the microbial agent or population, or when the microbial agent or population contains an activity or structural component different from a host that does not naturally have the microbial agent within the target environment to which the microbe is administered or thereafter disposed.

[0129] As used herein, the term "antioxidant" is understood to include any one or more of various substances such as beta-carotene (a vitamin A precursor), vitamin C, vitamin E, and selenium) that inhibit oxidation or reactions promoted by Reactive Oxygen Species ("ROS") and other radical and non-radical species. Additionally, antioxidants are molecules capable of slowing or preventing the oxidation of other molecules. Non-limiting examples of antioxidants include astaxanthin, carotenoids, coenzyme Q10 ("CoQ10"), flavonoids, glutathione, Goji (wolfberry), hesperidin, lactowolfberry, lignan, lutein, lycopene, polyphenols, selenium, vitamin A, vitamin C, vitamin E, zeaxanthin, or combinations thereof.

[0130] "Backbone Network Ecology" or simply "Backbone Network" or "Backbone" are compositions of microbes that form a foundational composition that can be built upon or subtracted from to optimize a Network Ecology or Functional Network Ecology to have specific biological characteristics or to comprise desired functional properties, respectively. Microbiome therapeutics can be comprised of these "Backbone Networks Ecologies" in their entirety, or the "Backbone Networks" can be modified by the addition or subtraction of "R-Groups" to give the network ecology desired characteristics and properties. "R-Groups" can be defined in multiple terms including, but not limited to: individual OTUs, individual or multiple OTUs derived from a specific phylogenetic clade or a desired phenotype such as the ability to form spores. or functional bacterial compositions. "Backbone Networks" can comprise a computationally derived Network Ecology in its entirety or can comprise subsets of the computed network that represent key nodes in the network that contribute to efficacy such as but not limited to a composition of Keystone OTUs. The number of organisms in a human gastrointestinal tract, as well as the diversity between healthy individuals, is indicative of the functional redundancy of a healthy gut microbiome ecology. See The Human Microbiome Consortia. 2012. Structure, function and diversity of the healthy human microbiome. Nature 486: 207-214. This redundancy makes it highly likely that non-obvious subsets of OTUs or functional pathways (i.e. "Backbone Networks") are critical to maintaining states of health and/or catalyzing a shift from a dysbiotic state to one of health. One way of exploiting this redundancy is through the substitution of OTUs that share a given clade (see below) or by adding members of a clade not found in the Backbone Network.

[0131] "Bacterial Composition" refers to a composition comprising bacteria, and/or bacterial spores. In some embodiments, a bacterial composition includes a consortium of microbes comprising two or more OTUs, Backbone Network Ecologies, Functional Network Ecologies, Network Classes, and Core Ecologies are all types of bacterial compositions. As used herein, Bacterial Composition includes a therapeutic microbial composition, a prophylactic microbial composition. a Spore Population, a Purified Spore Population, or an ethanol treated spore population.

[0132] "Bacterial translocation" refers to the passage of one or more bacteria across the epithelial layer of any organ of a human or non-human animal.

[0133] "Clade" refers to the OTUs or members of a phylogenetic tree that are downstream of a statistically valid node in a phylogenetic tree. The clade comprises a set of terminal leaves in the phylogenetic tree (i.e. tips of the tree) that are a

distinct monophyletic evolutionary unit and that share some extent of sequence similarity. Clades are hierarchical, in one embodiment, the node in a phylogenetic tree that is selected to define a clade is dependent on the level of resolution suitable for the underlying data used to compute the tree topology.

[0134] The "colonization" of a host organism includes the non-transitory residence of a bacterium or other microscopic organism. As used herein. "reducing colonization" of a host subject's gastrointestinal tract or vagina (or any other microbiota niche) by a pathogenic or non-pathogenic bacterium includes a reduction in the residence time of the bacterium in the gastrointestinal tract or vagina as well as a reduction in the number (or concentration) of the bacterium in the gastrointestinal tract or vagina, or adhered to the luminal surface of the gastrointestinal tract. The reduction in colonization can be permanent or occur during a transient period of time. Measuring reductions of adherent pathogens can be demonstrated directly, e.g., by determining pathogenic burden in a biopsy sample, or reductions may be measured indirectly, e.g., by measuring the pathogenic burden in the stool of a mammalian host.

[0135] A "Combination" of two or more bacteria includes the physical co-existence of the two bacteria, either in the same material or product or in physically connected products, as well as the temporal co-administration or co-localization of the two bacteria.

[0136] "Cytotoxic" activity of a bacterium includes the ability to kill a cell. e.g., a bacterial cell, such as a pathogenic bacterial cell, or a host cell. A "cytostatic" activity of a bacterium includes the ability to inhibit (e.g., partially or fully) the growth, metabolism, and/or proliferation of a cell, e.g., a bacterial cell, such as a pathogenic bacterial cell. Cytotoxic activity may also apply to other cell types such as but not limited to eukaryotic cells, e.g., host cells.

[0137] The term "distal" generally is used in relation to the gastrointestinal tract, specifically the intestinal lumen, of a human or other mammal. Thus, a "distal dysbiosis" includes a dysbiosis outside of the lumen of the gastrointestinal tract, and a "distal microbiota" includes a microbiota outside of the lumen of the gastrointestinal tract. In specified instances, the term "distal" may be used in relation to the site of administration, engraftment, or colonization of a composition, e.g., a probiotic composition, of the invention. For example, if a probiotic composition is administered vaginally, a "distal" effect of the composition would occur outside the vagina.

[0138] "Dysbiosis" refers to a state of the microbiota or microbiome of the gut or other body area, including, e.g., mucosal or skin surfaces (or any other microbiota niche) in which the normal diversity and/or function of the ecological network is disrupted. Any disruption from the preferred (e.g., ideal) state of the microbiota can be considered a dysbiosis, even if such dysbiosis does not result in a detectable decrease in health. This state of dysbiosis may be unhealthy (e.g., result in a diseased state), or it may be unhealthy under only certain conditions, or it may prevent a subject from becoming healthier. Dysbiosis may be due to a decrease in diversity of the microbiota population composition, the overgrowth of one or more population of pathogens (e.g., a population of pathogenic bacteria) or pathobionts, the presence of and/or overgrowth of symbiotic organisms able to cause disease only when certain genetic and/or environmental conditions are present in a patient. or the shift to an ecological network that no longer provides a beneficial function to the host and therefore no longer promotes health. A "distal dysbiosis" includes, but is not limited to, a dysbiosis outside of the lumen of the gastrointestinal tract.

[0139] "Germinant" is a material or composition. or a physical-chemical process. capable of inducing the germination of vegetative bacterial cells from dormant spores, or the proliferation of vegetative bacterial cells, either directly or indirectly in a host organism and/or in vitro.

[0140] "Graft versus host disease" as used herein is an immunological disorder in which the immune cells of a transplant attack the tissues of a transplant recipient. potentially leading to organ dysfunction.

[0141] "Acute GVHD" as used herein is GVHD that presents within the first 100 days of transplant.

[0142] "Chronic GVHD" as used herein is GVHD that presents after the first 100 days of transplant.

[0143] "Inhibit," "inhibiting," and "inhibition" mean to decrease an activity, response, condition, disease, or other biological parameter. This can include but is not limited to the complete ablation of the activity, response, condition, or disease. This may also include, for example, a 10% reduction in the activity, response, condition, or disease as compared to the native or control level. Thus, the reduction can be a 10, 20, 30, 40, 50, 60, 70, 80, 90, 100%, or any amount of reduction in between as compared to native or control levels.

[0144] "Inhibition" of a pathogen or non-pathogen encompasses the inhibition of any desired function or activity of the pathogen or non-pathogen by the probiotic. e.g., bacterial, compositions of the present invention. Demonstrations of inhibition, such as a decrease in the growth of a pathogenic bacterial cell population or a reduction in the level of colonization of a pathogenic bacterial species are provided herein and otherwise recognized by one of ordinary skill in the art. Inhibition of a pathogenic or non-pathogenic bacterial population's "growth" may include inhibiting an increase in the size of a pathogenic or non-pathogenic bacterial cell population and/or inhibiting the proliferation (or multiplication) of a pathogenic or non-pathogenic bacterial cell population. Inhibition of colonization of a pathogenic or non-pathogenic bacterial species may be demonstrated by measuring and comparing the amount or burden of the bacterial species before and after a treatment. An "inhibition" or the act of "inhibiting" includes the total cessation and partial reduction of one or more activities of a pathogen, such as growth. proliferation, colonization, and function. As used herein, inhibition includes cytostatic and/or cytotoxic activities. Inhibition of function includes, for example, the inhibition of expression of a pathogenic gene product (e.g., the genes encoding a toxin and/or toxin biosynthetic pathway, or the genes encoding a structure required for intracellular invasion (e.g., an invasive pilus)) induced by the bacterial composition.

[0145] "Isolated" encompasses a bacterium or other entity or substance that has been (1) separated from at least some of the components with which it was associated when initially produced (whether in nature or in an experimental setting), and/or (2) produced, prepared, purified. and/or manufactured by the hand of man. Isolated bacteria includes, for example, those bacteria that are cultured, even if such cultures are not monocultures. Isolated bacteria may be separated from at least about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%, about 90%, or more of the other components with which they were initially associated. In some embodiments, isolated bacteria are more than about 80%, about 85%, about 90%, about 91%, about 92%,

about 93%, about 94%, about 95%, about 96%, about 97%. about 98%. about 99%, or more than about 99% pure. As used herein, a substance is "pure" if it is substantially free of other components. The terms "purify." "purifying" and "purified" refer to a bacterium or other material that has been separated from at least some of the components with which it was associated either when initially produced or generated (e.g., whether in nature or in an experimental setting), or during any time after its initial production. A bacterium or a bacterial population may be considered purified if it is isolated at or after production, such as from a material or environment containing the bacterium or bacterial population, or by passage through culture, and a purified bacterium or bacterial population may contain other materials up to about 10%, about 20%, about 30%, about 40%, about 50%, about 60%, about 70%, about 80%. about 90%. or above about 90% o and still be considered "isolated." In some embodiments, purified bacteria and bacterial populations are more than about 80% o, about 85%, about 90%, about 91%, about 92%, about 93%. about 94%. about 95%. about 96%. about 97%, about 98%, about 99%, or more than about 99% pure. In the instance of bacterial compositions provided herein, the one or more bacterial types present in the composition can be independently purified from one or more other bacteria produced and/or present in the material or environment containing the bacterial type. In some embodiments, bacterial compositions and the bacterial components thereof are purified from residual habitat products. In other embodiments, bacterial compositions contain a defined mixture of isolated bacteria. For example, in some embodiments, the probiotic composition contains no more than 100 bacterial species. For example, in some embodiments, the probiotic composition contains no more than 75 bacterial species. In other embodiments, the probiotic composition contains no more than 50 bacterial species, e.g., no more than 40 bacterial species, no more than 30 bacterial species, no more than 25 bacterial species, no more than 20 bacterial species, no more than 15 bacterial species, no more than 10 bacterial species, etc. In other embodiments, the probiotic composition contains no more than 10 bacterial species, e.g., 10 bacterial species, 9 bacterial species, 8 bacterial species, 7 bacterial species, 6 bacterial species, 5 bacterial species, 4 bacterial species, 3 bacterial species, 2 bacterial species, 1 bacterial species. In some embodiments, the probiotic composition contains defined quantities of each bacterial species. In an exemplary embodiment, the probiotic composition contains isolated bacterial populations that are not isolated from fecal matter.

[0146] "Keystone OTU" or "Keystone Function" refers to one or more OTUs or Functional Pathways (e.g. KEGG or COG pathways) that are common to many network ecologies or functional network ecologies and are members of networks that occur in many subjects (i.e. "are pervasive). Due to the ubiquitous nature of Keystone OTUs and their associated Functions Pathways. they are central to the function of network ecologies in healthy subjects and are often missing or at reduced levels in subjects with disease. Keystone OTUs and their associated functions may exist in low, moderate, or high abundance in subjects. A "non-Keystone OTU" or "non-Keystone Function" refers to an OTU or Function that is observed in a Network Ecology or a Functional Network Ecology and is not a keystone OTU or Function.

[0147] "Metabolism" or "metabolic reaction" as used herein refers to any and all biomolecular catabolic or anabolic processes occurring or potentially occurring in mammalian cells or in microbes.

[0148] "Metabolite" as used herein refers to any and all molecular compounds, compositions, molecules, ions, co-factors, catalysts or nutrients used as substrates in any cellular or microbial metabolic reaction or resulting as product compounds, compositions, molecules, ions, co-factors, catalysts or nutrients from any cellular or microbial metabolic reaction.

[0149] "Microbiota" refers to the community of microorganisms that inhabit (sustainably or transiently) in and/or on a subject, (e.g, a mammal such as a human), including, but not limited to, eukaryotes (e.g., protozoa), archaea, bacteria, and viruses (including bacterial viruses, i.e., a phage).

[0150] "Microbiome" refers to the genetic content of the communities of microbes that live in and on the human body, both sustainably and transiently, including eukaryotes, archaea, bacteria, and viruses (including bacterial viruses (i.e., phage)), wherein "genetic content" includes genomic DNA, RNA such as ribosomal RNA, the epigenome, plasmids, and all other types of genetic information.

[0151] "Microbial Carriage" or simply "Carriage" refers to the population of microbes inhabiting a niche within or on a subject (e.g., a human subject). Carriage is often defined in terms of relative abundance. For example, OTU 1 comprises 60% of the total microbial carriage, meaning that OTU 1 has a relative abundance of 60% compared to the other OTUs in the sample from which the measurement is made. Carriage is most often based on genomic sequencing data where the relative abundance or carriage of a single OTU or group of OTUs is defined by the number of sequencing reads that are assigned to that OTU/s relative to the total number of sequencing reads for the sample.

[0152] "Microbial Augmentation" refers to the establishment or significant increase of a population of microbes that are (i) absent or undetectable (as determined by the use of standard genomic, biochemical and/or microbiological techniques) from the administered therapeutic microbial composition, and/or (ii) absent, undetectable, or present at low frequencies in the host niche (as an example: gastrointestinal tract, skin, anterior-nares, or vagina) before the delivery of the microbial composition; and (iii) are found, i.e, detectable, after the administration of the microbial composition or significantly increase, for instance increase in abundance by 2-fold, 5-fold, 1×10^2, 1×10^3, 1×10^4, 1×10^5, 1×10^6, 1×10^7, or greater than 1×10^8, in cases where they are present at low frequencies. The microbes that comprise an augmented ecology can be derived from exogenous sources such as food and the environment, or grow out from micro-niches within the host where they reside at low frequency.

[0153] The administration of the therapeutic composition can induce an environmental shift in the target niche that promotes favorable conditions for the growth of commensal microbes. In the absence of treatment with a therapeutic microbial composition, with or without one or more prebiotics, the host can be constantly exposed to these microbes; however, sustained growth and the positive health effects associated with the stable population of increased levels of the microbes comprising the augmented ecology are not observed.

[0154] "Microbial Engraftment" or simply "engraftment" refers to the establishment of OTUs comprised in a therapeutic microbial composition in a target niche. In one embodiment, the OTUs are absent in the treated host prior to treatment. The microbes that comprise the engrafted ecology are found in the therapeutic microbial composition and establish as constituents of the host microbial ecology upon treatment.

Engrafted OTUs can establish for a transient period of time, or demonstrate long-term stability in the microbial ecology that populates the host post-treatment with a therapeutic microbial composition. The engrafted ecology can induce an environmental shift in the target niche that promotes favorable conditions for the growth of commensal microbes capable of catalyzing a shift from a dysbiotic ecology to one representative of a healthy state.

[0155] As used herein, the term "minerals" is understood to include boron, calcium, chromium, copper. iodine, iron, magnesium, manganese, molybdenum, nickel, phosphorus. potassium, selenium. silicon, tin, vanadium, zinc, or combinations thereof.

[0156] "Network Ecology" refers to a consortium of clades or OTUs that co-occur in some number of subjects. As used herein, a "network" is defined mathematically by a graph delineating how specific nodes (i.e. clades or OTUs) and edges (connections between specific clades or OTUs) relate to one another to define the structural ecology of a consortium of clades or OTUs. Any given Network Ecology will possess inherent phylogenetic diversity and functional properties.

[0157] A Network Ecology can also be defined in terms of its functional capabilities where for example the nodes would be comprised of elements such as, but not limited to. enzymes, clusters of orthologous groups (COGS; http://www.ncbi.nlm.nih.gov books/NBK21090/). or KEGG Orthology Pathways (www.genome.jp/kegg/): these networks are referred to as a "Functional Network Ecology". Functional Network Ecologies can be reduced to practice by defining the group of OTUs that together comprise the functions defined by the Functional Network Ecology.

[0158] The terms "Network Class", "Core Network" and "Network Class Ecology" refer to a group of network ecologies that in general are computationally determined to comprise ecologies with similar phylogenetic and/or functional characteristics. A Network Class therefore contains important biological features, defined either phylogenetically or functionally, of a group (i.e., a cluster) of related network ecologies. One representation of a Core Network Ecology is a designed consortium of microbes, typically non-pathogenic bacteria, that represents core features of a set of phylogenetically or functionally related network ecologies seen in many different subjects. In many occurrences, a Core Network, while designed as described herein, exists as a Network Ecology observed in one or more subjects. Core Network ecologies are useful for reversing or reducing a dysbiosis in subjects where the underlying, related Network Ecology has been disrupted.

[0159] "Ecological Niche" or simply "Niche" refers to the ecological space that an organism or group of organisms (e.g., a bacterial population) occupies. Niche describes how an organism or population or organisms responds to the distribution of resources, physical parameters (e.g., host tissue space) and competitors (e.g., by growing when resources are abundant, and/or when predators, parasites and pathogens are scarce) and how it in turn alters those same factors (e.g., limiting access to resources by other organisms, acting as a food source for predators and a consumer of prey).

[0160] To be free of "non-comestible products" means that a bacterial composition or other material provided herein does not have a substantial amount of a non-comestible product, e.g., a product or material that is inedible, harmful or otherwise undesired in a product suitable for administration, e.g., oral administration, to a human subject.

[0161] "Operational taxonomic units," "OTU" (or plural, "OTUs") refer to a terminal leaf in a phylogenetic tree and is defined by a nucleic acid sequence, e.g., the entire genome, or a specific genetic sequence, and all sequences that share sequence identity to this nucleic acid sequence at the level of species. In some embodiments the specific genetic sequence may be the 16S sequence or a portion of the 16S sequence. In other embodiments, the entire genomes of two entities are sequenced and compared. In another embodiment, select regions such as multilocus sequence tags (MLST), specific genes, or sets of genes may be genetically compared. In 16S embodiments, OTUs that share ≥97% average nucleotide identity across the entire 16S or some variable region of the 16S are considered the same OTU (see e.g. Claesson M J, Wang Q, O'Sullivan O, Greene-Diniz R, Cole J R, Ros R P, and O'Toole P W. 2010. Comparison of two next-generation sequencing technologies for resolving highly complex microbiota composition using tandem variable 16S rRNA gene regions. *Nucleic Acids Res* 38: e200. Konstantinidis K T, Ramette A, and Tiedje J M. 2006. The bacterial species definition in the genomic era. *Philos Trans R Soc Lond B Biol Sci* 361: 1929-1940.). In embodiments involving the complete genome, MLSTs, specific genes, or sets of genes OTUs that share ≥95% average nucleotide identity are considered the same OTU (see e.g. Achtman M, and Wagner M. 2008. Microbial diversity and the genetic nature of microbial species. *Nat. Rev. Microbiol.* 6: 431-440. Konstantinidis K T, Ramette A, and Tiedje J M. 2006. The bacterial species definition in the genomic era. *Philos Trans R Soc Lond B Biol Sci* 361: 1929-1940.). OTUs are frequently defined by comparing sequences between organisms. Generally, sequences with less than 95% sequence identity are not considered to form part of the same OTU. OTUs may also be characterized by any combination of nucleotide markers or genes, in particular highly conserved genes (e.g., "house-keeping" genes), or a combination thereof. Such characterization employs, e.g., WGS data or a whole genome sequence.

[0162] "Pathobionts" or "Opportunistic Pathogens" refers to symbiotic organisms able to cause disease only when certain genetic and/or environmental conditions are present in a subject.

[0163] The term "Phylogenetic Diversity" refers to the biodiversity present in a given Network Ecology, Core Network Ecology or Network Class Ecology based on the OTUs that comprise the network. Phylogenetic diversity is a relative term, meaning that a Network Ecology, Core Network or Network Class that is comparatively more phylogenetically diverse than another network contains a greater number of unique species, genera, and taxonomic families. Uniqueness of a species, genera, or taxonomic family is generally defined using a phylogenetic tree that represents the genetic diversity all species, genera, or taxonomic families relative to one another. In another embodiment phylogenetic diversity may be measured using the total branch length or average branch length of a phylogenetic tree.

[0164] Phylogenetic Diversity may be optimized in a bacterial composition by including a wide range of biodiversity.

[0165] "Phylogenetic tree" refers to a graphical representation of the evolutionary relationships of one genetic sequence to another that is generated using a defined set of phylogenetic reconstruction algorithms (e.g. parsimony, maximum likelihood, or Bayesian). Nodes in the tree represent distinct ancestral sequences and the confidence of any

node is provided by a bootstrap or Bayesian posterior probability, which measures branch uncertainty.

[0166] As used herein "preventing" or "prevention" refers to any methodology where the disease state does not occur due to the actions of the methodology (such as, for example, administration of a probiotic and/or a prebiotic as described herein). In one aspect, it is understood that prevention can also mean that the disease is not established to the extent that occurs in untreated controls. For example, there can be a 5, 10, 15, 20, 25, 30, 35, 40, 50, 60, 70, 80, 90, or 100% reduction in the establishment of disease frequency relative to untreated controls. Accordingly, prevention of a disease encompasses a reduction in the likelihood that a subject will develop the disease, relative to an untreated subject (e.g. a subjece who does not receive a probiotic and/or a prebiotic as described herein).

[0167] "rDNA", "rRNA". "16S-rDNA", "16S-rRNA", "16S", "16S sequencing", "16S-NGS", "18S", "18S-rRNA", "18S-rDNA", "18S sequencing", and "18S-NGS" refer to the nucleic acids that encode for the RNA subunits of the ribosome. rDNA refers to the gene that encodes the rRNA that comprises the RNA subunits. There are two RNA subunits in the ribosome termed the small subunit (SSU) and large subunit (LSU); the RNA genetic sequences (rRNA) of these subunits are related to the gene that encodes them (rDNA) by the genetic code. rDNA genes and their complementary RNA sequences are widely used for determination of the evolutionary relationships amount organisms as they are variable, yet sufficiently conserved to allow cross organism molecular comparisons.

[0168] Typically 16S rDNA sequence (approximately 1542 nucleotides in length) of the 30S SSU is used for molecular-based taxonomic assignments of Prokaryotes and the 18S rDNA sequence (approximately 1869 nucleotides in length) of 40S SSU is used for Eukaryotes. 16S sequences are used for phylogenetic reconstruction as they are in general highly conserved, but contain specific hypervariable regions that harbor sufficient nucleotide diversity to differentiate genera and species of most bacteria.

[0169] "Residual habitat products" refers to material derived from the habitat for microbiota within or on a human or animal. For example, microbiota live in feces in the gastrointestinal tract, on the skin itself, in saliva, mucus of the respiratory tract, or secretions of the genitourinary tract (i.e., biological matter associated with the microbial community). Substantially free of residual habitat products means that the bacterial composition no longer contains the biological matter associated with the microbial environment on or in the human or animal subject and is 100% free, 99% free, 98% free, 97% free, 96% free, or 95% free, 94% free, 93% free, 92% free, 91% free, 90% free, 85% free, 80% free, 75% free, 70% free, 65% free, or 60% free of any contaminating biological matter associated with the microbial community. Residual habitat products can include abiotic materials (including undigested food) or it can include unwanted microorganisms. Substantially free of residual habitat products may also mean that the bacterial composition contains no detectable cells from a human or animal and that only microbial cells are detectable. In one embodiment, substantially free of residual habitat products may also mean that the bacterial composition contains no detectable viral (including bacterial viruses (i.e., phage)), fungal, mycoplasmal contaminants. In another embodiment, it means that fewer than 1×10^{-2}%, 1×10^{-3}%, 1×10^{-4}%, 1×10^{-5}%, 1×10^{-6}%, 1×10^{-7}%, 1×10^{-8}% of the viable cells in the bacterial composition are human or animal, as compared to microbial cells. There are multiple ways to accomplish this degree of purity, none of which are limiting. Thus, contamination may be reduced by isolating desired constituents through multiple steps of streaking to single colonies on solid media until replicate (such as, but not limited to, two) streaks from serial single colonies have shown only a single colony morphology. Alternatively, reduction of contamination can be accomplished by multiple rounds of serial dilutions to single desired cells (e.g., a dilution of 10^{-8} or 10^{-9}), such as through multiple 10-fold serial dilutions. This can further be confirmed by showing that multiple isolated colonies have similar cell shapes and Gram staining behavior. Other methods for confirming adequate purity include genetic analysis (e.g. PCR, DNA sequencing), serology and antigen analysis, enzymatic and metabolic analysis, and methods using instrumentation such as flow cytometry with reagents that distinguish desired constituents from contaminants.

[0170] In microbiology, "16S sequencing" or "16S-rRNA" or "16S" refers to sequence derived by characterizing the nucleotides that comprise the 16S ribosomal RNA gene(s). The bacterial 16S rDNA is approximately 1500 nucleotides in length and is used in reconstructing the evolutionary relationships and sequence similarity of one bacterial isolate to another using phylogenetic approaches. 16S sequences are used for phylogenetic reconstruction as they are in general highly conserved, but contain specific hypervariable regions that harbor sufficient nucleotide diversity to differentiate genera and species of most bacteria.

[0171] The "V1-V9 regions" of the 16S rRNA refers to the first through ninth hypervariable regions of the 16S rRNA gene that are used for genetic typing of bacterial samples. These regions in bacteria are defined by nucleotides 69-99, 137-242, 433-497, 576-682, 822-879, 986-1043, 1117-1173, 1243-1294 and 1435-1465 respectively using numbering based on the *E. coli* system of nomenclature. Brosius et al., Complete nucleotide sequence of a 16S ribosomal RNA gene from *Escherichia coli*, PNAS 75(10):4801-4805 (1978). In some embodiments, at least one of the V1, V2, V3, V4, V5, V6, V7, V8, and V9 regions are used to characterize an OTU. In one embodiment, the V1, V2, and V3 regions are used to characterize an OTU. In another embodiment, the V3, V4, and V5 regions are used to characterize an OTU. In another embodiment, the V4 region is used to characterize an OTU. A person of ordinary skill in the art can identify the specific hypervariable regions of a candidate 16S rRNA by comparing the candidate sequence in question to a reference sequence and identifying the hypervariable regions based on similarity to the reference hypervariable regions, or alternatively, one can employ Whole Genome Shotgun (WGS) sequence characterization of microbes or a microbial community.

[0172] The term "subject" refers to any organism or animal subject that is an object of a method or material, including mammals, e.g., humans, laboratory animals (e.g., primates, rats, mice, rabbits), livestock (e.g., cows, sheep, goats, pigs, turkeys, and chickens), household pets (e.g., dogs, cats, and rodents), horses, and transgenic non-human animals. The subject may be suffering from a dysbiosis, including, but not limited to, an infection due to a gastrointestinal pathogen or may be at risk of developing or transmitting to others an infection due to a gastrointestinal pathogen. Synonyms used herein include "patient" and "animal." In some embodiments, the subject or host may be suffering from a dysbiosis, that

contributes to or causes a condition classified as an autoimmune or inflammatory disease, graft-versus-host disease, Crohn's disease. Celiac disease, inflammatory bowel disease, ulcerative colitis, multiple sclerosis, systemic lupus erythematosus, Sjogren's syndrome, or type 1 diabetes. In some embodiments, the host may be suffering from including but not limited to mechanisms such as metabolic endotoxemia, altered metabolism of primary bile acids, immune system activation, or an imbalance or reduced production of short chain fatty acids including butyrate, propionate. acetate, and branched chain fatty acids.

[0173] The term "phenotype" refers to a set of observable characteristics of an individual entity. As example an individual subject may have a phenotype of "health" or "disease". Phenotypes describe the state of an entity and all entities within a phenotype share the same set of characteristics that describe the phenotype. The phenotype of an individual results in part, or in whole, from the interaction of the entities genome and/or microbiome with the environment.

[0174] "Spore" or "endospore" refers to an entity, particularly a bacterial entity, which is in a dormant, non-vegetative and non-reproductive stage. Spores are generally resistant to environmental stress such as radiation, desiccation, enzymatic treatment, temperature variation, nutrient deprivation, and chemical disinfectants.

[0175] A "spore population" refers to a plurality of spores present in a composition. Synonymous terms used herein include spore composition, spore preparation, ethanol treated spore fraction and spore ecology. A spore population may be purified from a fecal donation, e.g. via ethanol or heat treatment, or a density gradient separation or any combination of methods described herein to increase the purity, potency and/or concentration of spores in a sample. Alternatively, a spore population may be derived through culture methods starting from isolated spore former species or spore former OTUs or from a mixture of such species, either in vegetative or spore form.

[0176] A "sporulation induction agent" is a material or physical-chemical process that is capable of inducing sporulation in a bacterium, either directly or indirectly, in a host organism and/or in vitro.

[0177] To increase production of bacterial entities includes an activity or a sporulation induction agent. Production includes conversion of vegetative bacterial cells into spores and augmentation of the rate of such conversion, as well as decreasing the germination of bacteria in spore form, decreasing the rate of spore decay in vivo, or ex vivo, or to increasing the total output of spores (e.g. via an increase in volumetric output of fecal material).

[0178] "Synergy" or "synergistic interactions" refers to the interaction or cooperation of two or more microbes to produce a combined effect greater than the sum of their separate effects. In one embodiment, "synergy" between two or more microbes can result in the inhibition of a pathogens ability to grow.

[0179] "Treatment," "treat," or "treating" means a method of reducing the effects of a disease or condition. Treatment can also refer to a method of reducing the disease or condition itself rather than just the symptoms. The treatment can be any reduction from pre-treatment levels and can be but is not limited to the complete ablation of the disease, condition, or the symptoms of the disease or condition. Therefore, in the disclosed methods, treatment" can refer to a 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or 100% reduction in the severity of an established disease or the disease progression. For example, a disclosed method for reducing the effects of GVHD is considered to be a treatment if there is a 10% reduction in one or more symptoms of the disease in a subject with GVHD when compared to pre-treatment levels in the same subject or control subjects. Thus, the reduction can be a 10, 20, 30, 40, 50, 60, 70, 80, 90, 100%, or any amount of reduction in between as compared to native or control levels. It is understood and herein contemplated that "treatment" does not necessarily refer to a cure of the disease or condition, but an improvement in the outlook of a disease or condition (e.g., GVHD).

[0180] As used herein the term "vitamin" is understood to include any of various fat-soluble or water-soluble organic substances (non-limiting examples include vitamin A, Vitamin B1 (thiamine), Vitamin B2 (riboflavin), Vitamin B3 (niacin or niacinamide), Vitamin B5 (pantothenic acid), Vitamin B6 (pyridoxine, pyridoxal, or pyridoxamine, or pyridoxine hydrochloride), Vitamin B7 (biotin), Vitamin B9 (folic acid), and Vitamin B12 (various cobalamins; commonly cyanocobalamin in vitamin supplements), vitamin C, vitamin D, vitamin E, vitamin K, K1 and K2 (i.e. MK-4, MK-7), folic acid and biotin) essential in minute amounts for normal growth and activity of the body and obtained naturally from plant and animal foods or synthetically made, pro-vitamins, derivatives, analogs. As used herein, the term "recipient" refers to the subject receives a bone marrow or a solid organ transplantation.

III. Probiotic Compositions of the Invention

[0181] Disclosed herein are bacterial, e.g., probiotic, compositions comprising a non-pathogenic bacterial or fungal population, e.g., an immunomodulatory bacterial population, such as an anti-inflammatory bacterial population, with or without one or more prebiotics, for the prevention, control, and treatment of transplant disorders, and for general nutritional health in a subject receiving a transplant. These compositions are advantageous in being suitable for safe administration to humans and other mammalian subjects and are efficacious for the treatment, prevention, reduction and amelioration of graft versus host disease (GVHD), and complications associated therewith, such as transplant rejection. While spore-based compositions are known, these are generally prepared according to various techniques such as lyophilization or spray-drying of liquid bacterial cultures, resulting in poor efficacy, instability, substantial variability and lack of adequate safety and efficacy.

[0182] It has now been found that bacterial and fungal populations can be obtained from biological materials obtained from mammalian subjects, including humans. These populations are formulated into compositions as provided herein, and administered to mammalian subjects using the methods as provided herein.

[0183] As described in detail herein, alterations in the microbiota of a transplant recipient significantly impact the outcome for the subject. In particular, a dysbiosis in the gastrointestinal tract, or a dysbiosis distal to the gastrointestinal tract, can increase the likelihood that a subject will develop GVHD, and reduce the overall survival of the subject following the transplant. Outcome can be improved by administering a probiotic composition, optionally in combination with a prebiotic, to correct the dysbiosis. In particular, probiotic compositions that improve intestinal barrier integrity and/or

reduce inflammation in the subject can treat or prevent GVHD in a subject receiving a transplant.

[0184] In one embodiment, therapeutic compositions are provided for the treatment, prevention, reduction of onset and amelioration of inflammation or one or more symptom of a transplant disorder, such as, for example, GVHD. As used herein, "therapeutic" compositions include compositions that function in a prophylactic (e.g., preventative) manner. Therapeutic compositions can contain one or more populations of immunomodulatory bacteria and/or fungi, alone or in combination with one or more prebiotics. In one embodiment, the microbial entities can be produced by isolation and/or culture, using, for example, the following steps: a) providing fecal material and b) subjecting the material to a culture step and/or a treatment step resulting in purification and/or isolation of immunomodulatory bacteria and, optionally, c) formulating the purified population for administration, wherein the purified population is present in the composition in an amount effective to engraft and/or colonize in the gastrointestinal tract in order to treat, prevent or reduce the severity of inflammation or one or more symptom of GVHD in a mammalian recipient subject to whom the therapeutic composition is administered. Generally, the population is provided in an amount effective to treat (including to prevent) a disease, disorder or condition associated with or characterized by inflammation or dysbiosis, e.g., transplant rejection or GVHD. Such treatment may be effective to reduce the severity of at least one symptom of the dysbiosis, e.g., gastrointestinal or distal dysbiosis, thereby improving survival of the transplant recipient. Such treatment may be effective to modulate the microbiota diversity present in the mammalian recipient.

[0185] In embodiments, the probiotic compositions contain immunomodulatory microbes, e.g., immunomodulatory bacteria, which are capable of altering the immune activity of a mammalian subject. In exemplary embodiments, the immunomodulatory bacteria are capable of reducing inflammation in a mammalian subject. Such immunomodulatory bacteria are referred to herein as anti-inflammatory bacteria. Immunomodulatory bacteria can act to alter the immune activity of a subject directly or indirectly. For example, immunomodulatory bacteria can act directly on immune cells through receptors for bacterial components (e.g. Toll-like receptors) or by producing metabolites such as immunomodulatory short chain fatty acids (SCFAs). SCFAs produced by immunomodulatory bacteria can include, e.g., butyrate, acetate, propionate, or valerate, or combinations thereof. Such SCFAs can have many positive impacts on the health of the subject, by, for example, reducing inflammation, or improving intestinal barrier integrity. In one embodiment, the improvement of gut epithelium barrier integrity results in reduced trafficking of bacteria, bacterial components and/or bacterial metabolites into the blood. In one embodiment, a probiotic composition is administered to a subject in an amount effective to increase short chain fatty acid production by one or more organisms in the gut of a mammalian host. Immunomodulatory bacteria can also impact the immune activity of a subject by producing glutathione or gamma-glutamylcysteine. Probiotics containing such immunomodulatory bacteria can treat or prevent GVHD in a subject receiving a transplant.

[0186] Probiotic compositions containing immunomodulatory bacteria can additionally or alternatively impact the immune activity of a subject indirectly by modulating the activity of immune cells in the subject. For example, immunomodulatory bacteria may alter cytokine expression by host immune cells (e.g., macrophages, B lymphocytes, T lymphocytes, mast cells, peripherial blood mononuclear cells (PBMCs), etc.) or other types of host cells capable of cytokine secretion (e.g., endothelia cells, fibroblasts, stromal cells, etc.). In an exemplary embodiment, probiotic compositions contain anti-inflammatory immunomodulatory bacteria that are capable of inducing secretion of anti-inflammatory cytokines by host cells. For example, anti-inflammatory bacteria can induce secretion of one or more anti-inflammatory cytokines such as but not limited to IL-10, IL-13, IL-9, IL-4, IL-5, TGFβ, and combinations thereof, by host cells (e.g., host immune cells). In another exemplary embodiment, probiotic compositions contain anti-inflammatory immunomodulatory bacteria that are capable of reducing secretion of one or more pro-inflammatory cytokines by host cells (e.g., host immune cells). For example, anti-inflammatory bacteria can reduce secretion of one or more pro-inflammatory cytokines such as but not limited to IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. Other cytokines that may be modulated by immunomodulatory bacteria include, for example, IL-17A, IL-2, and IL-9. In some embodiments, the induction and/or secretion of pro-inflammatory cytokines may be induced by (e.g., in response to, either directly or indirectly) a bacteria (e.g., *Enterococcus faecalis*).

[0187] In some embodiments, immunomodulatory bacteria are selected for inclusion in a probiotic composition of the invention based on the desired effect of the probiotic composition on cytokine secretion by host cells, e.g., host immune cells. For example, in one embodiment, a probiotic composition contains anti-inflammatory bacteria that increase secretion of an anti-inflammatory cytokine, for example, IL-10, IL-13, IL-9, IL-4, IL-5, TGFβ, and combinations thereof. In some embodiments, the anti-inflammatory bacteria increase secretion of two or more anti-inflammatory cytokines. In some embodiments, the anti-inflammatory bacteria increase secretion of three or more anti-inflammatory cytokines. In some embodiments, the anti-inflammatory bacteria increase secretion of four or more anti-inflammatory cytokines. In some embodiments, the anti-inflammatory bacteria increase secretion of five or more anti-inflammatory cytokines. In exemplary embodiments, the increase is an increase of at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 80%, 100%, 200%, 300%, 500% or more. In another embodiment, a probiotic composition contains anti-inflammatory bacteria that decrease secretion of a pro-inflammatory cytokine, for example, IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. In some embodiments, the anti-inflammatory bacteria decrease secretion of two or more pro-inflammatory cytokines. In some embodiments, the anti-inflammatory bacteria decrease secretion of three or more pro-inflammatory cytokines. In some embodiments, the anti-inflammatory bacteria decrease secretion of four or more pro-inflammatory cytokines. In some embodiments, the anti-inflammatory bacteria decrease secretion of five or more pro-inflammatory cytokines. In exemplary embodiments, the decrease is a decrease of at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 80%, 100%, 200%, 300%, 500% or more. In another embodiment, the probiotic composition contains anti-inflammatory bacteria that increase secretion of one or more anti-inflammatory cytokines and reduce secretion of one or more pro-inflammatory

cytokines. Alterations in cytokine expression may occur locally, e.g., in the gastrointestinal tract of a subject, or at a site distal to the gastrointestinal tract. Such anti-inflammatory bacteria may be used to treat or prevent GVHD in a transplant recipient.

[0188] In other embodiments, probiotics containing immunomodulatory bacteria impact the immune activity of a subject by promoting the differentiation and/or expansion of particular subpopulations of immune cells. For example, immunomodulatory bacteria can increase or decrease the proportion of Treg cells, Th17 cells, Th1 cells, or Th2 cells in a subject. The increase or decrease in the proportion of immune cell subpopulations may be systemic, or it may be localized to a site of action of the probiotic, e.g., in the gastrointestinal tract or at the site of a distal dysbiosis. In some embodiments, immunomodulatory bacteria are selected for inclusion in a probiotic composition of the invention based on the desired effect of the probiotic composition on the differentiation and/or expansion of subpopulations of immune cells in the subject.

[0189] In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Treg cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Treg cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th17 cells in a subject (e.g., by inducing expansion of Th17 cells in the subject). In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th17 cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th1 cells in a subject (e.g., by inducing expansion of Th1 cells in the subject). In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th1 cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th2 cells in a subject (e.g., by inducing expansion of Th2 cells in the subject). In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th2 cells in a subject. The increase or decrease in the proportion of immune cell subpopulations (e.g., Th17 cells, Th1 cells and Th2 cells) may be localized or systemic.

[0190] In one embodiment, a probiotic composition contains immunomodulatory bacteria capable of modulating the proportion of one or more populations of Treg cells, Th17 cells, Th cells, Th2 cells, and combinations thereof in a subject. Certain immune cell profiles may be particularly desirable to treat or prevent particular disorders associated with a dysbiosis. For example, treatment or prevention of GVHD can be promoted by increased numbers of Treg cells and Th2 cells, and/or decreased numbers of Th17 cells and Th1 cells. Accordingly, probiotic compositions for the treatment or prevention of GVHD may contain probiotics capable of promoting Treg cells and Th2 cells, and reducing Th17 and Th1 cells.

[0191] In one embodiment, therapeutic probiotic compositions comprising a purified population of immunomodulatory microbes, e.g., bacteria, are provided, with or without one or more prebiotics, in an amount effective to i) treat or prevent dysbiosis, e.g., gastrointestinal or distal dysbiosis, inflammation, or an autoimmune or inflammatory disorder, and/or ii) augment at least one type of microbe, e.g., a bacterium, not present in the therapeutic composition in a mammalian recipient subject to whom the therapeutic composition is administered, and/or iii) engraft at least one type of microbe, e.g., a bacterium, present in the therapeutic composition but not present in a mammalian subject prior to treatment.

[0192] In another embodiment, therapeutic probiotic compositions comprising a purified population of immunomodulatory microbes are provided, in an amount effective to i) augment the microbiota diversity present in the mammalian recipient and/or ii) treat or prevent dysbiosis, e.g., gastrointestinal or distal dysbiosis, inflammation, or an autoimmune or inflammatory disorder in a mammalian recipient subject to whom the therapeutic composition is administered, wherein the purified population is obtained by separation of the population apart from at least one residual habitat product in a fecal material obtained from one or a plurality of mammalian donor subjects. In some embodiments, individual bacterial strains can be cultured from fecal material. These strains can then be purified or otherwise isolated and used singly or in combination. In one embodiment, the probiotic composition does not contain a fecal extract.

[0193] In one embodiment, the probiotic compositions described herein may be used to treat or correct a dysbiosis in a subject. The dysbiosis may be, for example, a local dysbiosis, or a distal dysbiosis. In another embodiment, the probiotic compositions described herein may be used to prevent a dysbiosis in a subject at risk for developing a dysbiosis.

[0194] In some embodiments, the purified population of immunomodulatory microbes described above is coadministered or coformulated with one or more prebiotics, e.g., carbohydrates.

[0195] In some embodiments, the purified population of immunomodulatory microbes described above is administered before one or more prebiotics are administered to a subject. In some embodiments the purified population of immunomodulatory microbes is administered after one or more prebiotics have been administered to a subject. In some embodiments, the purified population of immunomodulatory microbes is administered concurrently with one or more prebiotics. In other embodiments, the purified population of immunomodulatory microbes is administered sequentially with one or more prebiotics. In some embodiments, the purified population of immunomodulatory microbes is administered in a composition formulated to contain one or more pharmaceutical excipients, and optionally one or more prebiotics.

[0196] Microbes involved in modulation of the host immune system i) may be human commensals; ii) may be part of an organ's healthy-state microbiome; ii) may be part of a distal organ's healthy-state microbiome; iv) may be exogenous microbes; v) may be innocuous; vi) may be pathobionts; vii) may be pathogens; viii) may be opportunistic pathogens; or ix) any combination thereof. In some aspects, microbes are not required to be actively proliferating (e.g., spores, dormant cells, cells with reduced metabolic rate, or heat-killed cells) to have an immunomodulatory effect. In certain aspects, microbial cell components, rather than whole microbial cells, may have immunomodulatory effects. Non-limiting examples of microbial components are lipids, carbohydrates, proteins, nucleic acids, and small molecules.

[0197] Microbial compositions are provided herein, optionally comprising prebiotics, non-microbial immunomodulatory carbohydrates, or microbial immunomodulatory cell components, that are effective for the prevention or treat-

ment of an autoimmune or inflammatory disorder such as graft-versus-host disease (GVHD), and/or a dysbiosis which contributes to GVHD.

[0198] In certain embodiments, the compositions comprise at least one type of microbe and at least one type of carbohydrate (a prebiotic), and optionally further comprise microbial immunomodulatory cell components or substrates for the production of immunomodulatory metabolites, that are effective for the prevention or treatment of an autoimmune or inflammatory disorder such as graft-versus-host disease (GVHD). Methods for the prevention and/or treatment of GVHD in human subjects are also disclosed herein.

[0199] In some embodiments, the bacterial, e.g., probiotic, compositions of the invention comprise purified spore populations. As described herein, purified spore populations contain commensal bacteria of the human gut microbiota with the capacity to meaningfully provide one or more functions of a healthy microbiota when administered to a mammalian subject. Without being limited to a specific mechanism, it is thought that such compositions inhibit the growth of pathogens such as *C. difficile, Salmonella* spp., enteropathogenic *E. coli, Fusobacterium* spp., *Klebsiella* spp. and vancomycin-resistant *Enterococcus* spp., so that a healthy, diverse and protective microbiota can be maintained or, in the case of pathogenic bacterial infections, repopulate the intestinal lumen to reestablish ecological control over potential pathogens. In some embodiments, yeast spores and other fungal spores are also purified and selected for therapeutic use.

[0200] In one embodiment, the purified spore populations can engraft in the host and remain present for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 10 days, 14 days, 21 days, 25 days, 30 days, 60 days, 90 days, or longer than 90 days. Additionally, the purified spore populations can induce other healthy commensal bacteria found in a healthy gut to engraft in the host that are not present in the purified spore populations or present at lesser levels. Therefore, these species are considered to "augment" the delivered spore populations. In this manner, commensal species augmentation of the purified spore population in the recipient's gut leads to a more diverse population of gut microbiota than present initially.

[0201] In some embodiments, a probiotic composition of the invention contains a single species of bacteria. In other embodiments, the probiotic composition contains two or more species of bacteria, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 500, 1000 or more species of bacteria. In one embodiment, the probiotic composition contains no more than 20 species of bacteria, e.g., 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 species of bacteria. In exemplary embodiments, the probiotic composition contains 8 bacterial species. In other exemplary embodiments, the probiotic composition contains 9 bacterial species. In other embodiments, the probiotic composition contains or is administered in conjunction with a prebiotic, as described herein.

[0202] Preferred bacterial genera include *Acetanaerobacterium, Acetivibrio, Alicyclobacillus, Alkaliphilus, Anaerofustis, Anaerosporobacter, Anaerostipes, Anaerotruncus, Anoxybacillus, Bacillus, Bacteroides, Blautia, Brachyspira, Brevibacillus, Bryantella, Bulleidia, Butyricicoccus, Butyrivibrio, Catenibacterium, Chlamydiales, Clostridiaceae, Clostridiales, Clostridium, Collinsella, Coprobacillus, Coprococcus, Coxiella, Deferribacteres, Desulfitobacterium, Desulfotomaculum, Dorea, Eggerthella, Erysipelothrix, Erysipelotrichaceae, Ethanoligenens, Eubacterium, Faecalibacterium, Filifactor, Flavonifractor, Flexistipes, Fulvimonas, Fusobacterium, Gemmiger, Geobacillus, Gloeobacter, Holdemania, Hydrogenoanaerobacterium, Kocuria, Lachnobacterium, Lachnospira, Lachnospiraceae, Lactobacillus, Lactonifactor, Leptospira, Lutispora, Lysinibacillus, Mollicutes, Moorella, Nocardia, Oscillibacter, Oscillospira, Paenibacillus, Papillibacter, Pseudoflavonifractor, Robinsoniella, Roseburia, Ruminococcaceae, Ruminococcus, Saccharomonospora, Sarcina, Solobacterium, Sporobacter, Sporolactobacillus, Streptomyces, Subdoligranulum, Sutterella, Syntrophococcus, Thermoanaerobacter, Thermobifida*, and *Turicibacter.*

[0203] Preferred bacterial genera also include *Acetonema, Alkaliphilus, Amphibacillus, Ammonifex, Anaerobacter, Caldicellulosiruptor, Caloramator, Candidatus, Carboxydibrachium, Carboxydothermus, Cohnella, Dendrosporobacter Desulfitobacterium, Desulfosporosinus, Halobacteroides, Heliobacterium, Heliophilum, Heliorestis, Lachnoanaerobaculum, Lysinibacillus, Oceanobacillus, Orenia* (*S.*), *Oxalophagus, Oxobacter, Pelospora, Pelotomaculum, Propionispora, Sporohalobacter, Sporomusa, Sporosarcina, Sporotomaculum, Symbiobacterium, Syntrophobotulus, Syntrophospora, Terribacillus, Thermoanaerobacter*, and *Thermosinus.*

[0204] In another embodiment, a probiotic composition of the invention consists essentially of *Blautia.*

[0205] In one embodiment, a probiotic composition of the invention does not comprise *Blautia* alone.

[0206] As provided herein, therapeutic compositions comprise, or in the alternative, modulate, the colonization and/or engraftment, of the following exemplary bacterial entities: *Lactobacillus gasseri, Lactobacillus fermentum, Lactobacillus reuteri, Enterococcus faecalis, Enterococcus durans, Enterococcus villorum, Lactobacillus plantarum, Pediococcus acidilactici, Staphylococcus pasteuri, Staphylococcus cohnii, Streptococcus sanguinis, Streptococcus sinensis, Streptococcus mitis, Streptococcus* sp. SCA22, *Streptococcus* sp. CR-3145, *Streptococcus anginosus, Streptococcus mutans, Coprobacillus cateniformis, Clostridium saccharogumia, Eubacterium dolichum* DSM 3991, *Clostridium* sp. PPf35E6, *Clostridium sordelli* ATCC 9714, *Ruminococcus torques, Ruminococcus gnavus, Clostridium clostridioforme, Ruminococcus obeum, Blautia producta, Clostridium* sp. ID5, *Megasphaera micronuciformis, Veillonella parvula, Clostridium methylpentosum, Clostridium islandicum, Faecalibacterium prausnitzii, Bacteroides uniformmis, Bacteroides thetaiotaomicron, Bacteroides acidifaciens, Bacteroides ovatus, Bacteroides fragilis, Parabacteroides distasonis, Propinionibacteirum propionicum, Actinomycs hyovaginalis, Rothia mucilaginosa, Rothia aeria, Bifidobacterium breve, Scardovia inopinata* and *Eggerthella lenta.*

[0207] Preferred bacterial species are provided in Table 1, Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, Table 1F, and Table 5. Optionally, in some embodiments, preferred bacterial species are spore formers. Where specific strains of a species are provided, one of skill in the art will recognize that other strains of the species can be substituted for the named strain.

[0208] In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acidaminococcus intestine*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter baumannii*. In one embodiment, the bacterial entity, e.g., species

or strain, useful in the compositions and methods of the invention is *Acinetobacter lwoffii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Akkermansia muciniphila*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes putredinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes shahii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerostipes hadrus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerotruncus colihominis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides caccae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides cellulosilyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides dorei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides eggerthii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides finegoldii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides fragilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides massiliensis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides ovatus*. *In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bacteroides salanitronis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides salyersiae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. D20. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides uniformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides vulgatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium adolescentis*. *In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bifidobacterium bifidum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium breve*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium faecale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia glucerasea*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia wexlerae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Catenibacterium mitsuokai*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and

methods of the invention is *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium asparagiforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium bolteae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium clostridioforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium histolyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium indolis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium leptum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium perfringens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 14774. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. HGF2. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium symbiosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella aerofaciens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprobacillus* sp. D7. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus catus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus comes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea formicigenerans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea longicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecium*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Erysipelotrichaceae bacterium 3_1_53. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli* 588. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium eligens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium fissicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium ramulus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium rectale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Faecalibacterium prausnitzii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Flavonifractor plautii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium mortiferum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium nucleatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Holdemania filiformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Klebsiella oxytoca*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Lachnospiraceae bacterium 7_1_58FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus rhamnosus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus ruminis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactococcus casei. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Odoribacter splanchnicus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Oscillibacter valericigenes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides gordonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroi-*

des johnsonii. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides merdae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Pediococcus acidilactici*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Propionibacterium granulosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia inulinivorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus gnavus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus* sp. ID8. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus torques*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Slackia piriformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus epidermidis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus saprophyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus cristatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus infantis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus oralis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus sanguinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus viridans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus thermophiles*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Veillonella dispar*.

[0209] In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acidaminococcus intestine*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter baumannii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter lwoffii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Akkermansia muciniphila*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes putredinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes shahii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerostipes hadrus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerotruncus colihominis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides caccae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides cellulosilyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides dorei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides eggerthii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides finegoldii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides fragilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides massiliensis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides ovatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salanitronis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salyersiae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. D20. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides uniformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides vulgatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium adolescentis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium bifidum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium breve*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium faecale*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises

Blautia (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia glucerasea*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia wexlerae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Catenibacterium mitsuokai*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium asparagiforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium bolteae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium clostridioforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium histolyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium indolis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium leptum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium perfringens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 14774. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. HGF2. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium symbiosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella aerofaciens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprobacillus* sp. D7. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus catus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus comes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea formicigenerans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea longicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecium*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli* 588. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium eligens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium fissicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium ramulus*. In one embodiment, the bacterial population useful in the composi-

tions and methods of the invention comprises *Eubacterium* rectale. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Faecalibacterium prausnitzii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Flavonifractor plautii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium mortiferum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium nucleatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Holdemania filiformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Klebsiella oxytoca*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus rhamnosus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus ruminis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactococcus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Odoribacter splanchnicus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Oscillibacter valericigenes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides gordonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides johnsonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides merdae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Pediococcus acidilactici*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Propionibacterium granulosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia inulinivorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus gnavus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus* sp. ID8. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus torques*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Slackia piriformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus epidermidis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus saprophyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus cristatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus infantis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus oralis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus sanguinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus viridans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus thermophiles*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Veillonella dispar*.

[0210] In some embodiments, the therapeutic composition comprises engineered microbes. For example, engineered microbes include microbes harboring i) one or more genetic changes, such change being an insertion, deletion, translocation, or substitution, or any combination thereof, of one or more nucleotides contained on the bacterial chromosome or on an endogenous plasmid, wherein the genetic change may result in the alteration, disruption, removal, or addition of one or more protein coding genes, non-protein-coding genes, gene regulatory regions, or any combination thereof, and wherein such change may be a fusion of two or more separate genomic regions or may be synthetically derived; ii) one or more foreign plasmids containing a mutant copy of an endogenous gene, such mutation being an insertion, deletion, or substitution, or any combination thereof, of one or more nucleotides; and iii) one or more foreign plasmids containing a mutant or non-mutant exogenous gene or a fusion of two or more endogenous, exogenous, or mixed genes. The engineered microbe(s) may be produced using techniques including but not limited to site-directed mutagenesis, transposon mutagenesis, knock-outs, knock-ins, polymerase chain reaction mutagenesis, chemical mutagenesis, ultraviolet light mutagenesis, transformation (chemically or by electroporation), phage transduction, or any combination thereof. Suitable microbes for engineering are known in the art. For example, as described in PCT Publications Nos. WO/93/18163, DELIVERY AND EXPRESSION OF A HYBRID SURFACE PROTEIN ON THE SURFACE OF GRAM POSITIVE BACTERIA; WO/03/06593, METHODS FOR TREATING CANCER BY ADMINISTERING TUMOR-TARGETTED BACTERIA AND AN IMMUNOMODULATORY AGENT; and WO/2010/141143, ENGINEERED AVIRULENT BACTERIA STRAINS AND USE IN MEDICAL TREATMENTS.

[0211] In some embodiments, the engineered microbes are natural human commensals. In other embodiments, the engineered microbes are attenuated strains of pathogens, and may include, but are not limited to, *Pseudomonas aeruginosa, Salmonella* species, *Listeria monocytogenes, Mycoplasma hominis, Escherichia coli, Shigella* species, and *Streptococcus* species, see, e.g. PCT Publications No. WO/03/06593, METHODS FOR TREATING CANCER BY ADMINISTERING TUMOR-TARGETTED BACTERIA AND AN IMMUNOMODULATORY AGENT. Attenuated strains of pathogens will lack all or parts of virulence operons, may lack immune-stimulatory surface moieties (e.g. lipopolysaccharide for Gram-negative bacteria), and may contain one or more nutrient auxotrophies. In specific embodiments, the engineered microbes are attenuated intracellular pathogens, such as avirulent strains of *Listeria monocytogenes*.

[0212] In some embodiments, the composition of the invention comprises one or more types of microbe capable of producing butyrate in a mammalian subject. Butyrate-producing microbes may be identified experimentally, such as by NMR or gas chromatography analyses of microbial products or colorimetric assays (Rose I A. 1955. Methods Enzymol. Acetate kinase of bacteria. 1: 591-5). Butyrate-producing microbes may also be identified computationally, such as by the identification of one or more enzymes involved in butyrate synthesis. Non-limiting examples of enzymes found in butyrate-producing microbes include butyrate kinase, phosphotransbutyrylase, and butyryl CoA:acetate CoA transferase (Louis P., et al. 2004. Restricted Distribution of the Butyrate Kinase Pathway among Butyrate-Producing Bacteria from the Human Colon. J Bact. 186(7): 2099-2106). Butyrate-producing strains include, but are not limited to, *Faecalibacterium prausnitzii, Eubacterium* spp., *Butyrivibrio fibrisolvens, Roseburia intestinalis, Clostridium* spp., *Anaerostipes caccae*, and *Ruminococcus* spp. In some embodiments, the composition comprises two or more types of microbe, wherein at least two types of microbe are capable of producing butyrate in a mammalian subject. In other embodiments, the composition comprises two or more types of microbe, wherein two or more types of microbe cooperate (i.e., cross-feed) to produce an immunomodulatory SCFA (e.g., butyrate) in a mammalian subject. In a preferred embodiment, the composition comprises at least one type of microbe (e.g., *Bifidobacterium* spp.) capable of metabolizing a prebiotic, including but not limited to, inulin, inulin-type fructans, or oligofructose, such that the resulting metabolic product may be converted by a second type of microbe (e.g., a butyrate-producing microbe such as *Roseburia* spp.) to an immunomodulatory SCFA such as butyrate (Falony G., et al. 2006. Cross-Feeding between *Bifidobacterium longum* BB536 and Acetate-Converting, Butyrate-Producing Colon Bacteria during Grown on Oligofructose. Appl. Environ. Microbiol. 72(12): 7835-7841.) In other aspects, the composition comprises at least one acetate-producing microbe (e.g., *Bacteroides thetaiotaomicron*) and at least one acetate-consuming, butyrate-producing microbe (e.g., *Faecalibacterium prausnitzii*).

[0213] In some embodiments, the composition comprises one or more types of microbe capable of producing propionate in a mammalian subject, optionally further comprising a prebiotic or substrate appropriate for proprionate biosynthesis. Examples of prebiotics or substrates used for the production of propionate include, but are not limited to, L-rhamnose, D-tagalose, resistant starch, inulin, polydextrose, arabinoxylans, arabinoxylan oligosaccharides, mannooligosaccharides, and laminarans (Hosseini E., et al. 2011. Propionate as a health-promoting microbial metabolite in the human gut. Nutrition Reviews. 69(5): 245-258). Propionate-producing microbes may be identified experimentally, such as by NMR or gas chromatography analyses of microbial products or colorimetric assays (Rose I A. 1955. Methods Enzymol. Acetate kinase of bacteria. 1: 591-5). Propionate-producing microbes may also be identified computationally, such as by the identification of one or more enzymes involved in propionate synthesis. Non-limiting examples of enzymes found in propionate-producing microbes include enzymes of the succinate pathway, including but not limited to phophoenylpyrvate carboxykinase, pyruvate kinase, pyruvate carboxylase, malate dehydrogenase, fumarate hydratase, succinate dehydrogenase, succinyl CoA synthetase, methylmalonyl Coa decarboxylase, and propionate CoA transferase, as well as enzymes of the acrylate pathway, including but not limited to L-lactate dehydrogenase, propionate CoA transferase, lactoyl CoA dehydratase, acyl CoA dehydrogenase, phosphate acetyltransferase, and propionate kinase. Non-limiting examples of microbes that utilize the succinate pathway are *Bacteroides fragilis* and other species (including *B. vulgatus*), *Propionibacterium* spp. (including *freudenrichii* and *acidipropionici*), *Veillonella* spp. (including *gazogenes*), *Micrococcus lactilyticus, Selenomonas ruminantium, Escherichia coli*, and *Prevotella ruminocola*. Non-limiting examples of microbes that utilize the acrylate pathway are *Clostridium neopropionicum* X4, and *Megasphaera elsdenii*.

[0214] In preferred embodiments, the combination of a microbe or microbial composition and a prebiotic is selected based on the fermentation or metabolic preferences of one or more microbes capable of producing immunomodulatory SCFAs (e.g., preference for complex versus simple sugar or preference for a fermentation product versus a prebiotic). For example, *M. eldsenii* prefers lactate fermentation to glucose fermentation, and maximization of propionate production by *M. eldsenii* in a mammalian subject may therefore be achieved by administering along with *M. eldsenii* a favored substrate (e.g., lactate) or one or more microbes capable of fermenting glucose into lactate (e.g., *Streptococcus bovis*) (Hosseini E., et al. 2011. Propionate as a health-promoting microbial metabolite in the human gut. Nutrition Reviews. 69(5): 245-258). Thus, in some embodiments, the composition comprises at least one type of SCFA-producing microbe and a sugar fermentation product (e.g., lactate). In other embodiments, the composition comprises at least one type of SCFA-producing microbe and at least one type of sugar-fermenting microbe, wherein the fermentation product of the second, sugar-fermenting microbe is the preferred substrate of the SCFA-producing microbe.

[0215] Immunomodulation can also be achieved by the microbial production of glutathione or gamma-glutamylcysteine. Thus, in certain embodiments, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe capable of producing glutathione and/or gamma-glutamylcysteine in a mammalian subject. In some aspects, the composition comprises one or more microbes selected for the presence of glutamate cysteine ligase (e.g., *Lactobacillus fermentum*) and/or L-proline biosynthesis enzymes (e.g., *E. coli*) (Peran et al., 2006. *Lactobacillus fermenum*, a probiotic capable to release glutathione, prevents colonic inflammation in the TNBS model of rat colitis. Int J Colorectal Dis. 21(8):

737-746; Veeravalli et al., 2011. Laboratory evolution of glutathione biosynthesis reveals naturally compensatory pathways. Nat Chem Bio. 7(2): 101-105). In a preferred embodiment, at least one microbe in the composition is *L. fermentum.*

[0216] para-cresol (p-cresol) is a microbial product, via the fermentation of tyrosine or phenylalanine. Sulfated in the liver or colon to p-cresyl sulfate, this molecule reduces Th1-mediated responses (Shiba T. et al. 2014. Effects of intestinal bacteria-derived p-cresyl sulfate on Th1-type immune response in vivo and in vitro. Tox and Applied Pharm. 274(2): 191-199). In some embodiments, the composition comprises at least one type of microbe capable of fermenting tyrosine and/or phenylalanine to p-cresol in a mammalian subject. Non-limiting examples of such microbes include *Bacteroides fragilis, Clostridium difficile*, and *Lactobacillus* sp. Strain #11198-11201 (Yokoyama M T and Carlson J R. 1981. Production of Skatole and para-Cresol by a Rumen *Lactobacillus* sp. Applied and Environmental Microbiology. 41(1): 71-76.), and other microbes with p-hydroxylphenyl acetate decarboxylase activity.

IV. Methods of Making/Isolating Probiotic Compositions

[0217] In one embodiment, provided herein are therapeutic compositions containing a purified population of bacterial entities and/or fungal entities. The purified population can contain a single species, or multiple species. As used herein, the terms "purify", "purified" and "purifying" refer to the state of a population (e.g., a plurality of known or unknown amount and/or concentration) of desired bacterial entities and/or fungal entities, that have undergone one or more processes of purification, e.g., a selection or an enrichment of the desired bacterial, or alternatively a removal or reduction of residual habitat products as described herein. In some embodiments, a purified population has no detectable undesired activity or, alternatively, the level or amount of the undesired activity is at or below an acceptable level or amount. In other embodiments, a purified population has an amount and/or concentration of desired bacterial entities and/or fungal entities at or above an acceptable amount and/or concentration. In other embodiments, the ratio of desired-to-undesired activity (e.g., spores compared to vegetative bacteria), has changed by 2-, 5-, 10-, 30-, 100-, 300-, 1×10^4, 1×10^5, 1×10^6, 1×10^7, 1×10^8, or greater than 1×10^8. In other embodiments, the purified population of bacterial entities and/or fungal entities is enriched as compared to the starting material (e.g., a fecal material) from which the population is obtained. This enrichment may be by 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99%, 99.999%, 99.9999%, 99.9999%, or greater than 99.999999% as compared to the starting material.

[0218] In certain embodiments, the purified populations of bacterial entities and/or fungal entities have reduced or undetectable levels of one or more pathogenic activities, such as toxicity, an ability to cause infection of the mammalian recipient subject, an undesired immunomodulatory activity, an autoimmune response, a metabolic response, or an inflammatory response or a neurological response. Such a reduction in a pathogenic activity may be by 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99%, 99.999%, 99.9999%, or greater than 99.9999% as compared to the starting material. In other embodiments, the purified populations of bacterial entities and/or fungal entities have reduced sensory components as compared to fecal material, such as reduced odor, taste, appearance, and umami.

[0219] In another embodiment, the invention provides purified populations of bacterial entities and/or fungal entities that are substantially free of residual habitat products. In certain embodiments, this means that the bacterial composition no longer contains a substantial amount of the biological matter associated with the microbial community while living on or in the human or animal subject, and the purified population of spores may be 100% free, 99% free, 98% free, 97% free, 96% free, 95% free, 94% free, 93% free, 92% free, 91% free, 90% free, 85% free, 80% free, 75% free, 70% free, 60% free, or 50% free of any contamination of the biological matter associated with the microbial community. Substantially free of residual habitat products may also mean that the bacterial composition contains no detectable cells from a human or animal, and that only microbial cells are detectable, in particular, only desired microbial cells are detectable. In another embodiment, it means that fewer than 1×10^{-2}%, 1×10^{-3}%, 1×10^{-4}%, 1×10^{-5}%, 1×10^{-6}%, 1×10^{-7}%, 1×10^{-8}% of the cells in the bacterial composition are human or animal, as compared to microbial cells. In another embodiment, the residual habitat product present in the purified population is reduced at least a certain level from the fecal material obtained from the mammalian donor subject, e.g., reduced by at least about 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98%, 99%, 99.9%, 99.99%, 99.999%, 99.9999%, or greater than 99.9999%.

[0220] In one embodiment, substantially free of residual habitat products or substantially free of a detectable level of a pathogenic material means that the bacterial composition contains no detectable viral (including bacterial viruses (i.e., phage)), fungal, or mycoplasmal or toxoplasmal contaminants, or a eukaryotic parasite such as a helminth. Alternatively, the purified spore populations are substantially free of an acellular material, e.g., DNA, viral coat material, or non-viable bacterial material. Alternatively, the purified spore population may processed by a method that kills, inactivates, or removes one or more specific undesirable viruses, such as an enteric virus, including norovirus, poliovirus or hepatitis A virus.

[0221] As described herein, purified spore populations can be demonstrated by, for example, genetic analysis (e.g., PCR, DNA sequencing), serology and antigen analysis, microscopic analysis, microbial analysis including germination and culturing, or methods using instrumentation such as flow cytometry with reagents that distinguish desired bacterial entities and/or fungal entities from non-desired, contaminating materials.

[0222] In one embodiment, the spore preparation comprises spore-forming species wherein residual non-spore forming species have been inactivated by chemical or physical treatments including ethanol, detergent, heat, sonication, and the like; or wherein the non-spore forming species have been removed from the spore preparation by various separations steps including density gradients, centrifugation, filtration and/or chromatography; or wherein inactivation and separation methods are combined to make the spore preparation. In yet another embodiment, the spore preparation comprises spore-forming species that are enriched over viable non-spore formers or vegetative forms of spore formers. In this embodiment, spores are enriched by 2-fold, 5-fold, 10-fold, 50-fold, 100-fold, 1000-fold, 10,000-fold or greater

than 10,000-fold compared to all vegetative forms of bacteria. In yet another embodiment, the spores in the spore preparation undergo partial germination during processing and formulation such that the final composition comprises spores and vegetative bacteria derived from spore forming species.

[0223] In another embodiment, provided herein are methods for production of a composition, e.g., a probiotic composition, comprising a bacterial population, e.g., an anti-inflammatory bacterial population, or a fungal population, with or without one or more prebiotic, suitable for therapeutic administration to a mammalian subject in need thereof. In one embodiment, the composition can be produced by generally following the steps of: (a) providing a fecal material obtained from a mammalian donor subject; and (b) subjecting the fecal material to at least one purification treatment or step under conditions such that a population of bacterial entities and/or fungal entities is produced from the fecal material.

[0224] Individual bacterial strains can also be isolated from stool samples using culture methods. For example, 5 mls of phosphate-buffered saline (PBS) is added to 1 mg of frozen stool sample and homogenized by vortexing in an anaerobic chamber for isolation of anaerobic bacteria. The suspension is then serially diluted ten-fold (e.g. 10^{-1} to 10^{-9} dilutions) and 100 □l aliquots of each dilution are spread evenly over the surface of agar plates containing different formulations e.g. anaerobic blood agar plates, *Bacteroides* bile esculin plates, laked kanamycin vancomycin plates, egg yolk agar plates and de Man Rogosa and Sharpe agar plates. Inverted plates are incubated in an anaerobic chamber for 48 hr+/−4 hours. Colonies with different morphologies are picked and replated on anaerobic blood agar plates for further testing, PCR analysis and 16 S sequencing. Selected bacterial strains can be grown for therapeutic use singly or in combination.

[0225] In one embodiment, a probiotic composition of the invention is not a fecal transplant. In some embodiments all or essentially all of the bacterial entitites present in a purified population are originally obtained from a fecal material and subsequently, e.g., for production of pharmaceutical compositions, are grown in culture as described herein or otherwise known in the art. In one embodiment, the bacterial cells are cultured from a bacterial stock and purified as described herein. In one embodiment, each of the populations of bacterial cells are independently cultured and purified, e.g., each population is cultured separately and subsequently mixed together. In one embodiment, one or more of the populations of bacterial cells in the composition are co-cultured.

[0226] Donor Materials and Screening

[0227] Typically, bacteria and fungi are derived from biological samples, which may include one or more micriobiotal populations. Exemplary biological samples include fecal materials such as feces or materials isolated from the various segments of the small and large intestine. Fecal materials are obtained from a mammalian donor subject, or can be obtained from more than one donor subject, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, 100, 200, 300, 400, 500, 750, 1000 or from greater than 1000 donors, where such materials are then pooled prior to purification of the desired bacterial entities and/or fungal entities. In another embodiment, fecal materials can be obtained from a single donor subject over multiple times and pooled from multiple samples, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 32, 35, 40, 45, 48, 50, 100 samples from a single donor.

[0228] In alternative embodiments, the desired bacterial entities and/or fungal entities are purified from a single fecal material sample obtained from a single donor, and after such purification are combined with purified spore populations from other purifications, either from the same donor at a different time, or from one or more different donors, or both.

[0229] In some embodiments, all or essentially all of the bacterial entities and/or fungal entities present in a purified population are obtained from a fecal material treated as described herein or otherwise known in the art. In some embodiments all or essentially all of the bacterial entitites and/or fungal entities present in a purified population are obtained from a fecal material and subsequently are grown in culture as described herein or otherwise known in the art. In alternative embodiments, one or more than one bacterial entities and/or fungal entities or types of bacterial entities and/or fungal entities are generated in culture and combined to form a purified spore population. In other alternative embodiments, one or more of these culture-generated spore populations are combined with a fecal material-derived spore population to generate a hybrid spore population.

[0230] Preferably the biological sample includes a fecal material, such as obtained from a healthy mammalian donor subject or a plurality of mammalian donor subjects. In some embodiments, the biological material is not a fecal sample. Other appropriate biological samples include, but are not limited to, vaginal or cervical swabs, skin swabs, and bronchoalveolar lavage fluid (BALF).

[0231] In some embodiments, mammalian donor subjects are generally of good health and have microbiota consistent with such good health. In one embodiment, the donor subjects have not been administered antibiotic compounds within a certain period prior to the collection of the fecal material. In certain embodiments, the donor subjects are not obese or overweight, and may have body mass index (BMI) scores of below 25, such as between 18.5 and 24.9. In other embodiments, the donor subjects are not mentally ill or have no history or familial history of mental illness, such as anxiety disorder, depression, bipolar disorder, autism spectrum disorders, schizophrenia, panic disorders, attention deficit (hyperactivity) disorders, eating disorders or mood disorders. In other embodiments, the donor subjects do not have Irritable Bowel Disease (e.g., crohn's disease, ulcerative colitis), irritable bowel syndrome, celiac disease, colorectal cancer or a family history of these diseases. In other embodiments, donors have been screened for blood borne pathogens and fecal transmissible pathogens using standard techniques known to one in the art (e.g., nucleic acid testing, serological testing, antigen testing, culturing techniques, enzymatic assays, assays of cell free fecal filtrates looking for toxins on susceptible cell culture substrates).

[0232] In some embodiments, donors are also selected for the presence of certain genera and/or species that provide increased efficacy of therapeutic compositions containing these genera or species. In other embodiments, donors are preferred that produce relatively higher concentrations of spores in fecal material than other donors. In further embodiments, donors are preferred that provide fecal material from which spores having increased efficacy are purified; this increased efficacy is measured using in vitro or in animal studies as described below. In some embodiments, the donor may be subjected to one or more pre-donation treatments in order to reduce undesired material in the fecal material, and/or increase desired spore populations.

[0233] In one embodiment, it is advantageous to screen the health of the donor subject prior to and optionally, one or

more times after, the collection of the fecal material. Such screening identifies donors carrying pathogenic materials such as viruses (HIV, hepatitis, polio) and pathogenic bacteria. Post-collection, donors are screened about one week, two weeks, three weeks, one month, two months, three months, six months, one year or more than one year, and the frequency of such screening may be daily, weekly, bi-weekly, monthly, bi-monthly, semi-yearly or yearly. Donors that are screened and do not test positive, either before or after donation or both, are considered "validated" donors.

[0234] Methods for Purifying Spores

[0235] In one embodiment, treatment of fecal sample includes heating the material, e.g., above 25 degrees Celsius for at least 30 seconds, and/or contacting the material with a solvent, and/or and or contacting a chemical or providing a physical manipulation of the material. Culture of fecal material includes replicating the purified population in a liquid suspension and/or a solid medium. Optionally, one removes at least a portion of an acellular component of the fecal material, thereby separating immunomodulatory bacteria from acellular material. The treatment step may also include depleting or inactivating a pathogenic material.

[0236] Solvent Treatments.

[0237] The bacteria and/or fungi may contain a purified population obtained from a miscible solvent treatment of the fecal material or a fraction or derivative thereof. In one embodiment, to purify the bacterial entities and/or fungal entities, the fecal material can be subjected to one or more solvent treatments. A solvent treatment is a miscible solvent treatment (either partially miscible or fully miscible) or an immiscible solvent treatment. Miscibility is the ability of two liquids to mix with each to form a homogeneous solution. Water and ethanol, for example, are fully miscible such that a mixture containing water and ethanol in any ratio will show only one phase. Miscibility is provided as a wt/wt %, or weight of one solvent in 100 g of final solution. If two solvents are fully miscible in all proportions, their miscibility is 100%. Provided as fully miscible solutions with water are alcohols, e.g., methanol, ethanol, isopropanol, butanol, propanediol, butanediol, etc. The alcohols can be provided already combined with water; e.g., a solution containing 10%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 89%, 85%, 90%, 95% or greater than 95% water. Other solvents are only partially miscible, meaning that only some portion will dissolve in water. Diethyl ether, for example, is partially miscible with water. Up to 7 grams of diethyl ether will dissolve in 93 grams of water to give a 7% (wt/wt %) solution. If more diethyl ether is added, a two-phase solution will result with a distinct diethyl ether layer above the water. Other partially miscible materials include ethers, propanoate, butanoate, chloroform, dimethoxyethane, or tetrahydrofuran. In contrast, an oil such as an alkane and water are immiscible and form two phases. Further, immiscible treatments are optionally combined with a detergent, either an ionic detergent or a non-ionic detergent. Exemplary detergents include Triton X-100, Tween 20, Tween 80, Nonidet P40, a pluronic, or a polyol.

[0238] In one embodiment, the solvent treatment steps reduces the viability of non-spore forming bacterial species by 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95%, 99%, 99.9%, 99.99%, 99.999%, or 99.9999%, and it may optionally reduce the viability of contaminating protists, parasites and/or viruses.

[0239] Chromatography Treatments.

[0240] To purify spore populations, the fecal materials may be subjected to one or more chromatographic treatments, either sequentially or in parallel. In a chromatographic treatment, a solution containing the fecal material is contacted with a solid medium containing a hydrophobic interaction chromatographic (HIC) medium or an affinity chromatographic medium. In an alternative embodiment, a solid medium capable of absorbing a residual habitat product present in the fecal material is contacted with a solid medium that adsorbs a residual habitat product. In certain embodiments, the HIC medium contains sepharose or a derivatized sepharose such as butyl sepharose, octyl sepharose, phenyl sepharose, or butyl-s sepharose. In other embodiments, the affinity chromatographic medium contains material derivatized with mucin type I, II, III, IV, V, or VI, or oligosaccharides derived from or similar to those of mucins type I, II, III, IV, V, or VI. Alternatively, the affinity chromatographic medium contains material derivatized with antibodies that recognize immunomodulatory bacteria.

[0241] Mechanical Treatments.

[0242] In one embodiment, the fecal material can be physically disrupted, particularly by one or more mechanical treatment such as blending, mixing, shaking, vortexing, impact pulverization, and sonication. As provided herein, the mechanical disrupting treatment substantially disrupts a non-spore material present in the fecal material and does not substantially disrupt a spore present in the fecal material, or it may disrupt the spore material less than the non-spore material, e.g., 2-fold less, 5-, 10-, 30-, 100-, 300-, 1000- or greater than 1000-fold less. Furthermore, mechanical treatment homogenizes the material for subsequent sampling, testing, and processing. Mechanical treatments optionally include filtration treatments, where the desired spore populations are retained on a filter while the undesirable (non-spore) fecal components to pass through, and the spore fraction is then recovered from the filter medium. Alternatively, undesirable particulates and eukaryotic cells may be retained on a filter while bacterial cells including spores pass through. In some embodiments the spore fraction retained on the filter medium is subjected to a diafiltration step, wherein the retained spores are contacted with a wash liquid, typically a sterile saline-containing solution or other diluent such as a water compatible polymer including a low-molecular polyethylene glycol (PEG) solution, in order to further reduce or remove the undesirable fecal components.

[0243] Thermal Treatments.

[0244] In another embodiment, thermal disruption of the fecal material may be utilized. Generally, in one embodiment, the fecal material is mixed in a saline-containing solution such as phosphate-buffered saline (PBS) and subjected to a heated environment, such as a warm room, incubator, water-bath, or the like, such that efficient heat transfer occurs between the heated environment and the fecal material. Preferably the fecal material solution is mixed during the incubation to enhance thermal conductivity and disrupt particulate aggregates. Thermal treatments can be modulated by the temperature of the environment and/or the duration of the thermal treatment. For example, the fecal material or a liquid comprising the fecal material is subjected to a heated environment, e.g., a hot water bath of at least about 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100 or greater than 100 degrees Celsius, for at least about 1, 5, 10, 15, 20, 30, 45 seconds, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, or 50 minutes, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10 or more than 10 hours.

In certain embodiments the thermal treatment occurs at two different temperatures, such as 30 seconds in a 100 degree Celsius environment followed by 10 minutes in a 50 degree Celsius environment. In preferred embodiments the temperature and duration of the thermal treatment are sufficient to kill or remove pathogenic materials while not substantially damaging or reducing the germination-competency of the spores. In other preferred embodiments, the temperature and duration of the thermal treatment is short enough to reduce the germination of the spore population.

[0245] Irradiation Treatments.

[0246] In another embodiment, methods of treating the fecal material or separated contents of the fecal material with ionizing radiation, typically gamma irradiation, ultraviolet irradiation or electron beam irradiation provided at an energy level sufficient to kill pathogenic materials while not substantially damaging the desired spore populations may be used. For example, ultraviolet radiation at 254 nm provided at an energy level below about 22,000 microwatt seconds per cm^2 will not generally destroy desired spores.

[0247] Centrifugation and Density Separation Treatments.

[0248] In one embodiment, desired spore populations may be separated from the other components of the fecal material by centrifugation. For example, a solution containing the fecal material can be subjected to one or more centrifugation treatments, e.g., at about 200×g, 1000×g, 2000×g, 3000×g, 4000×g, 5000×g, 6000×g, 7000×g, 8000×g or greater than 8000×g. Differential centrifugation separates desired spores from undesired non-spore material; at low forces the spores are retained in solution, while at higher forces the spores are pelleted while smaller impurities (e.g., virus particles, phage, microscopic fibers, biological macromolecules such as free protein, nucleic acids and lipids) are retained in solution. For example, a first low force centrifugation pellets fibrous materials; a second, higher force centrifugation pellets undesired eukaryotic cells, and a third, still higher force centrifugation pellets the desired spores while smaller contaminants remain in suspension. In some embodiments density or mobility gradients or cushions (e.g., step cushions), such as CsCl, Percoll, Ficoll, Nycodenz, Histodenz or sucrose gradients, are used to separate desired spore populations from other materials in the fecal material.

[0249] Also provided herein are methods of producing spore populations that combine two or more of the treatments described herein in order to synergistically purify the desired spores while killing or removing undesired materials and/or activities from the spore population. It is generally desirable to retain the spore populations under non-germinating and non-growth promoting conditions and media, in order to minimize the growth of pathogenic bacteria present in the spore populations and to minimize the germination of spores into vegetative bacterial cells.

[0250] The bacteria and/or fungi may contain a spore population, e.g., spores and/or spore-formers, or a population containing vegetative cells.

[0251] Methods for Preparing a Bacterial Composition for Administration to a Subject.

[0252] In one embodiment, methods for producing bacterial compositions can include three main processing steps, combined with one or more mixing steps. For example, the steps can include organism banking, organism production, and preservation.

[0253] For banking, the strains included in the bacterial composition may be (1) isolated directly from a specimen or taken from a banked stock, (2) optionally cultured on a nutrient agar or broth that supports growth to generate viable biomass, and (3) the biomass optionally preserved in multiple aliquots in long-term storage.

[0254] In embodiments that use a culturing step, the agar or broth can contain nutrients that provide essential elements and specific factors that enable growth. An example includes a medium composed of 20 g/L glucose, 10 g/L yeast extract, 10 g/L soy peptone, 2 g/L citric acid, 1.5 g/L sodium phosphate monobasic, 100 mg/L ferric ammonium citrate, 80 mg/L magnesium sulfate, 10 mg/L hemin chloride, 2 mg/L calcium chloride, 1 mg/L menadione. A variety of microbiological media and variations are well known in the art (e.g. R. M. Atlas, *Handbook of Microbiological Media* (2010) CRC Press). Medium can be added to the culture at the start, may be added during the culture, or may be intermittently/continuously flowed through the culture. The strains in the bacterial composition may be cultivated alone, as a subset of the bacterial composition, or as an entire collection comprising the bacterial composition. As an example, a first strain may be cultivated together with a second strain in a mixed continuous culture, at a dilution rate lower than the maximum growth rate of either cell to prevent the culture from washing out of the cultivation.

[0255] The inoculated culture may be incubated under favorable conditions for a time sufficient to build biomass. For bacterial compositions for human use, this may be at 37° C., with pH, and other parameters having values similar to the normal human niche. The environment can be actively controlled, passively controlled (e.g., via buffers), or allowed to drift. For example, for anaerobic bacterial compositions (e.g., gut microbiota), an anoxic/reducing environment can be employed. This can be accomplished by addition of reducing agents such as cysteine to the broth, and/or stripping it of oxygen. As an example, a culture of a bacterial composition can be grown at 37° C., pH 7, in the medium above, pre-reduced with 1 g/L cysteine-HCl.

[0256] In one embodiment, when the culture has generated sufficient biomass, it can be preserved for banking. The organisms can be placed into a chemical milieu that protects from freezing (adding 'cryoprotectants'), drying ('lyoprotectants'), and/or osmotic shock ('osmoprotectants'), dispensing into multiple (optionally identical) containers to create a uniform bank, and then treating the culture for preservation. In one embodiment, containers can be generally impermeable and have closures that assure isolation from the environment. Cryopreservation treatment can be accomplished by freezing a liquid at ultra-low temperatures (e.g., at or below −80° C.). Dried preservation removes water from the culture by evaporation (in the case of spray drying or 'cool drying') or by sublimation (e.g., for freeze drying, spray freeze drying). Removal of water improves long-term bacterial composition storage stability at temperatures elevated above cryogenic. If the bacterial composition comprises spore forming species and results in the production of spores, the final composition can be purified by additional means, such as density gradient centrifugation preserved using the techniques described above. Bacterial composition banking can be done by culturing and preserving the strains individually, or by mixing the strains together to create a combined bank. As an example of cryopreservation, a bacterial composition culture can be harvested by centrifugation to pellet the cells from the culture medium, the supernate decanted and replaced with fresh culture broth containing 15% glycerol.

The culture can then be aliquoted into 1 mL cryotubes, sealed, and placed at −80° C. for long-term viability retention. This procedure achieves acceptable viability upon recovery from frozen storage.

[0257] Organism production can be conducted using similar culture steps to banking, including medium composition and culture conditions. In one embodiment, it can be conducted at larger scales of operation, especially for clinical development or commercial production. At larger scales, there can be several subcultivations of the bacterial composition prior to the final cultivation. At the end of cultivation, the culture can be harvested to enable further formulation into a dosage form for administration. This can involve concentration, removal of undesirable medium components, and/or introduction into a chemical milieu that preserves the bacterial composition and renders it acceptable for administration via the chosen route. For example, a bacterial composition can be cultivated to a concentration of 10^{10} CFU/mL, then concentrated 20-fold by tangential flow microfiltration; the spent medium can be exchanged by diafiltering with a preservative medium consisting of s2% gelatin, 100 mM trehalose, and 10 mM sodium phosphate buffer. The suspension can then be freeze-dried to a powder and titrated.

[0258] In one embodiment, after drying, the powder can be blended to an appropriate potency, and mixed with other cultures and/or a filler such as microcrystalline cellulose for consistency and ease of handling, and the bacterial composition formulated as provided herein.

[0259] Methods of Characterization of Compositions

[0260] In certain embodiments, methods are provided for testing certain characteristics of compositions comprising microbes or microbes and prebiotics. For example, the sensitivity of bacterial compositions to certain environmental variables is determined, e.g., in order to select for particular desirable characteristics in a given composition, formulation and/or use. For example, the bacterial constituents of the composition can be tested for pH resistance, bile acid resistance, and/or antibiotic sensitivity, either individually on a constituent-by-constituent basis or collectively as a bacterial composition comprised of multiple bacterial constituents (collectively referred to in this section as bacterial composition).

[0261] pH Sensitivity Testing.

[0262] If a microbial composition, with or without prebiotic, will be administered other than to the colon or rectum (i.e., for example, an oral route), optionally testing for pH resistance enhances the selection of microbes or therapeutic compositions that will survive at the highest yield possible through the varying pH environments of the distinct regions of the GI tract or vagina. Understanding how the bacterial compositions react to the pH of the GI tract or vagina also assists in formulation, so that the number of microbes in a dosage form can be increased if beneficial and/or so that the composition may be administered in an enteric-coated capsule or tablet or with a buffering or protective composition.

[0263] As the pH of the stomach can drop to a pH of 1 to 2 after a high-protein meal for a short time before physiological mechanisms adjust it to a pH of 3 to 4 and often resides at a resting pH of 4 to 5, and as the pH of the small intestine can range from a pH of 6 to 7.4, bacterial compositions can be prepared that survive these varying pH ranges (specifically wherein at least 1%, 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, or as much as 100% of the bacteria can survive gut transit times through various pH ranges). This can be tested by exposing the bacterial composition to varying pH ranges for the expected gut transit times through those pH ranges. Therefore, as a nonlimiting example only, 18-hour cultures of compositions comprising one or more bacterial species or strains can be grown in standard media, such as gut microbiota medium ("GMM", see Goodman et al., Extensive personal human gut microbiota culture collections characterized and manipulated in gnotobiotic mice, PNAS 108(15):6252-6257 (2011)) or another animal-products-free medium, with the addition of pH adjusting agents for a pH of 1 to 2 for 30 minutes, a pH of 3 to 4 for 1 hour, a pH of 4 to 5 for 1 to 2 hours, and a pH of 6 to 7.4 for 2.5 to 3 hours. An alternative method for testing stability to acid is described in U.S. Pat. No. 4,839,281. Survival of bacteria may be determined by culturing the bacteria and counting colonies on appropriate selective or non-selective media.

[0264] Bile Acid Sensitivity Testing.

[0265] Additionally, in some embodiments, testing for bile-acid resistance enhances the selection of microbes or therapeutic compositions that will survive exposures to bile acid during transit through the GI tract or vagina. Bile acids are secreted into the small intestine and can, like pH, affect the survival of bacterial compositions. This can be tested by exposing the compositions to bile acids for the expected gut exposure time to bile acids. For example, bile acid solutions can be prepared at desired concentrations using 0.05 mM Tris at pH 9 as the solvent. After the bile acid is dissolved, the pH of the solution may be adjusted to 7.2 with 10% HCl. Bacterial components of the therapeutic compositions can be cultured in 2.2 ml of a bile acid composition mimicking the concentration and type of bile acids in the patient, 1.0 ml of 10% sterile-filtered feces media and 0.1 ml of an 18-hour culture of the given strain of bacteria. Incubations may be conducted for from 2.5 to 3 hours or longer. An alternative method for testing stability to bile acid is described in U.S. Pat. No. 4,839,281. Survival of bacteria may be determined by culturing the bacteria and counting colonies on appropriate selective or non-selective media.

[0266] Antibiotic Sensitivity Testing.

[0267] As a further optional sensitivity test, the bacterial components of the microbial compositions, with or without prebiotics, can be tested for sensitivity to antibiotics. In one embodiment, the bacterial components can be chosen so that they are sensitive to antibiotics such that if necessary they can be eliminated or substantially reduced from the patient's gastrointestinal tract or vagina by at least one antibiotic targeting the bacterial composition.

[0268] Adherence to Gastrointestinal Cells.

[0269] The compositions may optionally be tested for the ability to adhere to gastrointestinal cells. A method for testing adherence to gastrointestinal cells is described in U.S. Pat. No. 4,839,281.

[0270] Identification of Immunomodulatory Bacteria.

[0271] In some embodiments, immunomodulatory bacteria are identified by the presence of nucleic acid sequences that modulate sporulation. In particular, signature sporulation genes are highly conserved across members of distantly related genera including *Clostridium* and *Bacillus*. Traditional approaches of forward genetics have identified many, if not all, genes that are essential for sporulation (spo). The developmental program of sporulation is governed in part by the successive action of four compartment-specific sigma factors (appearing in the order σF, σE, σG and σK), whose

activities are confined to the forespore (σF and σG) or the mother cell (σE and σK). In other embodiments, immunomodulatory bacteria are identified by the biochemical activity of DPA producing enzymes or by analyzing DPA content of cultures. As part of the bacterial sporulation, large amounts of DPA are produced, and comprise 5-15% of the mass of a spore. Because not all viable spores germinate and grow under known media conditions, it is difficult to assess a total spore count in a population of bacteria. As such, a measurement of DPA content highly correlates with spore content and is an appropriate measure for characterizing total spore content in a bacterial population.

[0272] In other embodiments, immunomodulatory bacteria are identified by screening bacteria to determine whether the bacteria induce secretion of pro-inflammatory or anti-inflammatory cytokines by host cells. For example, human or mammalian cells capable of cytokine secretion, such as immune cells (e.g., PBMCs, macrophages, T cells, etc.) can be exposed to candidate immunomodulatory bacteria, or supernatants obtained from cultures of candidate immunomodulatory bacteria, and changes in cytokine expression or secretion can be measured using standard techniques, such as ELISA, immunoblot, Luminex, antibody array, quantitative PCR, microarray, etc. Bacteria can be selected for inclusion in a probiotic composition based on the ability to induce a desired cytokine profile in human or mammalian cells. For example, anti-inflammatory bacteria can be selected for inclusion in a probiotic composition based on the ability to induce secretion of one or more anti-inflammatory cytokines, and/or the ability to reduce secretion of one or more pro-inflammatory cytokines. Anti-inflammatory cytokines include, for example, IL-10, IL-13, IL-9, IL-4, IL-5, and combinations thereof. Other inflammatory cytokines include, for example, TGFβ. Pro-inflammatory cytokines include, for example, IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. In some embodiments, anti-inflammatory bacteria may be selected for inclusion in a probiotic composition based on the ability to modulate secretion of one or more anti-inflammatory cytokines and/or the ability to reduce secretion of one or more pro-inflammatory cytokines by a host cell induced by a bacteria of a different type (e.g., a bacteria from a different species or from a different strain of the same species).

[0273] In other embodiments, immunomodulatory bacteria are identified by screening bacteria to determine whether the bacteria impact the differentiation and/or expansion of particular subpopulations of immune cells. For example, candidate bacteria can be screened for the ability to promote differentiation and/or expansion of Treg cells, Th17 cells, Th1 cells and/or Th2 cells from precursor cells, e.g. naive T cells. By way of example, naïve T cells can be cultured in the presence of candidate bacteria or supernatants obtained from cultures of candidate bacteria, and numbers of Treg cells, Th17 cells, Th1 cells and/or Th2 cells can be determined using standard techniques, such as FACS analysis. Markers indicative of Treg cells include, for example, $CD25^{+}CD127^{lo}$. Markers indicative of Th17 cells include, for example, $CXCR3^{-}CCR6^{+}$. Markers indicative of Th1 cells include, for example, $CXCR3^{+}CCR6^{-}$. Markers indicative of Th2 cells include, for example, $CXCR3^{-}CCR6^{-}$. Other markers indicative of particular T cells subpopulations are known in the art, and may be used in the assays described herein, e.g., to identify populations of immune cells impacted by candidate immunomodulatory bacteria. Bacteria can be selected for inclusion in a probiotic composition based on the ability to promote differentiation and/or expansion of a desired immune cell subpopulation.

[0274] In other embodiments, immunomodulatory bacteria are identified by screening bacteria to determine whether the bacteria secrete short chain fatty acids (SCFA), such as, for example, butyrate, acetate, propionate, or valerate, or combinations thereof. For example, secretion of short chain fatty acids into bacterial supernatants can be measured using standard techniques. In one embodiment, bacterial supernatants can be screened to measure the level of one or more short chain fatty acids using NMR, mass spectrometry (e.g., GC-MS, tandem mass spectrometry, matrix-assisted laser desorption/ionization, etc.), ELISA, or immunoblot. Expression of bacterial genes responsible for production of short chain fatty acids can also be determined by standard techniques, such as Northern blot, microarray, or quantitative PCR.

V. Mixtures of Bacteria and Microbial Networks

[0275] In one embodiment, provided herein are spore populations containing more than one type of bacterium. As used herein, a "type" or more than one "types" of bacteria may be differentiated at the genus level, the species level, the subspecies level, the strain level or by any other taxonomic method, as described herein and otherwise known in the art.

[0276] In one embodiment, the microbial, e.g., probiotic, population comprises a single microbial preparation or a combination of microbial preparations, wherein each microbial preparation can be purified from a fecal material obtained from a single mammalian donor subject, or from two or more donor subjects.

[0277] In some embodiments, all or essentially all of the bacterial entities and/or fungal entities present in an isolated population are obtained from a fecal material treated as described herein or otherwise known in the art. In alternative embodiments, one or more than one bacterial entities and/or fungal entities or types of bacterial entities and/or fungal entities are generated in culture and combined to form a purified spore population. In other alternative embodiments, one or more of these culture-generated spore populations are combined with one or more fecal material-derived spore population to generate a hybrid spore population.

[0278] In a preferred embodiment, a bacterial, e.g., probiotic, composition may contain one or at least two types of preferred bacteria, including strains of the same species or of different species. For instance, a bacterial composition may comprise 1, at least 2, at least 3, or at least 4 types of bacteria. In another embodiment, a bacterial composition may comprise 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 than 20 types of bacteria, as defined by species or operational taxonomic unit (OTU) encompassing such species. In a preferred embodiment, a bacterial composition comprises from 2 to no more than 40, from 2 to no more than 30, from 2 to no more than 20, from 2 to no more than 15, from 2 to no more than 10, from 2 to no more than 5, types of bacteria. In another preferred embodiment, a bacterial composition comprises a single type of bacteria.

[0279] In one embodiment, bacterial compositions may comprise two types of bacteria (termed "binary combinations" or "binary pairs") or greater than two types of bacteria. Bacterial compositions that comprise three types of bacteria are termed "ternary combinations".

[0280] Microbial compositions can comprise two types of microbes or a large number of microbe types. As used herein, a "type" or more than one "types" of microbes may be differentiated at the genus level, the species level, the sub-species level, the strain level or by any other taxonomic method, as described herein and otherwise known in the art. For instance, a microbial composition can 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, at least 20, or at least 21, 22, 23, 24, 25, 26, 27, 28, 29 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, or at least 40, at least 50 or greater than 50 types of microbes, e.g. as defined by species or operational taxonomic unit (OTU), or otherwise as provided herein. In some embodiments, the microbial composition includes at least 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, or greater numbers of types of microbes.

[0281] Alternatively, the number of types of microbes present in a microbial composition is at or below a known value. For example, the microbial composition comprises 1000, 900, 800, 700, 600, 500, 400, 300, 200, 100, 50 or fewer types of microbes, such as 49, 48, 47, 46, 45, 44, 43, 42, 41, 40, 39, 38, 37, 36, 35, 34, 33, 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, or 10 or fewer, or 9 or fewer types of microbes, 8 or fewer types of microbes, 7 or fewer types of microbes, 6 or fewer types of microbes, 5 or fewer types of microbes, 4 or fewer types of microbes, or 3 or fewer types of microbes. In a preferred embodiment, a bacterial composition comprises from 2 to no more than 40, from 2 to no more than 30, from 2 to no more than 20, from 2 to no more than 15, from 2 to no more than 10, from 2 to no more than 5, types of microbes. In another preferred embodiment, a bacterial composition comprises a single type of microbe.

[0282] In a preferred embodiment, the composition comprises about 20 or fewer isolated populations of bacterial cells. In another embodiment, the composition comprises about 15 or fewer isolated populations of bacterial cells. In another embodiment, the composition comprises about 10 or fewer isolated populations of bacterial cells. In another embodiment, the composition comprises about 5 or fewer isolated populations of bacterial cells. In another embodiment, the composition comprises about 4 or fewer isolated populations of bacterial cells. In another embodiment, the composition comprises about 3 or fewer isolated populations of bacterial cells. In another embodiment, the composition comprises about 2 isolated populations of bacterial cells. In another embodiment, the composition comprises between about 12 and 20 isolated populations of bacterial cells. In another embodiment, the composition comprises a single isolated population of bacterial cells. In another embodiment, the composition comprises at least two isolated populations of bacterial cells. In yet another embodiment, the composition comprises about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, or 20 isolated populations of bacterial cells.

[0283] Aspects of the invention relate to microbial compositions that are reconstituted from purified strains. Provided are microbial compositions comprising at least one, at least two or at least three microbes that are not identical and that are capable of decreasing the risk and/or severity of an autoimmune or inflammatory disease, symptom, condition, or disorder, or dysbiosis. In an embodiment, the microbial composition comprises at least about 2, 3, 4, 5, 6, 7, 8, 9, or 10 types of isolated microbes. In one embodiment, the microbial composition comprises at least about 4 types of isolated microbes or at least about 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more types of isolated microbes. In some embodiments, the above invention relates to microbial compositions further comprising one or more prebiotics.

[0284] Bacterial Compositions can be Described by Operational Taxonomic Units (OTUs).

[0285] Bacterial compositions may be prepared comprising one or at least two types of isolated bacteria, wherein a first type and a second type are independently chosen from the species or OTUs listed in Table 1. Certain embodiments of bacterial compositions with at least two types of isolated bacteria containing binary pairs are reflected herein. Additionally, a bacterial composition may be prepared comprising at least two types of isolated bacteria, wherein a first OTU and a second OTU are independently characterized by, i.e., at least 95%, 96%, 97%, 98%, 99% or including 100% sequence identity to, sequences listed.

[0286] Bacterial compositions may be prepared comprising one or at least two types of isolated bacteria, chosen from the species in Table 1, Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, Table 1F, or Table 5. Generally, the first bacteria and the second bacteria are not the same. The sequences provided in the sequencing listing file for OTUs in Table 1 are full 16S sequences. Therefore, in one embodiment, the first and/or second OTUs may be characterized by the full 16S sequences of OTUs listed in Table 1. In another embodiment, the first and/or second OTUs may be characterized by one or more of the variable regions of the 16S sequence (V1-V9). These regions in bacteria are defined by nucleotides 69-99, 137-242, 433-497, 576-682, 822-879, 986-1043, 1117-1173, 1243-1294 and 1435-1465 respectively using numbering based on the *E. coli* system of nomenclature. (See, e.g., Brosius et al., Complete nucleotide sequence of a 16S ribosomal RNA gene from *Escherichia coli*, PNAS 75(10):4801-4805 (1978)). In some embodiments, at least one of the V1, V2, V3, V4, V5, V6, V7, V8, and V9 regions are used to characterize an OTU. In one embodiment, the V1, V2, and V3 regions are used to characterize an OTU. In another embodiment, the V3, V4, and V5 regions are used to characterize an OTU. In another embodiment, the V4 region is used to characterize an OTU.

[0287] OTUs may be defined either by full 16S sequencing of the rRNA gene, by sequencing of a specific hypervariable region of this gene (i.e., V1, V2, V3, V4, V5, V6, V7, V8, or V9), or by sequencing of any combination of hypervariable regions from this gene (e.g. V1-3 or V3-5). The bacterial 16S rDNA is approximately 1500 nucleotides in length and is used in reconstructing the evolutionary relationships and sequence similarity of one bacterial isolate to another using phylogenetic approaches. 16S sequences are used for phylogenetic reconstruction as they are in general highly conserved, but contain specific hypervariable regions that harbor sufficient nucleotide diversity to differentiate genera and species of most microbes.

[0288] Using well known techniques, in order to determine the full 16S sequence or the sequence of any hypervariable region of the 16S sequence, genomic DNA is extracted from a bacterial sample, the 16S rDNA (full region or specific hypervariable regions) amplified using polymerase chain reaction (PCR), the PCR products cleaned, and nucleotide sequences delineated to determine the genetic composition of 16S gene or subdomain of the gene. If full 16S sequencing is

performed, the sequencing method used may be, but is not limited to, Sanger sequencing. If one or more hypervariable regions are used, such as the V4 region, the sequencing may be, but is not limited to being, performed using the Sanger method or using a next-generation sequencing method, such as an Illumina (sequencing by synthesis) method using barcoded primers allowing for multiplex reactions.

[0289] OTUs can be defined by a combination of nucleotide markers or genes, in particular highly conserved genes (e.g., "house-keeping" genes), or a combination thereof, full-genome sequence, or partial genome sequence generated using amplified genetic products, or whole genome sequence (WGS). Using well defined methods DNA extracted from a bacterial sample will have specific genomic regions amplified using PCR and sequenced to determine the nucleotide sequence of the amplified products. In the whole genome shotgun (WGS) method, extracted DNA will be directly sequenced without amplification. Sequence data can be generated using any sequencing technology including, but not limited to Sanger, Illumina, 454 Life Sciences, Ion Torrent, ABI, Pacific Biosciences, and/or Oxford Nanopore.

VI. Prebiotic Compositions

[0290] A prebiotic allows specific changes, both in the composition and/or activity in the gastrointestinal microbiota, that confers benefits upon host well-being and health. Prebiotics can include complex carbohydrates, amino acids, peptides, or other nutritional components useful for the survival of the bacterial composition. Prebiotics include, but are not limited to, amino acids, biotin, fructooligosaccharide, galactooligosaccharides, inulin, lactulose, mannan oligosaccharides, oligofructose-enriched inulin, oligofructose, oligodextrose, tagatose, trans-galactooligosaccharide, and xylooligosaccharides.

[0291] Suitable prebiotics are usually plant-derived complex carbohydrates, oligosaccharides or polysaccharides. Generally, prebiotics are indigestible or poorly digested by humans and serve as a food source for bacteria. Prebiotics which can be used in the pharmaceutical dosage forms, pharmaceutical compositions, and kits provided herein include, without limitation, galactooligosaccharides (GOS), trans-galactooligosaccharides, fructooligosaccharides or oligofructose (FOS), inulin, oligofructose-enriched inulin, lactulose, arabinoxylan, xylooligosaccharides (XOS), mannooligosaccharides, gum guar, gum Arabic, tagatose, amylose, amylopectin, xylan, pectin, and the like and combinations of thereof. Prebiotics can be found in certain foods, e.g. chicory root, Jerusalem artichoke, Dandelion greens, garlic, leek, onion, asparagus, wheat bran, wheat flour, banana, milk, yogurt, sorghum, burdock, broccoli, Brussels sprouts, cabbage, cauliflower, collard greens, kale, radish and rutabaga, and miso. Alternatively, prebiotics can be purified or chemically or enzymatically synthesized.

[0292] Prebiotics of the Invention

[0293] In some embodiments, the composition comprises at least one prebiotic. In one embodiment, the prebiotic is a carbohydrate. In some embodiments, the composition of the present invention comprises a prebiotic mixture, which comprises at least one carbohydrate. A "carbohydrate" refers to a sugar or polymer of sugars. The terms "saccharide," "polysaccharide," "carbohydrate," and "oligosaccharide" may be used interchangeably. Most carbohydrates are aldehydes or ketones with many hydroxyl groups, usually one on each carbon atom of the molecule. Carbohydrates generally have the molecular formula $(CH_2O)n$. A carbohydrate can be a monosaccharide, a disaccharide, trisaccharide, oligosaccharide, or polysaccharide. The most basic carbohydrate is a monosaccharide, such as glucose, sucrose, galactose, mannose, ribose, arabinose, xylose, and fructose. Disaccharides are two joined monosaccharides. Exemplary disaccharides include sucrose, maltose, cellobiose, and lactose. Typically, an oligosaccharide includes between three and six monosaccharide units (e.g., raffinose, stachyose), and polysaccharides include six or more monosaccharide units. Exemplary polysaccharides include starch, glycogen, and cellulose. Carbohydrates can contain modified saccharide units, such as 2'-deoxyribose wherein a hydroxyl group is removed, 2'-fluororibose wherein a hydroxyl group is replace with a fluorine, or N-acetylglucosamine, a nitrogen-containing form of glucose (e.g., 2'-fluororibose, deoxyribose, and hexose). Carbohydrates can exist in many different forms, for example, conformers, cyclic forms, acyclic forms, stereoisomers, tautomers, anomers, and isomers. Carbohydrates may be purified from natural (e.g., plant or microbial) sources (i.e., they are enzymatically synthetized), or they may be chemically synthesized or modified. Such prebiotics can optionally be used in conjunction with one or more probiotics in the compositions and methods of the invention. Exemplary prebiotics are provided in Table 7.

[0294] Suitable prebiotic carbohydrates can include one or more of a carbohydrate, carbohydrate monomer, carbohydrate oligomer, or carbohydrate polymer. In certain embodiments, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe and at least one type of non-digestible saccharide, which includes non-digestible monosaccharides, non-digestible oligosaccharides, or non-digestible polysaccharides. In one embodiment, the sugar units of an oligosaccharide or polysaccharide can be linked in a single straight chain or can be a chain with one or more side branches. The length of the oligosaccharide or polysaccharide can vary from source to source. In one embodiment, small amounts of glucose can also be contained in the chain. In another embodiment, the prebiotic composition can be partially hydrolyzed or contain individual sugar moieties that are components of the primary oligosaccharide (see U.S. Pat. No. 8,486,668, PREBIOTIC FORMULATIONS AND METHODS OF USE).

[0295] Prebiotic carbohydrates may include, but are not limited to monosaccharaides (e.g., trioses, tetroses, pentoses, aldopentoses, ketopentoses, hexoses, cyclic hemiacetals, ketohexoses, heptoses) and multimers thereof, as well as epimers, cyclic isomers, stereoisomers, and anomers thereof. Nonlimiting examples of monosaccharides include (in either the L- or D-conformation) glyceraldehyde, threose, ribose, altrose, glucose, mannose, talose, galactose, gulose, idose, lyxose, arabanose, xylose, allose, erythrose, erythrulose, tagalose, sorbose, ribulose, psicose, xylulose, fructose, dihydroxyacetone, and cyclic (alpha or beta) forms thereof. Multimers (disaccharides, trisaccharides, oligosaccharides, polysaccharides) thereof include but are not limited to sucrose, lactose, maltose, lactulose, trehalose, cellobiose, kojibiose, nigerose, isomaltose, sophorose, laminaribiose, gentioboise, turanose, maltulose, palatinose, gentiobiulose, mannobiose, melibiulose, rutinose, rutinulose, xylobiose, primeverose, amylose, amylopectin, starch (including resistant starch), chitin, cellulose, agar, agarose, xylan, glycogen, bacterial polysaccharides such as capsular polysaccharides, LPS, and peptodglycan, and biofilm exopolysaccharide (e.g.,

alginate, EPS), N-linked glycans, and O-linked glycans. Prebiotic sugars may be modified and carbohydrate derivatives include amino sugars (e.g., sialic acid, N-acetylglucosamine, galactosamine), deoxy sugars (e.g., rhamnose, fucose, deoxyribose), sugar phosphates, glycosylamines, sugar alcohols, and acidic sugars (e.g., glucuronic acid, ascorbic acid).

[0296] In one embodiment, the prebiotic carbohydrate component of the pharmaceutical composition, dosage form, or kit consists essentially of one or more non-digestible saccharides. In one embodiment, non-digestible oligosaccharides the non-digestible oligosaccharides are galactooligosaccharides (GOS). In another embodiment, the non-digestible oligosaccharides are fructooligosaccharides (FOS).

[0297] In one embodiment, the prebiotic carbohydrate component of the pharmaceutical composition, dosage form, or kit allows the commensal colonic microbiota, comprising microorganisms associated with a healthy-state microbiome or presenting a low risk of a patient developing an autoimmune or inflammatory condition, to be regularly maintained. In one embodiment, the prebiotic carbohydrate allows the co-administered or co-formulated microbe or microbes to engraft, grow, and/or be regularly maintained in a mammalian subject. In some embodiments, the mammalian subject is a human subject. In preferred embodiments, the mammalian subject suffers from or is at risk of developing an autoimmune or inflammatory disorder.

[0298] In some embodiments, the prebiotic favors the growth of an administered microbe, wherein the growth of the administered microbe and/or the fermentation of the administered prebiotic by the administered microbe slows or reduces the growth of a pathogen or pathobiont. For example, FOS, neosugar, or inuliri promotes the growth of acid-forming bacteria in the colon such as bacteria belonging to the genera *Lactobacillus* or *Bifidobacterium* and *Lactobacillus acidophilus* and *Bifidobacterium bifidus* can play a role in reducing the number of pathogenic bacteria in the colon (see U.S. Pat. No. 8,486,668, PREBIOTIC FORMULATIONS AND METHODS OF USE). Other polymers, such as various galactans, lactulose, and carbohydrate based gums, such as psyllium, guar, carrageen, gellan, and konjac, are also known to improve gastrointestinal (GI) health.

[0299] In some embodiments, the prebiotic composition of the invention comprises one or more of GOS, lactulose, raffinose, stachyose, lactosucrose, FOS (i.e., oligofructose or oligofructan), inulin, isomalto-oligosaccharide, xylo-oligosaccharide, paratinose oligosaccharide, transgalactosylated oligosaccharides (i.e., transgalacto-oligosaccharides), transgalactosylate disaccharides, soybean oligosaccharides (i.e., soyoligosaccharides), gentiooligosaccharides, glucooligosaccharides, pecticoligosaccharides, palatinose polycondensates, difructose anhydride III, sorbitol, maltitol, lactitol, polyols, polydextrose, reduced paratinose, cellulose, β-glucose, β-galactose, β-fructose, verbascose, galactinol, and β-glucan, guar gum, pectin, high, sodium alginate, and lambda carrageenan, or mixtures thereof. The GOS may be a short-chain GOS, a long-chain GOS, or any combination thereof. The FOS may be a short-chain FOS, a long-chain FOS, or any combination thereof.

[0300] In some embodiments, the prebiotic composition comprises two carbohydrate species (nonlimiting examples being a GOS and FOS) in a mixture of at least 1:1, at least 2:1, at least 5:1, at least 9:1, at least 10:1, about 20:1, or at least 20:1.

[0301] In some embodiments, the prebiotic composition of the invention comprises a mixture of one or more non-digestible oligosaccharides, non-digestible polysaccharides, free monosaccharides, non-digestible saccharides, starch, or non-starch polysaccharides. In one embodiment, a prebiotic component of a prebiotic composition is a GOS composition. In one embodiment, a prebiotic composition is a pharmaceutical composition. In one embodiment, a pharmaceutical composition is a GOS composition.

[0302] Oligosaccharides are generally considered to have a reducing end and a non-reducing end, whether or not the saccharide at the reducing end is in fact a reducing sugar. Most oligosaccharides described herein are described with the name or abbreviation for the non-reducing saccharide (e.g., Gal or D-Gal), preceded or followed by the configuration of the glycosidic bond (α or β), the ring bond, the ring position of the reducing saccharide involved in the bond, and then the name or abbreviation of the reducing saccharide (e.g., Glc or D-Glc). The linkage (e.g., glycosidic linkage, galactosidic linkage, glucosidic linkage) between two sugar units can be expressed, for example, as 1, 4, 1→4, or (1-4).

[0303] Both FOS and GOS are non-digestible saccharides. β glycosidic linkages of saccharides, such as those found in, but not limited to, FOS and GOS, make these prebiotics mainly non-digestible and unabsorbable in the stomach and small intestine α-linked GOS (α-GOS) is also not hydrolyzed by human salivary amylase, but can be used by *Bifidobacterium bifidum* and *Clostridium butyricum* (Yamashita A. et al., 2004. J. Appl. Glycosci. 51:115-122). FOS and GOS can pass through the small intestine and into the large intestine (colon) mostly intact, except where commensal microbes and microbes administered as part of a pharmaceutical composition are able to metabolize the oligosaccharides.

[0304] GOS (also known as galacto-oligosaccharides, galactooligosaccharides, trans-oligosaccharide (TOS), trans-galacto-oligosaccharide (TGOS), and trans-galactooligosaccharide) are oligomers or polymers of galactose molecules ending mainly with a glucose or sometimes ending with a galactose molecule and have varying degree of polymerization (generally the DP is between 2-20) and type of linkages. In one embodiment, GOS comprises galactose and glucose molecules. In another embodiment, GOS comprises only galactose molecules. In a further embodiment, GOS are galactose-containing oligosaccharides of the form of [β-D-Gal-(1-6)]$_n$-β-D-Gal-(1-4)-D-Glc wherein n is 2-20. In another embodiment, GOS are galactose-containing oligosaccharides of the form Glc α1-4-[β Gal 1-6)]$_n$ where n=2-20. In another embodiment, GOS are in the form of α-D-Glc (1-4)-[β-D-Gal-(1-6)-]$_n$ where n=2-20. Gal is a galactopyranose unit and Glc (or Glu) is a glucopyranose unit.

[0305] In one embodiment, a prebiotic composition comprises a GOS-related compound. A GOS-related compound can have the following properties: a) a "lactose" moiety; e.g., GOS with a gal-glu moiety and any polymerization value or type of linkage; or b) be stimulatory to "lactose fermenting" microbes in the human GI tract; for example, raffinose (gal-fru-glu) is a "related" GOS compound that is stimulatory to both lactobacilli and bifidobacteria.

[0306] In one embodiment, a prebiotic composition comprises GOS with a low degree of polymerization. In one embodiment a prebiotic composition comprising GOS with a low degree of polymerization increases growth of probiotic and select commensal bacteria to a greater extent than an equivalent amount of a prebiotic composition comprising

GOS with a high degree of polymerization. In one embodiment, a prebiotic composition comprising a high percentage of GOS with a low degree of polymerization increases growth of probiotic and beneficial commensal bacteria to a greater extent than an equivalent amount of a prebiotic composition comprising a low percentage of GOS with a low degree of polymerization (DP). In one embodiment a prebiotic composition comprises GOS with a DP less than 20, such as less than 10, less than 9, less than 8, less than 7, less than 6, less than 5, less than 4, or less than 3. In another embodiment a prebiotic composition comprising GOS with a low DP increases growth of co-formulated or co-administered microbes and/or beneficial commensal microbes in the GI tract of a subject.

[0307] Linkages between the individual sugar units found in GOS and other oligosaccharides include β-(1-6), β-(1-4), β-(1-3) and β-(1-2) linkages. In one embodiment, the administered oligosaccharides (e.g., GOS) are branched saccharides. In another embodiment, the administered oligosaccharides (e.g, GOS) are linear saccharides.

[0308] In some embodiments, the GOS comprises a disaccharide Gal α (1-6) Gal, at least one trisaccharide selected from Gal β (1-6)-Gal β (1-4)-Glc and Gal β (1-3)-Gal β (1-4)-Glc, the tetrasaccharide Gal β(1-6)-Gal β (1-6)-Gal β (1-4)-Glc and the pentasaccharide Gal β (1-6)-Gal β (1-6)-Gal β (1-6)-Gal β (1-4)-Glc.

[0309] In one embodiment, a GOS composition is a mixture of 10 to 45% w/v disaccharide, 10 to 45% w/v trisaccharide, 10 to 45% w/v tetrasaccharide and 10 to 45% w/v pentasaccharide. In another embodiment, a GOS composition is a mixture of oligosaccharides comprising 20-28% by weight of β (1-3) linkages, 20-25% by weight of β (1-4) linkages, and 45-55% by weight of β (1-6) linkages. In one embodiment, a GOS composition is a mixture of oligosaccharides comprising 26% by weight of β (1-3) linkages, 23% by weight of β (1-4) linkages, and 51% by weight of β (1-6) linkages.

[0310] Alpha-GOS (also called alpha-bond GOS or alpha-linked GOS) are oligosaccharides having an alpha-galactopyranosyl group. Alpha-GOS comprises at least one alpha glycosidic linkage between the saccharide units. Alpha-GOS are generally represented by α-(Gal)$_n$ (n usually represents an integer of 2 to 10) or α-(Gal)$_n$ Glc (n usually represents an integer of 1 to 9). Examples include a mixture of α-galactosylglucose, α-galactobiose, α-galactotriose, α-galactotetraose, and higher oligosaccharides. Additional non-limiting examples include melibiose, manninootriose, raffinose, stachyose, and the like, which can be produced from beat, soybean oligosaccharide, and the like.

[0311] Commercially available and enzyme synthesized alpha-GOS products are also useful for the compositions described herein. Synthesis of alpha-GOS with an enzyme is conducted utilizing the dehydration condensation reaction of α-galactosidase with the use of galactose, galactose-containing substance, or glucose as a substrate. The galactose-containing substance includes hydrolysates of galactose-containing substances, for example, a mixture of galactose and glucose obtained by allowing beta-galactosidase to act on lactose, and the like. Glucose can be mixed separately with galactose and be used as a substrate with α-galactosidase (see e.g., WO 02/18614). Methods of preparing alpha-GOS have been described (see e.g., EPI 514551 and EP2027863).

[0312] In one embodiment, a GOS composition comprises a mixture of saccharides that are alpha-GOS and saccharides that are produced by transgalactosylation using β-galactosidase. In another embodiment, GOS comprises alpha-GOS. In another embodiment, alpha-GOS comprises α-(Gal)$_2$ from 10% to 100% by weight. In one embodiment, GOS comprises only saccharides that are produced by transgalactosylation using β-galactosidase.

[0313] In one embodiment, a GOS composition can comprise GOS with alpha linkages and beta linkages.

[0314] In one embodiment, the pharmaceutical composition, dosage form, or kit comprises, in addition to one or more microbes, an oligosaccharide composition that is a mixture of oligosaccharides comprising 1-20% by weight of di-saccharides, 1-20% by weight tri-saccharides, 1-20% by weight tetra-saccharides, and 1-20% by weight penta-saccharides. In another embodiment, an oligosaccharide composition is a mixture of oligosaccharides consisting essentially of 1-20% by weight of di-saccharides, 1-20% by weight tri-saccharides, 1-20% by weight tetra-saccharides, and 1-20% by weight penta-saccharides.

[0315] In one embodiment, a prebiotic composition is a mixture of oligosaccharides comprising 1-20% by weight of saccharides with a degree of polymerization (DP) of 1-3, 1-20% by weight of saccharides with DP of 4-6, 1-20% by weight of saccharides with DP of 7-9, and 1-20% by weight of saccharides with DP of 10-12, 1-20% by weight of saccharides with DP of 13-15.

[0316] In another embodiment, a prebiotic composition comprises a mixture of oligosaccharides comprising 50-55% by weight of di-saccharides, 20-30% by weight tri-saccharides, 10-20% by weight tetra-saccharide, and 1-10% by weight penta-saccharides. In one embodiment, a GOS composition is a mixture of oligosaccharides comprising 52% by weight of di-saccharides, 26% by weight tri-saccharides, 14% by weight tetra-saccharide, and 5% by weight penta-saccharides. In another embodiment, a prebiotic composition comprises a mixture of oligosaccharides comprising 45-55% by weight tri-saccharides, 15-25% by weight tetra-saccharides, 1-10% by weight penta-saccharides.

[0317] In certain embodiments, the composition according to the invention comprises a mixture of neutral and acid oligosaccharides as disclosed in WO 2005/039597 (N.V. Nutricia) and US Patent Application 20150004130, which are hereby incorporated by reference. In one embodiment, the acid oligosaccharide has a degree of polymerization (DP) between 1 and 5000. In another embodiment, the DP is between 1 and 1000. In another embodiment, the DP is between 2 and 250. If a mixture of acid oligosaccharides with different degrees of polymerization is used, the average DP of the acid oligosaccharide mixture is preferably between 2 and 1000. The acid oligosaccharide may be a homogeneous or heterogeneous carbohydrate. The acid oligosaccharides may be prepared from pectin, pectate, alginate, chondroitine, hyaluronic acids, heparin, heparane, bacterial carbohydrates, sialoglycans, fucoidan, fucooligosaccharides or carrageenan, and are preferably prepared from pectin or alginate. The acid oligosaccharides may be prepared by the methods described in WO 01/60378, which is hereby incorporated by reference. The acid oligosaccharide is preferably prepared from high methoxylated pectin, which is characterized by a degree of methoxylation above 50%. As used herein, "degree of methoxylation" (also referred to as DE or "degree of esterification") is intended to mean the extent to which free carboxylic acid groups contained in the polygalacturonic acid chain have been esterified (e.g. by methylation). In some embodiments, the acid oligosaccharides have a degree of methoxylation above about 10%, above about 20%, above about 50%, above

about 70%. In some embodiments, the acid oligosaccharides have a degree of methylation above about 10%, above about 20%, above about 50%, above about 70%.

[0318] The term neutral oligosaccharides as used in the present invention refers to saccharides which have a degree of polymerization of monose units exceeding 2, exceeding 3, exceeding 4, or exceeding 10, which are not or only partially digested in the intestine by the action of acids or digestive enzymes present in the human upper digestive tract (small intestine and stomach) but which are fermented by the human intestinal flora and preferably lack acidic groups. The neutral oligosaccharide is structurally (chemically) different from the acid oligosaccharide. The term neutral oligosaccharides as used herein preferably refers to saccharides which have a degree of polymerization of the oligosaccharide below 60 monose units. The term monose units refers to units having a closed ring structure e.g., the pyranose or furanose forms. In come embodiments, the neutral oligosaccharide comprises at least 90% or at least 95% monose units selected from the group consisting of mannose, arabinose, fructose, fucose, rhamnose, galactose, -D-galactopyranose, ribose, glucose, xylose and derivatives thereof, calculated on the total number of monose units contained therein. Suitable neutral oligosaccharides are preferably fermented by the gut flora. Nonlimiting examples of suitable neutral oligosaccharides are cellobiose (4-O-β-D-glucopyranosyl-D-glucose), cellodextrins ((4-O-β-D-glucopyranosyl)n-D-glucose), B-cyclo-dextrins (Cyclic molecules of α-1-4-linked D-glucose; α-cyclodextrin-hexamer, β-cyclodextrin-heptamer and γ-cyclodextrin-octamer), indigestible dextrin, gentiooligosaccharides (mixture of β-1-6 linked glucose residues, some 1-4 linkages), glucooligosaccharides (mixture of α-D-glucose), isomaltooligosaccharides (linear α-1-6 linked glucose residues with some 1-4 linkages), isomaltose (6-O-α-D-glucopyranosyl-D-glucose); isomaltriose (6-O-α-D-glucopyranosyl-(1-6)-α-D-glucopyranosyl-D-glucose), panose (6-O-α-D-glucopyranosyl-(1-6)-α-D-glucopyranosyl-(1-4)-D-glucose), leucrose (5-O-α-D-glucopyranosyl-D-fructopyranoside), palatinose or isomaltulose (6-O-α-D-glucopyranosyl-D-fructose), theanderose (O-α-D-glucopyranosyl-(1-6)-O-α-D-glucopyranosyl-(1-2)-B-D-fructo furanoside), D-agatose, D-lyxo-hexylose, lactosucrose (O-β-D-galactopyranosyl-(1-4)-O-α-D-glucopyranosyl-(1-2)-β-D-fructofuranoside), α-galactooligosaccharides including raffinose, stachyose and other soy oligosaccharides (O-α-D-galactopyranosyl-(1-6)-α-D-glucopyranosyl-β-D-fructofuranoside), β-galactooligosaccharides or transgalacto-oligosaccharides (β-D-galactopyranosyl-(1-6)-[β-D-glucopyranosyl]n-(1-4) α-D glucose), lactulose (4-O-β-D-galactopyranosyl-D-fructose), 4'-galatosyllactose (O-D-galactopyranosyl-(1-4)-O-β-D-glucopyranosyl-(1-4)-D-glucopyranose), synthetic galactooligosaccharide (neogalactobiose, isogalactobiose, galsucrose, isolactose I, II and III), fructans-Levan-type (β-D-(2→6)-fructofuranosyl)n α-D-glucopyranoside), fructans-Inulin-type (β-D-((2→1)-fructofuranosyl)n α-D-glucopyranoside), 1 f-β-fructofuranosylnystose (B-D-((2→1)-fructofuranosyl)n B-D-fructofuranoside), xylooligo-saccharides (B-D-((1→4)-xylose)n, lafinose, lactosucrose and arabinooligosaccharides.

[0319] In some embodiments, the neutral oligosaccharide is selected from the group consisting of fructans, fructooligosaccharides, indigestible dextrins galactooligo-saccharides (including transgalactooligosaccharides), xylooligosaccharides, arabinooligo-saccharides, glucooligosaccharides, mannooligosaccharides, fucooligosaccharides and mixtures thereof.

[0320] Suitable oligosaccharides and their production methods are further described in Laere K. J. M. (Laere, K. J. M., Degradation of structurally different non-digestible oligosaccharides by intestinal bacteria: glycosylhydrolases of Bi. adolescentis. PhD-thesis (2000), Wageningen Agricultural University, Wageningen, The Netherlands), the entire content of which is hereby incorporated by reference. Transgalactooligosaccharides (TOS) are for example sold under the trademark Vivinal™ (Borculo Domo Ingredients, Netherlands). Indigestible dextrin, which may be produced by pyrolysis of corn starch, comprises α(1→4) and α(1→6) glucosidic bonds, as are present in the native starch, and contains 1→2 and 1→3 linkages and levoglucosan. Due to these structural characteristics, indigestible dextrin contains well-developed, branched particles that are partially hydrolysed by human digestive enzymes. Numerous other commercial sources of indigestible oligosaccharides are readily available and known to skilled persons in the art. For example, transgalactooligosaccharide is available from Yakult Honsha Co., Tokyo, Japan. Soybean oligosaccharide is available from Calpis Corporation distributed by Ajinomoto U.S.A. Inc., Teaneck, N.J.

[0321] In a further preferred embodiment, the prebiotic mixture of the pharmaceutical composition described herein comprises an acid oligosaccharide with a DP between 1 and 5000, prepared from pectin, alginate, and mixtures thereof; and a neutral oligosaccharide, selected from the group of fructans, fructooligosaccharides, indigestible dextrins, galactooligosaccharides including transgalacto-oligosaccharides, xylooligosaccharides, arabinooligosaccharides, glucooligosaccharides, manno-oligosaccharides, fucooligosaccharides, and mixtures thereof.

[0322] In certain embodiments, the prebiotic mixture comprises xylose. In other embodiments, the prebiotic mixture comprises a xylose polymer (i.e. xylan). In some embodiments, the prebiotic comprises xylose derivatives, such as xylitol, a sugar alcohol generated by reduction of xylose by catalytic hydrogenation of xylose, and also xylose oligomers (e.g., xylooligosaccharide). While xylose can be digested by humans, via xylosyltransferase activity, most xylose ingested by humans is excreted in urine. In contrast, some microorganisms are efficient at xylose metabolism or may be selected for enhanced xylose metabolism. Microbial xylose metabolism may occur by at least four pathways, including the isomerase pathway, the Weimburg pathway, the Dahms pathway, and, for eukaryotic microorganisms, the oxido-reductase pathway.

[0323] The xylose isomerase pathway involves the direct conversion of D-xylose into D-xylulose by xylose isomerase, after which D-xylulose is phosphorylated by xylulose kinase to yield D-xylolose-5-phosphate, an intermediate of the pentose phosphate pathway.

[0324] In the Weimberg pathway, D-xylose is oxidized to D-xylono-lactone by a D-xylose dehydrogenase. Then D-xylose dehydrogenase is hydrolyzed by a lactonase to yield D-xylonic acid, and xylonate dehydratase activity then yields 2-keto-3-deoxy-xylonate. The final steps of the Weimberg pathway are a dehydratase reaction to form 2-keto glutarate semialdehyde and an oxidizing reaction to form 2-ketoglutarate, an intermediate of the Krebs cycle.

[0325] The Dahms pathway follows the same mechanism as the Weimberg pathway but diverges once it has yielded

2-keto-3-deoxy-xylonate. In the Dahms pathway, an aldolase splits 2-keto-3-deoxy-xylonate into pyruvate and glycolaldehyde.

[0326] The xylose oxido-reductase pathway, also known as the xylose reductase-xylitol dehydrogenase pathway, begins by the reduction of D-xylose to xylitol by xylose reductase followed by the oxidation of xylitol to D-xylulose by xylitol dehydrogenase. As in the isomerase pathway, the next step in the oxido-reductase pathway is the phosphorylation of D-xylulose by xylulose kinase to yield D-xylolose-5-phosphate.

[0327] Xylose is present in foods like fruits and vegetables and other plants such as trees for wood and pulp production. Thus, xylose can be obtained in the extracts of such plants. Xylose can be obtained from various plant sources using known processes including acid hydrolysis followed by various types of chromatography. Examples of such methods to produce xylose include those described in Maurelli, L. et al. (2013), Appl. Biochem. Biotechnol. 170:1104-1118; Hooi H. T et al. (2013), Appl. Biochem. Biotechnol. 170:1602-1613; Zhang H-J. et al. (2014), Bioprocess Biosyst. Eng. 37:2425-2436.

[0328] Preferably, the metabolism of xylose and/or the shift in microbiota due to the metabolism of the xylose provided in a pharmaceutical composition of the invention confers a benefit to a host, e.g. immunological tolerance. For example, in aspects in which the patient is at risk or suffering from GVHD, the immunological tolerance may reduce graft-versus-host activity while maintaining graft-versus-leukemia activity. The xylose may be, e.g. i) cytotoxic for an autoimmune disease- and/or inflammatory disease-associated associated pathogen or pathobiont, ii) cytostatic for an autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, iii) capable of decreasing the growth of autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, iv) capable of inhibiting the growth of an autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, v) capable of decreasing the colonization of an autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, vi) capable of inhibiting the colonization of an autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, vii) capable of eliciting an immunomodulatory response in the host that reduces the risk of an autoimmune and/or inflammatory disorder, viii), capable of eliciting an immunomodulatory response in the host that reduces the severity of an autoimmune and/or inflammatory disorder, ix) capable of promoting barrier integrity directly or indirectly through its impact on microbiota, or x) any combination of i)-ix).

[0329] In some embodiments, the pharmaceutical composition or dosage form comprises a bacterial population and xylose in an amount effective to promote the growth of select bacteria of the family Clostridiacea, including members of the genus *Clostridium, Ruminococcus*, or *Blautia* or relatives thereof in a host. In some embodiments, the pharmaceutical composition or dosage form is further effective to promote the proliferation of select bacteria of the family Clostridiacea, including members of the genus *Clostridium, Ruminococcus*, or *Blautia* or relatives thereof in a host. In certain embodiments, the pharmaceutical composition or dosage form comprises a bacterial population and xylose in an amount effective to promote the colonization and/or engraftment of select bacteria of the family Clostridiacea, including members of the genus *Clostridium, Ruminococcus*, or *Blautia* or relatives thereof in a host. In preferred embodiments, the pharmaceutical composition or dosage form is further capable of altering a dysbiotic state such that the growth, proliferation, colonization, and/or engraftment of a host by a pathogen, pathobiont, disease-associated microbe, or a combination thereof such that the population of at least one pathogen, pathobiont, or disease-associated microbe is decreased 2-fold, 5-fold, 10-fold, 50-fold, 100-fold, 200-fold, 500-fold, 1000-fold, 10000-fold, or over 10000-fold. In one embodiment, the pharmaceutical composition or dosage form is capable of locally or systemically eliminating at least one pathogen, pathobiont, or disease-associated microbe from a host.

[0330] In some embodiments, the prebiotic mixture comprises a carbohydrate monomer or polymer that has been modified i.e., substituted with other substituents (e.g., acetyl group, glucuronic acid residue, arabinose residue, or the like) (see US Patent Application 20090148573, hereby incorporated by reference). The term "modified", as used herein, refers to a molecule modified from a reference molecule, and includes not only artificially produced molecules but also naturally occurring molecules. In preferred embodiments, the modification occurs at one or more hydroxyl groups of the reference carbohydrate. In some embodiments, the modification occurs at carbon-2 (C2), the modification occurs at carbon-6 (C6), or a combination thereof.

[0331] In some embodiments, a carbohydrate (a monomer or, preferably, a polymer) is modified with one or more hydrophilic groups. Nonlimiting examples of the hydrophilic groups include an acetyl group, a 4-O-methyl-α-D-glucuronic acid residue, an L-arabinofuranose residue, an L-arabinose residue, and an α-D-glucuronic acid residue. In some embodiments, the modification is the replacement of one or more hydroxyl groups with —H, —CH_2OH, —CH_3, or —NH_2.

[0332] In some embodiments, the composition comprises at least one carbohydrate that elicits an immunomodulatory response. Exemplary immunomodulary carbohydrates include (but are not limited to) fructo-oligosaccharides, glycosaminoglycans (e.g., heparin sulfate, chondroitin sulfate A, hyaluronan), O-glycans, and carrageenan oligosaccharides, and galacto-oligosaccharides. Immunomodulatory carbohydrates may be purified from plants or microbes or may be synthetically derived. Immunomodulatory carbohydrates may be effective to, for example, prevent disease, suppress symptoms, treat disease, or any combination thereof.

[0333] In some embodiments, immunomodulatory carbohydrates are C-type lectin receptor ligands. In preferred embodiments, the C-type lectin receptor ligands are produced by one or more fungal species. In other embodiments, the immunomodulatory carbohydrates are bacterial exopolysaccharides, such as (but not limited to) the exopolysaccharides (EPS) produced by *Bacillus subtilis, Bifidobacterium breve*, or *Bacteroides fragilis*. In some aspects, immunomodulatory carbohydrates are zwitterionic polysaccharides. In some aspects, immunomodulatory carbohydrates modulate toll-like receptor 2 (TLR2) and/or toll-like receptor 4 (TLR4) responses in a host. For example, autoimmune or inflammatory diseases characterized by intestinal inflammation may be prevented by a TLR4 agonist such as but not limited to *B. subtilis* EPS (Jones S, Paynich M L, Kearns D B, Knight K L, 2014. Protection from Intestinal Inflammation by Bacterial Exopolysaccharides. The Journal of Immunology. 192:4813-4820). Immunomodulatory carbohydrates may also activate CD4+ T cells and/or lead to an upregulation of the anti-

inflammatory cytokine interleukin-10 (Mazmanian S K, Kasper D L, 2006. The love-hate relationship between bacterial polysaccharides and the host immune system. Nat. Rev. Immunol. 6: 849-858). Immunomodulatory carbohydrates may be selected for administration to a patient based on the presence, abundance, distribution, modification and/or linkages of sugar residues. For example, immunomodulatory carbohydrates used in the prevention of intestinal disorders or autoimmune conditions that manifest in the gut (non-limiting examples being IBD and GVHD) may be selected based on i) a high abundance of mannose residues; ii) the presence of terminal mannopyransosyl (t-Man) residues and/or 2,6 linked mannopyranosyl residues (2,6-Man), iii) a ratio of mannose to glucose residues in the approximate range of 8:2 to 9:1, iv) the presence of galactose residues, v) areas of positive charge, or vi) a combination thereof.

[0334] Carbohydrates may be selected according to the fermentation or metabolic preferences of a microbe selected for administration to a mammalian subject. Selection criteria include but are not limited to sugar complexity (e.g., monosaccharides, including but not limited to glucose, versus oligosaccharides or starches) as well as by desired end-product. Non-limiting examples include the fermentation products ethanol and carbon dioxide (CO_2) (e.g., via ethanol fermentation by *Saccharomyces* sp. *Zymomonas* sp.), lactate (e.g., via homolactic acid fermentation by *Lactococcus* sp., *Streptococcus* sp., *Enterococcus* sp., *Pediococcus* sp. and some species *Lactobacillus*), lactate, ethanol, and CO_2 (e.g., via heterolactic acid fermentation (which includes the phosphoketolase pathway) by some species of *Lactobacillus* as well as *Leuconostoc* sp., *Oenococcus* sp., and *Weissella* sp.), butanol, acetone, CO_2 and H_2 (via acetone-butanol fermentation by some *Clostridium* sp.), and short chain fatty acids (with or without the production of other products) (Muller V, 2011. Bacterial Fermentation. Encyclopedia of Life Sciences). Examples of fermentation leading to short chain fatty acid production include homoacetic acid fermentation (e.g., by *Acetobacterium* sp., and resulting in acetate), propionic acid fermentation (e.g., by *Propionibacterium* sp., and resulting in propionate, acetate and CO_2) mixed acid fermentation (e.g., by *Escherichia* sp., and resulting in ethanol, lactate, acetate, succinate, formate, CO_2, and H_2), butyrate fermentation (e.g., by some *Clostridium* sp., resulting in butyrate, CO_2, and H_2), and 2,3-butanediol fermentation (e.g., by *Enterobacter* sp., resulting in ethanol, butanediol, lactate, formate, CO_2, and H_2). In some embodiments, selection of carbohydrates for co-formulation of co-administration with a type of microbe or types of microbe may be achieved by computational analysis of microbial enzymatic pathways, including but not limited to the presence of metabolic/fermentation pathway enzymes including but not limited to the enzymes provided in Table 4.

[0335] Other prebiotics include molecules capable of selective or semi-selective utilization by microbes of the composition contained herein. The ability of a microbe to utilize a metabolite of interest is determined by the genomic capacity of that microbe. Public databases have characterized many microbes and automate the annotation of the genome to allow a computational analysis of the metabolites a microbe is potentially able to utilize. Databases such as the Cluster of Orthologous Groups (COGs) database characterize genomes from a variety of species in this manner and are capable of characterizing newly sequenced genomes as well (e.g. see in this fashion (Tatusov et al 2000. Nucl Acid Res). Furthermore, pathway analysis classifies COGs into different categories with associated one letter codes including J, translation; L replication, recombination, and repair, K transcription; O molecular chaperones and related functions, M, cell wall structure and biogenesis and outer membrane, N secretion motility and chemotaxis; T signal Transduction; P inorganic ion transport and metabolism; C energy production and conversion; G, carbohydrate metabolism and transport; E amino acid metabolism and transport; F, nueclotide metabolism and transport; D cell Division and chromosome partitioning; R general functional prediction. In preferred embodiments, COGs of the categories, N, M, P, C, G, E, and F are selected as preferred COGs to both provide enhanced growth on specific substrates and modified behaviors relevant for anti-tumor properties. Other preferred embodiments, include COGs for C, G, E, and specific COG functions are listed in Table 4.

[0336] COGs are selected to be specific or semi enriched in the host or other microbes within a host by searching for specific functions present in the microbe of interest but absent from a large set of other competition organisms. Tissue specific analysis of the host for enzymes expressed within a tissue is performed to identify tissue specific enzymatic activities in the host. Specific functions are absent from at least 90%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40%, at least 30% at least 20% or at least 10% of the other organisms selected from the group of the host, the host tissue, the disease-associated microbiota, the host gut microbiota, the host niche specific to the engraftment of the microbial composition (e.g. GI tract, skin).

[0337] Once these COGs are identified, databases like KEGG were used to link the enzymatic functions to identify the metabolites that are substrates for these selective COGs. Furthermore, the selective analysis to generate selective metabolites is repeated on the set of substrate of COGs to validate that the pathways and metabolites are selective to the desired microbial composition.

[0338] Also provided are co-formulations of microbial populations and carbohydrates or other materials that foster desired microbial growth while, optionally, inhibiting undesired microbial growth. For example, one or more bacterial entites are encapsulated in a carbohydrate layer or coating (exemplary formulations include xylose-PEG and or xylose-PEG-PLGA).

[0339] Selecting Prebiotics for Particular Probiotics

[0340] It is well known that organisms, including bacteria, show a preferential and hierarchical utilization of different carbohydrates. Some bacteria will not respond at all to a sugar, while some bacterial will use a sugar preferentially. The metabolic effects of a sugar on a bacteria reflect how the bacteria senses and responds to its environment. Providing a sugar to a bacteria that has preferential utiliziation can encourage its growth/selection. Conversely, providing a sugar to a bacteria that is not preferred may lead to its down selection. For example, a particular sugar may not be a preferred substrate for metabolism, and thus may be utilized to bias for or enhance the growth and/or proliferation of particular microbial (e.g., bacterial) species or strains. Further, a particular sugar or the metabolism thereof may act as a selector to promote the survival, colonization, and/or engraftment of a desired microbial population in a host. Alternatively or simultaneously, a particular sugar or the metabolism thereof may act as a selector to reduce or eliminate the survival, colonization, and/or engraftment of an undesired microbial population in host.

[0341] Carbohydrates may be selected according to the fermentation or metabolic preferences of a microbe selected for administration to a mammalian subject. Selection criteria include but are not limited to sugar complexity (e.g., monosaccharides, including but not limited to glucose, versus oligosaccharides or starches) as well as by desired end-product. Non-limiting examples include the fermentation products ethanol and carbon dioxide (CO_2) (e.g., via ethanol fermentation by *Saccharomyces* sp. *Zymomonas* sp.), lactate (e.g., via homolactic acid fermentation by *Lactococcus* sp., *Streptococcus* sp., *Enterococcus* sp., *Pediococcus* sp. and some species *Lactobacillus*), lactate, ethanol, and CO_2 (e.g., via heterolactic acid fermentation (which includes the phosphoketolase pathway) by some species of *Lactobacillus* as well as *Leuconostoc* sp., *Oenococcus* sp., and *Weissella* sp.), butanol, acetone, CO_2 and H_2 (via acetone-butanol fermentation by some *Clostridium* sp.), and short chain fatty acids (with or without the production of other products) (Muller V, 2011. Bacterial Fermentation. Encyclopedia of Life Sciences). Examples of fermentation leading to short chain fatty acid production include homoacetic acid fermentation (e.g., by *Acetobacterium* sp., and resulting in acetate), propionic acid fermentation (e.g., by *Propionibacterium* sp., and resulting in propionate, acetate and CO_2) mixed acid fermentation (e.g., by *Escherichia* sp., and resulting in ethanol, lactate, acetate, succinate, formate, CO_2, and H_2), butyrate fermentation (e.g., by some *Clostridium* sp., resulting in butyrate, CO_2, and H_2), and 2,3-butanediol fermentation (e.g., by *Enterobacter* sp., resulting in ethanol, butanediol, lactate, formate, CO_2, and H_2). In some embodiments, selection of carbohydrates for co-formulation or co-administration with a type of microbe or types of microbe may be achieved by computational analysis of microbial enzymatic pathways, including but not limited to the presence of metabolic/fermentation pathway enzymes including but not limited to the enzymes provided in Table 4.

[0342] In preferred embodiments, the combination of a type of microbe or microbial composition and type of prebiotic mixture is selected based on the fermentation or metabolic preferences of one or more microbes capable of producing immunomodulatory SCFAs (e.g., preference for complex versus simple sugar or preference for a fermentation product versus a prebiotic). For example, *M. eldsenii* prefers lactate fermentation to glucose fermentation, and maximization of propionate production by *M. eldsenii* in a mammalian subject may therefore be achieved by administering along with *M. eldsenii* a favored substrate (e.g., lactate) or one or more microbes capable of fermenting glucose into lactate (e.g., *Streptococcus bovis*) (Hosseini E., et al. 2011. Propionate as a health-promoting microbial metabolite in the human gut. Nutrition Reviews. 69(5): 245-258).

[0343] Immunomodulation can also be achieved by the microbial production of glutathione or gamma-glutamylcysteine. Thus, in certain embodiments, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe capable of producing glutathione and/or gamma-glutamylcysteine

[0344] In some aspects, the composition, dosage form, or kit comprises one or more microbes selected for the presence of glutamate cysteine ligase (e.g., *Lactobacillus fermentum*) and/or L-proline biosynthesis enzymes (e.g., *E. coli*) (Peran et al., 2006. *Lactobacillus* fermenum, a probiotic capable to release glutathione, prevents colonic inflammation in the TNBS model of rat colitis. Int J Colorectal Dis. 21(8): 737-746; Veeravalli et al., 2011. Laboratory evolution of glutathione biosynthesis reveals naturally compensatory pathways. Nat Chem Bio. 7(2): 101-105). In a preferred embodiment, at least one microbe in the pharmaceutical composition, dosage form, or kit is *L. fermentum.*

VII. Methods of Altering the Microbiome Using Prebiotics and/or Probiotics

[0345] Disclosed herein are therapeutic compositions containing non-pathogenic, germination-competent bacterial entities and/or fungal entities, for the prevention, control, and treatment of immune and inflammatory diseases, disorders and conditions and for general nutritional health. These compositions are advantageous in being suitable for safe administration to humans and other mammalian subjects and are efficacious in numerous immune and inflammatory diseases, disorders and conditions and in general nutritional health. While spore-based compositions are known, these are generally prepared according to various techniques such as lyophilization or spray-drying of liquid bacterial cultures, resulting in poor efficacy, instability, substantial variability and lack of adequate safety.

[0346] It has now been found that populations of bacterial entities and/or fungal entities can be obtained from biological materials obtained from mammalian subjects, including humans. These populations are formulated into compositions as provided herein, and administered to mammalian subjects using the methods as provided herein.

[0347] Purified Spore Populations.

[0348] In some embodiments, the bacterial compositions comprise purified spore populations. As described herein, purified spore populations contain combinations of commensal bacteria of the human gut microbiota with the capacity to meaningfully provide functions of a healthy microbiota when administered to a mammalian subject. Without being limited to a specific mechanism, it is thought that such compositions inhibit the growth of a pathogen such as *C. difficile, Salmonella* spp., enteropathogenic *E. coli, Fusobacterium* spp., *Klebsiella* spp. and vancomycin-resistant *Enterococcus* spp., so that a healthy, diverse and protective microbiota can be maintained or, in the case of pathogenic bacterial infections, repopulate the intestinal lumen to reestablish ecological control over potential pathogens. In one embodiment, the purified spore populations can engraft in the host and remain present for 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 10 days, 14 days, 21 days, 25 days, 30 days, 60 days, 90 days, or longer than 90 days. Additionally, the purified spore populations can induce other healthy commensal bacteria found in a healthy gut to engraft in the host that are not present in the purified spore populations or present at lesser levels and therefore these species are considered to "augment" the delivered spore populations. In this manner, commensal species augmentation of the purified spore population in the recipient's gut leads to a more diverse population of gut microbiota then present initially.

[0349] Preferably, the one or more microbes provided in a therapeutic composition act additively, more preferably synergistically to confer a benefit to a host, e.g. immunological tolerance. For example, in aspects in which the patient is at risk or suffering from GVHD, the immunological tolerance may reduce graft-versus-host activity while maintaining graft-versus-leukemia activity. In another example, in aspects in which the patient suffers from Celiac disease, the immunological tolerance prevents an inappropriate immune

response to gluten. The microbes may additively or synergistically be, e.g. i) cytotoxic for an autoimmune disease- and/or inflammatory disease-associated associated pathogen or pathobiont, ii) cytostatic for an autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, iii) capable of decreasing the growth of autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, iv) capable of inhibiting the growth of an autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, v) capable of decreasing the colonization of an autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, vi) capable of inhibiting the colonization of an autoimmune disease- and/or inflammatory disease-associated pathogen or pathobiont, vii) capable of eliciting an immunomodulatory response in the host that reduces the risk of an autoimmune and/or inflammatory disorder, viii), capable of eliciting an immunomodulatory response in the host that reduces the severity of an autoimmue and/or inflammatory disorder, or ix) any combination of i)-viii).

[0350] The microbes described herein may additively or synergistically reduce the number of types of autoimmune disease- or inflammatory disease-associated pathogens or pathobionts either distally—e.g., orally-administered microbes reduce the total microbial burden in an organ not in the gastrointestinal tract, or intravaginally-administered microbes reduce the total microbial burden in an organ that is not the vagina—or locally, e.g., the intestines or vagina, respectively. Distal sites include but are not limited to the liver, spleen, fallopian tubes and uterus.

[0351] Thus provided are compositions formulated for vaginal administration, such as bacterial populations. The bacterial populations are capable of translocating across vaginal tissue to distal sites, or relocation from the vaginal canal into the gastrointestinal tract.

[0352] Similarly, the microbes described herein may additively or synergistically elicit an immunomodulatory response either distally, e.g., in which enteral administration of microbes results in altering the immune response at the skin or liver, or locally, e.g. the enteral administration of microbes results in altering the immune response in the intestines.

[0353] In some situations, the recipient subject is immunocompromised or immunosuppressed, or is at risk of developing an immune or inflammatory disorder.

[0354] Methods for Administrating Bacterial Compositions to Treat a Subject.

[0355] Administration of Microbial Compositions, with or without Prebiotics.

[0356] The microbial compositions of the invention, with or without one or more prebiotics, are suitable for administration to mammals and non-mammalian animals in need thereof. In certain embodiments, the mammalian subject is a human subject who has one or more symptoms of a dysbiosis, including but not limited to overgrowth of an undesired pathobiont or pathogen, reduced representation of key bacterial taxa such as the Bacteroidetes or Firmicutes or genera or species thereof, or reduced diversity of microbial species compared to a healthy individual, or reduced overall abundance of anaerobic bacteria.

[0357] When the mammalian subject is suffering from a disease, disorder or condition characterized by an aberrant microbiota, the bacterial compositions described herein are suitable for treatment thereof. In some embodiments, the mammalian subject has not received antibiotics in advance of treatment with the bacterial compositions. For example, the mammalian subject has not been administered at least two doses of vancomycin, metronidazole and/or or similar antibiotic compound within one week prior to administration of the therapeutic composition. In other embodiments, the mammalian subject has not previously received an antibiotic compound in the one month prior to administration of the therapeutic composition. In other embodiments, the mammalian subject has received one or more treatments with one or more different antibiotic compounds and such treatment(s) resulted in no improvement or a worsening of symptoms. In some embodiments, the composition is administered following a successful course of antibiotics to prevent dysbiosis and enhance recovery of a diverse, healthy microbiota.

[0358] In some embodiments, the disease, disorder or condition characterized by an aberrant microbiota is GVHD.

[0359] In some embodiments, the therapeutic composition is administered only once prior to improvement of the disease, disorder or condition. In some embodiments the therapeutic composition is administered at intervals greater than two days, such as once every three, four, five or six days, or every week or less frequently than every week. Or the preparation may be administered intermittently according to a set schedule, e.g., once a day, once weekly, or once monthly, or when the subject relapses from the primary illness. In another embodiment, the preparation may be administered on a long-term basis to individuals who are at risk for infection with or who may be carriers of these pathogens, including individuals who will have an invasive medical procedure (such as surgery), who will be hospitalized, who live in a long-term care or rehabilitation facility, who are exposed to pathogens by virtue of their profession (livestock and animal processing workers), or who could be carriers of pathogens (including hospital workers such as physicians, nurses, and other healthcare professionals).

[0360] In embodiments where a subject is administered a probiotic composition and a prebiotic composition, the probiotic and prebiotic can be administered simultaneously. For example, the probiotic composition can contain a prebiotic, or can be administered at the same time as a prebiotic. In other embodiments, the probiotic and the prebiotic are dosed on different regimens. For example, the prebiotic can be dosed prior to or after administration of the probiotic. In other embodiments, the prebiotic can be dosed regularly, and the probiotic is dosed at intervals of reduced frequency compared to dosing of the prebiotic.

[0361] Also provided are methods of treating or preventing a mammalian subject suffering from or at risk of developing a metabolic disease, and disorder or condition selected from the group consisting of diabetes, metabolic syndrome, obesity, heart disease, autoimmune disease, liver disease, and autism using the therapeutic compositions provided herein.

[0362] In embodiments, the microbial composition is administered enterically, with or without prebiotics. This preferentially includes oral administration, or by an oral or nasal tube (including nasogastric, nasojejunal, oral gastric, or oral jejunal). In other embodiments, administration includes rectal administration (including enema, suppository, or colonoscopy). The microbial composition may be administered to at least one region of the gastrointestinal tract, including the mouth, esophagus, stomach, small intestine, large intestine, and rectum. In some embodiments, it is administered to all regions of the gastrointestinal tract. The microbial

compositions may be administered orally in the form of medicaments such as powders, capsules, tablets, gels or liquids. The microbial compositions may also be administered in gel or liquid form by the oral route or through a nasogastric tube, or by the rectal route in a gel or liquid form, by enema or instillation through a colonoscope or by a suppository. In some embodiments, the microbial composition of the above invention is administered enterically with one ore more prebiotics.

[0363] If the composition is administered colonoscopically and, optionally, if the microbial composition, with or without one or more prebiotics, is administered by other rectal routes (such as an enema or suppository) or even if the subject has an oral administration, the subject may have a colonic-cleansing preparation. The colon-cleansing preparation can facilitate proper use of the colonoscope or other administration devices, but even when it does not serve a mechanical purpose it can also maximize the proportion of the bacterial composition relative to the other organisms previously residing in the gastrointestinal tract of the subject. Any ordinarily acceptable colonic-cleansing preparation may be used such as those typically provided when a subject undergoes a colonoscopy.

[0364] To evaluate the subject, symptoms of dysbiosis are evaluated post treatment ranging from 1 day to 6 months after administration of the purified bacterial population. Fecal material is collected during this period and the microbes present in the gastrointestinal tract can be assessed by 16S rDNA or metagenomic sequencing analysis or other analyses commonly used by the skilled artisan. Repopulation by species provided by the spore population as well as Augmentation by commensal microbes not present in the spore population will occur in this time as the spore population catalyzes a reshaping of the gut or vagina ecology to a state of healthy biosis.

[0365] Methods of Treating a Subject.

[0366] In some embodiments, the compositions disclosed herein are administered to a patient or a user (sometimes collectively referred to as a "subject"). As used herein "administer" and "administration" encompasses embodiments in which one person directs another to consume a bacterial composition in a certain manner and/or for a certain purpose, and also situations in which a user uses a bacteria composition in a certain manner and/or for a certain purpose independently of or in variance to any instructions received from a second person. Non-limiting examples of embodiments in which one person directs another to consume a bacterial composition in a certain manner and/or for a certain purpose include when a physician prescribes a course of conduct and/or treatment to a patient, when a parent commands a minor user (such as a child) to consume a bacterial composition, when a trainer advises a user (such as an athlete) to follow a particular course of conduct and/or treatment, and when a manufacturer, distributer, or marketer recommends conditions of use to an end user, for example through advertisements or labeling on packaging or on other materials provided in association with the sale or marketing of a product.

[0367] The microbial compositions, with or without one or more prebiotics, offer a protective and/or therapeutic effect against GVHD. In some embodiments, the compositions are administered to a subject before the subject receives a transplant. In other embodiments, the compositions are administered to a subject concurrently with receiving a transplant. In other embodiments, the compositions are administered to a subject after receiving a transplant. In other embodiments, the compositions are administered to a subject before and/or simultaneously with and/or after receiving a transplant. The compositions of the invention can be administered to a subject receiving a transplant before the subject has developed any signs or symptoms of developing GVHD. In this embodiment, the composition modulates the microbiome of the subject in a manner that prevents or reduces the likelihood that the subject will develop GVHD. In addition or alternatively, the compositions of the invention can be administered to a subject after the subject has developed GVHD, e.g., acute GVHD, or chronic GVHD. In this embodiment, the composition modulates the microbiome of the subject in a manner that treats or reduces the severity of GVHD. In another embodiment, the composition can be administered after GVHD has been resolved in order to prevent relapse or recurrence of GVHD.

[0368] The microbial compositions, with or without one or more prebiotics, offer a protective and/or therapeutic effect against infection by one or more GI pathogens of interest and can be administered after an acute case of infection has been resolved in order to prevent relapse, during an acute case of infection as a complement to antibiotic therapy if the bacterial composition is not sensitive to the same antibiotics as the GI pathogen, or to prevent infection or reduce transmission from disease carriers. In one embodiment, the subject is a transplant recipient. In another embodiment, the subject has or is at risk for developing GVHD.

[0369] The present microbial compositions, with or without one or more prebiotics, can be useful in a variety of clinical situations. For example, the compositions can be administered as a complementary treatment to antibiotics when a patient is suffering from an acute infection, to reduce the risk of recurrence after an acute infection has subsided, or when a patient will be in close proximity to others with or at risk of serious gastrointestinal infections (physicians, nurses, hospital workers, family members of those who are ill or hospitalized).

[0370] The present microbial compositions, with or without one or more prebiotics, can be administered to animals, including humans, laboratory animals (e.g., primates, rats, mice), livestock (e.g., cows, sheep, goats, pigs, turkeys, chickens), and household pets (e.g., dogs, cats, rodents).

[0371] In the present method, the microbial composition, with or without one or more prebiotics, can be administered enterically, in other words, by a route of access to the gastrointestinal tract or vagina. This includes oral administration, rectal administration (including enema, suppository, or colonoscopy), by an oral or nasal tube (nasogastric, nasojejunal, oral gastric, or oral jejunal), as detailed more fully herein.

[0372] Pretreatment Protocols.

[0373] Prior to administration of the microbial composition, with or without one or more prebiotics, the patient can optionally have a pretreatment protocol to prepare the gastrointestinal tract or vagina to receive the bacterial composition. In certain embodiments, the pretreatment protocol is advisable, such as when a patient has an acute infection with a highly resilient pathogen. In other embodiments, the pretreatment protocol is entirely optional, such as when the pathogen causing the infection is not resilient, or the patient has had an acute infection that has been successfully treated but where the physician is concerned that the infection may

recur. In these instances, the pretreatment protocol can enhance the ability of the bacterial composition to affect the patient's microbiome.

[0374] As one way of preparing the patient for administration of the microbial ecosystem, at least one antibiotic can be administered to alter the bacteria in the patient. As another way of preparing the patient for administration of the microbial ecosystem, a standard colon-cleansing preparation can be administered to the patient to substantially empty the contents of the colon, such as used to prepare a patient for a colonoscopy. By "substantially emptying the contents of the colon," this application means removing at least 75%, at least 80%, at least 90%, at least 95%, or about 100% of the contents of the ordinary volume of colon contents. Antibiotic treatment can precede the colon-cleansing protocol.

[0375] If a patient has received an antibiotic for treatment of an infection, or if a patient has received an antibiotic as part of a specific pretreatment protocol, in one embodiment, the antibiotic can be stopped in sufficient time to allow the antibiotic to be substantially reduced in concentration in the gut or vagina before the bacterial composition is administered. In one embodiment, the antibiotic can be discontinued 1, 2, or 3 days before the administration of the bacterial composition. In another embodiment, the antibiotic can be discontinued 3, 4, 5, 6, or 7 antibiotic half-lives before administration of the bacterial composition. In another embodiment, the antibiotic can be chosen so the constituents in the bacterial composition have an MIC50 that is higher than the concentration of the antibiotic in the gut or vagina.

[0376] MIC50 of a bacterial composition or the elements in the composition can be determined by methods well known in the art. Reller et al., Antimicrobial Susceptibility Testing: A Review of General Principles and Contemporary Practices, Clinical Infectious Diseases 49(11):1749-1755 (2009). In such an embodiment, the additional time between antibiotic administration and administration of the bacterial composition is not necessary. If the pretreatment protocol is part of treatment of an acute infection, the antibiotic can be chosen so that the infection is sensitive to the antibiotic, but the constituents in the bacterial composition are not sensitive to the antibiotic.

[0377] Routes of Administration.

[0378] As described above, the compositions can also be administered in vivo in a pharmaceutically acceptable carrier. By "pharmaceutically acceptable" is meant a material that is not biologically or otherwise undesirable, i.e., the material may be administered to a subject, along with the nucleic acid or vector, without causing any undesirable biological effects or interacting in a deleterious manner with any of the other components of the pharmaceutical composition in which it is contained. The carrier would naturally be selected to minimize any degradation of the active ingredient and to minimize any adverse side effects in the subject, as would be well known to one of skill in the art. Compositions can be administered by any route suitable for the delivery of disclosed compositions for treating, inhibiting, or preventing a dysbiosis. or diseases and disorders associated with a dysbiosis, including, but are not limited to orally, sublingually, rectally, parentally (e.g., intravenous injection (i.v.), intracranial injection (i.e.): intramuscular injection (i.m.), intraperitoneal injection (i.p.), and subcutaneous injection (s.c.) and intraosseous infusion (i.o.)), transdermally (using any standard patch), extracorporeally, inhalation, topically or the like, including topical intranasal administration or administration by inhalant. The compositions and dosage forms described herein can be administered by e.g., intradermal, ophthalmic, (intra)nasally, local, non-oral, such as aerosol, inhalation, subcutaneous, intramuscular, buccal, sublingual, (trans)rectal, vaginal, intra-arterial, and intrathecal, transmucosal (e.g., sublingual, lingual, (trans)buccal, (trans)urethral, vaginal (e.g., trans- and perivaginally), intravesical, intrapulmonary, intraduodenal, intragastrical, intrabronchial, etc. In preferred embodiments, the pharmaceutical compositions and dosage forms described herein are administered by routes selected from oral, topical, (trans)dermal, (intra)nasal, and rectal. In certain embodiments, the (intra)nasal administration is achieved via aerosol or inhalation.

[0379] The compositions of the invention are suitable for administration to mammals and non-mammalian animals in need thereof. In certain embodiments, the mammalian subject is a human subject who has one or more symptoms of a dysbiosis.

[0380] In some embodiments, the subject is fed a meal within one hour of administration of the probiotic composition. In another embodiment, the subject is fed a meal concurrently with administration of the probiotic composition.

[0381] When a mammalian subject is suffering from a disease, disorder or condition characterized by an aberrant microbiota, the bacterial compositions described herein are suitable for treatment thereof. In some embodiments, the mammalian subject has not received antibiotics in advance of treatment with the bacterial compositions. For example, the mammalian subject has not been administered at least two doses of vancomycin, metronidazole and/or or similar antibiotic compound within one week prior to administration of the therapeutic composition. In other embodiments, the mammalian subject has not previously received an antibiotic compound in the one month prior to administration of the therapeutic composition. In other embodiments, the mammalian subject has received one or more treatments with one or more different antibiotic compounds and such treatment(s) resulted in no improvement or a worsening of symptoms.

[0382] In some embodiments, the gastrointestinal disease, disorder or condition is a pathogen infection, ulcerative colitis, colitis, Crohn's disease, or irritable bowel disease. Beneficially, the therapeutic composition is administered only once prior to improvement of the disease, disorder or condition. In some embodiments, the therapeutic composition is administered at intervals greater than two days, such as once every three, four, five or six days, or every week or less frequently than every week. In other embodiments, the preparation can be administered intermittently according to a set schedule, e.g., once a day, once weekly, or once monthly, or when the subject relapses from the primary illness. In another embodiment, the preparation may be administered on a long-term basis to subjects who are at risk for infection with or who may be carriers of these pathogens, including subjects who will have an invasive medical procedure (such as surgery), who will be hospitalized, who live in a long-term care or rehabilitation facility, who are exposed to pathogens by virtue of their profession (livestock and animal processing workers), or who could be carriers of pathogens (including hospital workers such as physicians, nurses, and other health care professionals).

[0383] In certain embodiments, the microbial composition is administered enterically. This preferentially includes oral administration, or by an oral or nasal tube (including nasogastric, nasojejunal, oral gastric, or oral jejunal). In other

embodiments, administration includes rectal administration (including enema, suppository, or colonoscopy). The microbial composition can be administered to at least one region of the gastrointestinal tract, including the mouth, esophagus, stomach, small intestine, large intestine, and rectum. In some embodiments, it is administered to all regions of the gastrointestinal tract. The microbial compositions can be administered orally in the form of medicaments such as powders, capsules, tablets, gels or liquids. The bacterial compositions can also be administered in gel or liquid form by the oral route or through a nasogastric tube, or by the rectal route in a gel or liquid form, by enema or instillation through a colonoscope or by a suppository. In certain embodiments of the above invention, the microbial composition is administered enterically with one or more prebiotics.

[0384] If the composition is administered colonoscopically and, optionally, if the composition is administered by other rectal routes (such as an enema or suppository) or even if the subject has an oral administration, the subject can have a colon-cleansing preparation. The colon-cleansing preparation can facilitate proper use of the colonoscope or other administration devices, but even when it does not serve a mechanical purpose, it can also maximize the proportion of the bacterial composition relative to the other organisms previously residing in the gastrointestinal tract of the subject. For example, the colon cleansing preparation may maximize the amount of bacterial entities of the bacterial composition that reach and/or engraft in the gastrointestinal tract of the subject. Any ordinarily acceptable colon-cleansing preparation may be used such as those typically provided when a subject undergoes a colonoscopy.

[0385] Dosages and Schedule for Administration.

[0386] The dose administered to a subject should be sufficient to prevent a dysbiosis, partially reverse a dysbiosis, fully reverse a dysbiosis, or establish a healthy-state microbiome. In some aspects, the dose administered to a subject should be sufficient to prevent the onset of symptoms associated with an autoimmune, inflammatory, or barrier disorder, to reduces the symptoms associated with an autoimmune, inflammatory, or barrier disorder, to eliminate the symptoms associated with an autoimmune, inflammatory, or barrier disorder, or to prevent relapse or recurrence of an autoimmune, inflammatory, or barrier disorder.

[0387] One skilled in the art will recognize that dosage will depend upon a variety of factors including the strength of the particular active components employed, as well as the age, species, condition, and body weight of the subject. The size of the dose will also be determined by the route, timing, and frequency of administration as well as the existence, nature, and extent of any adverse side-effects that might accompany the administration of a particular composition and the desired physiological effect.

[0388] Suitable doses and dosage regimens can be determined by conventional range-finding techniques known to those of ordinary skill in the art. Generally, treatment is initiated with smaller dosages, which are less than the optimum dose of the active components. Thereafter, the dosage is increased by small increments until the optimum effect under the circumstances is reached. An effective dosage and treatment protocol can be determined by routine and conventional means, starting e.g. with a low dose in laboratory animals and then increasing the dosage while monitoring the effects, and systematically varying the dosage regimen as well. Animal studies are commonly used to determine the maximal tolerable dose ("MTD") of bioactive agent per kilogram weight. Those skilled in the art regularly extrapolate doses for efficacy, while avoiding toxicity, in other species, including humans.

[0389] Dosing may be in one or a combination of two or more administrations, e.g., daily, bi-daily, weekly, monthly, or otherwise in accordance with the judgment of the clinician or practitioner, taking into account factors such as age, weight, severity of the disease, and the dose administered in each administration.

[0390] In accordance with the above, in therapeutic applications, the dosages of the composition used in accordance with the invention vary depending on the form, depending on the age, weight, and clinical condition of the recipient patient, and depending on the experience and judgment of the clinician or practitioner administering the therapy, among other factors affecting the selected dosage. Generally, the dose should be sufficient to result in relieving, and preferably eliminating, a dysbiosis or disease-associated microbiome, most preferably causing complete recovery from the autoimmune, inflammatory, or barrier disorder. Relief or elimination of a dysbiosis or disease-associated microbiome may be measured by culturing and/or sequencing techniques, and well as by detection of microbial biomarkers in bodily fluids including but not limited to serum, urine, and feces, or by other techniques known in the art. Relief or elimination of an autoimmune, inflammatory, or barrier disease, condition, or disorder may be indicated by biopsy and subsequent analysis of immune cells, microbial cells, and/or TEER, by local or systemic measurement of cytokine levels, by detection of biomarkers for immune cells, by a lactulose/mannitol test, or by other techniques known in the art.

[0391] In some embodiments, the microbes, carbohydrates, and microbial and prebiotic compositions are provided in a dosage form. In certain embodiments, the dosage form is designed for administration of at least one OTU or combination thereof disclosed herein, wherein the total amount of bacterial composition administered is selected from 0.1 ng to 10 g, 10 ng to 1 g, 100 ng to 0.1 g, 0.1 mg to 500 mg, 1 mg to 100 mg, or from 10-15 mg. In other embodiments, the bacterial composition is consumed at a rate of from 0.1 ng to 10 g a day, 10 ng to 1 g a day, 100 ng to 0.1 g a day, 0.1 mg to 500 mg a day, 1 mg to 100 mg a day, or from 10-15 mg a day, or more.

[0392] In certain embodiments, the treatment period is at least 1 day, at least 2 days, at least 3 days, at least 4 days, at least 5 days, at least 6 days, at least 1 week, at least 2 weeks, at least 3 weeks, at least 4 weeks, at least 1 month, at least 2 months, at least 3 months, at least 4 months, at least 5 months, at least 6 months, or at least 1 year. In some embodiments the treatment period is from 1 day to 1 week, from 1 week to 4 weeks, from 1 month, to 3 months, from 3 months to 6 months, from 6 months to 1 year, or for over a year.

[0393] In one embodiment, between about 10^5 and about 10^{12} microorganisms (e.g., CFUs) total can be administered to the patient in a given dosage form. In another embodiment, an effective amount can be provided in from 1 to 500 ml or from 1 to 500 grams of the bacterial composition having from 10^7 to 10^{11} bacteria per ml or per gram, or a capsule, tablet or suppository having from 1 mg to 1000 mg lyophilized powder having from 10^7 to 10^{11} bacteria. Those receiving acute treatment can receive higher doses than those who are receiving chronic administration (such as hospital workers or those admitted into long-term care facilities).

[0394] Any of the preparations described herein can be administered once on a single occasion or on multiple occasions, such as once a day for several days or more than once a day on the day of administration (including twice daily, three times daily, or up to five times daily). In another embodiment, the preparation can be administered intermittently according to a set schedule, e.g., once weekly, once monthly, or when the patient relapses from the primary illness. In one embodiment, the preparation can be administered on a long-term basis to individuals who are at risk for infection with or who may be carriers of these pathogens, including individuals who will have an invasive medical procedure (such as surgery), who will be hospitalized, who live in a long-term care or rehabilitation facility, who are exposed to pathogens by virtue of their profession (livestock and animal processing workers), or who could be carriers of pathogens (including hospital workers such as physicians, nurses, and other health care professionals).

[0395] Patient Selection.

[0396] Particular microbial compositions, with or without one or more prebiotic, can be selected for individual patients or for patients with particular profiles. For example, 16S sequencing can be performed for a given patient to identify the bacteria present in his or her microbiota. The sequencing can either profile the patient's entire microbiome using 16S sequencing (to the family, genera, or species level), a portion of the patient's microbiome using 16S sequencing, or it can be used to detect the presence or absence of specific candidate bacteria that are biomarkers for health or a particular disease state, such as markers of multi-drug resistant organisms or specific genera of concern such as *Escherichia*. Based on the biomarker data, a particular composition can be selected for administration to a patient to supplement or complement a patient's microbiota in order to restore health or treat or prevent disease. In another embodiment, patients can be screened to determine the composition of their microbiota to determine the likelihood of successful treatment.

[0397] In some embodiments, metabolite profiles of patient tissue samples or microbes cultures from patient tissue are used to identify risk factors for developing a gastrointestinal, autoimmune or inflammatory response, to diagnose a gastrointestinal, autoimmune or inflammatory disease, to evaluate the prognosis or severity of said disease, to evaluate the success of a treatment regimen, or any combination thereof. Exemplary metabolites for the purposes of diagnosis, prognostic risk assessment, or treatment assessment purposes include short chain fatty acids, bile acids, and lactate. In preferred embodiments, metabolite profiles are taken at different time points during a patient's disease and treatment in order to better evaluate the patient's disease state including recovery or relapse events. Such monitoring is also important to lower the risk of a patient developing a new autoimmune condition following immunomodulatory treatment. In some embodiments, metabolite profiles inform subsequent treatment, including but not limited to alterations in dosage of therapeutic compositions, formations of prebiotic, or the administration of a particular prebiotic or bacterial population, in order to promote the growth, proliferation, colonization, and/or engraftment of a desired microbial population in the host. In some embodiments, a patient has a deficiency of a desired microbial population which is enhanced by treatment. In some embodiments, a patient has a excess of a desired microbial population which is decreased by treatment.

[0398] Pharmaceutical Compositions and Formulations of the Invention

[0399] Formulations. Provided are formulations for administration to humans and other subjects in need thereof. Generally the microbial compositions are combined with additional active and/or inactive materials in order to produce a final product, which may be in single dosage unit or in a multi-dose format. In some embodiments of the invention, the microbial compositions are comprised of microbes. In some embodiments of the invention, the microbial compositions are comprised of microbes and one or more prebiotics.

[0400] As described herein, the composition comprises at least one prebiotic carbohydrate.

[0401] A "carbohydrate" refers to a sugar or polymer of sugars. The terms "saccharide," "polysaccharide," "carbohydrate," and "oligosaccharide" may be used interchangeably. Most carbohydrates are aldehydes or ketones with many hydroxyl groups, usually one on each carbon atom of the molecule. Carbohydrates generally have the molecular formula $C_nH_{2n}O_n$. A carbohydrate can be a monosaccharide, a disaccharide, trisaccharide, oligosaccharide, or polysaccharide. The most basic carbohydrate is a monosaccharide, such as glucose, sucrose, galactose, mannose, ribose, arabinose, xylose, and fructose. Disaccharides are two joined monosaccharides. Exemplary disaccharides include sucrose, maltose, cellobiose, and lactose. Typically, an oligosaccharide includes between three and six monosaccharide units (e.g., raffinose, stachyose), and polysaccharides include six or more monosaccharide units. Exemplary polysaccharides include starch, glycogen, and cellulose. Carbohydrates can contain modified saccharide units, such as 2'-deoxyribose wherein a hydroxyl group is removed, 2'-fluororibose wherein a hydroxyl group is replace with a fluorine, or N-acetylglucosamine, a nitrogen-containing form of glucose (e.g., 2'-fluororibose, deoxyribose, and hexose). Carbohydrates can exist in many different forms, for example, conformers, cyclic forms, acyclic forms, stereoisomers, tautomers, anomers, and isomers.

[0402] In some embodiments, the composition comprises at least one lipid. As used herein, a "lipid" includes fats, oils, triglycerides, cholesterol, phospholipids, fatty acids in any form including free fatty acids. Fats, oils and fatty acids can be saturated, unsaturated (cis or trans) or partially unsaturated (cis or trans). In some embodiments, the lipid comprises at least one fatty acid selected from lauric acid (12:0), myristic acid (14:0), palmitic acid (16:0), palmitoleic acid (16:1), margaric acid (17:0), heptadecenoic acid (17:1), stearic acid (18:0), oleic acid (18:1), linoleic acid (18:2), linolenic acid (18:3), octadecatetraenoic acid (18:4), arachidic acid (20:0), eicosenoic acid (20:1), eicosadienoic acid (20:2), eicosatetraenoic acid (20:4), eicosapentaenoic acid (20:5) (EPA), docosanoic acid (22:0), docosenoic acid (22:1), docosapentaenoic acid (22:5), docosahexaenoic acid (22:6) (DHA), and tetracosanoic acid (24:0). In other embodiments, the composition comprises at least one modified lipid, for example, a lipid that has been modified by cooking.

[0403] In some embodiments, the composition comprises at least one supplemental mineral or mineral source. Examples of minerals include, without limitation: chloride, sodium, calcium, iron, chromium, copper, iodine, zinc, magnesium, manganese, molybdenum, phosphorus, potassium, and selenium. Suitable forms of any of the foregoing minerals include soluble mineral salts, slightly soluble mineral salts, insoluble mineral salts, chelated minerals, mineral com-

plexes, non-reactive minerals such as carbonyl minerals, and reduced minerals, and combinations thereof.

[0404] In certain embodiments, the composition comprises at least one supplemental vitamin. The at least one vitamin can be fat-soluble or water soluble vitamins. Suitable vitamins include but are not limited to vitamin C, vitamin A, vitamin E, vitamin B12, vitamin K, riboflavin, niacin, vitamin D, vitamin B6, folic acid, pyridoxine, thiamine, pantothenic acid, and biotin. Suitable forms of any of the foregoing are salts of the vitamin, derivatives of the vitamin, compounds having the same or similar activity of the vitamin, and metabolites of the vitamin.

[0405] The composition(s) may include different types of carriers depending on whether it is to be administered in solid, liquid or aerosol form, and whether it needs to be sterile for such routes of administration such as injection. The present invention can be administered intravenously, intradermally, intraarterially, intraperitoneally, intralesionally, intracranially, intraarticularly, intraprostaticaly, intrapleurally, intratracheally, intranasally, intravitreally, intravaginally, intrarectally, topically, intratumorally, intramuscularly, intraperitoneally, subcutaneously, subconjunctival, intravesicularlly, mucosally, intlrapericardially, intraumbilically, intraocularally, orally, topically, locally, as an injection, infusion, continuous infusion, localized perfusion bathing target cells directly, via a catheter, via a lavage, in lipid compositions (e.g., liposomes), as an aerosol, or by other method or any combination of the foregoing as would be known to one of ordinary skill in the art (see, for example, Remington's Pharmaceutical Sciences, 18th Ed. Mack Printing Company, 1990, incorporated herein by reference).

[0406] In other embodiments, the composition comprises an excipient. Non-limiting examples of suitable excipients include a buffering agent, a preservative, a stabilizer, a binder, a compaction agent, a lubricant, a dispersion enhancer, a disintegration agent, a flavoring agent, a sweetener, and a coloring agent.

[0407] In another embodiment, the excipient is a buffering agent. Non-limiting examples of suitable buffering agents include sodium citrate, magnesium carbonate, magnesium bicarbonate, calcium carbonate, and calcium bicarbonate.

[0408] In some embodiments, the excipient comprises a preservative. Non-limiting examples of suitable preservatives include antioxidants, such as alpha-tocopherol and ascorbate, and antimicrobials, such as parabens, chlorobutanol, and phenol.

[0409] In cases where a probiotic formulation contains anerobic bacterial strains, the pharmaceutical formulation and excipients can be selected to prevent exposure of the bacterial strains to oxygen.

[0410] In other embodiments, the composition comprises a binder as an excipient. Non-limiting examples of suitable binders include starches, pregelatinized starches, gelatin, polyvinylpyrolidone, cellulose, methylcellulose, sodium carboxymethylcellulose, ethylcellulose, polyacrylamides, polyvinyloxoazolidone, polyvinylalcohols, C_{12}-C_{18} fatty acid alcohol, polyethylene glycol, polyols, saccharides, oligosaccharides, and combinations thereof.

[0411] In another embodiment, the composition comprises a lubricant as an excipient. Non-limiting examples of suitable lubricants include magnesium stearate, calcium stearate, zinc stearate, hydrogenated vegetable oils, sterotex, polyoxyethylene monostearate, talc, polyethyleneglycol, sodium benzoate, sodium lauryl sulfate, magnesium lauryl sulfate, and light mineral oil.

[0412] In other embodiments, the composition comprises a dispersion enhancer as an excipient. Non-limiting examples of suitable dispersants include starch, alginic acid, polyvinylpyrrolidones, guar gum, kaolin, bentonite, purified wood cellulose, sodium starch glycolate, isoamorphous silicate, and microcrystalline cellulose as high HLB emulsifier surfactants.

[0413] In some embodiments, the composition comprises a disintegrant as an excipient. In other embodiments, the disintegrant is a non-effervescent disintegrant. Non-limiting examples of suitable non-effervescent disintegrants include starches such as corn starch, potato starch, pregelatinized and modified starches thereof, sweeteners, clays, such as bentonite, micro-crystalline cellulose, alginates, sodium starch glycolate, gums such as agar, guar, locust bean, karaya, pecitin, and tragacanth. In another embodiment, the disintegrant is an effervescent disintegrant. Non-limiting examples of suitable effervescent disintegrants include sodium bicarbonate in combination with citric acid, and sodium bicarbonate in combination with tartaric acid.

[0414] In another embodiment, the excipient comprises a flavoring agent. Flavoring agents can be chosen from synthetic flavor oils and flavoring aromatics; natural oils; extracts from plants, leaves, flowers, and fruits; and combinations thereof. In some embodiments the flavoring agent is selected from cinnamon oils; oil of wintergreen; peppermint oils; clover oil; hay oil; anise oil; eucalyptus; vanilla; citrus oil such as lemon oil, orange oil, grape and grapefruit oil; and fruit essences including apple, peach, pear, strawberry, raspberry, cherry, plum, pineapple, and apricot.

[0415] In other embodiments, the excipient comprises a sweetener. Non-limiting examples of suitable sweeteners include glucose (corn syrup), dextrose, invert sugar, fructose, and mixtures thereof (when not used as a carrier); saccharin and its various salts such as the sodium salt; dipeptide sweeteners such as aspartame; dihydrochalcone compounds, glycyrrhizin; *Stevia Rebaudiana* (Stevioside); chloro derivatives of sucrose such as sucralose; and sugar alcohols such as sorbitol, mannitol, sylitol, and the like. Also contemplated are hydrogenated starch hydrolysates and the synthetic sweetener 3,6-dihydro-6-methyl-1,2,3-oxathiazin-4-one-2,2-dioxide, particularly the potassium salt (acesulfame-K), and sodium and calcium salts thereof.

[0416] In yet other embodiments, the composition comprises a coloring agent. Non-limiting examples of suitable color agents include food, drug and cosmetic colors (FD&C), drug and cosmetic colors (D&C), and external drug and cosmetic colors (Ext. D&C). The coloring agents can be used as dyes or their corresponding lakes.

[0417] The weight fraction of the excipient or combination of excipients in the formulation is usually about 99% or less, such as about 95% or less, about 90% or less, about 85% or less, about 80% or less, about 75% or less, about 70% or less, about 65% or less, about 60% or less, about 55% or less, 50% or less, about 45% or less, about 40% or less, about 35% or less, about 30% or less, about 25% or less, about 20% or less, about 15% or less, about 10% or less, about 5% or less, about 2% or less, or about 1% or less of the total weight of the composition.

[0418] The compositions disclosed herein can be formulated into a variety of forms and administered by a number of

different means. The compositions can be administered orally, rectally, or parenterally, in formulations containing conventionally acceptable carriers, adjuvants, and vehicles as desired. The term "parenteral" as used herein includes subcutaneous, intravenous, intramuscular, or intrasternal injection and infusion techniques. In an exemplary embodiment, the composition is administered orally.

[0419] Solid dosage forms for oral administration include capsules, tablets, caplets, pills, troches, lozenges, powders, and granules. A capsule typically comprises a core material comprising a bacterial composition and a shell wall that encapsulates the core material. In some embodiments, the core material comprises at least one of a solid, a liquid, and an emulsion. In other embodiments, the shell wall material comprises at least one of a soft gelatin, a hard gelatin, and a polymer. Suitable polymers include, but are not limited to: cellulosic polymers such as hydroxypropyl cellulose, hydroxyethyl cellulose, hydroxypropyl methyl cellulose (HPMC), methyl cellulose, ethyl cellulose, cellulose acetate, cellulose acetate phthalate, cellulose acetate trimellitate, hydroxypropylmethyl cellulose phthalate, hydroxypropylmethyl cellulose succinate and carboxymethylcellulose sodium; acrylic acid polymers and copolymers, such as those formed from acrylic acid, methacrylic acid, methyl acrylate, ammonio methylacrylate, ethyl acrylate, methyl methacrylate and/or ethyl methacrylate (e.g., those copolymers sold under the trade name "Eudragit"); vinyl polymers and copolymers such as polyvinyl pyrrolidone, polyvinyl acetate, polyvinylacetate phthalate, vinylacetate crotonic acid copolymer, and ethylene-vinyl acetate copolymers; and shellac (purified lac). In yet other embodiments, at least one polymer functions as taste-masking agents.

[0420] Tablets, pills, and the like can be compressed, multiply compressed, multiply layered, and/or coated. The coating can be single or multiple. In one embodiment, the coating material comprises at least one of a saccharide, a polysaccharide, and glycoproteins extracted from at least one of a plant, a fungus, and a microbe. Non-limiting examples include corn starch, wheat starch, potato starch, tapioca starch, cellulose, hemicellulose, dextrans, maltodextrin, cyclodextrins, inulins, pectin, mannans, gum arabic, locust bean gum, mesquite gum, guar gum, gum karaya, gum ghatti, tragacanth gum, funori, carrageenans, agar, alginates, chitosans, or gellan gum. In some embodiments the coating material comprises a protein. In another embodiment, the coating material comprises at least one of a fat and an oil. In other embodiments, the at least one of a fat and an oil is high temperature melting. In yet another embodiment, the at least one of a fat and an oil is hydrogenated or partially hydrogenated. In one embodiment, the at least one of a fat and an oil is derived from a plant. In other embodiments, the at least one of a fat and an oil comprises at least one of glycerides, free fatty acids, and fatty acid esters. In some embodiments, the coating material comprises at least one edible wax. The edible wax can be derived from animals, insects, or plants. Non-limiting examples include beeswax, lanolin, bayberry wax, carnauba wax, and rice bran wax. Tablets and pills can additionally be prepared with enteric coatings.

[0421] Alternatively, powders or granules embodying the bacterial compositions disclosed herein can be incorporated into a food product. In some embodiments, the food product is a drink for oral administration. Non-limiting examples of a suitable drink include fruit juice, a fruit drink, an artificially flavored drink, an artificially sweetened drink, a carbonated beverage, a sports drink, a liquid diary product, a shake, an alcoholic beverage, a caffeinated beverage, infant formula and so forth. Other suitable means for oral administration include aqueous and nonaqueous solutions, emulsions, suspensions and solutions and/or suspensions reconstituted from non-effervescent granules, containing at least one of suitable solvents, preservatives, emulsifying agents, suspending agents, diluents, sweeteners, coloring agents, and flavoring agents.

[0422] In some embodiments, the food product can be a solid foodstuff. Suitable examples of a solid foodstuff include without limitation a food bar, a snack bar, a cookie, a brownie, a muffin, a cracker, an ice cream bar, a frozen yogurt bar, and the like.

[0423] In other embodiments, the compositions disclosed herein are incorporated into a therapeutic food. In some embodiments, the therapeutic food is a ready-to-use food that optionally contains some or all essential macronutrients and micronutrients. In another embodiment, the compositions disclosed herein are incorporated into a supplementary food that is designed to be blended into an existing meal. In one embodiment, the supplemental food contains some or all essential macronutrients and micronutrients. In another embodiment, the bacterial compositions disclosed herein are blended with or added to an existing food to fortify the food's protein nutrition. Examples include food staples (grain, salt, sugar, cooking oil, margarine), beverages (coffee, tea, soda, beer, liquor, sports drinks), snacks, sweets and other foods.

[0424] In one embodiment, the formulations are filled into gelatin capsules for oral administration. An example of an appropriate capsule is a 250 mg gelatin capsule containing from 10 (up to 100 mg) of lyophilized powder (10^8 to 10^{11} bacteria), 160 mg microcrystalline cellulose, 77.5 mg gelatin, and 2.5 mg magnesium stearate. In an alternative embodiment, from 10^5 to 10^{12} bacteria may be used, 10^5 to 10^7, 10^6 to 10^7, or 10^8 to 10^{10}, with attendant adjustments of the excipients if necessary. In an alternative embodiment, an enteric-coated capsule or tablet or with a buffering or protective composition can be used.

[0425] The microbial compositions, with or without one or more prebiotics, are generally formulated for oral or gastric administration, typically to a mammalian subject. In particular embodiments, the composition is formulated for oral administration as a solid, semi-solid, gel, or liquid form, such as in the form of a pill, tablet, capsule, or lozenge. In some embodiments, such formulations contain or are coated by an enteric coating to protect the bacteria through the stomach and small intestine, although spores are generally resistant to the stomach and small intestines. In other embodiments, the microbial compositions, with or without one or more prebiotics, may be formulated with a germinant to enhance engraftment, or efficacy. In yet other embodiments, the bacterial compositions may be co-formulated or co-administered with prebiotic substances, to enhance engraftment or efficacy. In some embodiments, bacterial compositions may be co-formulated or co-administered with prebiotic substances, to enhance engraftment or efficacy.

[0426] The microbial compositions, with or without one or more prebiotics, may be formulated to be effective in a given mammalian subject in a single administration or over multiple administrations. For example, a single administration is substantially effective to reduce inflammatory and immune response in a mammalian subject to whom the composition is administered. Substantially effective means that inflamma-

tory and/or immune response in the subject is reduced by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99% or greater than 99% following administration of the composition. For example, a single administration is substantially effective to reduce *Cl. difficile* and/or *Cl. difficile* toxin content in a mammalian subject to whom the composition is administered. Substantially effective means that *Cl. difficile* and/or *Cl. difficile* toxin content in the subject is reduced by at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 98%, 99% or greater than 99% following administration of the composition. In some embodiments, microbial and prebiotic compositions may be formulated as described above.

[0427] The composition is formulated such that a single oral dose contains at least about 1×10^4 colony forming units of the bacterial entities and/or fungal entities, and a single oral dose will typically contain about 1×10^4, 1×10^5, 1×10^6, 1×10^7, 1×10^8, 1×10^9, 1×10^{10}, 1×10^{11}, 1×10^{12}, 1×10^{13}, 1×10^{14}, 1×10^{15}, or greater than 1×10^{15} CFUs of the bacterial entities and/or fungal entities. The presence and/or concentration of a given type of bacterial may be known or unknown in a given purified spore population. If known, for example the concentration of spores of a given strain, or the aggregate of all strains, is e.g., 1×10^4, 1×10^5, 1×10^6, 1×10^7, 1×10^8, 1×10^9, 1×10^{10}, 1×10^{11}, 1×10^{12}, 1×10^{13}, 1×10^{14}, 1×10^{15}, or greater than 1×10^{15} viable bacterial entities (e.g., CFUs) and/or fungal entities per gram of composition or per administered dose.

[0428] In some formulations, the composition contains at least about 0.5%, 1%, 2%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90% or greater than 90% spores on a mass basis. In some formulations, the administered dose does not exceed 200, 300, 400, 500, 600, 700, 800, 900 milligrams or 1, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, or 1.9 grams in mass.

[0429] The bacteria and/or fungi may contain a purified population that includes a substantial enrichment of bacterial entities present in the fecal material, and wherein the composition optionally comprises a germinant, such as BHIS oxgall, CaDPA, one or more amino acids, a sugar, a nucleoside, a bile salt, a metal or a metal cation, a fatty acid, and a long-chain alkyl amine, or a combination thereof.

[0430] It has recently come to light that the DNA of commensal microbes, including many species of *Lactobacillus* protect against activation of lamina propia dendritic cells and sustain regulatory T cell conversion (Bouladoux N, Hall J A, Grainger J R, dos Santos L M, Kann M G, Nagarajan V, Verthelyi D, and Belkaid Y, 2012. Regulatory role of suppressive motifs from commensal DNA. Mucosal Immunol. 5: 623-634). Thus commensal DNA may protect against colitis, IBD, and/or other immunological intolerances in the gut. Furthermore, *Lactobacillus* species are prevalent in the healthy vaginal microbiome. Thus, DNA from *Lactobacillus* or other vaginal microbiome commensals may suppress immune responses in the vagina that could disrupt the normal healthy-state vaginal microbiome and lead to complications such as chronic HPV, infertility, miscarriages, or UTIs. As such, in certain embodiments, the microbial composition, pharmaceutical composition, dosage form, or kit additionally comprises DNA isolated from one or more host commensals.

[0431] Combination Therapy.

[0432] The microbial compositions, with or without one or more prebiotics, can be administered with other agents in a combination therapy mode, including anti-microbial agents. Administration can be sequential, over a period of hours or days, or simultaneous.

[0433] In one embodiment, the microbial compositions, with or without one or more prebiotics, are included in combination therapy with one or more anti-microbial agents, which include anti-bacterial agents, anti-fungal agents, anti-viral agents and anti-parasitic agents.

[0434] Anti-bacterial agents can include cephalosporin antibiotics (cephalexin, cefuroxime, cefadroxil, cefazolin, cephalothin, cefaclor, cefamandole, cefoxitin, cefprozil, and ceftobiprole); fluoroquinolone antibiotics (cipro, Levaquin, floxin, tequin, avelox, and norflox); tetracycline antibiotics (tetracycline, minocycline, oxytetracycline, and doxycycline); penicillin antibiotics (amoxicillin, ampicillin, penicillin V, dicloxacillin, carbenicillin, vancomycin, and methicillin); and carbapenem antibiotics (ertapenem, doripenem, imipenem/cilastatin, and meropenem).

[0435] Anti-viral agents can include Abacavir, Acyclovir, Adefovir, Amprenavir, Atazanavir, Cidofovir, Darunavir, Delavirdine, Didanosine, Docosanol, Efavirenz, Elvitegravir, Emtricitabine, Enfuvirtide, Etravirine, Famciclovir, Foscarnet, Fomivirsen, Ganciclovir, Indinavir, Idoxuridine, Lamivudine, Lopinavir Maraviroc, MK-2048, Nelfinavir, Nevirapine, Penciclovir, Raltegravir, Rilpivirine, Ritonavir, Saquinavir, Stavudine, Tenofovir Trifluridine, Valaciclovir, Valganciclovir, Vidarabine, Ibacitabine, Amantadine, Oseltamivir, Rimantidine, Tipranavir, Zalcitabine, Zanamivir and Zidovudine.

[0436] Examples of antifungal compounds include, but are not limited to polyene antifungals such as natamycin, rimocidin, filipin, nystatin, amphotericin B, candicin, and hamycin; imidazole antifungals such as miconazole, ketoconazole, clotrimazole, econazole, omoconazole, bifonazole, butoconazole, fenticonazole, isoconazole, oxiconazole, sertaconazole, sulconazole, and tioconazole; triazole antifungals such as fluconazole, itraconazole, isavuconazole, ravuconazole, posaconazole, voriconazole, terconazole, and albaconazole; thiazole antifungals such as abafungin; allylamine antifungals such as terbinafine, naftifine, and butenafine; and echinocandin antifungals such as anidulafungin, caspofungin, and micafungin. Other compounds that have antifungal properties include, but are not limited to polygodial, benzoic acid, ciclopirox, tolnaftate, undecylenic acid, flucytosine or 5-fluorocytosine, griseofulvin, and haloprogin.

[0437] In one embodiment, the bacterial compositions are included in combination therapy with one or more corticosteroids, mesalazine, mesalamine, sulfasalazine, sulfasalazine derivatives, immunosuppressive drugs, cyclosporin A, mercaptopurine, azathiopurine, prednisone, methotrexate, antihistamines, glucocorticoids, epinephrine, theophylline, cromolyn sodium, anti-leukotrienes, anti-cholinergic drugs for rhinitis, anti-cholinergic decongestants, mast-cell stabilizers, monoclonal anti-IgE antibodies, vaccines, and combinations thereof.

[0438] In one embodiment, the bacterial compositions are included in a combination or adjuvant therapy with one or more additional treatments for GVHD. For example, the bacterial compositions can be administered to a transplant subject who has been or currently is being treated with an immunosuppressive treatment like cyclosporine, high dose steroids, methotrexate, or methylprednisolone.

[0439] A prebiotic is an ingredient that can allow specific changes in both the composition and/or activity in the gas-

trointestinal microbiota that confers benefits upon host well-being and health. Prebiotics can include complex carbohydrates, amino acids, peptides, or other essential nutritional components for the survival of the bacterial composition. Prebiotics include, but are not limited to, amino acids, biotin, fructooligosaccharide, galactooligosaccharides, inulin, lactulose, mannan oligosaccharides, oligofructose-enriched inulin, oligofructose, oligodextrose, tagatose, trans-galactooligosaccharide, and xylooligosaccharides.

[0440] Methods for Testing Compositions for Populating Effect

[0441] In Vivo Assay for Determining Whether a Composition Populates a Subject's Gastrointestinal Tract or Vagina.

[0442] In order to determine that the composition populates the gastrointestinal tract or vagina of a subject, an animal model, such as a mouse model, can be used. The model can begin by evaluating the microbiota of the mice. Qualitative assessments can be accomplished using 16S profiling of the microbial community in the feces of normal mice. It can also be accomplished by full genome sequencing, whole genome shotgun sequencing (WGS), or traditional microbiological techniques. Quantitative assessments can be conducted using quantitative PCR (qPCR), described below, or by using traditional microbiological techniques and counting colony formation.

[0443] Optionally, the mice can receive an antibiotic treatment to mimic the condition of dysbiosis. Antibiotic treatment can decrease the taxonomic richness, diversity, and evenness of the community, including a reduction of abundance of a significant number of bacterial taxa. Dethlefsen et al., The pervasive effects of an antibiotic on the human gut microbiota, as revealed by deep 16S rRNA sequencing, PLoS Biology 6(11):3280 (2008). At least one antibiotic can be used, and antibiotics are well known. Antibiotics can include aminoglycoside antibiotic (amikacin, arbekacin, gentamicin, kanamycin, neomycin, netilmicin, paromomycin, rhodostreptomycin, streptomycin, tobramycin, and apramycin), amoxicillin, ampicillin, Augmentin (an amoxicillin/clavulanate potassium combination), cephalosporin (cefaclor, defadroxil, cefazolin, cefixime, fefoxitin, cefprozil, ceftazimdime, cefuroxime, cephalexin), clavulanate potassium, clindamycin, colistin, gentamycin, kanamycin, metronidazole, or vancomycin. As an individual, nonlimiting specific example, the mice can be provided with drinking water containing a mixture of the antibiotics kanamycin, colistin, gentamycin, metronidazole and vancomycin at 40 mg/kg, 4.2 mg/kg, 3.5 mg/kg, 21.5 mg/kg, and 4.5 mg/kg (mg per average mouse body weight), respectively, for 7 days. Alternatively, mice can be administered ciprofloxacin at a dose of 15-20 mg/kg (mg per average mouse body weight), for 7 days.

[0444] If the mice are provided with an antibiotic, a wash out period of from one day to three days may be provided with no antibiotic treatment and no bacterial composition treatment.

[0445] Subsequently, the composition is administered to the mice by oral gavage. The composition may be administered in a volume of 0.2 ml containing 10^4 CFUs of each type of bacteria in the therapeutic composition. Dose-response may be assessed by using a range of doses, including, but not limited to 10^2, 10^3, 10^4, 10^5, 10^6, 10^7, 10^8, 10^9, and/or 10^{10}.

[0446] The mice can be evaluated using 16S sequencing, full genome sequencing, whole genome shotgun sequencing (WGS), or traditional microbiological techniques to determine whether administering the composition has resulted in the population by one or more administered bacteria in the gastrointestinal tract or vagina of the mice. For example only, one day, three days, one week, two weeks, and one month after administration of the bacterial composition to the mice, 16S profiling is conducted to determine whether administering the composition has resulted in population by one or more administered bacteria in the gastrointestinal tract or vagina of the mice. Quantitative assessments, including qPCR and traditional microbiological techniques such as colony counting, can additionally or alternatively be performed, at the same time intervals.

[0447] Furthermore, the number of sequence counts that correspond exactly to those in the composition over time can be assessed to determine specifically which components of the bacterial composition reside in the gastrointestinal tract or vagina over a particular period of time. In one embodiment, the bacterial strains of the composition persist for a desired period of time. In another embodiment, the bacterial strains of the composition persist for a desired period of time, while also increasing the ability of other microbes (such as those present in the environment, food, etc.) to populate the gastrointestinal tract or vagina, further increasing overall diversity, as discussed below.

[0448] Ability of Compositions to Populate Different Regions of the Gastrointestinal Tract or Vagina.

[0449] The present microbial compositions can also be assessed for their ability to populate different regions on the gastrointestinal tract or vagina. In one embodiment, a microbes of the therapeutic composition can be chosen for its ability to populate one or more than one region of the gastrointestinal tract, including, but not limited to the stomach, the small intestine (duodenum, jejunum, and ileum), the large intestine (the cecum, the colon (the ascending, transverse, descending, and sigmoid colon), and the rectum). In another embodiment, the bacterial composition can be chosen for its ability to populate one or more than one region of the vagina. In some embodiments of the above invention, the microbial compositions comprise microbes and one or more prebiotics.

[0450] An in vivo study can be conducted to determine which regions of the gastrointestinal tract or vagina a given bacterial composition will populate. A mouse model similar to the one described above can be conducted, except instead of assessing the feces produced by the mice, particular regions of the gastrointestinal tract or vagina can be removed and studied individually. For example, at least one particular region of the gastrointestinal tract or vagina can be removed and a qualitative or quantitative determination can be performed on the contents of that region of the gastrointestinal tract or vagina. In another embodiment, the contents can optionally be removed and the qualitative or quantitative determination may be conducted on the tissue removed from the mouse.

[0451] qPCR.

[0452] As one quantitative method for determining whether a microbial composition, with or without one or more prebiotics, populates the gastrointestinal tract or vagina, quantitative PCR (qPCR) can be performed. Standard techniques can be followed to generate a standard curve for the bacterial composition of interest, either for all of the components of the bacterial composition collectively, individually, or in subsets (if applicable). Genomic DNA can be extracted from samples using commercially-available kits, such as the Mo Bio Powersoil®-htp 96 Well Soil DNA Isolation Kit (Mo Bio Laboratories, Carlsbad, Calif.), the Mo Bio Powersoil®

DNA Isolation Kit (Mo Bio Laboratories, Carlsbad, Calif.), or the QIAamp DNA Stool Mini Kit (QIAGEN, Valencia, Calif.) according to the manufacturer's instructions.

[0453] In some embodiments, qPCR can be conducted using HotMasterMix (5PRIME, Gaithersburg, Md.) and primers specific for the bacterial composition of interest, and may be conducted on a MicroAmp® Fast Optical 96-well Reaction Plate with Barcode (0.1 mL) (Life Technologies, Grand Island, N.Y.) and performed on a BioRad C1000™ Thermal Cycler equipped with a CFX96™ Real-Time System (BioRad, Hercules, Calif.), with fluorescent readings of the FAM and ROX channels. The Cq value for each well on the FAM channel is determined by the CFX Manager™ software version 2.1. The $\log_{10}$(cfu/ml) of each experimental sample is calculated by inputting a given sample's Cq value into linear regression model generated from the standard curve comparing the Cq values of the standard curve wells to the known $\log_{10}$(cfu/ml) of those samples. The skilled artisan may employ alternative qPCR modes.

VIII. Distal Dysbiosis

[0454] The probiotic compositions described herein have beneficial effects for the subject locally, at the site of administration (e.g., in the gastrointestinal tract for compositions administered orally, or in the vagina for compositions administered vaginally), as previously described. Surprisingly, the probiotic compositions described herein may also be used to correct or prevent a dysbiosis at a site distal to the site of administration.

[0455] "Dysbiosis" refers to a state of the microbiota of the gut or other body area in a subject, including mucosal or skin surfaces in which the normal diversity and/or function of the ecological network is disrupted. This unhealthy state can be due to a decrease in diversity, the overgrowth of one or more pathogens or pathobionts, symbiotic organisms able to cause disease only when certain genetic and/or environmental conditions are present in a subject, or the shift to an ecological microbial network that no longer provides an essential function to the host subject, and therefore no longer promotes health. Accordingly, a "gastrointestinal dysbiosis" refers to a state of the microbiota or microbiome of the gut in which the normal diversity and/or function of the ecological network or niche is disrupted. The term "gut" as used herein is meant to refer to the entire gastrointestinal or digestive tract (also referred to as the alimentary canal) and it refers to the system of organs within multi-cellular animals which takes in food, digests it to extract energy and nutrients, and expels the remaining waste. As used herein the term "gastrointestinal tract" refers to the entire digestive canal, from the oral cavity to the rectum. The term "gastrointestinal tract" includes, but is not limited to, mouth and proceeds to the esophagus, stomach, small intestine, large intestine, rectum and, finally, the anus.

[0456] The term "distal" generally is used in relation to the gastrointestinal tract, specifically the intestinal lumen, of a human or other mammal, which represent the intended sites of engraftment or colonization for probiotics administered orally. Thus, in relation to probiotics administered to the gastrointestinal tract, a "distal dysbiosis" includes a dysbiosis outside of the lumen of the gastrointestinal tract. In other instances, the term "distal" may be used in relation to the site of administration, intended engraftment, or intended colonization of a composition, e.g., a probiotic composition, of the invention. For example, if a probiotic composition is administered vaginally, a distal effect of the composition would occur outside the vagina. Similarly, if a probiotic composition is administered to the skin, e.g., through a skin patch, transdermal lotion, etc., a distal effect of the composition would occur in a niche other than the skin. If a probiotic composition is administered to the lungs, e.g., in an inhalable formulation, a distal effect of the composition would occur outside the lungs. If a probiotic composition is administered to the ear, eye, nose, etc., a distal effect of the composition would occur at a site other than the site of administration, engraftment, or colonization of the composition (i.e., distal to the ear, distal to the eye, distal to the nose, etc.).

[0457] Distal sites include but are not limited to the liver, spleen, fallopian tubes and uterus. Other distal sites include skin, blood and lymph nodes. In other embodiments, the distal site is placenta, spleen, liver, uterus, blood, eyes, ears, lungs, liver, pancreas, brain, embryonic sac, or vagina. In another embodiment, the distal site is vagina, skin, lungs, brain, nose, ear, eyes/conjunctiva, mouth, circulatory system, e.g., blood, placenta, reproductive tract, cardiovascular system, and/or nervous system. A probiotic composition may have an effect on the microbiota of more than one distal site in a subject. For example, in some embodiments, a probiotic composition modulates the microbiota of one or more sites distal to the site of administration, engraftment, or colonization, e.g., one or more of placenta, spleen, liver, uterus, blood, eyes, ears, lungs, liver, pancreas, brain, embryonic sac, vagina, skin, brain, nose, mouth, reproductive tract, cardiovascular system, and/or nervous system.

[0458] Any disruption from a preferred (e.g., ideal, normal, or beneficial) state of the microbiota can be considered a dysbiosis, even if such dysbiosis does not result in a detectable disease or disorder, or decrease in health. This state of dysbiosis may lead to a disease or disorder (e.g. GVHD, transplant rejection, and related conditions), or the state of dysbiosis may lead to a disease or disorder (e.g. GVHD, transplant rejection, and related conditions) only under certain conditions, or the state of dysbiosis may prevent a subject from responding to treatment or recovering from a disease or disorder (e.g. GVHD, transplant rejection, and related conditions). In the case of GVHD, a gastrointestinal dysbiosis can contribute to the pathology of GVHD by increasing inflammation and/or reducing intestinal barrier integrity. A dysbiosis distal to the gastrointestinal tract can also contribute to GVHD pathology, for example, by increasing systemic inflammation in the subject. In one embodiment, the distal dysbiosis is at or near the site of the transplant. Accordingly, probiotic compositions of the invention that modulate the microbiome, e.g., to correct a dysbiosis, can be used to prevent or treat GVHD in a transplant recipient. In addition, probiotic compositions that reduce inflammation and/or increase intestinal barrier integrity can be used to prevent or treat GVHD in a transplant recipient.

[0459] In certain aspects, the present invention is directed to a method of reconstituting, modulating, or creating a beneficial bacterial flora in the gastrointestinal tract of a mammalian host in need thereof, comprising administering to the mammalian host a composition comprising at least one isolated bacterial population. In one embodiment, the at least one bacterial population is coadministered or coformulated with one or more prebiotic, e.g, at least one polymer or monomer. In one embodiment, the prebiotic is a carbohydrate, e.g., xylose. In one embodiment, the subject is a transplant recipient. In one embodiment, the subject has or is at

risk for developing GVHD. In certain embodiments the gastrointestinal disease, disorder or condition is a disease or disorder associated with or characterized by reduced intestinal integrity.

[0460] In certain other aspects, the present invention is directed to a method of treating or alleviating a transplant disorder, e.g., GVHD or transplant rejection, in a subject in need thereof, the method comprising a administering to the subject at least one isolated bacterial population. In one embodiment, the at least one bacterial population is coadministered or coformulated with one or more prebiotic, e.g, at least one polymer or monomer. In one embodiment, the one or more prebiotic is a carbohydrate, e.g., xylose.

[0461] Provided are compositions and methods to provide modulation, engraftment and/or augmentation of one or more bacterial and/or fungal entities to a distal site. In order to characterize the alteration of a target niche, such as by engraftment and/or augmentation of a bacteria within the niche, provided are methods of detecting, quantifying and characterizing 16S, 18S and ITS signatures in skin, vagina, etc. Moreover, provided are methods of detecting bacterial and fungal components typically associated with one microbiota in a distal site, often associating with (in a physiological or manner) with the microbiota of that distal site. For example, following administration of a composition, bacteria detectably present in the GI tract or vagina prior to administration are detected in distal sites, for example, the blood, or another niche outside the GI lumen. For example, changes in the microbiome at a given site (e.g. GI tract) lead to changes in the microbiome at a distal site (e.g. vagina).

[0462] Accordingly, detecting and quantifying 16S, 18S and ITS signatures of the microbial network at a distal site can be used to characterize the components of the microbiome at the distal site under normal, healthy conditions, and can also be used to detect a dysbiosis at the distal site, when the components of the microbiome at the distal site are disrupted.

[0463] In order to characterize a distal dysbiosis, provided are methods of detecting, quantifying and characterizing 16S, 18S and ITS signatures in immune organs, such as the lymph nodes, spleen, etc. Moreover, provided are methods of detecting bacterial and fungal components typically associated with one microbiota in a distal site, often associating (in a physiological or pathological manner) with the microbiota of that distal site. For example, bacteria normally detected in the GI tract or vagina are detected in distal sites, for example, the blood.

[0464] A distal dysbiosis includes disruptions in the normal diversity and/or function of the microbial network in a subject at a site other than the gastrointestinal tract, which is generally the site of administration of probiotics provided orally. In cases where a probiotic composition is administered to a site other than the gastrointestinal tract, a distal dysbiosis can include disruptions in the normal diversity and/or function of the microbial network in a subject at a site other than the site of administration, colonization or engraftment.

[0465] Probiotic compositions described herein can correct or treat a distal dysbiosis by correcting the imbalance in microbial diversity that is present at the distal site. Bacteria contained in the probiotic composition can correct the distal dysbiosis directly, by translocating to the distal site. Bacteria contained in the probiotic composition can also correct the distal dysbiosis indirectly, by promoting translocation of other gut commensals to the distal site, or by modifying the microenvironment of the distal site to create conditions that restore a healthy microbiome, e.g., by reducing inflammation.

[0466] Without wishing to be bound by theory, the probiotic compositions of the invention may impact distal sites in several ways.

[0467] In one embodiment, a bacterial strain present in the probiotic composition engrafts in the gastrointestinal tract of a subject, and translocates to a distal site, thereby augmenting the bacterial strain present in the probiotic composition at the distal site. In one embodiment, the bacterial strain present in the probiotic composition is not detectably present at the distal site prior to administration of the probiotic.

[0468] In another embodiment, a bacterial strain present in the probiotic composition is augmented in the gastrointestinal tract of a subject without engraftment, and translocates to a distal site, thereby augmenting the bacterial strain present in the probiotic composition at the distal site. In one embodiment, the bacterial strain present in the probiotic composition is not detectably present at the distal site prior to administration of the probiotic.

[0469] In another embodiment, a bacterial strain present in the probiotic composition modulates the microenvironment of the gut, augmenting a second bacterial strain present within the gut microbiota. The second bacterial strain augmented in the gut translocates to a distal site, thereby augmenting the second bacterial strain at the distal site. In embodiments, the second bacterial strain is not present in the probiotic composition. In some embodiments, the bacterial strain present in the probiotic composition is an immunomodulatory bacteria, e.g., an anti-inflammatory bacteria. Modulation of the microenvironment of the gut may include, for example, alteration of cytokines secreted by host cells in and around the gut, reducing inflammation in the gut, increasing secretion of short chain fatty acids in the gut, or altering the proportion of immune cell subpopulations in the gut, each of which impacts the gut microbiome. Modulation of the microenvironment of the gut can include increasing or decreasing overall microbial diversity.

[0470] In another embodiment, a bacterial strain present in the probiotic composition modulates the microenvironment at a distal site in a subject, thereby augmenting a second bacterial strain at the distal site. In embodiments, the second bacterial strain is not present in the probiotic composition. In some embodiments, the bacterial strain present in the probiotic composition is an immunomodulatory bacteria, e.g., an anti-inflammatory bacteria. Immunomodulatory bacteria can modulate the microenvironment at a site distal to the gastrointestinal tract in a subject by, for example, reducing systemic inflammation. This can be achieved by altering the profile of cytokine expression by immune cells, or altering the proportion of immune cell subpopulations. Bacterial strains present in the probiotic composition can also modulate intestinal permeability, e.g., by secretion of short chain fatty acids, which impacts the microenvironment of distal sites. In addition or alternatively, bacterial strains present in the probiotic composition can increase or decrease overall microbial diversity.

[0471] Accordingly, the probiotic compositions described herein may additively or synergistically elicit an immunomodulatory response either distally, e.g., in which enteral administration of microbes results in altering the immune response at a site outside the gastrointestinal tract such as the skin or liver, or locally, e.g. the enteral administration of

microbes results in altering the immune response in the gastrointestinal tract, e.g., in the intestines.

[0472] The immune system of a subject and the microbiome of the subject are closely linked, and interact systemically. Disruptions to the microbiome, both in the gastrointestinal tract and at distal sites, can have profound effects throughout the body of the subject. In particular, disruptions to the microbiome increase systemic inflammation and intestinal barrier dysfunction in a subject. Increased inflammation and intestinal barrier dysfunction negatively impact the health of the subject in many ways, by contributing to a wide range of inflammatory and autoimmune conditions distal to the gastrointestinal tract. Conversely, increased inflammation in a subject leads to disruptions in the subject's microbiome, and disruptions to the microbiome lead in turn to further increases in inflammation. Administration of a probiotic composition containing immunomodulatory bacteria can reduce inflammation in the gastrointestinal tract and restore intestinal barrier integrity, resulting in a reduction in inflammation at sites distal to the gastrointestinal tract, and improvement in the symptoms of autoimmune or inflammatory disorders associated with systemic inflammation. Administration of a probiotic composition containing bacterial strains that secrete short chain fatty acids are also capable of reducing inflammation restoring intestinal barrier integrity.

[0473] In other embodiments, the probiotic compositions of the invention improve blood/brain barrier integrity. In other embodiments, the probiotic compositions of the invention improve lung epithelium integrity.

[0474] The probiotic compositions and methods described herein can prevent or treat the loss or reduction of barrier function recognized to occur during dysbiosis or in the shift in one or more microbiotal populations that give rise to the dysbiosis. The loss of barrier function results in systemic seeding of bacterial populations resulting in dysbiotic activity, and in some events, the loss of barrier function results in a local reseeding of the bacterial populations. In both situations, the resulting immune activation leads to pathogenic inflammatory and immune responses. In response, provided are compositions that are capable of restoring barrier function, restoring the normal microbiotal components, and reducing (e.g., suppressing) immune/inflammatory response. In one embodiment, the improvement of gut epithelium barrier integrity results in reduced trafficking of bacteria, bacterial components and/or bacterial metabolites into the blood. In some compositions, provided are antibiotic agents that remove the existing microflora in a target niche, while newly administered or recruited bacteria and fungi populate (or re-populate) the target niche. The combination with carbohydrates (e.g., by co-administration or co-formulation) may synergistically affect this population/repopulation technique.

[0475] Disorders associated with a dysbiosis, i.e., a gastrointestinal dysbiosis or a distal dysbiosis, which increases systemic inflammation and/or reduces intestinal barrier integrity include, for example, autoimmune or inflammatory disorders, Crohn's Disease, vaginal dysbiosis, and transplant disorders such as graft-versus-host disease. These disorders can be treated by administration (e.g., oral administration) of probiotic compositions containing immunomodulatory (e.g., anti-inflammatory) bacterial strains.

[0476] In some embodiments, the probiotic compositions described herein may additively or synergistically reduce the number of types of autoimmune disease- or inflammatory disease-associated pathogens or pathobionts either distally—e.g., orally-administered microbes reduce the total microbial burden in an organ not in the gastrointestinal tract, or intravaginally-administered microbes reduce the total microbial burden in an organ that is not the vagina—or locally, e.g., the intestines or vagina, respectively.

[0477] Accordingly, in one aspect, the invention provides a method of reducing inflammation in a subject, comprising administering to the subject a probiotic composition comprising an isolated, anti-inflammatory bacterial population, such that inflammation in the subject is reduced. A systemic reduction in inflammation can modulate the microbiome of niches distal to the site of administration, intended engraftment, or intended colonization of the bacterial population. The probiotic composition can contain an excipient useful for formulation as a pharmaceutical composition. In instances where the bacterial population includes anaerobic bacteria, the excipient can, in one embodiment, reduce exposure of the bacterial population to oxygen.

[0478] In a preferred embodiment, administration of the probiotic composition can reduce inflammation at a site distal to the site of administration, engraftment, or colonization, such as, for example, vagina, skin, lungs, brain, nose, ear, eyes/conjunctiva, mouth, circulatory system, e.g., blood, placenta, embryonic sac, reproductive tract, cardiovascular system, and/or nervous system. In one embodiment, administration of the probiotic composition can reduce inflammation at a site selected from blood, skin, vagina, liver, spleen, fallopian tubes, uterus, or a combination thereof. In one embodiment, administration of the probiotic composition modulates the microbiome at a distal site.

[0479] The anti-inflammatory bacterial population can induce a decrease in secretion of pro-inflammatory cytokines and/or an increase in secretion of anti-inflammatory cytokines by host cells. The anti-inflammatory properties of the bacterial population can be determined by methods described herein or known in the art, for example, by measuring alterations in cytokine secretion by peripheral blood mononuclear cells (PBMCs) exposed to the bacterial population. Anti-inflammatory bacteria can be selected for inclusion in the probiotic formulation based on modulation of particular cytokines of interest. For example, anti-inflammatory bacteria can be selected based on the ability to decrease secretion of one or more pro-inflammatory cytokines, e.g., IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof, and/or the ability to increase secretion of one or more anti-inflammatory cytokines, e.g., IL-10, IL-13, IL-4, IL-5, and combinations thereof.

[0480] In another aspect, the invention provides methods of treating or preventing a distal dysbiosis in a subject, by administering to the subject a probiotic composition comprising an isolated bacterial population in an amount sufficient to alter the microbiome at a site distal to the site of administration, engraftment, or colonization of the bacterial population, such that the distal dysbiosis is treated. For example, administration of the probiotic composition may modulate a first microbiome at the site of administration, engraftment or colonization of the bacterial population, causing subsequent modulation of a second microbiome at a site that is distinct from the first microbiome, e.g., a distal site.

[0481] In one embodiment, the invention provides methods of treating or preventing a distal dysbiosis, by orally administering a probiotic composition which alters the microbiome at a site distal to the gastrointestinal tract.

[0482] In another aspect, the invention provides a method of treating or preventing a disorder associated with a distal dysbiosis in a subject in need thereof, comprising administering to the subject a probiotic composition comprising an isolated bacterial population in an amount sufficient to alter the microbiome at a site of the distal dysbiosis, such that the disorder associated with the distal dysbiosis is treated. Disorders associated with distal dysbiosis, including disruptions to the systemic microbiome, are described herein and include, for example, autoimmune or inflammatory disorders such as graft-versus-host disease (GVHD), an inflammatory bowel disease (IBD), ulterative colitis, Crohn's disease, multiple sclerosis (MS), systemic lupus erythematosus (SLE), type I diabetes, rheumatoid arthritis, Sjogren's syndrome, and Celiac disease; transplant disorders such as graft-versus-host disease; and vaginal dysbiosis. In one embodiment, the disorder associated with distal dysbiosis occurs in the respiratory tract (e.g., lung), including but not limited to Cystic Fibrosis and chronic obstructive pulmonary disorder (COPD).

[0483] In one embodiment, the probiotic composition contains a species of bacteria that is deficient at the site of the distal dysbiosis. Administration of the probiotic composition can increase the quantity of the deficient species in the distal microbiome. In one embodiment, the deficient species is not detectably present at the site of the distal dysbiosis prior to administration of the probiotic composition. In one embodiment, the species of bacteria in the probiotic composition translocates to the site of the distal dysbiosis.

[0484] In another embodiment, the probiotic composition results in augmentation of a species of bacteria not present in the probiotic composition at a distal site. This augmentation can result from, for example, translocation of a species of bacteria not present in the probiotic composition to the distal site, and/or modulation of the microenvironment of the distal site in a manner that alters the microbiome.

[0485] In preferred embodiments, the probiotic composition contains immunomodulatory bacteria, e.g., anti-inflammatory bacteria.

[0486] In another aspect, the invention provides a method of reducing intestinal permeability in a subject, by administering a probiotic composition comprising an isolated bacterial population, wherein administration of the probiotic composition augments a species of bacteria that produces short chain fatty acids, such that the intestinal permeability of the subject is reduced. In other embodiments, intestinal permeability and disorders associated therewith is improved by administering a probiotic composition containing mucin-containing bacteria, and/or anti-inflammatory bacteria.

[0487] Probiotic compositions useful for correcting or treating a distal dysbiosis, or for treating a disorder distal to the gastrointestinal tract associated with a dysbiosis, can include any of the probiotic compositions described herein. In exemplary embodiments, a probiotic composition useful for correcting or treating a distal dysbiosis includes one or more bacterial strains from Table 1. In other embodiments, the probiotic composition useful for correcting or treating a distal dysbiosis includes one or more bacterial strains from Table 1A. In other embodiments, the probiotic composition useful for correcting or treating a distal dysbiosis includes one or more bacterial strains from Table 1B. In other embodiments, the probiotic composition useful for correcting or treating a distal dysbiosis includes one or more bacterial strains from Table 1C. In other embodiments, the probiotic composition useful for correcting or treating a distal dysbiosis includes one or more bacterial strains from Table 1D. In other embodiments, the probiotic composition useful for correcting or treating a distal dysbiosis includes one or more bacterial strains from Table 1E. In other embodiments, the probiotic composition useful for correcting or treating a distal dysbiosis includes one or more bacterial strains from Table 1F. In some embodiments, the probiotic composition contains a single strain of bacteria. In other embodiments, the probiotic composition contains two or more strains of bacteria, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 500, 1000 or more strains of bacteria. In other embodiments, the probiotic composition contains or is administered in conjunction with a prebiotic, as described herein.

[0488] Preferred bacterial genera include *Acetanaerobacterium, Acetivibrio, Alicyclobacillus, Alkaliphilus, Anaerofustis, Anaerosporobacter, Anaerostipes, Anaerotruncus, Anoxybacillus, Bacillus, Bacteroides, Blautia, Brachyspira, Brevibacillus, Bryantella, Bulleidia, Butyricicoccus, Butyrivibrio, Catenibacterium, Chlamydiales, Clostridiaceae, Clostridiales, Clostridium, Collinsella, Coprobacillus, Coprococcus, Coxiella, Deferribacteres, Desulfitobacterium, Desulfotomaculum, Dorea, Eggerthella, Erysipelothrix, Erysipelotrichaceae, Ethanoligenens, Eubacterium, Faecalibacterium, Filifactor, Flavonifractor, Flexistipes, Fulvimonas, Fusobacterium, Gemmiger, Geobacillus, Gloeobacter, Holdemania, Hydrogenoanaerobacterium, Kocuria, Lachnobacterium, Lachnospira, Lachnospiraceae, Lactobacillus, Lactonifactor, Leptospira, Lutispora, Lysinibacillus, Mollicutes, Moorella, Nocardia, Oscillibacter, Oscillospira, Paenibacillus, Papillibacter, Pseudoflavonifractor, Robinsoniella, Roseburia, Ruminococcaceae, Ruminococcus, Saccharomonospora, Sarcina, Solobacterium, Sporobacter, Sporolactobacillus, Streptomyces, Subdoligranulum, Sutterella, Syntrophococcus, Thermoanaerobacter, Thermobifida*, and *Turicibacter.*

[0489] Preferred bacterial genera also include *Acetonema, Alkaliphilus, Amphibacillus, Ammonifex, Anaerobacter, Caldicellulosiruptor, Caloramator, Candidatus, Carboxydibrachium, Carboxydothermus, Cohnella, Dendrosporobacter Desulfitobacterium, Desulfosporosinus, Halobacteroides, Heliobacterium, Heliophilum, Heliorestis, Lachnoanaerobaculum, Lysinibacillus, Oceanobacillus, Orenia* (*S.*), *Oxalophagus, Oxobacter, Pelospora, Pelotomaculum, Propionispora, Sporohalobacter, Sporomusa, Sporosarcina, Sporotomaculum, Symbiobacterium, Syntrophobotulus, Syntrophospora, Terribacillus, Thermoanaerobacter, Thermosinus* and *Heliobacillus.*

[0490] As provided herein, therapeutic compositions comprise, or in the alternative, modulate, the colonization and/or engraftment, of the following exemplary bacterial entities: *Lactobacillus gasseri, Lactobacillus fermentum, Lactobacillus reuteri, Enterococcus faecalis, Enterococcus durans, Enterococcus villorum, Lactobacillus plantarum, Pediococcus acidilactici, Staphylococcus pasteuri, Staphylococcus cohnii, Streptococcus sanguinis, Streptococcus sinensis, Streptococcus mitis, Streptococcus* sp. SCA22, *Streptococcus* sp. CR-3145, *Streptococcus anginosus, Streptococcus mutans, Coprobacillus cateniformis, Clostridium saccharogumia, Eubacterium dolichum* DSM 3991, *Clostridium* sp. PPf35E6, *Clostridium sordelli* ATCC 9714, *Ruminococcus torques, Ruminococcus gnavus, Clostridium clostridioforme, Ruminococcus obeum, Blautia producta, Clostridium* sp. ID5, *Megasphaera micronuciformis, Veillonella parvula,*

Clostridium methylpentosum, Clostridium islandicum, Faecalibacterium prausnitzii, Bacteroides uniformmis, Bacteroides thetaiotaomicron, Bacteroides acidifaciens, Bacteroides ovatus, Bacteroides fragilis, Parabacteroides distasonis, Propinionibacteirum propionicum, Actinomycs hyovaginalis, Rothia mucilaginosa, Rothia aeria, Bifidobacterium breve, Scardovia inopinata and *Eggerthella lenta.*

[0491] Preferred bacterial species are provided in Table 1, Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, Table 1F, and Table 5. Optionally, in some embodiments, preferred bacterial species are spore formers. The bacterial species may be used in vegetative form and/or in spore form. Thus, in some embodiments, the bacteria present in a composition are solely in spore form. In some embodiments, the bacteria present in a composition are solely in vegetative form. In some embodiments, the bacteria present in a composition are in a combination of vegetative form and spore form. Where specific strains of a species are provided, one of skill in the art will recognize that other strains of the species can be substituted for the named strain.

[0492] In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acidaminococcus intestine*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter baumannii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter lwoffii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Akkermansia muciniphila*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes putredinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes shahii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerostipes hadrus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerotruncus colihominis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides caccae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides cellulosilyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides dorei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides eggerthii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides finegoldii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides fragilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides massiliensis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides ovatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bacteroides salanitronis. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides salyersiae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. D20. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides uniformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides vulgatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium adolescentis. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bifidobacterium bifidum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium breve*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium faecale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia glucerasea*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one

embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia wexlerae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Catenibacterium mitsuokai*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium asparagiforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium bolteae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium clostridioforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium histolyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium indolis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium leptum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium perfringens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 14774. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. HGF2. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium symbiosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella aerofaciens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprobacillus* sp. D7. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus catus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus comes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea formicigenerans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea longicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecium*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli* 588. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium eligens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium fissicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium ramulus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium rectale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Faecalibacterium prausnitzii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Flavonifractor plautii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium mortiferum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium nucleatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Holdemania filiformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Klebsiella oxytoca*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods

of the invention is *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus rhamnosus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus ruminis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactococcus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Odoribacter splanchnicus. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Oscillibacter valericigenes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides gordonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides johnsonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides merdae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Pediococcus acidilactici*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Propionibacterium granulosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia inulinivorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus gnavus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus* sp. ID8. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus torques*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Slackia piriformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus epidermidis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus saprophyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus cristatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus infantis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus oralis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus sanguinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus viridans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus thermophiles*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Veillonella dispar.*

[0493] In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acidaminococcus intestine*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter baumannii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter lwoffii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Akkermansia muciniphila*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes putredinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes shahii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerostipes hadrus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerotruncus colihominis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides caccae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides cellulosilyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides dorei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides eggerthii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides finegoldii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides fragilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides massiliensis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides ovatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salanitronis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salyersiae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. D20. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroi-*

des thetaiotaomicrond. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides uniformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides vulgatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium adolescentis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium bifidum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium breve*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium faecale*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia glucerasea*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia wexlerae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Catenibacterium mitsuokai*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium asparagiforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium bolteae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium clostridioforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium histolyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium indolis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium leptum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium perfringens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 14774. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. HGF2. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium symbiosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella aerofaciens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprobacillus* sp. D7. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus catus*. In one

embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus comes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea formicigenerans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea longicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecium*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli* 588. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium eligens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium fissicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium ramulus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium* rectale. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Faecalibacterium prausnitzii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Flavonifractor plautii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium mortiferum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium nucleatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Holdemania filiformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Klebsiella oxytoca*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus rhamnosus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus ruminis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactococcus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Odoribacter splanchnicus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Oscillibacter valericigenes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides gordonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides johnsonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides merdae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Pediococcus acidilactici*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Propionibacterium granulosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia inulinivorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus gnavus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus* sp. ID8. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus torques*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Slackia piriformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus epidermidis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus saprophyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus cristatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus infantis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus oralis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus sanguinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus viridans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus thermophiles*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Veillonella dispar*.

[0494] Exemplary probiotic compositions useful for treatment of disorders associated with a distal dysbiosis contain bacterial strains capable of reducing inflammation in a subject. As described herein, such immunomodulatory (anti-inflammatory) bacteria can modulate cytokine expression by host immune cells, resulting in an overall increase in secretion of anti-inflammatory cytokines and/or an overall decrease in secretion of pro-inflammatory cytokines, systemically reducing inflammation in the subject. In exemplary

embodiments, probiotic compositions useful for treatment of disorders associated with a distal dysbiosis stimulate secretion of one or more anti-inflammatory cytokines by host immune cells, such as PBMCs. Anti-inflammatory cytokines include, but are not limited to, IL-10, IL-13, IL-9, IL-4, IL-5, TGFβ, and combinations thereof. In other exemplary embodiments, probiotic compositions useful for treatment of disorders associated with a distal dysbiosis inhibit secretion of one or more pro-inflammatory cytokines by host immune cells, such as PBMCs. Pro-inflammatory cytokines include, but are not limited to, IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. Other exemplary cytokines are known in the art and are described herein. Probiotic compositions containing anti-inflammatory bacteria reduce inflammation at the site of administration, e.g., in the gastrointestinal tract, as well as at distal sites throughout the body of the subject.

[0495] Other exemplary probiotic compositions useful for treatment of disorders associated with a dysbiosis distal to the gastrointestinal tract contain bacterial strains capable of altering the proportion of immune subpopulations, e.g., T cell subpopulations, in the subject.

[0496] For example, immunomodulatory bacteria can increase or decrease the proportion of Treg cells, Th17 cells, Th1 cells, or Th2 cells in a subject. The increase or decrease in the proportion of immune cell subpopulations may be systemic, or it may be localized to a site of action of the probiotic, e.g., in the gastrointestinal tract or at the site of a distal dysbiosis. In some embodiments, a probiotic composition comprising immunomodulatory bacteria is used for treatment of disorders associated with a dysbiosis distal to the gastrointestinal tract based on the desired effect of the probiotic composition on the differentiation and/or expansion of subpopulations of immune cells in the subject.

[0497] In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Treg cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Treg cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th17 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th17 cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th1 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th1 cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th2 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th2 cells in a subject.

[0498] In one embodiment, a probiotic composition contains immunomodulatory bacteria capable of modulating the proportion of one or more of Treg cells, Th17 cells, Th1 cells, and combinations thereof in a subject. Certain immune cell profiles may be particularly desirable to treat or prevent particular disorders associated with a dysbiosis. For example, treatment or prevention of autoimmune or inflammatory disorders can be promoted by increasing numbers of Treg cells and Th2 cells, and decreasing numbers of Th17 cells and Th1 cells. Accordingly, probiotic compositions for the treatment or prevention of autoimmune or inflammatory disorders may contain probiotics capable of promoting Treg cells and Th2 cells, and reducing Th17 and Th1 cells.

[0499] Short chain fatty acids (SCFAs) can have immunomodulatory (i.e., immunosuppressive) effects and therefore their production (i.e., biosynthesis or conversion by fermentation) is advantageous for the prevention, control, mitigation, and treatment of autoimmune and/or inflammatory disorders (Lara-Villoslada F. et al., 2006. Short-chain fructooligosaccharides, in spite of being fermented in the upper part of the large intestine, have anti-inflammatory activity in the TNBS model of colitis. Eur J Nutr. 45(7): 418-425). In germ-free mice and vancomycin-treated conventional mice, administration of SCFA (acetate, propionate, or butyrate) restored normal numbers of Tregs in the large intestine (Smith P M, et al. Science. 2013; 569-573). Short-chain fatty acids (SCFA) are produced by some bacteria as a byproduct of xylose fermentation. SCFA are one of the most abundant metabolites produced by the gut microbiome, particularly the family Clostridiacea, including members of the genus *Clostridium, Ruminococcus*, or *Blautia*. In some aspects, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe (e.g., one or more microbial species, such as a bacterial species, or more than one strain of a particular microbial species) and at least one type of prebiotic such that the composition, dosage form, or kit is capable of increasing the level of one or more immunomodulatory SCFA (e.g., acetate, propionate, butyrate, or valerate) in a mammalian subject. Optionally, the pharmaceutical composition, dosage form, or kit further comprises one or more substrates of one or more SCFA-producing fermentation and/or biosynthesis pathways. In certain embodiments, the administration of the composition, dosage form, or kit to a mammalian subject results in the increase of one or more SCFAs in the mammalian subject by approximately 1.5-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater than 100-fold. In some embodiments, the dysbiosis is caused by a deficiency in microbes that produce short chain fatty acids. Accordingly, in some embodiments, the probiotic composition can contain a species of bacteria that produce short chain fatty acids.

[0500] Aspects of this invention also include medium chain triglycerides (MCTs). MCTs passively diffuse from the GI tract to the portal system (longer fatty acids are absorbed into the lymphatic system) without requirement for modification like long-chain fatty acids or very-long-chain fatty acids. In addition, MCTs do not require bile salts for digestion. Patients who have malnutrition or malabsorption syndromes are treated with MCTs because they do not require energy for absorption, use, or storage. Medium-chain triglycerides are generally considered a good biologically inert source of energy that the human body finds reasonably easy to metabolize. They have potentially beneficial attributes in protein metabolism, but may be contraindicated in some situations due to their tendency to induce ketogenesis and metabolic acidosis. Due to their ability to be absorbed rapidly by the body, medium-chain triglycerides have found use in the treatment of a variety of malabsorption ailments. MCT supplementation with a low-fat diet has been described as the cornerstone of treatment for primary intestinal lymphangiectasia (Waldmann's disease). MCTs are an ingredient in parenteral nutritional emulsions. Accordingly, in some embodiments, the xylose compositions are capable of increasing the level of one or more medium chain triglycerides in a mammalian subject. In certain embodiments, the administration of the

xylose composition to a mammalian subject results in the increase of one or more medium chain triglycerides in the mammalian subject by approximately 1.5-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater than 100-fold.

[0501] Distal disorders associated with loss of intestinal barrier function can be treated or improved by administration of probiotic compositions containing bacterial strains that produce short chain fatty acids (SCFAs), such as, for example, butyrate, acetate, propionate, or valerate, or combinations thereof. Distal disorders associated with loss of intestinal barrier function can be treated or improved by administration of probiotic compositions containing bacterial strains that reduce inflammation, as described herein.

[0502] In other embodiments, the distal dysbiosis is caused by a deficiency in microbes that produce lactic acid. Accordingly, in one embodiment, the probiotic composition can contain a species of bacteria that produce lactic acid.

[0503] Probiotic compositions for modulating a distal microbiome may optionally be administered in conjunction with a prebiotic. For example, a prebiotic can be selected which augments the growth of the anti-inflammatory bacterial population present in the probiotic composition. Exemplary prebiotics are provided in Table 7. Exemplary prebiotics which may augment the growth of exemplary bacterial species are provided in FIG. **29**. In one embodiment, the prebiotic can be a monomer or polymer selected from the group consisting of arabinoxylan, xylose, soluble fiber dextran, soluble corn fiber, polydextrose, lactose, N-acetyl-lactosamine, glucose, or combinations thereof. In another embodiment, the prebiotic can be a monomer or polymer, such as galactose, fructose, rhamnose, mannose, uronic acids, 3'-fucosyllactose, 3'sialylactose, 6'-sialyllactose, lacto-N-neotetraose, 2'-2'-fucosyllactose, or combinations thereof. In one embodiment, the prebiotic can include a monosaccharide selected from the group consisting of arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, and combinations thereof. In another embodiment, the prebiotic can include a disaccharide selected from the group consisting of xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, or a combination thereof. In another embodiment, the prebiotic comprises a polysaccharide, for example, a xylooligosaccharide. Exemplary prebiotics include sugars such as arabinose, fructose, fucose, lactose, galactose, glucose, mannose, D-xylose, xylitol, ribose, xylobiose, sucrose, maltose, lactose, lactulose, trehalose, cellobiose, and xylooligosaccharide, or combinations thereof.

[0504] The foregoing probiotic compositions (and optional prebiotic compositions) can be used for treatment of the following disorders associated with dysbiosis of the microbiome at particular niches within the subject, or with disorders of the systemic microbiome.

IX. Autoimmune/Inflammatory Diseases

[0505] Herein, we disclose probiotic microbial compositions, optionally comprising prebiotics, non-microbial immunomodulatory carbohydrates, or microbial immunomodulatory cell components, that are effective for the prevention or treatment of transplant disorders in a transplant recipient. Such disorders, e.g., GVHD, transplant rejection, sepsis, etc. are associated with systemic inflammation and/or loss of intestinal barrier function. In one embodiment, the transplant recipient has an autoimmune or inflammatory disorder. For example, a subject with an autoimmune or inflammatory disorder may receive a transplant, e.g., a hematopoietic stem cell transplant, for example, and autologous hematopoietic stem cell transplant, as a treatment modality for the autoimmune or inflammatory disorder. In this embodiment, administration of the probiotic (and optional prebiotic) compositions of the invention can be used to prevent or treat GVHD in the subject receiving the transplant, and can additionally or alternatively be used to treat the underlying autoimmune or inflammatory disorder. Exemplary autoimmune or inflammatory disorders include, for example, lupus, multiple sclerosis, systemic sclerosis, Crohn's disease, type I diabetes, or juvenile idiopathic arthritis. Additional autoimmune or inflammatory disorders include, for example, an inflammatory bowel disease (IBD) including but not limited to ulterative colitis and Crohn's disease, multiple sclerosis (MS), systemic lupus erythematosus (SLE), type I diabetes, rheumatoid arthritis, Sjogren's syndrome, and Celiac disease. In certain embodiments, the compositions comprise at least one type of microbe and at least one type of carbohydrate (a prebiotic), and optionally further comprise microbial immunomodulatory cell components or substrates for the production of immunomodulatory metabolites, that are effective for the prevention or treatment of an autoimmune or inflammatory disorder. We also disclose herein methods for the prevention and/or treatment of autoimmune and inflammatory diseases in human subjects, e.g., transplant recipients.

[0506] In one embodiment, the subject is receiving a hematopoietic stem cell transplant. In other embodiments, the subject is receiving a bone marrow transplant. In other embodiments, the subject is receiving a solid organ transplant, e.g., a kidney transplant, a heart transplant, a lung transplant, a skin transplant, a liver transplant, a pancreas transplant, an intestinal transplant, an endocrine gland transplant, a bladder transplant, and/or a skeletal muscle transplant.

[0507] Autoimmune and inflammatory diseases include, but are not limited to: Acute Disseminated Encephalomyelitis, Acute necrotizing hemorrhagic leukoencephalitis, Addison's disease, adhesive capsulitis, Agammaglobulinemia, Alopecia areata, Amyloidosis, Ankylosing spondylitis, Anti-GBM nephritis, Anti-TBM nephritis, Antiphospholipid syndrome, arthofibrosis, atrial fibrosis, autoimmune angioedema, autoimmune aplastic anemia, autoimmune dusautonomia, autoimmune hepatitis, autoimmune hyperlipidemia, autoimmune immunodeficiency, autoimmune inner ear disease, autoimmune myocarditis, autoimmune oophoritis, autoimmune pancreatitis, autoimmune retinopathy, autoimmune thrombocytopenic purpura, autoimmune thyroid disease, autoimmune urticaria, axonal and neuronal neuropathies, Balo disease, Behçet's disease, benign mucosal pemphigold, Bullous pemphigold, cardiomyopathy, Castleman disease, Celiac Disease, Chagas disease, chronic fatigue syndrome, chronic inflammatory demyelinating polyneuropathy, chronic Lyme disease, chronic recurrent multifocal osteomyelitis, Churg-Strauss syndrome, cicatricial pemphigold, cirrhosis, Cogans syndrome, cold agglutinin disease, congenital heart block, Coxsackle myocarditis, CREST disease, Crohn's disease, Cystic Fibrosis, essential mixed cryoglobulinemia, deficiency of the interleukin-1 receptor antagonist, demyelinating neuropathies, dermatitis herpetiformis, dermatomyosis, Devic's disease, discoid lupus, Dressler's syndrome, Dupuytren's contracture, endometriosis, endomyocardial fibrosis, eosinophilic esophagitis, eosinophilic facsciitis, erythema nodosum, experimental allergic

encephalomyelitis, Evans syndrome, Familial Mediterranean Fever, fibromyalgia, fibrosing alveolitis, giant cell arteritis, giant cell myocarditis, glomerulonephritis, Goodpasture's syndrome, Graft-versus-host disease (GVHD), granulomatosus with polyanglitis, Graves' disease, Guillain-Bare syndrome, Hashimoto's encephalitis, Hashimoto's thyroiditis, hemolytic anemia, Henoch-Schonlein purpura, hepatitis, herpes gestationis, hypogammaglobulinemia, idiopathic thrombocytopenic purpura, IgA nephropathy, IgG4-related sclerosing disease, immunoregulatory lipoproteins, inclusion body myositis, inflammatory bowel disorders, interstitial cystitis, juvenile arthritis, juvenile myositis, Kawasaki syndrome, keloid, Lambert-Eaton syndrome, leukocytoclastic vasculitis, lichen planus, lichen sclerosus, ligneous conjunctivitis, linear IgA disease, mediastinal fibrosis, Meniere's disease, microscopic polyanglitis, mixed connective tissue disease, Mooren's ulcer, Mucha-Hamermann disease, Multiple Sclerosis (MS), Myasthenia gravis, myelofibrosis, Myositis, narcolepsy, Neonatal Onset Multisystem Inflammatory Disease, nephrogenic systemic fibrosis, neutropenia, nonalcoholic fatty liver disease, nonalcoholic steatohepatitis (NASH), ocular-cicatricial pemphigold, optic neuritis, palindromic rheumatism, Pediatric Autoimmune Neuropsychiatric Disorders Associated with *Streptococcus* (PANDAS), paraneoplastic cerebellar degeneration, paroxysmal nocturnal nemoglobinuria, Parry Romberg syndrome, Parsonnage-Turner syndrome, Pars planitis, Pemphigus, Peripheral neuropathy, perivenous encephalomyelitis, pernicious anemia, Peyronie's disease, POEMS syndrome, polyarteritis nodosa, progressive massive fibrosis, Tumor Necrosis Factor Receptor-assoicated Periodic Syndrome, Type I autoimmune polyglandular syndrome, Type II autoimmune polyglandular syndrome, Type III autoimmune polyglandular syndrome, polymyalgia rhematica, polymyositis, postmyocardial infarction syndrome, postpericardiotomy syndrome, progesterone dermatitis, primary biliary cirrhosis, primary sclerosing cholangitis, psoriasis, psoriatic arthritis, idiopathic pulmonary fibrosis, pyoderma gangrenosum, pure red cell aplasia, Raynauds phenomenon, reactic arthritis, reflex sympathetic dystrophy, Reiter's syndrome, relapsing polychondritis, restless legs syndrome, retroperitoneal fibrosis, rheumatic fever, rheumatoid arthritis, sarcoidosis, Schmidt syndrome, scleritis, scleroderma, Sjogren's syndrome, sperm and testicular autoimmunity, stiff person syndrome, subacute bacterial endocarditis, Susac's syndrome, sympathetic ophthalmia, systemic lupus erythematosus (SLE), Takayasu's arthritis, temporal arteritis, thrombocytopenic purpura, Tolosa-Hunt syndrome, transverse myelitis, Type 1 diabetes, ulcerative colitis, undifferentiated connective tissue disease, uveitis, vasculitis, vesiculobullous dermatosis, and Vitiligo.

[0508] In some aspects, the administered microbes and/or carbohydrates modulate the release of immune stimulatory cytokines. In preferred embodiments, the administered microbes and/or carbohydrates inhibit or reduce the release of immune stimulatory cytokines. Non-limiting examples of immune modulating cytokines and ligands include B lymphocyte chemoattractant ("BLC"), C-C motif chemokine 11 ("Eotaxin-1"), Eosinophil chemotactic protein 2 ("Eotaxin-2"), Granulocyte colony-stimulating factor ("G-CSF"), Granulocyte macrophage colony-stimulating factor ("GM-CSF"), 1-309, Intercellular Adhesion Molecule 1 ("ICAM-1"), Interferon gamma ("IFN-γ"), Interlukin-1 alpha ("IL-1α"), Interlukin-1β ("IL-1β"), Interleukin 1 receptor antagonist ("IL-1 ra"), Interleukin-2 ("IL-2"), Interleukin-4 ("IL-4"), Interleukin-5 ("IL-5"), Interleukin-6 ("IL-6"), Interleukin-6 soluble receptor ("IL-6 sR"), Interleukin-7 ("IL-7"), Interleukin-8 ("IL-8"), Interleukin-10 ("IL-10"), Interleukin-11 ("IL-11"), Subunit 3 of Interleukin-12 ("IL-12 p40" or "IL-12 p70"), Interleukin-13 ("IL-13"), Interleukin-15 ("IL-15"), Interleukin-16 ("IL-16"), Interleukin-17 ("IL-17"), Chemokine (C-C motif) Ligand 2 ("MCP-1"), Macrophage colony-stimulating factor ("M-CSF"), Monokine induced by gamma interferon ("MIG"), Chemokine (C-C motif) ligand 2 ("MIP-1 alpha"), Chemokine (C-C motif) ligand 4 ("MIP-1β"), Macrophage inflammatory protein-1-δ ("MIP-1δ"), Platelet-derived growth factor subunit B ("PDGF-BB"), Chemokine (C-C motif) ligand 5, Regulated on Activation, Normal T cell Expressed and Secreted ("RANTES"), TIMP metallopeptidase inhibitor 1 ("TIMP-1"), TIMP metallopeptidase inhibitor 2 ("TIMP-2"), Tumor necrosis factor, lymphotoxin-α ("TNF-α"), Tumor necrosis factor, lymphotoxin-β ("TNF β"), Soluble TNF receptor type 1 ("sTNFRI"), sTNFRIIAR, Brain-derived neurotrophic factor ("BDNF"), Basic fibroblast growth factor ("bFGF"), Bone morphogenetic protein 4 ("BMP-4"), Bone morphogenetic protein 5 ("BMP-5"), Bone morphogenetic protein 7 ("BMP-7"), Nerve growth factor ("b-NGF"), Epidermal growth factor ("EGF"), Epidermal growth factor receptor ("EGFR"), Endocrine-gland-derived vascular endothelial growth factor ("EG-VEGF"), Fibroblast growth factor 4 ("FGF-4"), Keratinocyte growth factor ("FGF-7"), Growth differentiation factor 15 ("GDF-15"), Glial cell-derived neurotrophic factor ("GDNF"), Growth Hormone, Heparin-binding EGF-like growth factor ("HB-EGF"), Hepatocyte growth factor ("HGF"), Insulin-like growth factor binding protein 1 ("IGFBP-1"), Insulin-like growth factor binding protein 2 ("IGFBP-2"), Insulin-like growth factor binding protein 3 ("IGFBP-3"), Insulin-like growth factor binding protein 4 ("IGFBP-4"), Insulin-like growth factor binding protein 6 ("IGFBP-6"), Insulin-like growth factor 1 ("IGF-1"), Insulin, Macrophage colony-stimulating factor ("M-CSF R"), Nerve growth factor receptor ("NGF R"), Neurotrophin-3 ("NT-3"), Neurotrophin-4 ("NT-4"), Osteoclastogenesis inhibitory factor ("Osteoprotegerin"), Platelet-derived growth factor receptors ("PDGF-AA"), Phosphatidylinositol-glycan biosynthesis ("PIGF"), Skp, Cullin, F-box containing comples ("SCF"), Stem cell factor receptor ("SCF R"), Transforming growth factor α ("TGF-α"), Transforming growth factor β-1 ("TGF β1"), Transforming growth factor β-3 ("TGF β3"), Vascular endothelial growth factor ("VEGF"), Vascular endothelial growth factor receptor 2 ("VEGFR2"), Vascular endothelial growth factor receptor 3 ("VEGFR3"), VEGF-D 6Ckine, Tyrosine-protein kinase receptor UFO ("Axl"), Betacellulin ("BTC"), Mucosae-associated epithelial chemokine ("CCL28"), Chemokine (C-C motif) ligand 27 ("CTACK"), Chemokine (C-X-C motif) ligand 16 ("CXCL16"), C-X-C motif chemokine 5 ("ENA-78"), Chemokine (C-C motif) ligand 26 ("Eotaxin-3"), Granulocyte chemotactic protein 2 ("GCP-2"), GRO, Chemokine (C-C motif) ligand 14 ("HCC-1"), Chemokine (C-C motif) ligand 16 ("HCC-4"), Interleukin-9 ("IL-9"), Interleukin-17 F ("IL-17F"), Interleukin-18-binding protein ("IL-18 BPa"), Interleukin-28 A ("IL-28A"), Interleukin 29 ("IL-29"), Interleukin 31 ("IL-31"), C-X-C motif chemokine 10 ("IP-10"), Chemokine receptor CXCR3 ("I-TAC"), Leukemia inhibitory factor ("LIF"), Light, Chemokine (C motif) ligand ("Lymphotactin"), Monocyte chemoattractant protein 2 ("MCP-2"), Monocyte chemoattractant protein 3 ("MCP-3"), Monocyte chemoattractant

protein 4 ("MCP-4"), Macrophage-derived chemokine ("MDC"), Macrophage migration inhibitory factor ("MIF"), Chemokine (C-C motif) ligand 20 ("MIP-3α"), C-C motif chemokine 19 ("MIP-3β"), Chemokine (C-C motif) ligand 23 ("MPIF-1"), Macrophage stimulating protein alpha chain ("MSP-α"), Nucleosome assembly protein 1-like 4 ("NAP-2"), Secreted phosphoprotein 1 ("Osteopontin"), Pulmonary and activation-regulated cytokine ("PARC"), Platelet factor 4 ("PF4"), Stroma cell-derived factor-1α ("SDF-1α"), Chemokine (C-C motif) ligand 17 ("TARC"), Thymus-expressed chemokine ("TECK"), Thymic stromal lymphopoietin ("TSLP 4-IBB"), CD 166 antigen ("ALCAM"), Cluster of Differentiation 80 ("B7-1"), Tumor necrosis factor receptor superfamily member 17 ("BCMA"), Cluster of Differentiation 14 ("CD14"), Cluster of Differentiation 30 ("CD30"), Cluster of Differentiation 40 ("CD40 Ligand"), Carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) ("CEACAM-1"), Death Receptor 6 ("DR6"), Deoxythymidine kinase ("Dtk"), Type 1 membrane glycoprotein ("Endoglin"), Receptor tyrosine-protein kinase erbB-3 ("ErbB3"), Endothelial-leukocyte adhesion molecule 1 ("E-Selectin"), Apoptosis antigen 1 ("Fas"), Fms-like tyrosine kinase 3 ("Flt-3L"), Tumor necrosis factor receptor superfamily member 1 ("GITR"), Tumor necrosis factor receptor superfamily member 14 ("HVEM"), Intercellular adhesion molecule 3 ("ICAM-3"), IL-1 R4, IL-1 RI, IL-10 Rβ, IL-17R, IL-2Rγ, IL-21R, Lysosome membrane protein 2 ("LIMPII"), Neutrophil gelatinase-associated lipocalin ("Lipocalin-2"), CD62L ("L-Selectin"), Lymphatic endothelium ("LYVE-1"), MHC class I polypeptide-related sequence A ("MICA"), MHC class I polypeptide-related sequence B ("MICB"), NRGl-βl, Beta-type platelet-derived growth factor receptor ("PDGF Rβ"), Platelet endothelial cell adhesion molecule ("PECAM-1"), RAGE, Hepatitis A virus cellular receptor 1 ("TIM-1"), Tumor necrosis factor receptor superfamily member IOC ("TRAIL R3"), Trappin protein transglutaminase binding domain ("Trappin-2"), Urokinase receptor ("uPAR"), Vascular cell adhesion protein 1 ("VCAM-1"), XEDARActivin A, Agouti-related protein ("AgRP"), Ribonuclease 5 ("Angiogenin"), Angiopoietin 1, Angiostatin, Catheprin S, CD40, Cryptic family protein IB ("Cripto-1"), DAN, Dickkopf-related protein 1 ("DKK-1"), E-Cadherin, Epithelial cell adhesion molecule ("EpCAM"), Fas Ligand (FasL or CD95L), Fcg RIIB/C, FoUistatin, Galectin-7, Intercellular adhesion molecule 2 ("ICAM-2"), IL-13 R1, IL-13R2, IL-17B, IL-2 Ra, IL-2 Rb, IL-23, LAP, Neuronal cell adhesion molecule ("NICAM"), Plasminogen activator inhibitor-1 ("PAI-1"), Platelet derived growth factor receptors ("PDGF-AB"), Resistin, stromal cell-derived factor 1 ("SDF-1β"), sgpl30, Secreted frizzled-related protein 2 ("ShhN"), Sialic acid-binding immunoglobulin-type lectins ("Siglec-5"), ST2, Transforming growth factor-β2 ("TGF β 2"), Tie-2, Thrombopoietin ("TPO"), Tumor necrosis factor receptor superfamily member 10D ("TRAIL R4"), Triggering receptor expressed on myeloid cells 1 ("TREM-1"), Vascular endothelial growth factor C ("VEGF-C"), VEGFR1Adiponectin, Adipsin ("AND"), α-fetoprotein ("AFP"), Angiopoietin-like 4 ("ANGPTL4"), β-2-microglobulin ("B2M"), Basal cell adhesion molecule ("BCAM"), Carbohydrate antigen 125 ("CA125"), Cancer Antigen 15-3 ("CA15-3"), Carcinoembryonic antigen ("CEA"), cAMP receptor protein ("CRP"), Human Epidermal Growth Factor Receptor 2 ("ErbB2"), Follistatin, Follicle-stimulating hormone ("FSH"), Chemokine (C-X-C motif) ligand 1 ("GRO α"), human chorionic gonadotropin ("β HCG"), Insulin-like growth factor 1 receptor ("IGF-1 sR"), IL-1 sRII, IL-3, IL-18 Rb, IL-21, Leptin, Matrix metalloproteinase-1 ("MMP-1"), Matrix metalloproteinase-2 ("MMP-2"), Matrix metalloproteinase-3 ("MMP-3"), Matrix metalloproteinase-8 ("MMP-8"), Matrix metalloproteinase-9 ("MMP-9"), Matrix metalloproteinase-10 ("MMP-10"), Matrix metalloproteinase-13 ("MMP-13"), Neural Cell Adhesion Molecule ("NCAM-1"), Entactin ("Nidogen-1"), Neuron specific enolase ("NSE"), Oncostatin M ("OSM"), Procalcitonin, Prolactin, Prostate specific antigen ("PSA"), Sialic acid-binding Ig-like lectin 9 ("Siglec-9"), ADAM 17 endopeptidase ("TACE"), Thyroglobulin, Metalloproteinase inhibitor 4 ("TIMP-4"), TSH2B4, Disintegrin and metalloproteinase domain-containing protein 9 ("ADAM-9"), Angiopoietin 2, Tumor necrosis factor ligand superfamily member 13/Acidic leucine-rich nuclear phosphoprotein 32 family member B ("APRIL"), Bone morphogenetic protein 2 ("BMP-2"), Bone morphogenetic protein 9 ("BMP-9"), Complement component 5a ("C5a"), Cathepsin L, CD200, CD97, Chemerin, Tumor necrosis factor receptor superfamily member 6B ("DcR3"), Fatty acid-binding protein 2 ("FABP2"), Fibroblast activation protein, alpha ("FAP"), Fibroblast growth factor 19 ("FGF-19"), Galectin-3, Hepatocyte growth factor receptor ("HGF R"), IFN-γα/β R2, Insulin-like growth factor 2 ("IGF-2"), Insulin-like growth factor 2 receptor ("IGF-2 R"), Interleukin-1 receptor 6 ("IL-1R6"), Interleukin 24 ("IL-24"), Interleukin 33 ("IL-33", Kallikrein 14, Asparaginyl endopeptidase ("Legumain"), Oxidized low-density lipoprotein receptor 1 ("LOX-"), Mannose-binding lectin ("MBL"), Neprilysin ("NEP"), Notch homolog 1, translocation-associated (*Drosophila*) ("Notch-1"), Nephroblastoma overexpressed ("NOV"), Osteoactivin, Programmed cell death protein 1 ("PD-1"), N-acetylmuramoyl-L-alanine amidase ("PGRP-5"), Serpin A4, Secreted frizzled related protein 3 ("sFRP-3"), Thrombomodulin, Toll-like receptor 2 ("TLR2"), Tumor necrosis factor receptor superfamily member 10A ("TRAIL Rl"), Transferrin ("TRF"), WIF-lACE-2, Albumin, AMICA, Angiopoietin 4, B-cell activating factor ("BAFF"), Carbohydrate antigen 19-9 ("CA19-9"), CD 163, Clusterin, CRT AM, Chemokine (C-X-C motif) ligand 14 ("CXCL14"), Cystatin C, Decorin ("DCN"), Dickkopf-related protein 3 ("Dkk-3"), Delta-like protein 1 ("DLL1"), Fetuin A, Heparin-binding growth factor 1 ("aFGF"), Folate receptor c ("FOLR1"), Furin, GPCR-associated sorting protein 1 ("GASP-I"), GPCR-associated sorting protein 2 ("GASP-2"), Granulocyte colony-stimulating factor receptor ("GCSF R"), Serine protease hepsin ("HAI-2"), Interleukin-17B Receptor ("IL-17B R"), Interleukin 27 ("IL-27"), Lymphocyte-activation gene 3 ("LAG-3"), Apolipoprotein A-V ("LDL R"), Pepsinogen I, Retinol binding protein 4 ("RBP4"), SOST, Heparan sulfate proteoglycan ("Syndecan-1"), Tumor necrosis factor receptor superfamily member 13B ("TACI"), Tissue factor pathway inhibitor ("TFPI"), TSP-1, Tumor necrosis factor receptor superfamily, member 10b ("TRAIL R2"), TRANCE, Troponin I, Urokinase Plasminogen Activator ("uPA"), Cadherin 5, type 2 or VE-cadherin (vascular endothelial) also known as CD144 ("VE-Cadherin"), WNTl-inducible-signaling pathway protein 1 ("WISP-1"), and Receptor Activator of Nuclear Factor κ B ("RANK").

[0509] Exemplary probiotic compositions useful for treatment or prevention of autoimmune or inflammatory disorders contain bacterial strains capable of reducing inflammation in a subject. Such immunomodulatory (anti-inflammatory) bac-

teria can modulate cytokine expression by host immune cells, resulting in an overall increase in secretion of anti-inflammatory cytokines and/or an overall decrease in secretion of pro-inflammatory cytokines, systemically reducing inflammation in the subject. In exemplary embodiments, probiotic compositions useful for treatment of immune or inflammatory disorders stimulate secretion of one or more anti-inflammatory cytokines by host immune cells, such as PBMCs. Anti-inflammatory cytokines include, but are not limited to, IL-10, IL-13, IL-9, IL-4, IL-5, TGFβ and combinations thereof. In other exemplary embodiments, probiotic compositions useful for treatment of autoimmune or inflammatory disorders inhibit secretion of one or more pro-inflammatory cytokines by host immune cells, such as PBMCs. Pro-inflammatory cytokines include, but are not limited to, IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. Other exemplary cytokines are known in the art and are described herein. Probiotic compositions containing anti-inflammatory bacteria reduce inflammation at the site of administration, e.g., in the gastrointestinal tract, as well as at distal sites throughout the body of the subject.

[0510] Other exemplary probiotic compositions useful for treatment of autoimmune or inflammatory disorders contain bacterial strains capable of altering the proportion of immune subpopulations, e.g., T cell subpopulations, in the subject.

[0511] For example, immunomodulatory bacteria can increase or decrease the proportion of Treg cells, Th17 cells, Th1 cells, or Th2 cells in a subject. The increase or decrease in the proportion of immune cell subpopulations may be systemic, or it may be localized to a site of action of the probiotic, e.g., in the gastrointestinal tract or at the site of a distal dysbiosis. In some embodiments, a probiotic composition comprising immunomodulatory bacteria is used for treatment of an autoimmune or inflammatory disorder based on the desired effect of the probiotic composition on the differentiation and/or expansion of subpopulations of immune cells in the subject.

[0512] In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Treg cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Treg cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th17 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th17 cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th1 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th1 cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th2 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th2 cells in a subject.

[0513] In one embodiment, a probiotic composition contains immunomodulatory bacteria capable of modulating the proportion of one or more of Treg cells, Th17 cells, Th1 cells, and combinations thereof in a subject. Certain immune cell profiles may be particularly desirable to treat or prevent autoimmune or inflammatory disorders. For example, in some embodiments, treatment or prevention of autoimmune or inflammatory disorders can be promoted by increasing numbers of Treg cells and Th2 cells, and decreasing numbers of Th17 cells and Th1 cells. Accordingly, probiotic compositions for the treatment or prevention of autoimmune or inflammatory disorders may contain probiotics capable of promoting Treg cells and Th2 cells, and reducing Th17 and Th1 cells.

[0514] Probiotic compositions useful for treating or preventing the autoimmune or inflammatory disorders described herein include, in exemplary embodiments, one or more bacterial strains from Table 1. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1A. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1B. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1C. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1D. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1E. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1F. In some embodiments, the probiotic composition contains a single strain of bacteria. In other embodiments, the probiotic composition contains two or more strains of bacteria, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 500, 1000 or more strains of bacteria. In other embodiments, the probiotic composition contains or is administered in conjunction with a prebiotic, as described herein.

[0515] Preferred bacterial genera include *Acetanaerobacterium, Acetivibrio, Alicyclobacillus, Alkaliphilus, Anaerofustis, Anaerosporobacter, Anaerostipes, Anaerotruncus, Anoxybacillus, Bacillus, Bacteroides, Blautia, Brachyspira, Brevibacillus, Bryantella, Bulleidia, Butyricicoccus, Butyrivibrio, Catenibacterium, Chlamydiales, Clostridiaceae, Clostridiales, Clostridium, Collinsella, Coprobacillus, Coprococcus, Coxiella, Deferribacteres, Desulfitobacterium, Desulfotomaculum, Dorea, Eggerthella, Erysipelothrix, Erysipelotrichaceae, Ethanoligenens, Eubacterium, Faecalibacterium, Filifactor, Flavonifractor, Flexistipes, Fulvimonas, Fusobacterium, Gemmiger, Geobacillus, Gloeobacter, Holdemania, Hydrogenoanaerobacterium, Kocuria, Lachnobacterium, Lachnospira, Lachnospiraceae, Lactobacillus, Lactonifactor, Leptospira, Lutispora, Lysinibacillus, Mollicutes, Moorella, Nocardia, Oscillibacter, Oscillospira, Paenibacillus, Papillibacter, Pseudoflavonifractor, Robinsoniella, Roseburia, Ruminococcaceae, Ruminococcus, Saccharomonospora, Sarcina, Solobacterium, Sporobacter, Sporolactobacillus, Streptomyces, Subdoligranulum, Sutterella, Syntrophococcus, Thermoanaerobacter, Thermobifida*, and *Turicibacter.*

[0516] Preferred bacterial genera also include *Acetonema, Alkaliphilus, Amphibacillus, Ammonifex, Anaerobacter, Caldicellulosiruptor, Caloramator, Candidatus, Carboxydibrachium, Carboxydothermus, Cohnella, Dendrosporobacter Desulfitobacterium, Desulfosporosinus, Halobacteroides, Heliobacterium, Heliophilum, Heliorestis, Lachnoanaerobaculum, Lysinibacillus, Oceanobacillus, Orenia* (*S.*), *Oxalophagus, Oxobacter, Pelospora, Pelotomaculum, Propionispora, Sporohalobacter, Sporomusa, Sporosarcina, Sporotomaculum, Symbiobacterium, Syntrophobotulus, Syntrophospora, Terribacillus, Thermoanaerobacter*, and *Thermosinus.*

[0517] As provided herein, therapeutic compositions comprise, or in the alternative, modulate, the colonization and/or engraftment, of the following exemplary bacterial entities:

Lactobacillus gasseri, Lactobacillus fermentum, Lactobacillus reuteri, Enterococcus faecalis, Enterococcus durans, Enterococcus villorum, Lactobacillus plantarum, Pediococcus acidilactici, Staphylococcus pasteuri, Staphylococcus cohnii, Streptococcus sanguinis, Streptococcus sinensis, Streptococcus mitis, Streptococcus sp. SCA22, *Streptococcus* sp. CR-3145, *Streptococcus anginosus, Streptococcus mutans, Coprobacillus cateniformis, Clostridium saccharogumia, Eubacterium dolichum* DSM 3991, *Clostridium* sp. PPf35E6, *Clostridium sordelli* ATCC 9714, *Ruminococcus torques, Ruminococcus gnavus, Clostridium clostridioforme, Ruminococcus obeum, Blautia producta, Clostridium* sp. ID5, *Megasphaera micronuciformis, Veillonella parvula, Clostridium methylpentosum, Clostridium islandicum, Faecalibacterium prausnitzii, Bacteroides uniformmis, Bacteroides thetaiotaomicron, Bacteroides acidifaciens, Bacteroides ovatus, Bacteroides fragilis, Parabacteroides distasonis, Propinionibacteirum propionicum, Actinomycs hyovaginalis, Rothia mucilaginosa, Rothia aeria, Bifidobacterium breve, Scardovia inopinata* and *Eggerthella lenta.*

[0518] Preferred bacterial species are provided in Table 1, Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, Table 1F, and Table 5. Optionally, in some embodiments, preferred bacterial species are spore formers. Where specific strains of a species are provided, one of skill in the art will recognize that other strains of the species can be substituted for the named strain.

[0519] In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acidaminococcus intestine*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter baumannii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter lwoffii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Akkermansia muciniphila*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes putredinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes shahii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerostipes hadrus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerotruncus colihominis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides caccae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides cellulosilyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides dorei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides eggerthii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides finegoldii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides fragilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides massiliensis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides ovatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bacteroides salanitronis. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides salyersiae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. D20. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides uniformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides vulgatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium adolescentis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bifidobacterium bifidum. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium breve*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium faecale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia glucerasea*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the composi-

tions and methods of the invention is *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia wexlerae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Catenibacterium mitsuokai*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium asparagiforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium bolteae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium clostridioforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium histolyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium indolis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium leptum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium perfringens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 14774. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. HGF2. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium symbiosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella aerofaciens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprobacillus* sp. D7. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus catus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus comes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea formicigenerans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea longicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecium*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli* 588. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium eligens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium fissicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium ramulus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium rectale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Faecalibacterium prausnitzii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Flavonifractor plautii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium mortiferum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium nucleatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Holdemania*

filiformis. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Klebsiella oxytoca*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus rhamnosus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus ruminis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactococcus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Odoribacter splanchnicus. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Oscillibacter valericigenes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides gordonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides johnsonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides merdae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Pediococcus acidilactici*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Propionibacterium granulosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia inulinivorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus gnavus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus* sp. ID8. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus torques*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Slackia piriformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus epidermidis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus saprophyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus cristatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus infantis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus oralis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus sanguinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus viridans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus thermophiles*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Veillonella dispar.*

[0520] In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acidaminococcus intestine*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter baumannii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter lwoffii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Akkermansia muciniphila*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes putredinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes shahii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerostipes hadrus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerotruncus colihominis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides caccae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides cellulosilyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides dorei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides eggerthii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides finegoldii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides fragilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides massiliensis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides ovatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salanitronis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salyersiae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention com-

prises *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. D20. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides uniformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides vulgatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium adolescentis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium bifidum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium breve*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium faecale*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia glucerasea*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia wexlerae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Catenibacterium mitsuokai*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium asparagiforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium bolteae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium clostridioforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium histolyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium indolis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium leptum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium perfringens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 14774. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. HGF2. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium symbiosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella aerofaciens*.

In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprobacillus* sp. D7. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus catus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus comes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea formicigenerans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea longicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecium*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli* 588. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium eligens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium fissicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium ramulus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium* rectale. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Faecalibacterium prausnitzii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Flavonifractor plautii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium mortiferum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium nucleatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Holdemania filiformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Klebsiella oxytoca*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus rhamnosus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus ruminis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactococcus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Odoribacter splanchnicus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Oscillibacter valericigenes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides gordonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides johnsonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides merdae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Pediococcus acidilactici*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Propionibacterium granulosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia inulinivorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus gnavus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus* sp. ID8. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus torques*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Slackia piriformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus epidermidis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus saprophyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus cristatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus infantis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus oralis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus sanguinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus viridans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus thermophiles*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Veillonella dispar*.

[0521] In one embodiment, the prebiotic carbohydrate component of the pharmaceutical composition, dosage form,

or kit allows the commensal colonic microbiota, comprising microorganisms associated with a healthy-state microbiome or presenting a low risk of a patient developing an autoimmune or inflammatory condition, to be regularly maintained. In one embodiment, the prebiotic carbohydrate component of the pharmaceutical composition, dosage form, or kit allows the co-administered or co-formulated microbe or microbes to engraft, grow, and/or be regularly maintained in a mammalian subject. In some embodiments, the mammalian subject is a human subject. In preferred embodiments, the mammalian subject suffers from or is at risk of developing an autoimmune or inflammatory disorder. In some embodiments, the prebiotic component of the invention favors the growth of an administered microbe, wherein the growth of the administered microbe and/or the fermentation of the administered prebiotic by the administered microbe slows or reduces the growth of a pathogen or pathobiont. For example, FOS, neosugar, or inuliri promotes the growth of acid-forming bacteria in the colon such as bacteria belonging to the genera *Lactobacillus* or *Bifidobacterium* and *Lactobacillus acidophilus* and *Bifidobacterium bifidus* can play a role in reducing the number of pathogenic bacteria in the colon (U.S. Pat. No. 8,486,668 PREBIOTIC FORMULATIONS AND METHODS OF USE). Other polymers, such as various galactans, lactulose, and carbohydrate based gums, such as psyllium, guar, carrageen, gellan, and konjac, are also known to improve gastrointestinal (GI) health.

[0522] Short chain fatty acids (SCFAs) can have immunomodulatory (i.e., immunosuppressive) effects and therefore their production (i.e., biosynthesis or conversion by fermentation) is advantageous for the prevention, control, mitigation, and treatment of autoimmune and/or inflammatory disorders (Lara-Villoslada F. et al., 2006. Short-chain fructooligosaccharides, in spite of being fermented in the upper part of the large intestine, have anti-inflammatory activity in the TNBS model of colitis. Eur J Nutr. 45(7): 418-425). In some aspects, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe and at least one type of prebiotic such that the composition, dosage form, or kit is capable of increasing the level of one or more immunomodulatory SCFA (e.g., acetate, propionate, butyrate, or valerate) in a mammalian subject. Optionally, the pharmaceutical composition, dosage form, or kit further comprises one or more substrates of one or more SCFA-producing fermentation and/or biosynthesis pathways. In certain embodiments, the administration of the composition, dosage form, or kit to a mammalian subject results in the increase of one or more SCFAs in the mammalian subject by approximately 1.5-fold, 2-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater than 100-fold.

[0523] In some embodiments, the prebiotic mixture is selected to favor the production of a particular immunomodulatory SCFA, including but not limited to butyrate, propionate, or acetate. In preferred embodiments, the fermentation product is butyrate or propionate. Non-limiting examples are resistant starch and carbohydrates with highly organized structures, such as high amylose maize starch, that are more likely to be fermented by microbes to produce butyrate than other SCFAs (Zhou Z et al. 2013. Starch structure modulates metabolic activity and gut microbiota profile. Anaerobe. 24:71-78). In some embodiments, one or more components of a prebiotic mixture is subjected to denaturation (e.g., thermal treatment) to favor the production of a SCFA (e.g., acetate) or a non-SCFA species including but not limited to lactate or succinate.

[0524] In some embodiments, the pharmaceutical composition, dosage form, or kit comprises one or more types of microbe capable of producing butyrate in a mammalian subject. Butyrate-producing microbes may be identified experimentally, such as by NMR or gas chromatography analyses of microbial products or colorimetric assays (Rose I A. 1955. Methods Enzymol. Acetate kinase of bacteria. 1: 591-5). Butyrate-producing microbes may also be identified computationally, such as by the identification of one or more enzymes involved in butyrate synthesis. Non-limiting examples of enzymes found in butyrate-producing microbes include butyrate kinase, phosphotransbutyrylase, and butyryl CoA:acetate CoA transferase (Louis P., et al. 2004. Restricted Distribution of the Butyrate Kinase Pathway among Butyrate-Producing Bacteria from the Human Colon. J Bact. 186(7): 2099-2106). Butyrate-producing strains include, but are not limited to, *Faecalibacterium prausnitzii, Eubacterium* spp., *Butyrivibrio fibrisolvens, Roseburia intestinalis, Clostridium* spp., *Anaerostipes caccae*, and *Ruminococcus* spp. In some embodiments, the pharmaceutical composition, dosage form, or kit comprises two or more types of microbe, wherein at least two types of microbe are capable of producing butyrate in a mammalian subject. In other embodiments, the pharmaceutical composition, dosage form, or kit comprises two or more types of microbe, wherein two or more types of microbe cooperate (i.e., cross-feed) to produce an immunomodulatory SCFA (e.g., butyrate) in a mammalian subject. In a preferred embodiment, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe (e.g., *Bifidobacterium* spp.) capable of metabolizing a prebiotic, including but not limited to, inulin, inulin-type fructans, or oligofructose, such that the resulting metabolic product may be converted by a second type of microbe (e.g, a butyrate-producing microbe such as *Roseburia* spp.) to an immunomodulatory SCFA such as butyrate (Falony G., et al. 2006. Cross-Feeding between *Bifidobacterium longum* BB536 and Acetate-Converting, Butyrate-Producing Colon Bacteria during Grown on Oligofructose. Appl. Environ. Microbiol. 72(12): 7835-7841.) In other aspects, the pharmaceutical composition, dosage form, or kit comprises at least one acetate-producing microbe (e.g., *Bacteroides thetaiotaomicron*) and at least one acetate-consuming, butyrate-producing microbe (e.g., *Faecalibacterium prausnitzii*).

[0525] In some embodiments, the pharmaceutical composition, dosage form, or kit comprises one or more types of microbe capable of producing propionate in a mammalian subject, optionally further comprising a prebiotic or substrate appropriate for proprionate biosynthesis. Examples of prebiotics or substrates used for the production of propionate include, but are not limited to, L-rhamnose, D-tagalose, resistant starch, inulin, polydextrose, arabinoxylans, arabinoxylan oligosaccharides, mannooligosaccharides, and laminarans (Hosseini E., et al. 2011. Propionate as a health-promoting microbial metabolite in the human gut. Nutrition Reviews. 69(5): 245-258). Propionate-producing microbes may be identified experimentally, such as by NMR or gas chromatography analyses of microbial products or colorimetric assays (Rose I A. 1955. Methods Enzymol. Acetate kinase of bacteria. 1: 591-5). Propionate-producing microbes may also be identified computationally, such as by the identification of one or more enzymes involved in propionate synthesis. Non-

limiting examples of enzymes found in propionate-producing microbes include enzymes of the succinate pathway, including but not limited to phophoenylpyrvate carboxykinase, pyruvate kinase, pyruvate carboxylase, malate dehydrogenase, fumarate hydratase, succinate dehydrogenase, succinyl CoA synthetase, methylmalonyl Coa decarboxylase, and propionate CoA transferase, as well as enzymes of the acrylate pathway, including but not limited to L-lactate dehydrogenase, propionate CoA transferase, lactoyl CoA dehydratase, acyl CoA dehydrogenase, phosphate acetyltransferase, and propionate kinase. Non-limiting examples of microbes that utilize the succinate pathway are *Bacteroides fragilis* and other species (including *B. vulgatus*), *Propionibacterium* spp. (including *freudenrichii* and *acidipropionici*), *Veillonella* spp. (including *gazogenes*), *Micrococcus lactilyticus, Selenomonas ruminantium, Escherichia coli*, and *Prevotella ruminocola*. Non-limiting examples of microbes that utilize the acrylate pathway are *Clostridium neopropionicum* X4, and *Megasphaera elsdenii*. In preferred embodiments, the combination of a type of microbe or microbial composition and type of prebiotic mixture is selected based on the fermentation or metabolic preferences of one or more microbes capable of producing immunomodulatory SCFAs (e.g., preference for complex versus simple sugar or preference for a fermentation product versus a prebiotic). For example, *M. eldsenii* prefers lactate fermentation to glucose fermentation, and maximization of propionate production by *M. eldsenii* in a mammalian subject may therefore be achieved by administering along with *M. eldsenii* a favored substrate (e.g., lactate) or one or more microbes capable of fermenting glucose into lactate (e.g., *Streptococcus bovis*) (Hosseini E., et al. 2011. Propionate as a health-promoting microbial metabolite in the human gut. Nutrition Reviews. 69(5): 245-258). Thus, in some embodiments, the pharmaceutical composition, dosage form, or kit comprises at least one type of SCFA-producing microbe and a sugar fermentation product (e.g., lactate). In other embodiments, the pharmaceutical composition, dosage form, or kit comprises at least one type of SCFA-producing microbe and at least one type of sugar-fermenting microbe, wherein the fermentation product of the second, sugar-fermenting microbe is the preferred substrate of the SCFA-producing microbe.

[0526] In some embodiments, the pharmaceutical composition, dosage form, or kit comprises two or more types of microbe, wherein at least two types of microbe are capable of producing propionate in a mammalian subject. In other embodiments, the pharmaceutical composition, dosage form, or kit comprises two or more types of microbe, wherein two or more types of microbe cooperate (i.e., cross-feed) to produce an immunomodulatory SCFA (e.g., propionate) in a mammalian subject. In a preferred embodiment, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe (e.g., *Ruminococcus* spp. or *Bacteroides* spp.) capable of metabolizing a prebiotic into succinate, and a second type of microbe (e.g., *S. ruminantium*) capable of converting succinate (via the succinate pathway) into propionate in the mammalian subject.

[0527] Immunomodulation can also be achieved by the microbial production of glutathione or gamma-glutamylcysteine. Thus, in certain embodiments, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe capable of producing glutathione and/or gamma-glutamylcysteine in a mammalian subject. In some aspects, the composition, dosage form, or kit comprises one or more microbes selected for the presence of glutamate cysteine ligase (e.g., *Lactobacillus fermentum*) and/or L-proline biosynthesis enzymes (e.g., *E. coli*) (Peran et al., 2006. *Lactobacillus* fermenum, a probiotic capable to release glutathione, prevents colonic inflammation in the TNBS model of rat colitis. Int J Colorectal Dis. 21(8): 737-746; Veeravalli et al., 2011. Laboratory evolution of glutathione biosynthesis reveals naturally compensatory pathways. Nat Chem Bio. 7(2): 101-105). In a preferred embodiment, at least one microbe in the pharmaceutical composition, dosage form, or kit is *L fermentum*. para-cresol (p-cresol) is a microbial product, via the fermentation of tyrosine or phenylalanine.
Sulfated in the liver or colon to p-cresyl sulfate, this molecule reduces Th1-mediated responses (Shiba T. et al. 2014. Effects of intestinal bacteria-derived p-cresyl sulfate on Th1-type immune response in vivo and in vitro. Tox and Applied Pharm. 274(2): 191-199). In some embodiments, the pharmaceutical composition, dosage form, or kit comprises at least one type of microbe capable of fermenting tyrosine and/or phenylalanine to p-cresol in a mammalian subject. Non-limiting examples of such microbes include *Bacteroides fragilis, Clostridium difficile*, and *Lactobacillus* sp. Strain #11198-11201 (Yokoyama M T and Carlson J R. 1981. Production of Skatole and para-Cresol by a Rumen *Lactobacillus* sp. Applied and Environmental Microbiology. 41(1): 71-76.), and other microbes with p-hydroxylphenyl acetate decarboxylase activity.

[0528] It has recently come to light that the DNA of commensal microbes, including many species of *Lactobacillus* protect against activation of lamina propia dendritic cells and sustain regulatory T cell conversion (Bouladoux N, Hall J A, Grainger J R, dos Santos L M, Kann M G, Nagarajan V, Verthelyi D, and Belkaid Y, 2012. Regulatory role of suppressive motifs from commensal DNA. Mucosal Immunol. 5: 623-634). Thus commensal DNA may protect against colitis, IBD, and/or other immunological intolerances in the gut. Furthermore, *Lactobacillus* species are prevalent in the healthy vaginal microbiome. Thus, DNA from *Lactobacillus* or other vaginal microbiome commensals may suppress immune responses in the vagina that could disrupt the normal healthy-state vaginal microbiome and lead to complications such as chronic HPV, infertility, miscarriages, or UTIs. As such, in certain embodiments, the microbial composition, pharmaceutical composition, dosage form, or kit additionally comprises DNA isolated from one or more host commensals.

X. Crohn's Disease

[0529] Crohn's disease and ulcerative colitis are types of IBDs. While both illness share elements of their characteristic immune responses (e.g., high TNF-α, which can be detected in a patient's feces), their associated immune responses can also have distinguishing markers. For example, interleukin-16 (IL-16) levels are high and T-bet is overexpressed the lamina propia T cell nucleus in patients with Crohn's disease, but not in those suffering from ulcerative colitis. Notably T-bets produce the pro-inflammatory cytokine IFN-γ. One similarity among IBDs is high IFN-γ (by about 4-fold), caused in part due to high TL1A and TNF-α. Moreover, the levels of these cytokines correlate with the severity of the IBD.

[0530] Early Crohn's disease has a different immunological signature than does chronic Crohn's disease. In aspects in which a patient presents with early lesions, the microbial composition may be selected, with or without one or more

prebiotics, to counteract a T helper cell 2-mediated response. For example, the microbial composition, optionally combined with immunomodulatory molecules such as nucleotides or carbohydrates, may decrease interleukin-4 (IL-4) levels or increase IFN-γ. In aspects in which a patient presents with chronic lesions, the microbial composition may be selected to counteract a T helper cell 1-mediated response. For example, the microbial composition, optionally combined with immunomodulatory molecules such as nucleotides or carbohydrates, may decrease IL-2, IFN-γ, TNF-α, TL1A, IL-12, and/or IL-18. In some embodiments, in which a patient suffers from an IBD including but not limited to Crohn's disease, a probiotic microbial composition, with or without one or more prebiotics, is administered to the patient such that it is effective to reduce TNF-α levels, as detectable in feces samples, by approximately 5-fold, 10-fold, 25-fold, 50-fold, or 100-fold. Crohn's disease patients tend to present with low plasma levels of vitamins or minerals including but not limited to vitamin A, vitamin E, vitamin C, lycopene, carotenoids, and/or selenium. Patients eligible for immunomodulatory treatment may thus be administered an immunomodulatory microbe, molecule, and/or microbial component optionally combined with an appropriate vitamin or mineral supplement, as determined by plasma deficiency.

[0531] Probiotic compositions useful for treating or preventing Crohn's disease include, in exemplary embodiments, one or more bacterial strains from Table 1. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1A. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1B. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1C. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1D. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1E. In other embodiments, the probiotic composition includes one or more bacterial strains from Table 1F. In some embodiments, the probiotic composition contains a single strain of bacteria. In other embodiments, the probiotic composition contains two or more strains of bacteria, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 500, 1000 or more strains of bacteria. In other embodiments, the probiotic composition contains or is administered in conjunction with a prebiotic, as described herein.

[0532] Preferred bacterial genera include *Acetanaerobacterium, Acetivibrio, Alicyclobacillus, Alkaliphilus, Anaerofustis, Anaerosporobacter, Anaerostipes, Anaerotruncus, Anoxybacillus, Bacillus, Bacteroides, Blautia, Brachyspira, Brevibacillus, Bryantella, Bulleidia, Butyricicoccus, Butyrivibrio, Catenibacterium, Chlamydiales, Clostridiaceae, Clostridiales, Clostridium, Collinsella, Coprobacillus, Coprococcus, Coxiella, Deferribacteres, Desulfitobacterium, Desulfotomaculum, Dorea, Eggerthella, Erysipelothrix, Erysipelotrichaceae, Ethanoligenens, Eubacterium, Faecalibacterium, Filifactor, Flavonifractor, Flexistipes, Fulvimonas, Fusobacterium, Gemmiger, Geobacillus, Gloeobacter, Holdemania, Hydrogenoanaerobacterium, Kocuria, Lachnobacterium, Lachnospira, Lachnospiraceae, Lactobacillus, Lactonifactor, Leptospira, Lutispora, Lysinibacillus, Mollicutes, Moorella, Nocardia, Oscillibacter, Oscillospira, Paenibacillus, Papillibacter, Pseudoflavonifractor, Robinsoniella, Roseburia, Ruminococcaceae, Ruminococcus, Saccharomonospora, Sarcina, Solobacterium, Sporobacter, Sporolactobacillus, Streptomyces, Subdoligranulum, Sutterella, Syntrophococcus, Thermoanaerobacter, Thermobifida*, and *Turicibacter.*

[0533] Preferred bacterial genera also include *Acetonema, Alkaliphilus, Amphibacillus, Ammonifex, Anaerobacter, Caldicellulosiruptor, Caloramator, Candidatus, Carboxydibrachium, Carboxydothermus, Cohnella, Dendrosporobacter Desulfitobacterium, Desulfosporosinus, Halobacteroides, Heliobacterium, Heliophilum, Heliorestis, Lachnoanaerobaculum, Lysinibacillus, Oceanobacillus, Orenia* (*S.*), *Oxalophagus, Oxobacter, Pelospora, Pelotomaculum, Propionispora, Sporohalobacter, Sporomusa, Sporosarcina, Sporotomaculum, Symbiobacterium, Syntrophobotulus, Syntrophospora, Terribacillus, Thermoanaerobacter*, and *Thermosinus.*

[0534] As provided herein, therapeutic compositions comprise, or in the alternative, modulate, the colonization and/or engraftment, of the following exemplary bacterial entities: *Lactobacillus gasseri, Lactobacillus fermentum, Lactobacillus reuteri, Enterococcus faecalis, Enterococcus durans, Enterococcus villorum, Lactobacillus plantarum, Pediococcus acidilactici, Staphylococcus pasteuri, Staphylococcus cohnii, Streptococcus sanguinis, Streptococcus sinensis, Streptococcus mitis, Streptococcus* sp. SCA22, *Streptococcus* sp. CR-3145, *Streptococcus anginosus, Streptococcus mutans, Coprobacillus cateniformis, Clostridium saccharogumia, Eubacterium dolichum* DSM 3991, *Clostridium* sp. PPf35E6, *Clostridium sordelli* ATCC 9714, *Ruminococcus torques, Ruminococcus gnavus, Clostridium clostridioforme, Ruminococcus obeum, Blautia producta, Clostridium* sp. ID5, *Megasphaera micronuciformis, Veillonella parvula, Clostridium methylpentosum, Clostridium islandicum, Faecalibacterium prausnitzii, Bacteroides uniformmis, Bacteroides thetaiotaomicron, Bacteroides acidifaciens, Bacteroides ovatus, Bacteroides fragilis, Parabacteroides distasonis, Propinionibacteirum propionicum, Actinomycs hyovaginalis, Rothia mucilaginosa, Rothia aeria, Bifidobacterium breve, Scardovia inopinata* and *Eggerthella lenta.*

[0535] Preferred bacterial species are provided in Table 1, Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, Table 1F, and Table 5. Optionally, in some embodiments, preferred bacterial species are spore formers. Where specific strains of a species are provided, one of skill in the art will recognize that other strains of the species can be substituted for the named strain.

[0536] In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acidaminococcus intestine*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter baumannii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter lwoffii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Akkermansia muciniphila*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes putredinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes shahii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerostipes hadrus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of

the invention is *Anaerotruncus colihominis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides caccae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides cellulosilyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides dorei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides eggerthii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides finegoldii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides fragilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides massiliensis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides ovatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bacteroides salanitronis. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides salyersiae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. D20. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides uniformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides vulgatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium adolescentis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bifidobacterium bifidum. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium breve*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium faecale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia glucerasea*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia wexlerae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Catenibacterium mitsuokai*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium asparagiforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium bolteae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium clostridioforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of

the invention is *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium histolyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium indolis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium leptum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium perfringens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 14774. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. HGF2. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium symbiosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella aerofaciens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprobacillus* sp. D7. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus catus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus comes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea formicigenerans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea longicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecium*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli* 588. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium eligens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium fissicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium ramulus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium rectale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Faecalibacterium prausnitzii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Flavonifractor plautii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium mortiferum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium nucleatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Holdemania filiformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Klebsiella oxytoca*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus rhamnosus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus ruminis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactococcus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Odoribacter splanchnicus. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Oscillibacter valericigenes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides gordonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides johnsonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides merdae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Pediococcus acidilactici*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Propionibacterium granulosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia intestinalis*. In one

embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia inulinivorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus gnavus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus* sp. ID8. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus torques*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Slackia piriformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus epidermidis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus saprophyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus cristatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus infantis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus oralis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus sanguinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus viridans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus thermophiles*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Veillonella dispar*.

[0537] In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acidaminococcus intestine*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter baumannii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter lwoffii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Akkermansia muciniphila*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes putredinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes shahii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerostipes hadrus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerotruncus colihominis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides caccae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides cellulosilyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides dorei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides eggerthii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides finegoldii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides fragilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides massiliensis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides ovatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salanitronis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salyersiae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. D20. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides uniformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides vulgatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium adolescentis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium bifidum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium breve*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium faecale*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia glucerasea*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *luti*. In one

embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia wexlerae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Catenibacterium mitsuokai*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium asparagiforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium bolteae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium clostridioforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium histolyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium indolis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium leptum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium perfringens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 14774. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. HGF2. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium symbiosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella aerofaciens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprobacillus* sp. D7. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus catus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus comes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea formicigenerans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea longicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecium*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli* 588. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium eligens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium fissicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium ramulus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium* rectale. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Faecalibacterium prausnitzii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Flavonifractor plautii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium mortiferum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium nucleatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Holdemania filiformis*. In one embodi-

ment, the bacterial population useful in the compositions and methods of the invention comprises *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Klebsiella oxytoca*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus rhamnosus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus ruminis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactococcus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Odoribacter splanchnicus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Oscillibacter valericigenes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides gordonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides johnsonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides merdae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Pediococcus acidilactici*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Propionibacterium granulosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia inulinivorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus gnavus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus* sp. ID8. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus torques*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Slackia piriformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus epidermidis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus saprophyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus cristatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus infantis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus oralis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus sanguinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus viridans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus thermophiles*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Veillonella dispar*.

XI. Transplant Disorders and Graft Versus Host Disease (GVHD)

[0538] Graft-versus-host disease (GVHD) is a common complication for patients who have received an allogeneic transplant (e.g., allogeneic bone marrow transplant or allogeneic stem cell transplant). GVHD may also develop in patients who have received a blood transfusion with blood products that had not been irradiated. Patients suffering from GVHD have elevated levels of pro-inflammatory cytokines, particularly interleukin-6 (IL-6), as well as others including tumor necrosis factor-alpha (TNF-α), interleukin-1 (IL-1), interleukin-12 (IL-12), interferon-gamma (IFN-γ), and interleukin-2 (IL-2). GVHD is also associated with low interleukin-22 (IL-22) and the loss of interleukin-23 (IL-23)-responsive or Lgr5+ innate lymphoid cells. Furthermore, GVHD patients have reduced numbers of intestinal stem cells, fewer or less active Paneth cells, and lower Foxp3 expression in T cells.

[0539] For over 40 years, it has been known that the bacteria inhabiting our intestines are important modulators of the biology of hematopoietic cell transplantation (HCT) and impact the development of graft versus host disease. Studies in mice have shown reduction of GVHD with gut-decontaminating antibiotics (van Bekkum et al., 1974) and transplantation in germ-free conditions (Jones et al., 1971). This led to clinical attempts to eliminate intestinal bacterial colonization in allogenic BMT patients with a combination of gut decontamination practices and maintenance of a near-sterile environment (Storb et al., 1983). Initial clinical studies employing strategies to suppress the intestinal microbiota showed considerable promise, but later reports failed to demonstrate a clear and consistent benefit.

[0540] The recent understanding of the microbiota that inhabit the human gastrointestinal tract, skin, lungs, vagina, and other niches is being appreciated in their role in health and disease of dysbiosis (e.g. see Human Microbiome Project Consortium 2012, Structure, function, and diversity of the healthy human microbiome. Nature 486(7402):207-14). Several groups have reported preliminary data on the significance of the gut microbiota in HCT patients and in the development of GVHD. Collectively these reports show, using murine and human studies, that there is a significant decreased in diversity of gut microbiome following HCT accompanied by marked changes in the population (Taur et al., 2012; Jenq et al., 2012; Taur et al., 2014). Most notably, we have found that as much as 90% of allo BMT patients demonstrate a loss of diversity and a corresponding expansion of a single type of

bacteria that takes up much of the "space" within the intestinal flora compartment (Taur Y, et al. Clin Infect Dis. 2012).

[0541] Aspects of the invention are based, in part, on the realization that microbes play an important role in the prevention, initiation and development of graft versus host disease (GVHD). The presence of certain microbial populations correlate with the initiation and development of the disease. More importantly, the presence of some species correlates with reduced severity or mortality associated with the disease or protection from GVHD altogether.

[0542] In some aspects, the invention is a composition or method for the treatment of GVHD in patients suffering from chronic or acute GVHD. In certain embodiments, the pharmaceutical composition, dosage form, or kit comprises one or more microbes, with or without one or more prebiotics, capable of decreasing the expression or release of one or more of IL-6, IL-1, IL-12, IL-2, IFN-γ, and TNF-α. In some embodiments, the pharmaceutical composition, dosage form, or kit comprises one or more microbes capable of increasing the expression or release of IL-22. The microbial composition, with or without one or more prebiotics, may also be selected such that it is effective to stimulate or favor the survival of Paneth cells, intestinal stem cells, FoxP3+ Treg cells (e.g., CD4+ CD25+ FoxP3+ Treg cells), IL-23-responsive innate lymphoid cells, and/or Lgr5+ innate lymphoid cells. In some embodiments, the microbial composition, with or without one or more prebiotics, regulates expression of Foxp3 by modulating (de)methylation of the Foxp3 locus. In preferred embodiments, the immunological tolerance elicited by the microbial composition, with or without one or more prebiotics, does not reduce graft-vs-leukemia activity by the immune system.

[0543] In some aspects, the invention is a composition or method for the prevention of GVHD. Recent work has shown that small doses of IL-2 may be able to restore T cell homeostasis in patients at risk for GVHD (Kennedy-Nasser et al., 2014. Ultra low-dose IL-2 for GVHD prophylaxis after allogeneic hematopoietic stem cell transplantation mediates expansion of regulatory T cells without diminishing antiviral or antileukemic activity. Clin Cancer Res. 20:2215-2225). Thus in certain embodiments, the pharmaceutical composition, dosage form, or kit comprises one or more microbes capable of slightly increasing IL-2 levels in a patient such that the abundance of $CD4^{+}CD25+$ FoxP3+ Treg cells increases by 1.5-fold, 2-fold, or more than 5-fold. In a preferred embodiment, the IL-2-level enhancing treatment is administrated between one week and one month following the patient's transplant procedure.

[0544] Aspects of this invention are based at least in part on the discovery that presence of certain bacterial populations can protect from GVHD and that supplementation with such or similar bacterial compositions can prevent, treat or inhibit GVHD. Similarly, aspects of this invention also includes approaches used for augmentation of such bacterial compositions using various techniques including substrates for bacterial fermentation and propagation as well as delivery of key end products or metabolites of such bacteria which reconstitute needed functionality of a bacterial community can also be used to prevent, treat or inhibit GVHD. Other aspects of this invention include agents for targeting bacteria that increase GVHD mortality or exacerbate clinical GVHD.

[0545] Herein, we disclose methods for identifying bacterial subsets that increased or decreased GVHD related mortality in order to identify subsets that may modulate GVHD severity Stool specimen was collected from patients who underwent conventional (non-T cell depleted) allo BMT. Fecal samples were collected and stored weekly over the course of the transplant hospitalization this included prior to conditioning, as well as on days 0, 7, 14, 21, 30, 60, and 100. GVHD was diagnosed clinically, confirmed pathologically by biopsy whenever possible, and classified according to standard criteria. Patients who engrafted were evaluable for acute GVHD based on historical consensus criteria as described previously (see Rowlings P A, Przepiorka D, Klein J P, et al. IBMTR Severity Index for grading acute graft-versus-host disease: retrospective comparison with Glucksberg grade. *Br J Haematol.* 1997). These criteria were applied to GVHD with purely acute features that occurred after day 100. Cases of GVHD were further categorized by treatment with or without systemic steroids (prednisone or methylprednisolone, 0.5 mg/kg daily or higher). Cause of death was determined using a standard algorithm where outcomes were prioritized in the following order: 1) primary disease recurrence, 2) graft failure, 3) GVHD, 4) infection, and 5) organ failure; thus in patients without disease recurrence or graft failure, those who were being treated for GVHD at the time of death were considered to have succumbed to GVHD-related mortality, including those who died from infections. In some embodiments, the abundances of bacterial genera from patients who did or did not die from GVHD by linear discriminant analysis (LDA) effect size (LEfSe) was compared to identify bacterial subsets associated with either increased or decreased GVHD-related mortality.

[0546] Provided herein are probiotic compositions of bacteria that modulate GVHD severity and related mortality and thus can be used to prevent, treat or inhibit GVHD. In one embodiment, a probiotic composition is administered to a subject in an amount effective to increase short chain fatty acid production by one or more organisms in the gut of a mammalian host.

[0547] In certain aspects, the invention relates to microbial compositions. In certain embodiments, the microbial compositions can be used for the prevention, treatment or inhibition of GVHD. Aspects of the invention relate to microbial compositions that are being isolated from a subject's microbiota. In some embodiments, the subject is a healthy mammal. In other embodiments, the subject is the recipient of the transplant prior itself prior to inception of the conditioning regimen. In some embodiments, the microbial compositions comprise of bacteria that are enriched in alive GVHD patients. These bacteria are strongly predictive of improved overall survival following allo BMT and largely driven by reduced GVHD-related mortality.

[0548] In some embodiments, the microbial composition comprises bacteria that are associated with and can reduce clinical acute GVHD. In some embodiments, the microbial composition comprises of bacteria that can reduce acute GVHD grades 2-4. In some embodiments, the microbial composition comprises of bacteria that can reduce acute GVHD responsive to treatment with systemic corticosteroids. In some embodiments, the microbial composition comprises of bacteria that can reduce systemic corticosteroid treatment refractory acute GVHD. In some embodiments, the microbial composition comprises of bacteria that are associated with reduced lower gut GVHD. In some embodiments, the microbial composition comprises of bacteria that are associated

with reduced liver GVHD. In some embodiments, the microbial composition comprises of bacteria that are associated with reduced skin GVHD.

[0549] In some embodiments, the microbial composition comprises bacteria that are associated with and can reduce clinical chronic GVHD in a subject. In some embodiments, the subject has chronic GVHD. The subject with chronic GVHD may be receiving an immunosuppressive treatment. The immunosuppressive treatment may be one or more of methotrexate, cyclosporine, a corticosteroid, and antithymocyte globulin. The corticosteroid may be methylprednisolone. In some embodiments, the subject requires or has required immunosuppressive treatment for a period of one or more years. In further embodiments, the subject has steroid-refractory GVHD. The subject may be receiving one or more of extracorporeal photophoresis, anti-TNF alpha antibody, mammalian target of rapamycin (mTOR) inhibitor, mycophenolate mofetil, interleukin-2 receptor antibody, alemtuzumab pentostatin, mesenchymal stem cells, and methotrexate.

[0550] Aspects of this intervention also includes identification of antimicrobial agents that increase GVHD incidence and severity by impacting bacteria that are protective against GVHD. Identification of such bacteria can be used as a guide to alter clinical practice to reduce GVHD incidence/severity. Antibiotics are used in BMT patients either for gut decontamination purposes or to treat neutropenic fever. In some embodiments, BMT patients were analyzed to identify if antibiotics they were administered such as piperacillin-tazobactam, imipenem-cilastatin, metronidazole, aztreonam and oral vancomycin lead to reduction in bacteria protective against GVHD including clostridiales such as *blautia*. In some embodiments, BMT patients were analyzed to identify if antibiotics they were administered such as piperacillin-tazobactam, imipenem-cilastatin, metronidazole, aztreonam and oral vancomycin lead to increase in bacteria that exacerbate GVHD. In some embodiments, BMT patients were retroactively analyzed to see if exposure to antibiotics with or without anaerobic coverage could impact on GVHD. In some embodiments, the microbial composition comprises bacteria that are associated with GVHD-related mortality. Aspects of this invention also includes agents that targets bacterial populations exacerbate clinical GVHD, increase incidence or severity of GVHD or increase GVHD related mortality.

[0551] Aspects of this invention also includes approaches used for augmentation of bacterial compositions that prevent or mitigate GVHD using various techniques including substrates for bacterial fermentation and propagation. It was noted that patients undergoing BMT can lose GVHD protective bacteria without any exposure to antibiotics. This phenomenon was also noted in murine models with experimental GVHD. In some embodiments, the composition of the invention comprises substrates that augment bacterial compositions that prevent or mitigate GVHD. Given diet and nutrition has a tremendous impact on gut microbiome composition and that oral nutrition intake is commonly reduced in allo BMT patients, the impact of nutrition on GVHD protective bacteria abundance was analyzed. In some embodiments, the effect of reduced oral caloric consumption, particularly below 500 kcal/day, on *Blautia* abundance was analyzed. A pilot experiment of daily nutritional and flora monitoring in five patients undergoing allo BMT showed that a reduction in oral caloric consumption, particularly below 500 kcal/day, was associated with a reduction in *Blautia* abundance. Given *blautia*'s ability to mitigate GVHD, a nutrition method to augment *blautia* levels in BMT patients would be a rationale strategy for mitigating GVHD. The ability of *blautia* to ferment a variety of sugars was thus analyzed using pH and optical density to evaluate bacterial growth in media lacking glucose. In one embodiment, the growth of *blautia* was analyzed. In another embodiment, bacteria that are potentially competing with *blautia* such as *lactobacillus johnsonii*. *Lactobacillus johnsonii* was evaluated. *Lactobacillus johnsonii* expands in the setting of calorie restriction at the expense of Clostridia (Jenq et al., 2012) and is thus presumably a direct competitor for nutrients in the murine intestine. Using such strategies, specific substrates or sugars were identified that are fermentable by *blautia* but not *lactobacillus*. In one embodiment, the substrate that specifically augments *blautia* but not *lactobacillus* was xylose. In another embodiment, the substrate that specifically augments *blautia* but not *lactobacillus* was rhamnose. In another embodiment, the effect of administration of such substrates on *blautia* level was investigated in experimental GVHD models. Administration of xylose in the drinking water of mice was found to lead to an expansion of *Blautia* in the intestinal flora de-spite the presence of GVHD on day 14 after BMT. In another embodiment, long term effect of xylose administration was evaluated to investigate effects on GVHD related survival. Long-term administration of xylose led to improved survival of mice with GVHD.

[0552] Aspects of this invention also include compositions of bacterial end products or metabolites that are responsible or can impart the functionality of a bacterial compositions that prevent or mitigate GVHD. Short-chain fatty acids (SCFA), which are produced by many bacteria as a byproduct of carbohydrate fermentation. SCFA are one of the most abundant metabolites produced by the gut microbiome, particularly the class clostridia. SCFA have been found to be important modulators of the immune system. In germ-free mice and vancomycin-treated conventional mice, administration of SCFA (acetate, propionate, or butyrate) restored normal numbers of Tregs in the large intestine (Smith P M, et al. Science. 2013; 569-573). In some embodiments, the SCFA levels of stool specimens from GVHD patients were analyzed for associations with *blautia* abundance. Samples with reduced abundance of *Blautia* were also found to have reduced abundance of the SCFA butyrate and acetate. In some embodiments, SCFA will be administered post BMT to reduce incidence and severity of GVHD. In some embodiment, the SFCA administered is acetate. In some embodiment, the SFCA administered is butyrate while in other embodiments it is propionate. In some embodiments, SCFA will reduce GVHD without impacting graft versus tumor effects. In some embodiments, SCFA administration increases the number of peripheral tregs and leads to induction of Foxp3 expression. In some embodiments, SCFA administration reduces donor alloreactive T cells.

[0553] In some embodiments, metabolite profiles of patient tissue samples or microbes cultures from patient tissue are used to identify risk factors for developing an autoimmune or inflammatory response, to diagnose an autoimmune or inflammatory disease, to evaluate the prognosis or severity of said disease, to evaluate the success of a treatment regimen, or any combination thereof. Exemplary metabolites for the purposes of diagnosis, prognostic risk assessment, or treatment assessment purposes include short chain fatty acids, bile acids, and lactate. In preferred embodiments, metabolite profiles are taken at different time points during a patient's dis-

ease and treatment in order to better evaluate the patient's disease state including recovery or relapse events. Such monitoring is also important to lower the risk of a patient developing a new autoimmune condition following immunomodulatory treatment. In some embodiments, metabolite profiles inform subsequent treatment. For example, patients at risk for developing GVHD and presenting low levels of butyrate may be administered a microbial composition comprising microbes that produce butyrate (e.g., *Blautia* species) and excluding microbes capable of depleting butyrate (e.g. *Methanobacterium* species). Probiotic compositions that produce SCFA in the gut of a subject are particularly useful for the treatment of GVHD, because they improve intestinal barrier integrity, which is associated with improvement in overall survival in patients receiving a transplant.

[0554] In some embodiments, the administration is preventative or prophylactic in that the subject has not yet developed a detectable GVHD. In some embodiments, the preventative/prophylactic microbial composition will be administered prior after the completion of conditioning region but prior to the transplant. Typically, it takes 2-3 weeks for engraftment of the transplant to be completed. In some embodiments, the preventative/prophylactic microbial composition will be administered once prior to transplant and then again on day 17 after completion of antibiotics prescribed to prevent or treat neutropenic fever or other infections.

[0555] The classical definition of Graft versus host disease (GVHD) is that it is an immunological disorder in which the immune cells of a transplant attack the tissues of a transplant recipient and lead to organ dysfunction. In the case of allogeneic bone marrow (BM) transplantation, T-cells from the transplanted BM recognize the host (the bone marrow-transplanted patient i.e., the recipient) as non-self and attack its tissues and organs. The organs most commonly attacked are the gastrointestinal (GI) tract, skin, liver, and lungs. Historical data, however, says it is not only immune cells that are involved in disease pathogenesis and points to the importance of the resident host gut microbes in the development of GVHD.

[0556] GVHD can be mild, moderate, or severe, depending on the extent of damage inflicted to different organs. The disease is divided into acute and chronic GVHD according to clinical manifestations. Patients with acute GVHD typically suffer damage to the skin, GI tract, and liver. Skin damage ranges from redness to exfoliation. Insult to the GI tract can result in bloody diarrhea and blood loss. Liver manifestations, though usually cholestatic in nature, can include liver failure in rare cases.

[0557] Acute GVHD usually develops within the first 100 days after transplantation, but it can also occur later. The clinical manifestations of chronic GVHD include red and itchy skin, dry eyes, dry mouth, abnormal liver function with jaundice, and lung damage due to bronchiolitis obliterans. Chronic GVHD is the major cause of non-relapse mortality after allogeneic hematopoietic transplantations. Chronic GVHD usually develops more than 100 days after transplantation, but it can appear sooner.

[0558] Patients with chronic GVHD require prolonged immunosupressive treatment, averaging two to three years in length. The mechanisms underlying chronic GVHD are considered to be somewhat distinct from those of acute GVHD. Thus, chronic GVHD is not simply an end-stage of acute GVHD.

[0559] Clinical Staging of Acute GVHD (aGVHD)—There are two systems for quantifying the severity of aGVHD, namely, the International Bone Marrow Transplant Registry (IBMTR) grading system and the Glucksberg grading system. For both systems, the stage of aGVHD is first determined separately in the three main target organs (skin, liver and gut). These grades are then used to determine an overall aGVHD grade, using either the International Bone Marrow Transplant Registry (IBMTR) or Glucksberg criteria.

[0560] For each grading system, the acute GVHD stage for each target organ is first determined according to certain clinical measures, as provided in Table 3.

[0561] The invention also provides, in one aspect, a method of increasing the duration of survival of a subject receiving a bone marrow transplant, by administering to the subject a probiotic composition comprising an isolated bacterial population, such that the duration of survival of the subject is increased. In a preferred embodiment, the bacterial population is a human-derived bacterial population. A human-derived bacterial population includes bacterial strains that natively inhabit a human host, as opposed to a non-human mammalian host. Administration of the probiotic composition can reduce the likelihood that the subject will develop sepsis following the bone marrow transplant. Administration of the probiotic composition can also reduce the likelihood that the subject will develop graft versus host disease (GVHD) following the bone marrow transplant. The probiotic composition can be administered to the subject prior to, after, or concurrently with receiving the bone marrow transplant.

[0562] In one embodiment, the probiotic composition reduces intestinal permeability in the subject. This can be achieved by, for example, administering a probiotic composition that contains bacteria which produce short chain fatty acids, which increase intestinal barrier integrity in a subject. In exemplary embodiments, the bacteria produce butyrate, acetate, propionate, or valerate, or combinations thereof. Also provided is a method of reducing intestinal permeability in a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population and a pharmaceutically acceptable excipient, such that the intestinal permeability of the subject of the subject receiving the transplant is reduced.

[0563] In another embodiment, the probiotic composition reduces inflammation in the subject, e.g., in the gastrointestinal tract, or in a distal location. The probiotic composition can contain anti-inflammatory bacteria. Anti-inflammatory bacteria are described herein. For example, anti-inflammatory bacteria included in the probiotic composition can decrease secretion of pro-inflammatory cytokines (e.g., IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof) and/or increase secretion of anti-inflammatory cytokines (e.g., IL-10, IL-13, IL-4, IL-5, TGFβ, and combinations thereof) by human host cells, such as human epithelial cells or immune cells, e.g., peripheral blood mononuclear cells (PBMCs). Bacteria which produce short chain fatty acids also have anti-inflammatory properties.

[0564] In some embodiments, the subject has received or will receive a hematopoietic stem cell transplant. In some embodiments, the subject will receive a hematopoietic stem cell transplant that is T cell depleted.

[0565] In exemplary embodiments, the subject has a disorder such as a hematopoietic neoplastic disorder, leukemia, lymphoma, and multiple myeloma. In some embodiments, the subject has a hematopoietic neoplastic disorder. The subject may have leukemia. The leukemia may be chronic myelogeneous leukemia or chronic lymphocytic leukemia. In some embodiments, the subject has lymphoma. The lymphoma may be Hodgkin's disease or non-Hodgkin's lymphoma. In some cases, the subject has multiple myeloma. The subject may receive or will receive a bone marrow, peripheral blood stem cell, or cord blood transplant. In some embodiments, the subject has received or will receive whole body irradiation. In further embodiments, the subject is female.

[0566] Due to the unique mechanism of action of probiotic compositions in the treatment or prevention of GVHD, probiotic compositions can be selected which minimize GVHD, but do not significantly reduce or eliminate the graft versus tumor (GVT) effect of the bone marrow transplant.

[0567] In other embodiments, the subject receiving the transplant has an autoimmune disorder, such as, for example, lupus, multiple sclerosis, systemic sclerosis, Crohn's disease, type I diabetes, and juvenile idiopathic arthritis. In another embodiment, the subject receiving the transplant has sickle cell disease or sickle cell anemia.

[0568] In an exemplary embodiment, the invention provides a method of increasing the duration of survival of a subject receiving a bone marrow transplant, comprising administering to the subject a probiotic composition comprising an isolated population of anti-inflammatory bacteria capable of decreasing secretion of pro-inflammatory cytokines and/or increasing secretion of anti-inflammatory cytokines by human peripheral blood mononuclear cells (PBMCs), and a pharmaceutically acceptable excipient, in an amount effective to reduce inflammation in the gastrointestinal tract of the subject, such that the duration of survival of the subject is increased.

[0569] In some embodiments, the subject has received or will receive a transplant from an HLA-matched related donor or an HLA-matched unrelated donor. The subject may also have received or may receive a transplant from an HLA-mismatched related or unrelated donor. In some embodiments, the subject will receive an autologous transplant. In some embodiments, the microbial composition will augment an autologous or allogeneic transplant. In some embodiments, the microbial composition will improve engraftment after an autologous or allogeneic transplant. In some embodiments, the microbial composition will improve neutropenic recovery after an autologous or allogeneic transplant. In some embodiments, the microbial composition will reduce complications after an allogeneic transplant. In some embodiments, the microbial composition will reduce complications after an autologous transplant. Complications after allogeneic transplant may include but are not limited to infections, organ failure, Veno-occlusive disease (VOD) of the liver, and/or Interstitial Pneumonia Syndrome (IPS).

[0570] In some embodiments, the subject will receive GVHD prophylaxis regimen that are standardly used in the clinic in addition to the microbial composition. This may include administering immunosuppressive treatment such as methotrexate, cyclosporine, corticosteroids, or anti-thymocyte globulin.

[0571] In some embodiments, the subject will receive GVHD treatment regimen that are standardly used in the clinic in addition to the microbial composition for management of graft versus host disease. The joint working group established by the Haemato-oncology subgroup of the British Committee for Standards in Haematology (BCSH) and the British Society for Bone Marrow Transplantation (BSBMT) reviewed the available literature and made recommendations in 2012 for the management of acute graft-versus-host disease. Their recommendations are as follows: (1) The management of grade I disease should include topical therapy and optimizing levels of calcineurin inhibitors without the need for additional systemic immunosuppression. (2) The use of systemic corticosteroids is recommended for first line therapy for grade II-IV GVHD. (3) The following agents are suggested for use in the second line treatment of steroid-refractory acute GVHD: extracorporeal photopheresis, anti-tumour necrosis factor a antibodies, mammalian target of rapamycin (mTOR) inhibitors, mycophenolate mofetil, interleukin-2 receptor antibodies. (4) The following agents are suggested as third line treatment options in acute steroid-refractory GVHD: alemtuzumab pentostatin, mesenchymal stem cells and methotrexate. In one aspect, disclosed herein are methods of treating, inhibiting, or preventing GVHD in a subject wherein the subject has acute steroid-refractory GVHD. In such methods, the method can further comprise administering to the subject extracorporeal photopheresis, anti-tumour necrosis factor a antibodies, mammalian target of rapamycin (mTOR) inhibitors, mycophenolate mofetil, interleukin-2 receptor antibodies, alemtuzumab pentostatin, mesenchymal stem cells, methotrexate, or any combination thereof.

[0572] In other embodiments, the subject is administered a prebiotic composition in conjunction with the probiotic composition. For example, in one aspect, the invention provides method of increasing the duration of survival of a subject receiving a bone marrow transplant, by administering to the subject a probiotic composition comprising an isolated bacterial population, wherein the probiotic composition reduces intestinal permeability in the subject, and administering a prebiotic that enhances the activity of the bacterial population, such that the duration of survival of the subject is increased. Prebiotic compositions of the invention are described herein. Exemplary prebiotics are provided in Table 7, and in FIG. **29**.

[0573] The invention also provides, in certain aspects, method of preventing or treating graft versus host disease (GVHD) in a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population, such that GVHD is prevented or treated. The probiotic composition can increase the duration of survival of the transplant recipient, by preventing GVHD, and/or preventing the development of sepsis. Preferably the bacterial population is a human-derived bacterial population. As noted above, the subject may be receiving a hematopoietic stem cell transplant or a bone marrow transplant. In other embodiments, the subject is receiving a solid organ transplant.

[0574] GVHD commonly develops after an allogeneic bone marrow transplant (BMT) but it can also appear after solid organ transplantation. The exact incidence rate of GVHD after solid organ transplantation is unknown. Mild cases likely remain undiagnosed because the clinical features of fever, rash, and diarrhea can be misinterpreted as related to post-transplantation infections. The incidence rate of GVHD is highest after small bowel transplantation (about 5%), followed by liver transplantation. But in general, the incidence rate for solid organ transplantation is very small relative to

bone marrow transplantation. In embodiments, the microbial composition is used to prevent or treat GVHD in solid organ transplant recipients.

[0575] In some embodiments, the microbial composition will be administered to subjects receiving solid organ transplantation. Transplanted solid organs may include a kidney, heart, skin, a lung, a liver, a pancreas, an intestine, an endocrine gland, a bladder, or a skeletal muscle. In some embodiments, microbial composition will be used to prevent graft rejection in a recipient of a transplanted solid organ. In some embodiments, microbial composition will be used to prevent other complications of solid organ transplantation such as infections.

[0576] In exemplary embodiments, the subject has a hematopoietic neoplastic disorder such as, for example, leukemia, lymphoma, or multiple myeloma, an autoimmune disorder such as, for example, lupus, multiple sclerosis, systemic sclerosis, Crohn's disease, type I diabetes, or juvenile idiopathic arthritis, or a sickle cell disorder such as, for example, sickle cell disease or sickle cell anemia.

[0577] Aspects of this invention also include an immune mechanism via which acute or chronic GVHD or solid organ transplant recipients are managed. In some embodiments, a test article inhibits the functionality of antigen presenting cells such as dendritic cells where the test article is the microbial composition, prebiotics, microbial composition plus prebiotics or microbial metabolites. In some embodiments, a test article inhibits maturation of antigen presenting cells such that levels of CD40, CD80, CD86, PD-L1 and PD-L2 are modulated. In some embodiments, test article inhibits activity of antigen presenting cells such that production of cytokines such as TGFβ, IL-10, IL-4, IL-12 are modulated. In some embodiments, test article inhibits activity of antigen presenting cells such as their endocytic/phagocytic capacity is hindered. In some embodiments, test article inhibits activity of antigen presenting cells such that their ability to activate naïve T cells is hindered.

[0578] In some embodiments, test article inhibits the functionality of T cells where the test article is the microbial composition, prebiotics, microbial composition plus prebiotics or microbial metabolites. In some embodiments, test article alters the functionality of CD4+ T cells such that their activation status is altered affecting surface levels of CD25. In some embodiments, test article alters the functionality of CD4+ T cells such that their proliferative capacity is inhibited. In some embodiments, test article increases the number and differentiation of peripheral regulatory T cells. In some embodiments, the test article affects production of cytokines by T cells such as but not limited to IL-6, TNF-alpha, IFN-γ, IL-10, IL-4. In some embodiments, the test article reduces the cytotoxic capacity of effector CD8+ cells.

[0579] As described herein, reducing systemic or local inflammation in a subject reduces the likelihood that a subject will develop GVHD. Accordingly, in another embodiment, the invention provides a method of reducing inflammation in the gastrointestinal tract of a subject receiving a transplant, by administering to the subject a probiotic composition comprising an isolated, anti-inflammatory bacterial population and a pharmaceutically acceptable excipient, such that inflammation in the gastrointestinal tract of the subject receiving the transplant is reduced. Probiotic compositions containing anti-inflammatory bacterial populations described herein are suitable for the practice of this embodiment.

[0580] Additional probiotic compositions useful for treatment or prevention of GVHD contain bacterial strains capable of reducing inflammation in a subject. Such immunomodulatory (anti-inflammatory) bacteria can modulate cytokine expression by host immune cells, resulting in an overall increase in secretion of anti-inflammatory cytokines and/or an overall decrease in secretion of pro-inflammatory cytokines, systemically reducing inflammation in the subject. In exemplary embodiments, probiotic compositions useful for treatment or prevention of GVHD stimulate secretion of one or more anti-inflammatory cytokines by host immune cells, such as PBMCs. Anti-inflammatory cytokines include, but are not limited to, IL-10, IL-13, IL-9, IL-4, IL-5, TGFβ, and combinations thereof. In other exemplary embodiments, probiotic compositions useful for treatment or prevention of GVHD inhibit secretion of one or more pro-inflammatory cytokines by host immune cells, such as PBMCs. Pro-inflammatory cytokines include, but are not limited to, IFNγ, IL-12p70, IL-1α, IL-6, IL-8, MCP1, MIP1α, MIP1β, TNFα, and combinations thereof. Other exemplary cytokines are known in the art and are described herein. Probiotic compositions containing anti-inflammatory bacteria reduce inflammation and restore barrier function at the site of administration, e.g., in the gastrointestinal tract, as well as at distal sites throughout the body of the subject.

[0581] Other exemplary probiotic compositions useful for treatment or prevention of GVHD contain bacterial strains capable of altering the proportion of immune subpopulations, e.g., T cell subpopulations, in the subject.

[0582] For example, immunomodulatory bacteria can increase or decrease the proportion of Treg cells, Th17 cells, Th1 cells, or Th2 cells in a subject. The increase or decrease in the proportion of immune cell subpopulations may be systemic, or it may be localized to a site of action of the probiotic, e.g., in the gastrointestinal tract or at the site of a distal dysbiosis. In some embodiments, a probiotic composition comprising immunomodulatory bacteria is used for treatment or prevention of GVHD based on the desired effect of the probiotic composition on the differentiation and/or expansion of subpopulations of immune cells in the subject.

[0583] In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Treg cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Treg cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th17 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th17 cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th1 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th1 cells in a subject. In one embodiment, a probiotic composition contains immunomodulatory bacteria that increase the proportion of Th2 cells in a subject. In another embodiment, a probiotic composition contains immunomodulatory bacteria that decrease the proportion of Th2 cells in a subject.

[0584] In one embodiment, a probiotic composition contains immunomodulatory bacteria capable of modulating the proportion of one or more of Treg cells, Th17 cells, Th1 cells, and combinations thereof in a subject. Certain immune cell profiles may be particularly desirable to treat or prevent

GVHD. For example, in some embodiments, treatment or prevention of GVHD can be promoted by increasing numbers of Treg cells and Th2 cells, and decreasing numbers of Th17 cells and Th1 cells. Accordingly, probiotic compositions for the treatment or prevention of GVHD may contain probiotics capable of promoting Treg cells and Th2 cells, and reducing Th17 and Th1 cells.

[0585] Probiotic compositions useful for treating or preventing GVHD include, in exemplary embodiments, one or more bacterial species from Table 1. In other embodiments, the probiotic composition includes one or more bacterial species from Table 1A. In other embodiments, the probiotic composition includes one or more bacterial species from Table 1B. In other embodiments, the probiotic composition includes one or more bacterial species from Table 1C. In other embodiments, the probiotic composition includes one or more bacterial species from Table 1D. In other embodiments, the probiotic composition includes one or more bacterial species from Table 1E. In other embodiments, the probiotic composition includes one or more bacterial species from Table 1F. In other embodiments, the probiotic composition includes one or more bacterial species from Table 5. In some embodiments, the probiotic composition contains a single species of bacteria. In other embodiments, the probiotic composition contains two or more species of bacteria, e.g., 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 30, 40, 50, 60, 70, 80, 90, 100, 500, 1000 or more species of bacteria. In one embodiment, the probiotic composition contains no more than 20 species of bacteria, e.g., 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 species of bacteria. In exemplary embodiments, the probiotic composition contains 8 bacterial species. In other exemplary embodiments, the probiotic composition contains 9 bacterial species. In other embodiments, the probiotic composition contains or is administered in conjunction with a prebiotic, as described herein.

[0586] Preferred bacterial genera include *Acetanaerobacterium, Acetivibrio, Alicyclobacillus, Alkaliphilus, Anaerofustis, Anaerosporobacter, Anaerostipes, Anaerotruncus, Anoxybacillus, Bacillus, Bacteroides, Blautia, Brachyspira, Brevibacillus, Bryantella, Bulleidia, Butyricicoccus, Butyrivibrio, Catenibacterium, Chlamydiales, Clostridiaceae, Clostridiales, Clostridium, Collinsella, Coprobacillus, Coprococcus, Coxiella, Deferribacteres, Desulfitobacterium, Desulfotomaculum, Dorea, Eggerthella, Erysipelothrix, Erysipelotrichaceae, Ethanoligenens, Eubacterium, Faecalibacterium, Filifactor, Flavonifractor, Flexistipes, Fulvimonas, Fusobacterium, Gemmiger, Geobacillus, Gloeobacter, Holdemania, Hydrogenoanaerobacterium, Kocuria, Lachnobacterium, Lachnospira, Lachnospiraceae, Lactobacillus, Lactonifactor, Leptospira, Lutispora, Lysinibacillus, Mollicutes, Moorella, Nocardia, Oscillibacter, Oscillospira, Paenibacillus, Papillibacter, Pseudoflavonifractor, Robinsoniella, Roseburia, Ruminococcaceae, Ruminococcus, Saccharomonospora, Sarcina, Solobacterium, Sporobacter, Sporolactobacillus, Streptomyces, Subdoligranulum, Sutterella, Syntrophococcus, Thermoanaerobacter, Thermobifida*, and *Turicibacter.*

[0587] Preferred bacterial genera also include *Acetonema, Alkaliphilus, Amphibacillus, Ammonifex, Anaerobacter, Caldicellulosiruptor, Caloramator, Candidatus, Carboxydibrachium, Carboxydothermus, Cohnella, Dendrosporobacter Desulfitobacterium, Desulfosporosinus, Halobacteroides, Heliobacterium, Heliophilum, Heliorestis, Lachnoanaerobaculum, Lysinibacillus, Oceanobacillus, Orenia* (*S.*), *Oxalophagus, Oxobacter, Pelospora, Pelotomaculum, Propionispora, Sporohalobacter, Sporomusa, Sporosarcina, Sporotomaculum, Symbiobacterium, Syntrophobotulus, Syntrophospora, Terribacillus, Thermoanaerobacter*, and *Thermosinus.*

[0588] In one embodiment, a probiotic composition for the treatment or prevention of GVHD consists essentially of *Blautia.*

[0589] In another embodiment, a probiotic composition for the treatment or prevention of GVHD does not contain *Blautia* alone.

[0590] As provided herein, therapeutic compositions comprise, or in the alternative, modulate, the colonization and/or engraftment, of the following exemplary bacterial entities: *Lactobacillus gasseri, Lactobacillus fermentum, Lactobacillus reuteri, Enterococcus faecalis, Enterococcus durans, Enterococcus villorum, Lactobacillus plantarum, Pediococcus acidilactici, Staphylococcus pasteuri, Staphylococcus cohnii, Streptococcus sanguinis, Streptococcus sinensis, Streptococcus mitis, Streptococcus* sp. SCA22, *Streptococcus* sp. CR-3145, *Streptococcus anginosus, Streptococcus mutans, Coprobacillus cateniformis, Clostridium saccharogumia, Eubacterium dolichum* DSM 3991, *Clostridium* sp. PPf35E6, *Clostridium sordelli* ATCC 9714, *Ruminococcus torques, Ruminococcus gnavus, Clostridium clostridioforme, Ruminococcus obeum, Blautia producta, Clostridium* sp. ID5, *Megasphaera micronuciformis, Veillonella parvula, Clostridium methylpentosum, Clostridium islandicum, Faecalibacterium prausnitzii, Bacteroides uniformmis, Bacteroides thetaiotaomicron, Bacteroides acidifaciens, Bacteroides ovatus, Bacteroides fragilis, Parabacteroides distasonis, Propinionibacteirum propionicum, Actinomycs hyovaginalis, Rothia mucilaginosa, Rothia aeria, Bifidobacterium breve, Scardovia inopinata* and *Eggerthella lenta.*

[0591] Preferred bacterial species are provided in Table 1, Table 1A, Table 1B, Table 1C, Table 1D, Table 1E, Table 1F, and Table 5. Optionally, in some embodiments, preferred bacterial species are spore formers. Where specific strains of a species are provided, one of skill in the art will recognize that other strains of the species can be substituted for the named strain.

[0592] In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acidaminococcus intestine*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter baumannii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Acinetobacter lwoffii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Akkermansia muciniphila*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes putredinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Alistipes shahii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerostipes hadrus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Anaerotruncus colihominis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides caccae*. In one embodiment, the bacterial entity, e.g., species

or strain, useful in the compositions and methods of the invention is *Bacteroides cellulosilyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides dorei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides eggerthii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides finegoldii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides fragilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides massiliensis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides ovatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bacteroides salanitronis. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides salyersiae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides* sp. D20. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides uniformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bacteroides vulgatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium adolescentis. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Bifidobacterium bifidum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium breve*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium faecale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Bifidobacterium stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia glucerasea*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia stercoris*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Blautia wexlerae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Catenibacterium mitsuokai*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium asparagiforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium bolteae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium clostridioforme*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium histolyticum*. In one embodiment, the bacterial

entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium indolis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium leptum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium perfringens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 14774. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium* sp. HGF2. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium symbiosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella aerofaciens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Collinsella intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprobacillus* sp. D7. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus catus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Coprococcus comes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea formicigenerans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Dorea longicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Enterococcus faecium*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Escherichia coli* 588. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium eligens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium fissicatena*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium ramulus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Eubacterium rectale*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Faecalibacterium prausnitzii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Flavonifractor plautii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium mortiferum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Fusobacterium nucleatum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Holdemania filiformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Klebsiella oxytoca*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus rhamnosus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactobacillus ruminis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Lactococcus casei*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is Odoribacter splanchnicus. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Oscillibacter valericigenes*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides gordonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides johnsonii*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Parabacteroides merdae*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Pediococcus acidilactici*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Propionibacterium granulosum*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia intestinalis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Roseburia inulinivorans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods

of the invention is *Ruminococcus faecis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus gnavus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus* sp. ID8. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Ruminococcus torques*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Slackia piriformis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus epidermidis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Staphylococcus saprophyticus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus cristatus*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus infantis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus oralis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus sanguinis*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus viridans*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Streptococcus thermophiles*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Veillonella dispar.*

[0593] In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acidaminococcus intestine*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter baumannii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Acinetobacter lwoffii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Akkermansia muciniphila*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes putredinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Alistipes shahii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerostipes hadrus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Anaerotruncus colihominis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides caccae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides cellulosilyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides dorei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides eggerthii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides finegoldii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides fragilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides massiliensis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides ovatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salanitronis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides salyersiae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 1_1_6. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. 3_1_23. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides* sp. D20. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides thetaiotaomicrond*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides uniformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bacteroides vulgatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium adolescentis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium bifidum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium breve*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium faecale*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium kashiwanohense*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium longum* subsp. *Longum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium pseudocatenulatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Bifidobacterium stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *coccoides*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia glucerasea*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *hansenii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *luti*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *obeum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention

comprises *Blautia producta* (*Ruminococcus productus*). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* (*Ruminococcus*) *schinkii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia stercoris*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2). In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Blautia wexlerae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Candidatus Arthromitus* sp. SFB-mouse-Yit. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Catenibacterium mitsuokai*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridiales* bacterium 1_7_47FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium asparagiforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium bolteae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium clostridioforme*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium glycyrrhizinilyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Hungatella*) *hathewayi*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium histolyticum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium indolis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium leptum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Tyzzerella*) *nexile*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium perfringens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* (*Erysipelatoclostridium*) *ramosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium scindens*. In one embodiment, the bacterial entity, e.g., species or strain, useful in the compositions and methods of the invention is *Clostridium septum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 14774. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. 7_3_54FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium* sp. HGF2. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Clostridium symbiosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella aerofaciens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Collinsella intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprobacillus* sp. D7. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus catus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Coprococcus comes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea formicigenerans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Dorea longicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Enterococcus faecium*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Erysipelotrichaceae* bacterium 3_1_53. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Escherichia coli* 588. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium eligens*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium fissicatena*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium ramulus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Eubacterium* rectale. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Faecalibacterium prausnitzii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Flavonifractor plautii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium mortiferum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Fusobacterium nucleatum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Holdemania filiformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Hydrogenoanaerobacterium saccharovorans*. In one embodiment, the bacterial population useful in the compositions and methods of the

invention comprises *Klebsiella oxytoca*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 3_1_57FAA_CT1. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 7_1_58FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lachnospiraceae* bacterium 5_1_57FAA. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus rhamnosus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactobacillus ruminis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Lactococcus casei*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Odoribacter splanchnicus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Oscillibacter valericigenes*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides gordonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides johnsonii*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Parabacteroides merdae*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Pediococcus acidilactici*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Peptostreptococcus asaccharolyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Propionibacterium granulosum*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia intestinalis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Roseburia inulinivorans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus faecis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus gnavus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus* sp. ID8. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Ruminococcus torques*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Slackia piriformis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus epidermidis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Staphylococcus saprophyticus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus cristatus*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus dysgalactiae* subsp. *Equisimilis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus infantis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus oralis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus sanguinis*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus viridans*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Streptococcus thermophiles*. In one embodiment, the bacterial population useful in the compositions and methods of the invention comprises *Veillonella dispar*.

XII. Diagnostic Methods

[0594] In some embodiments, metabolite profiles of patient tissue samples or microbes cultures from patient tissue are used to identify risk factors for developing an autoimmune or inflammatory response, to diagnose an autoimmune or inflammatory disease, to evaluate the prognosis or severity of said disease, to evaluate the success of a treatment regimen, or any combination thereof. Exemplary metabolites for the purposes of diagnosis, prognostic risk assessment, or treatment assessment purposes include short chain fatty acids, bile acids, and lactate. In preferred embodiments, metabolite profiles are taken at different time points during a patient's disease and treatment in order to better evaluate the patient's disease state including recovery or relapse events. Such monitoring is also important to lower the risk of a patient developing a new autoimmune condition following immunomodulatory treatment. In some embodiments, metabolite profiles inform subsequent treatment. For example, patients at risk for developing GVHD and presenting low levels of butyrate may be administered a microbial composition comprising microbes that produce butyrate (e.g., *Blautia* species) and excluding microbes capable of depleting butyrate (e.g. *Methanobacterium* species). In another example, patients experiencing bacterial vaginosis—which increases the risk that a woman will suffer from a sexually transmitted disease or experience fertility issues—often presents with abnormally low lactic acid levels. Thus, patients with low lactic acid production in the vagina may be administered a microbial composition comprising lactic acid producing microbes (e.g., *Lactobacillus* species) to restore a healthy microbiome state.

[0595] Patient Selection.

[0596] Particular bacterial compositions can be selected for individual patients or for patients with particular profiles. For example, 16S sequencing can be performed for a given patient to identify the bacteria present in his or her microbiota. The sequencing can either profile the patient's entire microbiome using 16S sequencing (to the family, genera, or species level), a portion of the patient's microbiome using 16S sequencing, or it can be used to detect the presence or absence of specific candidate bacteria that are biomarkers for health or a particular disease state, such as markers of multidrug resistant organisms or specific genera of concern such as *Escherichia*. Based on the biomarker data, a particular composition can be selected for administration to a patient to supplement or complement a patient's microbiota in order to restore health or treat or prevent disease. In another embodiment, patients can be screened to determine the composition of their microbiota to determine the likelihood of successful treatment.

XIII. Kits

[0597] In certain aspects, the invention relates to kits for the treatment of an autoimmune disease and/or inflammatory disease. The kits may comprise a microbial composition and an immunomodulatory carbohydrate, a prebiotic, microbial DNA, a mucolytic agent or a combination thereof. Optionally, the microbial composition, the immunomodulatory carbohydrate, the prebiotic, microbial DNA, and/or the mucolytic agent are matched to exhibit a synergistic treatment effect in a subject when employing an appropriate treatment regimen or preventative measure for an autoimmune and/or inflammatory disease.

[0598] The kits provided may comprise one or more containers. The containers may comprise singly isolated microbial compositions comprising one or more microbes and/or singly isolated prebiotic compositions comprising one or more carbohydrates. The microbial compositions, with or without one or more prebiotics, in the different containers may be administered at the same time or at different times, and may be administered in a specific order.

[0599] The compositions may, optionally, additively, or synergistically provide immunomodulatory effects when administered to a subject. The microbial composition, with or without one or more prebiotics, may comprise live microbes, microbes that are lyophilized, freeze-dried, and/or substantially dehydrated, or the composition may comprise bacterial or fungal spores or virions. In some embodiments, the kit further comprises an effective amount of one or more immunomodulary carbohydrates in one or more containers. In some embodiments, the kit further comprises in one or more containers an effective amount of an anti-mucolytic agent. In some embodiments, the kit further comprises one or more containers an effective amount of a prebiotic. In some embodiments, the kit further comprises an effective amount of a pro-inflammatory or anti-inflammatory agent. In some embodiments, the kit further comprises a pharmaceutically acceptable excipient or diluent.

EXAMPLES

[0600] The invention is further illustrated by the following examples. The examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way. The entire contents of all references, patents, and published patent applications cited throughout this application are hereby incorporated by reference in their entirety.

[0601] The practice of the present invention will employ, unless otherwise indicated, conventional methods of protein chemistry, biochemistry, recombinant DNA techniques and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, e.g., T. E. Creighton, *Proteins: Structures and Molecular Properties* (W.H. Freeman and Company, 1993); A. L. Lehninger, Biochemistry (Worth Publishers, Inc., current addition); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Methods In Enzymology* (S. Colowick and N. Kaplan eds., Academic Press, Inc.); *Remington's Pharmaceutical Sciences,* 18th Edition (Easton, Pa.: Mack Publishing Company, 1990); Carey and Sundberg *Advanced Organic Chemistry* 3rd Ed. (Plenum Press, Vols A and B, 1992). Enzyme Linked Immunosorbent Assays (ELISAs) and Western blots described below are performed using kits according to the manufacturers' (e.g., Life Technologies, Thermo Fisher Scientific, New York, USA) instructions.

Example 1

Assessment of Intestinal Permeability after Administration of Bacteria Prebiotic or Combinations Thereof

[0602] The main function of the gastrointestinal (GI) tract is to digest and absorb nutrients from food. The mucosa of the GI tract forms a selective barrier between the host and the environment of the gut lumen. The mucosa allows transport of nutrients while restricting passage of larger molecules and bacteria. Impaired barrier integrity is believed to contribute to the pathogenesis of many disorders including autoimmune diseases, including transplant disorders such as graft-versus-host-disease (GVHD), and neurological disorders. Disruption of the intestinal barrier due to toxins, dysbiosis, inflammation or other factors is believed to result in the passage and presentation of environmental antigens to the immune system leading to aberrant immune responses. Similarly, the leakage of bacterial endotoxin or other toxic metabolites into the circulation can lead to systemic inflammation promoting the development of autoimmunity and neuroinflammation.

[0603] Restoration of GI barrier integrity through the administration of selected prebiotics and/or probiotics represents an approach to correct a basic defect underlying multiple pathological conditions.

In a first set of experiments, intestinal permeability was assessed using serum endotoxin levels as a marker of gut permeability in mice treated with xylose and/or antibiotics. Basal levels of intestinal permeability can be measured under disease or normal conditions. Intestinal permeability can be induced in mice through administration of inflammatory stimuli such as cholera toxin (3 oral gavages of 10 μg cholera toxin, 5 days apart), Poly I:C (3 intraperioneal injections of 1 mg/kg, 3 days apart) or dextran sulfate (3% dextran sulfate sodium salt in drinking water for 7 days). Quantitation of intestinal permeability was carried out by quantitatively measuring plasma levels of endotoxin originating from gut bacteria using a commercially available chromogenic assay (Lonza, Rockland, Me.). The results of these experiments are shown in FIG. **1**.

[0604] Quantitation of intestinal permeability can also be conducted using a number of alternative methods (reviewed in Bischoff et al, 2014) for example, by quantifying leakage of fluorescently-labeled high molecular weight dextran (FITC-dextran) into the plasma following oral administration (oral gavage with 0.6 g/kg 4 kDa FITC-dextran, serum samples collected 4 hours later and read for fluorescence intensity at 521 nm; Hsiao et al, 2013). To study the effect of bacterial strains on intestinal permeability, mice are gavaged orally with 10^7-10^{10} bacterial cells for an average of 5 administrations, typically daily or 2 days apart. Bacteria can be administered as single strains or combinations of strains. The bacteria can be administered alone or in combination with a pre-biotic(s). The pre-biotic can be xylose or xylose-containing molecules as a preferred carbon source for anaerobic bacteria. Other prebiotics that can be used include, for example, those described in Table 7. After administration of bacteria+/−pre-biotic, intestinal permability is assessed using the preferred method at the desired time point(s) starting on day 1 post-treatment.

[0605] As shown in FIG. **1**, C57BL/6 mice were either left untreated or were treated with xylose at 10 g/L in drinking water from day −7 to day 14; ciprofloxacin (cipro) at 0.25 g/L in drinking water from day −7 to day −2; enrofloxacin (enro) at 0.25 g/L in drinking water from day −7 to day −2; xylose+cipro or xylose+enro. Analysis of serum samples collected on days 0 and 14 showed that basal levels of serum endotoxin are present in normal mice that remained unchanged in untreated mice. Xylose treatment reduced these basal levels over time, suggesting an increase in gut barrier integrity even in normal animals. Antibiotic treatment with cipro, a broad spectrum quinolone antibiotic, or enro, an anaerobe-sparing antibiotic, led to an increase in serum endotoxin levels (measured 2 days after a 5 day course), likely due to disruption of the microbiota. Serum endotoxin levels returned to baseline over time. As shown in FIG. **1**, xylose appeared to counteract the increase in serum endotoxin level caused by cipro, but not enro. The differential effect of xylose on these 2 antibiotics may relate to its ability to preserve/promote expansion of anaerobic bacteria, which are killed by cipro but not enro.

Example 2

Immunomodulatory Properties of Different Human Commensal Bacteria on Human Peripheral Blood Mononuclear Cells

[0606] The microbiota of mammalian hosts is composed of bacterial species that possess both pro- and anti-inflammatory properties. In healthy individuals, a balance or state of eubiosis is maintained that supports gut barrier integrity, immune containment of commensal bacteria and promotion of a tolerogenic environment. Under disease conditions, dysbiosis characterized by an imbalance in pro- and anti-inflammatory bacteria results in local inflammation and compromised gut barrier integrity, leading to systemic inflammation and aberrant immune responses. Administration of selected probiotic bacterial strains (+/−prebiotics) that possess anti-inflammatory activity and promote immune tolerance represents an approach to correct a basic defect underlying multiple pathological conditions.

[0607] An in vitro system was developed to efficiently test the inflammatory and immunomodulatory properties of different human commensal bacteria on human peripheral blood mononuclear cells (PBMCs). Experiments were carried out with 21 bacterial candidates to profile their anti-inflammatory properties against human PBMCs. The innate properties of bacteria alone on human PBMCs were tested as well as their ability to counteract the pro-inflammatory activity of *Enterococcus feacalis*.

[0608] Human PBMCs were isolated from fresh blood by density-gradient centrifugation using Ficoll (1-4). Freshly isolated PBMCs were plated at 1.5×10^6 cells per ml per well of a 24-well plate in a total volume of 2 mls RPMI-1640 medium+5% human serum, and incubated at 37° C./5% CO_2 with the following:

[0609] (1) 500 □l of different commensal bacteria suspensions at OD 0.8

[0610] (2) *E. faecalis* at 10^7 colony-forming units (cfu)

[0611] (3) A combination of commensal bacteria (OD 0.8)+E. *Faecalis* (10^7 cfu)

[0612] (4) Complete medium alone as a negative control

[0613] (5) Bacterial lipopolysaccharide (LPS; 100 ng/ml) as an immunomodulatory "positive" control

Culture supernatants were collected at 24, 48 and 72 h, and the cytokine profile was analyzed by Luminex technology according to manufacturer's instruction (EMD Millipore, Danvers, Mass.). Cytokine production was detectable in culture supernatants by 24 h with levels increasing over 48-72 h and sometimes exceeding the range of quantitation. The results are presented in FIGS. **2-5** for all time points. The 24 h time point was chosen as the optimal time point for further analysis. The 24 h results are shown as a composite in FIG. **6** and with statistical analysis on individual cytokines in FIGS. **7-10**. The results represent the properties of each bacterial species against human PBMCs and their ability to counteract inflammatory stimulation with *E. faecalis* in vitro. It was found that the commensal bacteria tested have distinct immunomodulatory properties, and most appear to counteract the inflammatory activity of *E. faecalis* for at least one cytokine.

[0614] FIG. **2** shows the time course of Th1 related cytokines that were released by human PBMCs incubated with *Ruminococcus gnavus* (Epv 1), *Eubacterium rectale* (Epv 2), *Blautia luti* (Epv 3), *Blautia wexlerae* (Epv 5) and *Enterococcus faecalis* (Epv 8), or combinations of each bacterium with *E. faecalis*. Amounts of Th1-related pro-inflammatory cytokines interferon gamma (IFN-γ), interleukin-12 p70 (IL-12p70), interleukin-6 (IL-6), interleukin-2 (IL-2) and tumor necrosis factor alpha (TNFα) released by PBMCs were measured after 24, 48 and 72 hours. As shown in FIG. **2**, all commensals have unique immunomodulatory properties. As expected, *E. faecalis* induced high levels of these pro-inflammatory cytokines. By comparison, most of the other bacterial candidates induced lower levels of Th1-related cytokines and were able to counteract the induction of one or more inflammatory cytokines by *E. faecalis*. In particular, *Blautia luti* (Epv 3), showed minimal induction of Th1-related cytokines on its own and was most effective in counteracting induction of these cytokines by *E. faecalis* (Epv 8). This profile is desirable for disease indications which are primarily driven by Th1 immune responses, such as GVHD.

[0615] FIG. **3** shows the time course of Th2 related cytokines that were released in cells treated with *R. gnavus* (Epv 1), *E. rectale* (Epv 2), *B. luti* (Epv 3), *B. wexlerae* (Epv 5) and *E. faecalis* (Epv 8), or combinations thereof. Amounts of anti-inflammatory cytokines interleukin-13 (IL-13), interleukin-4 (IL-4) and interleukin-5 (IL-5) released by PBMCs were measured after 24, 48 and 72 hours. Each bacterium displayed detectable pattern of cytokine induction and ability to modulate the effect of *E. faecalis*. Th2-related cytokines are beneficial in counteracting Th1 responses. Bacteria capable of promoting Th2 cytokine release are therefore of interest in Th1-driven diseases. *R. gnavus* appeared the most active in terms of eliciting Th2 cytokine on its own or in the presence of *E. faecalis*.

[0616] FIG. **4** shows the time course of Th9, Th17 and Treg cytokines that were released in cells treated with *R. gnavus* (Epv 1), *E. rectale* (Epv 2), *B. luti* (Epv 3), *B. wexlerae* (Epv 5) and *E. faecalis* (Epv 8), or combinations thereof. Amounts of interleukin-9 (IL-9), interleukin-17 (IL-17) and interleukin-10 (IL-10) released by PBMCs were measured after 24, 48 and 72 hours. The activity of IL-9 and IL-17 is context-dependent in that these cytokines can be beneficial under some conditions but detrimental under other conditions depending on the mechanisms responsible for disease pathogenesis. For example, IL-17 is expected to contribute to disease pathogenesis in GVHD but could provide a benefit in Th2-driven disorders. IL-10 produced by regulatory T cells

(Treg) is generally immunosuppressive and is expected to provide a benefit in most inflammatory disorders whether Th—or Th2-driven. As shown in FIG. **4**, all bacterial candidates elicited IL-9 and IL-17 to varying degrees and *B. wexlerae* (Epv 5) was the most potent in inducing IL-10.

[0617] FIG. **5** shows the time course of monocyte, macrophage and neutrophil-related inflammatory cytokines that were released by PBMCs treated with *R. gnavus* (Epv 1), *E. rectale* (Epv 2), *B. luti* (Epv 3), *B. wexlerae* (Epv 5) and *E. faecalis* (Epv 8), or combinations thereof. Amounts of monocyte chemotactic protein 1 (MCP-1), macrophage inflammatory protein 1β (MIP10), macrophage inflammatory protein 1α (MIP1α), regulated on activation, normal T expressed and secreted protein (RANTES), interleukin-1α (IL-1α), interleukin-1β (IL1β), interferon α2 (IFN-α2) and interleukin-8 (IL-8) that were released were measured after 24, 48 and 72 hours. In general, these cytokines contribute to inflammation by innate immune effector cells. The bacteria tested showed different degrees of induction and effects on *E. faecalis*. *Overall, E. rectale* (Epv 2) and *B. luti* (Epv 3) were the least inflammatory and the most effective at countering the effect of *E. faecalis* (Epv 8).

[0618] A composite illustration of the secretion of each of the pro-inflammatory and anti-inflammatory cytokines described above in the presence of each commensal alone or in combination with EPV8 is graphed relative to the pro-inflammatory bacterial strain *E. faecalis* (Epv 8) in FIG. **6**. In the context of GVHD, IFNγ (IFNg), IL-12p70, IL-1α (IL-1a), IL-6, IL-8, MCP1, MIP1α (MIP1a), MIP1β (MIP1b) and TNFα (TNFα) are considered pro-inflammatory cytokines. IL-10, IL-13, IL-9, IL-4 and IL-5 are considered anti-inflammatory cytokines. IL-17 (IL-17A), IL-9 and IL-2 have context dependent activity. The results are shown as a percentage of Epv 8, where cytokine levels in the presence of *E. faecalis* after 24 hours is set at 100%. Each commensal has a unique signature and each one added alone to human PBMCs appeared to be less inflammatory than *E. fecalis* (below 100% for pro-inflammatory cytokines), except for *B. wexlerae* (Epv 5). When added to PBMCs in combination with *E. faecalis*, most commensals tested (except for Epv 5) also counteracted the pro-inflamamtory activity of *E. faecalis* (below 100% for pro-inflammatory cytokines).

[0619] FIGS. **7-10** detail individual cytokine profiles of PBMCs following exposure to various commensals, alone or in combination with the pro-inflammatory bacterium *E. faecalis* (Epv8). In particular, FIG. **7** shows the effect of *R. gnavus* (EPV 1) on cytokine concentration (pg/ml) either alone or in combination with Epv 8 (*E. faecalis*).

[0620] FIG. **8** shows the effect of *E. rectale* (EPV 2) on cytokine concentration (pg/ml) either alone or in combination with Epv 8 (*E. faecalis*). FIG. **9** shows the effect of *B. luti* (EPV 3) on cytokine concentration (pg/ml) either alone or in combination with Epv 8 (*E. faecalis*). FIG. **10** shows the effect of *B. wexlerae* (EPV 5) on cytokine concentration (pg/ml) either alone or in combination with Epv 8 (*E. faecalis*).

[0621] Overall, the foregoing data indicate that, among the bacteria tested, EPV3 has a significantly desirable anti-inflammatory profile for a Th-1-driven condition, such as GVHD while EPV5 has a suboptimal anti-inflammatory profile for GVHD. As shown in FIG. **11**, EPV3 has relatively low intrinsic inflammatory activity compared to EPV 8 and is able to reduce the induction of pro-inflammatory cytokines by EPV 8, including IL-6, MCP-1, IL-12p70, and IFNγ which are believed to contribute to the pathogenesis of GVHD. By comparison, EPV 5 is similar to EPV 8 in terms of induction of pro-inflammatory cytokines and shows little ability to counteract the induction of pro-inflammatory cytokines by EPV 8.

[0622] Additional bacteria were profiled using this methodology including: *Clostridium leptum* (EPV 6), *Blautia faecis* (EPV15), *Blautia/Ruminococcus obeum* ATCC 29174 (EPV 20), *Blautia* product ATCC 27340 (EPV 21), *Blautia coccoides* ATCC 29236 (EPV 22), *Blautia hydrogenotrophica* ATCC BAA-2371 (EPV-23) and *Blautia Hansenii* ATCC27752 (EPV 24). Strains freshly isolated by Epiva from the stool of a normal healthy volunteer were also profiled and included: *Eubacterium rectale* (EPV 35), a previously uncultured *Blautia*, similar to GQ898099_s S1-5 (EPV 47), a previously uncultured *Blautia*, similar to SJTU_C_14_16 (EPV 51), *Blautia wexlerae* (SJTU_B_09_77) (EPV 52), *Blautia luti* ELU0087-T13-S-NI_000247 (EPV 54), *Blautia wexlerae* WAL 14507 (EPV 64), *Blautia obeum* (EPV 78), *Ruminococcus gnavus* (EPV 102) and *Blautia luti* (BlnIX) (EPV 114). Results focusing on key pro-inflammatory (IL-12p70, IFNγ, IP-10, IL-1RA) and anti-inflammatory (IL-10, IL-4, IL-13) cytokines are shown in FIGS. **12-27**. As observed with the initial set of bacterial candidates, each isolate displayed a defined signature. Candidates for treatment of autoimmune or inflammatory disorders, such as GVHD, displayed low induction of pro-inflammatory cytokines and/or positive induction of anti-inflammatory cytokines, and had ability to counteract the inflammatory activity of *E. faecalis*. Bacterial candidates meeting these criteria include, for example, EPV 35, 51, 78 and 114.

[0623] Taken together, these results show that commensals have distinct immunomodulatory properties and display a definable signature in terms of their ability to induce cytokines in human host cells, or counteract the pro-inflammatory activity of another bacterium (*E. faecalis*). Accordingly, bacterial compositions may be selected in order to achieve a desired modulation of pro- and anti-inflammatory cytokines. For example, anti-inflammatory bacterial strains may be selected based on their ability to reduce key pro-inflammatory cytokines such as interferon gamma, IL-12p70, IP-10 and IL-1RA and/or increase anti-inflammatory cytokines such as IL-13, IL-10 and IL-4.

Example 3

Effect of Commensal Human Bacteria on T-Cell Polarization

[0624] In order to determine whether exposure to commensal bacteria may polarize T cells toward a particular phenotype, flow cytometry analysis was performed on human PBMCs cultured with various commensal bacteria as described above. The cells recovered from culture were washed in phosphate-buffered saline and stained with a cocktail of fluorescently labeled antibodies against specific cell surface protein markers to allow for the detection of Th1 cells ($CXCR3^+CCR6^-$), Th2 cells ($CXCR3^-CCR6^-$), Th17 cells ($CXCR3^-CCR6^+$) and Tregs ($CD25^+CD127^{lo}$). Negative control wells contained PBMCs in culture medium alone and positive control wells contained PBMCs+LPS (100 ng/ml) as a known immune stimulus. The commensal bacteria examined included: Epv 1*: R. gnavus*; Epv 3*: B. luti*; Epv 2*: E. rectale*; Epv 5*: B. wexlerae*; Epv. 8: *E. faecalis*; Epv 20: *B. obeum*, ATCC 29174; Epv 21*: B. product*, ATCC 27340; Epv

24: *B. hansenii*, ATCC 27752. As shown in FIG. **28**, exposure of human PBMCs to bacteria did result in a shift in the relative proportion of T cell populations compared to the PBMCs alone (control) although statistical significance was not achieved in every case. Overall, most bacteria tested caused an increase in the proportion of T cells with a regulatory phenotype (Tregs) with EPV 21 and EPV 24 having the greatest impact and EPV8 (*E. faecalis*) causing little or no increase in Tregs. Most bacteria also caused a decrease in the proportion of Th17 cells, an increase in Th2 cells and had little or no effect on the proportion of Th1 cells. This type of analysis indicates that commensal bacteria can modulate the proportions of effector T cell types and can be used to select the desired phenotype for a given disease application. For example, the optimal T cell profile to address pro-inflammatory disorders such as GVHD would consist of ↑Treg, ↓Th17, ↓ or unchanged Th1, and ↑Th2. This phenotype was induced by many of the bacteria tested.

Example 4

Pattern of Carbon Source Utilization by Commensal Bacteria

[0625] Modulation of the microbiota to correct a dysbiosis associated with pathological conditions can potentially be achieved through administration of bacteria (or bacterial combinations) and prebiotic(s) as a carbon source to promote endogenous expansion of beneficial bacteria. Alternatively, prebiotics can be administered in combination with bacteria to promote their growth or create a favorable environment for their growth. Profiling of carbon source usage by bacterial isolates can be used to customize and optimize selection of prebiotics for particular bacterial strains. Profiling of carbon source usage was conducted on 21 anaerobic commensal bacteria (Table 6) using 96 well plates from Biolog (Hayward, Calif.) where each well contains a different carbon source for a total of 192 different carbon sources (PM01 and PM02A plates). The carbon sources tested are listed in Table 7. The assay was conducted according to manufacturer's instructions. Briefly, pre-cultured bacteria were suspended in Biolog assay medium at a 750 nm optical density (OD) of 0.3-0.4, and 100 μl of the suspension was transferred to each well of the 96 well PM01 and PM02 assay plates. The plates were then incubated at 37° C. in an anaerobic chamber for 24 hr or longer. The amount of growth on each carbon source was evaluated by measuring the optical density (OD) of each well at 750 nm. The results are summarized in FIG. **29**, and indicate that each individual strain displays a unique pattern of carbon source usage. Interestingly, different isolates of the same species (e.g. *B. luti* and *B. wexlerae*) show related (albeit distinct) patterns. Overall, these results indicate that characterization of carbon source usage for profiling of bacterial candidates allows optimal selection of prebiotics. Preferred prebiotics can be selected which increase the growth (indicated by an increase in optical density) of bacterial species contained in probiotic compositions.

Example 5

Normal Human Volunteer Study of a Prebiotic Formulation Containing Xylose

[0626] D-xylose is a carbon source generally preferred by anaerobic bacteria. Preliminary results in the mouse indicate that it may act to promote gut barrier integrity (FIG. **1**). It is also used as a carbon source by several bacterial strains (FIG. **29**) that were determined to possess a desirable immunological profile for target indications such as GVHD (FIG. **19**, **25**, **27**). A parallel, double-blind, 5 cohort escalation food safety study was conducted to examine D-xylose in normal human volunteers. The study was a double-blind, single-center, parallel group study designed to evaluate the tolerability and potential microbiome changes induced by ingestion of D-xylose at 5 different amounts in healthy, adult volunteers enrolled at 1 study center in the United States (US).

[0627] Subjects were screened for eligibility within 21 days prior to the first planned ingestion of study sweetener on Day 1 (Baseline). Within each of 5 cohorts, eligible subjects were randomly assigned in a double-blinded, 6:2 ratio to ingest either D-xylose or the GRAS sweetener Splenda® (control), dissolved into 2 to 6 oz of sterile water and ingested TID with meals for a total of 82 ingestions taken over 28 consecutive days. D-xylose ingestion amounts ranged from 1 to 15 g TID (total daily amount of 3 to 45 g), and all subjects randomized to Splenda® ingested 1 dissolved, commercially available packet TID (3 packets total per day).

[0628] Subjects returned to the study center weekly on Days 8, 15, 22, and 28 for ingestion, tolerability, and compliance evaluations. Safety was evaluated on a continual basis through adverse events (AE) monitoring, clinical laboratory measurements, vital sign monitoring, physical examinations, electrocardiograms (ECGs), telephone follow-up, and electronic subject ingestion diaries. Stool was collected pre-ingestion and at pre-specified time points, and post-ingestion samples were evaluated for changes in the gut microbiome compared with Baseline for all subjects. For subjects who consented to further sampling, additional stool specimens were used to potentially isolate living bacteria that could be categorized for research and potential commercialization purposes. Serum and urine were collected for measurement of D-xylose levels and pharmacokinetic (PK) assessments and PK/pharmacodynamics (PD) correlations. Telephone follow-up was conducted as needed, but minimally once per week. The total duration for each participant was up to 60 days, including the Screening period (Day −21 to 0), the ingestion period (Day 1 to 28), and an End-of-Study (EOS) follow-up visit conducted 7 (+3) days after the last ingestion of study sweetener.

[0629] Criteria for Evaluation

[0630] Safety

[0631] Safety was evaluated on a continual basis through AE monitoring, clinical laboratory measurements, vital sign monitoring, physical examinations, ECGs, telephone follow-up, and electronic subject ingestion diaries.

[0632] Immunology and Other Assessments

[0633] Stool was collected at pre-specified pre- and post-ingestion time points and post-ingestion samples were evaluated for changes in the gut microbiome compared with Baseline. Additional optional specimens were collected to potentially isolate living bacteria that could be categorized for research and potential commercialization purposes.

[0634] Blood was collected at pre-specified pre- and post-ingestion time points to evaluate C-reactive protein (CRP), serum cytokines (tumor necrosis factor alpha [TNF-α], interleukin [IL]-2, IL-6, interferon gamma [IFN-γ], and IL-10), and T-cell markers CD3, CD4, CD8, CD25, and FOXP3. Plasma was also stored and may be tested for biomarkers and/or metabolic markers for up to 7 years.

[0635] Pharmacokinetics

[0636] Blood and urine were collected at pre-specified pre- and post-ingestion time points to measure D-xylose levels and to characterize the systemic absorption profiles of D-xylose.

[0637] Statistical Methods

[0638] Statistical analyses were conducted using SAS®, Version 9.2 (SAS Institute, Inc., Cary, N.C., USA). The sample size calculations were empiric and based on an estimation of normal healthy volunteer variability in reported symptoms and side effects and not on a statistical method. A weighted randomization scheme was implemented such that more subjects were enrolled at the higher D-xylose ingestion amounts to account for potential toxicity-related effects that could have resulted in withdrawal and/or analysis ineligibility, and to enable collection of more data at ingestion amounts for which limited data were available.

[0639] Analysis Populations

[0640] The safety population comprised all subjects who ingested any amount of study sweetener.

[0641] Safety

[0642] AEs were coded using the Medical Dictionary for Regulatory Activities (MedDRA), Version 18.0 (Northrup Grumman Corporation, Chantilly, Va., USA), and summarized by cohort. Laboratory, vital sign, and physical examination data were summarized by cohort using descriptive statistics over time, including statistics for changes from Baseline. ECG findings were also summarized by cohort over time as well as using frequency counts and percentages, as normal or abnormal, with the relevance of abnormalities categorized by clinical significance.

[0643] Immunology and Other Assessments

[0644] Stool sample compliance was summarized by cohort, using the following calculation for each subject:

$$\text{Percentage compliance} = \frac{\text{Total number of stool samples collected}}{\text{Total number of stool samples expected}} \times 100$$

[0645] A total of 7 stool samples were expected to be collected for each subject. Evaluation of changes in the gut microbiome were evaluated in stool samples through taxonomic classification, relative and statistical differential abundance analyses by cohort and time point, an alpha diversity analysis calculated using the Shannon diversity index by cohort and time point, a beta diversity analysis using Bray-Curtis dissimilarity and Unifrac distance by subject and time point, and a principal coordinates analysis using the beta diversity data.

[0646] Summary statistics (n, mean, standard deviation, median, minimum, and maximum) were presented for serum concentrations of CRP, flow cytometry T-cell markers (CD3, CD4, CD8, CD25, and FOXP3), and cytokines (TNF-α, IL-2, IL-6, IFN-γ, and IL-10) as per their nominal time points.

[0647] Pharmacokinetics

[0648] Phoenix® WinNonLin®, Version 6.2.1, was used for PK analyses.

[0649] Serum D-xylose concentrations were summarized by cohort using nominal sample times according to actual amount received using summary statistics (n, coefficient of variation [CV], mean, standard deviation [SD], median, minimum, and maximum). Evidence for the occurrence of steady-state was assessed graphically by comparing the time course of either trough or 2-hour post-ingestion serum concentrations of D-xylose as different levels of D-xylose. Accumulation was assessed by comparing the 2-hour post-first-ingestion serum levels with those observed at Week 2 (Day 15) and Week 4 (Day 28).

[0650] The total amount of D-xylose excreted in urine was analyzed for all subjects over 5 hours post-ingestion and pooled for analysis; the pooling for analysis reflected the subject mean within a given time of collection (e.g., Day 15 and then Day 28) sorted by ingested amount. Urine PK parameters for D-xylose levels included $A_{(0\text{-}t)}$ (cumulative amount of sweetener recovered in urine) and percent sweetener amount excreted over a 5-hour period.

[0651] Summary of Results

[0652] Forty-eight subjects were randomized to ingest either 1 packet of commercially-available Splenda® TID (n=12) or D-xylose TID at the following ingestion amounts (n=36 total):

1 g: 6 subjects
2 g: 6 subjects
8 g: 7 subjects
12.5 g: 8 subjects
15 g: 9 subjects

[0653] Over the 28-day ingestion period, study sweetener ingestion compliance was >90% for all subjects. Two subjects (4.2%) discontinued from the study prematurely; primary reasons for discontinuation were a protocol violation (positive urine drug screen) and withdrawal of consent. The proportion of males (47.9%) and females (52.1%) was balanced, and the majority of subjects were White (89.6%) and not Hispanic or Latino (77.1%). Subject ages spanned a wide range, with a median of 38.3 (range 22.5 to 60.5) years for the combined D-xylose cohorts and 43.6 (range 24.9 to 64.3) years for the Splenda® cohort.

[0654] Safety

[0655] D-xylose and Splenda® were both well tolerated, with no new safety concerns identified. One subject required a D-xylose reduction from 15 g to 12.5 g TID at the Week 1 (Day 8) visit due to AEs of moderate abdominal distension, diarrhea, and GI pain; no other modifications to sweetener ingestion amounts were implemented.

[0656] Overall, 17 subjects (35.4%) experienced at least 1 AE, including a higher proportion of subjects who ingested any amount of D-xylose (14 subjects [38.9%]) than Splenda® (3 subjects [25.0%]). Reported AE rates increased with increasing D-xylose ingestion amounts, with incidences ranging from 16.7% in subjects who ingested the 2 lowest amounts (1 and 2 g TID) to 66.7% in subjects who ingested the highest amount (15 g TID). AEs reported for more than 1 subject in the D-xylose cohorts included diarrhea (3 subjects [8.3%]) and flatulence and GI pain (2 subjects [5.6%] each). AEs in the Splenda® cohort included abdominal distension, flatulence, increased blood creatinine, infrequent bowel movements, and rhinitis. The incidence of AEs was highest during Weeks 1 and 2 (Days 2 through 15), regardless of sweetener type or ingestion amount. During this 2-week period, 18 subjects overall (37.5%) experienced AEs, compared with 7 subjects (14.6%) overall who experienced AEs either on Day 1 or after Week 2.

[0657] All AEs were mild in severity with the exception of moderate AEs reported for 4 subjects (11.1%) in the D-xylose cohorts. These moderate AEs included abdominal distension, concussion/post-concussion syndrome, diarrhea, GI pain, increased blood bilirubin, and neutropenia.

[0658] No SAEs, severe AEs, or subject deaths were reported. One subject in the 8 g TID D-xylose cohort experienced non-serious, moderate AEs of concussion and post-concussion syndrome that were noted to have contributed to study discontinuation; however, this subject's primary reason for discontinuation was withdrawal of consent.

[0659] GI-related AEs, which were of special interest, were reported for 7 subjects (19.4%) in the D-xylose cohorts and 2 subjects (16.7%) in the Splenda® cohort. GI-related events were mild for all but 1 subject in the 15 g TID D-xylose cohort who experienced moderate GI-related AEs of abdominal distension, diarrhea, and GI pain that required reduction of the D-xylose ingestion amount to 12.5 g TID.

[0660] Eleven subjects (22.9%) experienced at least 1 AE that was considered by the Investigator to be related to study sweetener, including 9 subjects (25.0%) in the D-xylose cohorts and 2 subjects (16.7%) in the Splenda® cohort. The incidence of sweetener-related AEs appeared to increase with increasing D-xylose ingestion amounts. Sweetener-related AEs reported for more than 1 subject in the D-xylose cohorts included diarrhea (3 subjects [8.3%]) and flatulence and GI pain (2 subjects [5.6%] each). Sweetener-related AEs reported in the Splenda® cohort were abdominal distension, flatulence, and infrequent bowel movements.

[0661] No fluctuations in clinical laboratory measurements over time were considered to be clinically meaningful. Categorical shifts from Baseline that occurred in >10% of subjects in either the combined D-xylose or Splenda® cohorts included decreased or increased glucose (27.7% D-xylose and 16.7% Splenda®) and decreased absolute neutrophil count (ANC) (13.9% and 8.3%); these shifts were not associated with sweetener type or ingestion amount.

[0662] Immunology and Other Assessments

[0663] To assess the effect of D-xylose on the gut microbiome, this study incorporated an analysis of alpha diversity, beta diversity, and differentially abundant taxa. These factors were assessed both across cohorts and over time. Regardless of sweetener ingestion amount, no apparent significant impact on the intra-sample alpha diversity of the gut microbiome was observed, and no significant changes in community composition were observed over time on study. Numerous taxa were identified as differentially abundant, but these findings may reflect the relatively small sample sizes in each cohort.

[0664] Across all D-xylose cohorts, 8.3% of subjects with normal serum CRP at Baseline experienced at least 1 post-ingestion CRP value >2.9 mg/L. A substantially higher proportion of subjects in the Splenda® cohort (41.7%) had normal serum CRP at Baseline and experienced at least 1 post-ingestion CRP value >2.9 mg/L. None of the post-ingestion CRP values for any subject were deemed clinically significant.

[0665] Because most individual cytokine data points were below the limit of quantitation (BLQ) and therefore set to zero, cytokine summary statistics were limited and did not indicate any consistent or clinically meaningful changes over time for either sweetener or any D-xylose ingestion amount. There was a trend for reduced levels of serum interferon gamma over time in the 2 g and 15 g D-xylose cohorts (FIG. **30**). No consistent or clinically meaningful changes over time in total T-cells or any T-cell subsets were observed for either sweetener or any D-xylose ingestion amount.

[0666] Pharmacokinetics

[0667] Serum D-xylose concentrations increased linearly with increasing ingestion amounts. Little to no accumulation of serum D-xylose occurred at Day 15 following 1 g to 12.5 g TID ingestion, while an approximately 1.9-fold accumulation ratio was observed in the 15 mg TID cohort (although variability was high). On Day 28, the accumulation ratio ranged from 1.08 to 1.31 following 1 g to 12.5 g TID ingestion and 1.68 following 15 g TID ingestion, although variability was moderate to high in all but the 8 g TID cohort.

[0668] In the 1 g TID cohort, approximately 40% of the ingested amount of D-xylose was recovered in urine within 5 hours post-ingestion on Days 1, 15, and 28. In the 2 g through 15 g TID cohorts, between 23% and 32% of the ingested amount of D-xylose was recovered in urine within 5 hours post-ingestion on Days 1, 15, and 28. The fraction excreted in urine was similar among Days 1, 15, and 28.

[0669] A review of the time course of serum D-xylose concentrations and the corresponding urinary excretion profiles indicated high ingestion compliance.

[0670] Changes in the Gut Microbiome

[0671] A total of 344 stool samples were collected in OMNIgene•GUT collection kits and shipped to the GenoFIND laboratory for DNA extraction and V3-V4 16S amplicon sequencing. There were no major shifts in the microbiome alpha diversity between the different treatment groups (absolute number of OTUs, abundance of OTUs) or over time on study. There was an overall decrease in the Chao diversity index over time (indicator of community richness—# of singleton, doubleton OTUs), as shown in FIG. **31**. Numerous taxa were identified as differentially abundant, but this finding may be attributable to the relatively small sample sizes of each cohort. Similar observations were made in the mouse study, e.g., xylose treatment did not cause major shifts in the gut microbiome but showed some differences at the family level. Overall, these results suggest that, under the conditions tested in normal individuals and normal mice, ingestion of xylose exerts subtle changes in the gut microbiome. The impact of xylose on the microbiome under disease conditions remains to be determined.

[0672] Taken together, the results of this trial show that D-xylose is safe and well-tolerated, and indicate that prebiotic formulations containing xylose may reduce inflammation in a subject, resulting in reduction of serum levels of pro-inflammatory cytokines.

Example 6

Distal Augmentation

[0673] The trillions of organisms forming the microbiome function as an organ system interconnected throughout the body. The possibility that modification of the microbiome in a given physical location may influence the microbiome at other sites in the body (distal augmentation) was investigated. Seven week old C57B1/6 female mice were acclimatized for 7 days prior to the start of the study by daily handling and shuffling between cages. All mice were housed at three mice per cage in individually vented cages (Thoren, Hazleton, Pa.). At day 0, baseline fresh fecal pellets, and vaginal lavages with 100 μL of sterile double-distilled water were collected and immediately frozen at −80° C. for microbiome analysis. After baseline collection, mice were given to drink either autoclaved water (N=6) or 0.5 mg/L of the antibiotic vancomycin in autoclaved water (N=6) ad libitum. Water alone is not expected to influence the microbiome and acted as a negative

control. Oral vancomycin is poorly absorbed from the gut and its ingestion does not result in significant levels of drug in the body (Rao et al, 2011). The impact of oral vancomycin is therefore expected to be limited to the gastrointestinal tract such that microbiome changes elsewhere in the body (e.g. vagina) would be attributable to distal augmentation. At day 6, fresh fecal pellets and vaginal lavages with 100 μL of sterile double-distilled water were collected and immediately stored at −80° C. for microbiome analysis.

[0674] Isolation and sequencing of microbial DNA from the stool and vaginal samples was performed by DNA Genotek (Ottawa, ON, Canada). The V3-V4 region of the 16S ribosomal subunit was amplified with custom PCR primers and sequenced on an Illumina MiSeq to a minimum acceptable read depth of 25,000 sequences per sample. The widely accepted read depth requirement for accurate taxonomic profiling is 15,000-100,000 reads (Illumina, 2014). A closed-reference taxonomic classification was performed, where each sequence was aligned to the SILVA reference database, version 123. Sequences were aligned using the UCLUST algorithm included in QIIME version 1.9.1 (Caporaso et al., 2010). A minimum threshold of 97% sequence identity was used to classify sequences according to representative sequences in the database. At 97% sequence identity, each OTU represents a genetically unique group of biological organisms. These OTU's were then assigned a curated taxonomic label based on the seven level SILVA taxonomy.

[0675] As expected, oral vancomycin treatment had a strong impact on the microbiome of the gut. As shown by principal component analysis (PCA) at the family level, the day 0 to day 6 pattern in fecal samples was clearly different in the control vs oral vancomycin group (FIG. **32**). Interestingly, the day 0 to day 6 pattern in the vaginal samples also showed an overall difference between the PBS and oral vancomycin groups even though the vaginal environment is not exposed to vancomycin following oral administration of the antibiotic (FIG. **32**). In addition, some bacterial species were detected at low frequency in vaginal samples of the vancomycin-treated group at day 6 (median abundance of approximately 0.00002%) that were not present at day 0 (Table 8). These results support the concept of distal augmentation whereby modification of the microbiome at one site also has an impact at a distal site(s). This finding opens the possibility of modulating the microbiome, for example at the level of the gut, to effect therapeutic changes in the microbiome at other sites, for example the lung.

Example 7

Provision of Fecal Material

[0676] Fresh fecal samples are obtained from healthy human donors who have been screened for general good health and for the absence of infectious diseases, and meet inclusion and exclusion criteria, inclusion criteria include being in good general health, without significant medical history, physical examination findings, or clinical laboratory abnormalities, regular bowel movements with stool appearance typically Type 2, 3, 4, 5 or 6 on the Bristol Stool Scale, and having a BMI≥18 kg/m^2 and ≤25 kg/m^2. Exclusion criteria generally include significant chronic or acute medical conditions including renal, hepatic, pulmonary, gastrointestinal, cardiovascular, genitourinary, endocrine, immunologic, metabolic, neurologic or hematological disease, a family history of, inflammatory bowel disease including Crohn's disease and ulcerative colitis, Irritable bowel syndrome, colon, stomach or other gastrointestinal malignancies, or gastrointestinal polyposis syndromes, or recent use of yogurt or commercial probiotic materials in which an organism(s) is a primary component. Samples are collected directly using a commode specimen collection system, which contains a plastic support placed on the toilet seat and a collection container that rests on the support. Feces are deposited into the container, and the lid is then placed on the container and sealed tightly. The sample is then delivered on ice within 1-4 hours for processing. Samples are mixed with a sterile disposable tool, and 2-4 g aliquots are weighed and placed into tubes and flash frozen in a dry ice/ethanol bath. Aliquots are frozen at −80 degrees Celsius until use.

[0677] Optionally, the fecal material is suspended in a solution, and/or fibrous and/or particulate materials are removed. A frozen aliquot containing a known weight of feces is removed from storage at −80 degrees Celsius and allowed to thaw at room temperature. Sterile 1×PBS is added to create a 10% w/v suspension, and vigorous vortexing is performed to suspend the fecal material until the material appeared homogeneous. The material is then left to sit for 10 minutes at room temperature to sediment fibrous and particulate matter. The suspension above the sediment is then carefully removed into a new tube and contains a purified spore population. Optionally, the suspension is then centrifuged at a low speed, e.g., 1000×g, for 5 minutes to pellet particulate matter including fibers. The pellet is discarded and the supernatant, which contained vegetative organisms and spores, is removed into a new tube. The supernatant is then centrifuged at 6000×g for 10 minutes to pellet the vegetative organisms and spores. The pellet is then resuspended in 1×PBS with vigorous vortexing until the material appears homogenous.

Example 8

Spore Purification from Alcohol Treatment of Fecal Material

[0678] A 10% w/v suspension of human fecal material in PBS is mixed with absolute ethanol in a 1:1 ratio and vortexed to mix for 1 minute. The suspension is incubated at 37 degrees Celsius for 1 hour. After incubation the suspension is centrifuged at 13,000 rpm for 5 minutes to pellet spores. The supernatant is discarded and the pellet is resuspended in an equal volume of PBS. Glycerol is added to a final concentration of 15% and then the purified spore fraction is stored at −80 degrees Celsius.

Example 9

Generation of a Spore Preparation from Alcohol Treatment of Fecal Material

[0679] A 10% w/v suspension of human fecal material in PBS is mixed with absolute ethanol in a 1:1 ratio and vortexed to mix for 1 minute. The suspension is incubated at 37 degrees Celsius for 1 hour. After incubation the suspension is centrifuged at 13,000 rpm for 5 minutes to concentrate spores into a pellet containing a purified sprore-containing preparation. The supernatant is discarded and the pellet resuspended in an equal volume of PBS. Glycerol is added to a final concentration of 15% and then the purified spore preparation is stored at −80 degrees Celsius.

Example 10

Spore Purification from Thermal Treatment of Fecal Material

[0680] A 10% w/v suspension of human fecal material in PBS is incubated in a water bath at 80 degrees Celsius for 30 minutes. Glycerol is added to a final concentration of 15% and then the enriched spore containing material is stored at −80 degrees Celsius.

Example 11

Spore Purification from Alcohol Treatment and Thermal Treatment of Fecal Material

[0681] A 10% w/v suspension of human feces in PBS is mixed with absolute ethanol in a 1:1 ratio and vortexed to mix for 1 minute. The suspension is incubated in a water bath under aerobic conditions at 37 degrees Celsius for 1 hour. After incubation the suspension is centrifuged at 13,000 rpm for 5 minutes to pellet spores. The supernatant is discarded and the pellet is resuspended in equal volume PBS. The ethanol treated spore population is then incubated in a water bath at 80 degrees Celsius for 30 minutes. Glycerol is added to a final concentration of 15% and the purified spore fraction is stored at −80 C.

Example 12

Construction of Binary and Ternary Combinations in a High-Throughput 96-Well Format

[0682] To allow high-throughput screening of binary and ternary combinations, vials of −80° C. glycerol stock banks are thawed and diluted to 1e8 CFU/mL. Each strain is then diluted 10× (to a final concentration of 1e7 CFU/mL of each strain) into 200 uL of PBS+15% glycerol in the wells of a 96-well plate. Plates are then frozen at −80° C. When needed for the assay, plates are removed from −80° C. and thawed at room temperature under anaerobic conditions when testing in a plate assay with various pathogens.

Example 13

Spore Purification from Detergent Treatment of Fecal Material

[0683] A 10% w/v suspension of human feces in PBS is prepared to contain a final concentration of 0.5 to 2% Triton X-100. After shaking incubation for 30 minutes at 25 to 37 degrees Celsius, the sample is centrifuged at 1000 g for 5-10 minutes to pellet particulate matter and large cells. The bacterial entities are recovered in the supernatant fraction, where the purified spore population is optionally further treated, such as in Example 11. Without being bound by theory, detergent addition to the fecal mixture produces better spore populations, at least in part by enhancing separation of the spores from particulates thereby resulting in higher yields of spores. In some embodiments, the purified spore population is further treated, such as by thermal treatment and/or ethanol treatment as described above.

Example 14

Spore Purification by Chromatographic Separation of Fecal Material

[0684] A spore-enriched population such as obtained from Examples 7-12 above, is mixed with NaCl to a final concentration of 4M total salt and contacted with octyl Sepharose 4 Fast Flow to bind the hydrophobic spore fraction. The resin is washed with 4M NaCl to remove less hydrophobic components, and the spores are eluted with distilled water, and the desired enriched spore fraction is collected via UV absorbance.

Example 15

Spore Purification by Filtration of Fecal Material

[0685] A spore-enriched population such as obtained from Examples 8-13 above is diluted 1:10 with PBS, and placed in the reservoir vessel of a tangential flow microfiltration system. A 0.2 μm pore size mixed cellulose ester hydrophilic tangential flow filter is connected to the reservoir such as by a tubing loop. The diluted spore preparation is recirculated through the loop by pumping, and the pressure gradient across the walls of the microfilter forces the supernatant liquid through the filter pores. By appropriate selection of the filter pore size the desired bacterial entities are retained, while smaller contaminants such as cellular debris, and other contaminants in feces such as bacteriophage pass through the filter. Fresh PBS buffer is added to the reservoir periodically to enhance the washout of the contaminants. At the end of the diafiltration, the spores are concentrated approximately ten-fold to the original concentration. The purified spores are collected from the reservoir and stored as provided herein.

Example 16

Characterization of Purified Spore Populations

[0686] Counts of viable spores are determined by performing 10 fold serial dilutions in PBS and plating to Brucella Blood Agar Petri plates or applicable solid media. Plates are incubated at 37 degrees Celsius for 2 days. Colonies are counted from a dilution plate with 50-400 colonies and used to back-calculate the number of viable spores in the population. The ability to germinate into vegetative bacteria is also demonstrated. Visual counts are determined by phase contrast microscopy. A spore preparation is either diluted in PBS or concentrated by centrifugation, and a 5 microliter aliquot is placed into a Petroff Hauser counting chamber for visualization at 400× magnification. Spores are counted within ten 0.05 mm×0.05 mm grids and an average spore count per grid is determined and used to calculate a spore count per ml of preparation. Lipopolysaccharide (LPS) reduction in purified spore populations is measured using a Limulus amebocyte lysate (LAL) assay such as the commercially available ToxinSensor™ Chromogenic LAL Endotoxin Assay Kit (GenScript, Piscataway, N.J.) or other standard methods known to those skilled in the art.

Example 17

Quantification of *C. difficile* using Quantitative PCR (qPCR)

[0687] A. Standard Curve Preparation

[0688] The standard curve is generated from a well on each assay plate containing only pathogenic *C. difficile* grown in

SweetB+FosIn media as provided herein and quantified by selective spot plating. Serial dilutions of the culture are performed in sterile phosphate-buffered saline. Genomic DNA is extracted from the standard curve samples along with the other wells.

[0689] B. Genomic DNA Extraction

[0690] Genomic DNA is extracted from 5 μl of each sample using a dilution, freeze/thaw, and heat lysis protocol. 5 μL of thawed samples are added to 45 μL of UltraPure water (Life Technologies, Carlsbad, Calif.) and mixed by pipetting. The plates with diluted samples are frozen at −20° C. until use for qPCR which includes a heated lysis step prior to amplification. Alternatively the genomic DNA could be isolated using the Mo Bio Powersoil®-htp 96 Well Soil DNA Isolation Kit (Mo Bio Laboratories, Carlsbad, Calif.), Mo Bio Powersoil® DNA Isolation Kit (Mo Bio Laboratories, Carlsbad, Calif.), or the QIAamp DNA Stool Mini Kit (QIAGEN, Valencia, Calif.) according to the manufacturer's instructions.

[0691] C. qPCR Composition and Conditions

[0692] The qPCR reaction mixture contained 1× SsoAdvanced Universal Probes Supermix, 900 nM of Wr-tcdB-F primer (AGCAGTTGAATATAGTGGTTTAGTTAGAGTTG, IDT, Coralville, Iowa), 900 nM of Wr-tcdB-R primer (CATGCITIITrAGTTCTGGATTGAA, IDT, Coralville, Iowa), 250 nM of Wr-tcdB-P probe (6FAM-CATCCAGTCTCAATTGTATATGTTTCTCCA-MGB, Life Technologies, Grand Island, N.Y.), and Molecular Biology Grade Water (Mo Bio Laboratories, Carlsbad, Calif.) to 18 μl (Primers adapted from: Wroblewski, D. et al., Rapid Molecular Characterization of *Clostridium difficile* and Assessment of Populations of *C. difficile* in Stool Specimens, Journal of Clinical Microbiology 47:2142-2148 (2009)). This reaction mixture is aliquoted to wells of a Hard-shell Low-Profile Thin Wall 96-well Skirted PCR Plate (BioRad, Hercules, Calif.). To this reaction mixture, 2 μl of diluted, frozen, and thawed samples are added and the plate sealed with a Microseal 'B' Adhesive Seal (BioRad, Hercules, Calif.). The qPCR is performed on a BioRad C1000™ Thermal Cycler equipped with a CFX96™ Real-Time System (BioRad, Hercules, Calif.). The thermocycling conditions are 95° C. for 15 minutes followed by 45 cycles of 95° C. for 5 seconds, 60° C. for 30 seconds, and fluorescent readings of the FAM channel. Alternatively, the qPCR could be performed with other standard methods known to those skilled in the art.

Example 18

16S Sequencing to Determine Operational Taxonomic Unit (OTU) Method for Determining 16S Sequence

[0693] OTUs may be defined either by full 16S sequencing of the rDNA gene. by sequencing of a specific hypervariable region of this gene (i.e. V1, V2, V3, V4, V5, V6, V7, V8, or V9), or by sequencing of any combination of hypervariable regions from this gene (e.g. V1-3 or V3-5). The bacterial 16S rDNA is approximately 1500 nucleotides in length and is used in reconstructing the evolutionary relationships and sequence similarity of one bacterial isolate to another using phylogenetic approaches. 16S sequences are used for phylogenetic reconstruction as they are in general highly conserved, but contain specific hypervariable regions that harbor sufficient nucleotide diversity to differentiate genera and species of most microbes.

[0694] rDNA gene sequencing methods are applicable to both the analysis of non-enriched samples, but also for identification of microbes after enrichment steps that either enrich the microbes of interest from the microbial composition and/or the nucleic acids that harbor the appropriate rDNA gene sequences as described below. For example, enrichment treatments prior to 16S rDNA gene characterization will increase the sensitivity of 16S as well as other molecular-based characterization nucleic acid purified from the microbes.

[0695] Using well known techniques, in order to determine the full 16S sequence or the sequence of any hypervariable region of the 16S rRNA sequence, genomic DNA is extracted from a bacterial sample, the 16S rDNA (full region or specific hypervariable regions) amplified using polymerase chain reaction (PCR), the PCR products cleaned, and nucleotide sequences delineated to determine the genetic composition of 16S gene or subdomain of the gene. If full 16S sequencing is performed, the sequencing method used may be, but is not limited to, Sanger sequencing. If one or more hypervariable regions are used, such as the V4 region, the sequencing may be, but is not limited to being, performed using the Sanger method or using a next-generation sequencing method, such as an Illumina (sequencing by synthesis) method using barcoded primers allowing for multiplex reactions.

Method for Determining 18S rDNA and ITS Gene Sequence

[0696] Methods to assign and identify fungal OTUs by genetic means can be accomplished by analyzing 18S sequences and the internal transcribed spacer (ITS). The rRNA of fungi that forms the core of the ribosome is transcribed as a signal gene and consists of the 8S, 5.8S and 28S regions with ITS4 and 5 between the 8S and 5.8S and 5.8S and 28S regions, respectively. These two intercistronic segments between the 18S and 5.8S and 5.8S and 28S regions are removed by splicing and contain significant variation between species for barcoding purposes as previously described (Schoch et al Nuclear ribosomal internal transcribed spacer (ITS) region as a universal DNA barcode marker for Fungi. PNAS 109:6241-6246. 2012). 18S rDNA is traditionally used for phylogenetic reconstruction however the ITS can serve this function as it is generally highly conserved but contains hypervariable regions that harbor sufficient nucleotide diversity to differentiate genera and species of most fungus.

[0697] Using well known techniques, in order to determine the full 18S and ITS sequences or a smaller hypervariable section of these sequences, genomic DNA is extracted from a microbial sample, the rDNA amplified using polymerase chain reaction (PCR), the PCR products cleaned, and nucleotide sequences delineated to determine the genetic composition rDNA gene or subdomain of the gene. The sequencing method used may be, but is not limited to, Sanger sequencing or using a next-generation sequencing method, such as an Illumina (sequencing by synthesis) method using barcoded primers allowing for multiplex reactions.

Method for Determining Other Marker Gene Sequences

[0698] In addition to the 16S rRNA gene, one may define an OTU by sequencing a selected set of genes that are known to be marker genes for a given species or taxonomic group of OTUs.

[0699] These genes may alternatively be assayed using a PCR-based screening strategy. As example, various strains of pathogenic *Escherichia coli* can be distinguished using DNAs from the genes that encode heat-labile (LTI, LTIIa, and LTIIb) and heat-stable (STI and STII) toxins, verotoxin types 1, 2, and 2e (VT1, VT2, and VT2e, respectively), cytotoxic necrotizing factors (CNF1 and CNF2), attaching and effacing mechanisms (eaeA), enteroaggregative mechanisms (Eagg), and enteroinvasive mechanisms (Einv). The optimal genes to utilize for taxonomic assignment of OTUs by use of marker genes will be familiar to one with ordinary skill of the art of sequence based taxonomic identification.

Genomic DNA Extraction

[0700] Genomic DNA is extracted from pure microbial cultures using a hot alkaline lysis method. 1 μl of microbial culture is added to 9 μl of Lysis Buffer (25 mM NaOH, 0.2 mM EDTA) and the mixture is incubated at 95° C. for 30 minutes. Subsequently, the samples are cooled to 4° C. and neutralized by the addition of 10 μl of Neutralization Buffer (40 mM Tris-HCl) and then diluted 10-fold in Elution Buffer (10 mM Tris-HCl). Alternatively, genomic DNA is extracted from pure microbial cultures using commercially available kits such as the Mo Bio Ultraclean® Microbial DNA Isolation Kit (Mo Bio Laboratories, Carlsbad, Calif.) or by standard methods known to those skilled in the art. For fungal samples, DNA extraction can be performed by methods described previously (US20120135127) for producing lysates from fungal fruiting bodies by mechanical grinding methods.

Amplification of 16S Sequences for Downstream Sanger Sequencing

[0701] To amplify bacterial 16S rDNA, 2 μl of extracted gDNA is added to a 20 μl final volume PCR reaction. For full-length 16 sequencing the PCR reaction also contains 1× HotMasterMix (5PRIME, Gaithersburg, Md.), 250 nM of 27f (AGRGTTTGATCMTGGCTCAG, IDT, Coralville, Iowa), and 250 nM of 1492r (TACGGYTACCTTGTTAYGACTT, IDT, Coralville, Iowa), with PCR Water (Mo Bio Laboratories, Carlsbad, Calif.) for the balance of the volume. Alternatively, other universal bacterial primers or thermostable polymerases known to those skilled in the art are used. For example primers are available to those skilled in the art for the sequencing of the "V1-V9 regions" of the 16S rRNA. These regions refer to the first through ninth hypervariable regions of the 16S rRNA gene that are used for genetic typing of bacterial samples. These regions in bacteria are defined by nucleotides 69-99, 137-242, 433-497, 576-682, 822-879, 986-1043, 1117-1173, 1243-1294 and 1435-1465 respectively using numbering based on the *E. coli* system of nomenclature. Brosius et al., Complete nucleotide sequence of a 16S ribosomal RNA gene from *Escherichia coli*, PNAS 75(10): 4801-4805 (1978).

[0702] In some embodiments, OTUs may be defined either by full 16S sequencing of the rRNA gene, by sequencing of a specific hypervariable region of this gene (i.e., V1, V2, V3, V4, V5, V6, V7, V8, or V9), or by sequencing any combination of hypervariable regions from this gene (e.g., V1-3 or V3-5). In one embodiment, the V1, V2, and V3 regions are used to characterize an OTU. In another embodiment, the V3, V4, and V5 regions are used to characterize an OTU. In another embodiment, the V4 region is used to characterize an OTU. A person of ordinary skill in the art can identify the specific hypervariable regions of a candidate 16S rRNA by comparing the candidate sequence in question to the reference sequence and identifying the hypervariable regions based on similarity to the reference hypervariable regions.

[0703] The PCR is performed on commercially available thermocyclers such as a BioRad MyCycler™ Thermal Cycler (BioRad, Hercules, Calif.). The reactions are run at 94° C. for 2 minutes followed by 30 cycles of 94° C. for 30 seconds, 51° C. for 30 seconds, and 68° C. for 1 minute 30 seconds, followed by a 7 minute extension at 72° C. and an indefinite hold at 4° C. Following PCR, gel electrophoresis of a portion of the reaction products is used to confirm successful amplification of a ~1.5 kb product.

[0704] To remove nucleotides and oligonucleotides from the PCR products, 2 μl of HT ExoSap-IT (Affymetrix, Santa Clara, Calif.) is added to 5 μl of PCR product followed by a 15 minute incubation at 37° C. and then a 15 minute inactivation at 80° C.

Amplification of 16S Sequences for Downstream Characterization by Massively Parallel Sequencing Technologies

[0705] Amplification performed for downstream sequencing by short read technologies such as Illumina require amplification using primers known to those skilled in the art that additionally include a sequence-based barcoded tag. As example, to amplify the 16s hypervariable region V4 region of bacterial 16S rDNA, 2 μl of extracted gDNA is added to a 20 μl final volume PCR reaction. The PCR reaction also contains 1× HotMasterMix (5PRIME, Gaithersburg, Md.), 200 nM of V4_515f_adapt

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(AATGATACGGCGACCACCGAGATCTACACTATGGTAATTGTGT
GCCAGCMGCCGCGGTAA,, IDT, Coralville, IA),
and

200 nM of barcoded 806 rbc
(CAAGCAGAAGACGGCATACGAGAT_12bpGolayBarcode_A
GTCAGTCAGCCGGACTACHVGGGTWTCTAAT, IDT,
Coralville, IA),
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with PCR Water (Mo Bio Laboratories, Carlsbad, Calif.) for the balance of the volume. These primers incorporate barcoded adapters for Illumina sequencing by synthesis. Optionally, identical replicate, triplicate, or quadruplicate reactions may be performed. Alternatively other universal bacterial primers or thermostable polymerases known to those skilled in the art are used to obtain different amplification and sequencing error rates as well as results on alternative sequencing technologies.

[0706] The PCR amplification is performed on commercially available thermocyclers such as a BioRad MyCycler™ Thermal Cycler (BioRad, Hercules, Calif.). The reactions are run at 94° C. for 3 minutes followed by 25 cycles of 94° C. for 45 seconds, 50° C. for 1 minute, and 72° C. for 1 minute 30 seconds, followed by a 10 minute extension at 72° C. and a indefinite hold at 4° C. Following PCR, gel electrophoresis of a portion of the reaction products is used to confirm successful amplification of a ~1.5 kb product. PCR cleanup is performed as specified in the previous example.

Sanger Sequencing of Target Amplicons from Pure Homogeneous Samples

[0707] To detect nucleic acids for each sample, two sequencing reactions are performed to generate a forward and

reverse sequencing read. For full-length 16s sequencing primers 27f and 1492r are used. 40 ng of ExoSap-IT-cleaned PCR products are mixed with 25 pmol of sequencing primer and Mo Bio Molecular Biology Grade Water (Mo Bio Laboratories, Carlsbad, Calif.) to 15 μl total volume. This reaction is submitted to a commercial sequencing organization such as Genewiz (South Plainfield, N.J.) for Sanger sequencing.

[0708] In order to determine the full 16S sequence or the sequence of any hypervariable region of the 16S rRNA sequence, genomic DNA is extracted from a bacterial sample, the 16S rDNA (full region or specific hypervariable regions) is amplified using polymerase chain reaction (PCR), the PCR products are cleaned, and nucleotide sequences delineated to determine the genetic composition of 16S gene or subdomain of the gene. If full 16S sequencing is performed, the sequencing method used may be, but is not limited to, Sanger sequencing. If one or more hypervariable regions are used, such as the V4-V5 region, the sequencing may be, but is not limited to being, performed using the Sanger method or using a next-generation sequencing method, such as an Illumina (sequencing by synthesis) method using barcoded primers allowing for multiplex reactions.

Amplification of 18S and ITS regions for Downstream Sequencing and Characterization

[0709] To amplify the 18S or ITS regions, 2 μL fungal DNA were amplified in a final volume of 30 μL with 15 μL AmpliTaq Gold 360 Mastermix. PCR primers, and water. The forward and reverse primers for PCR of the ITS region are 5'-TCCTCCGCTTATTGATATGC-3' and 5'-GGAAGTAAAAGTCGTAACAAGG-3' and are added at 0.2 uM concentration each. The forward and reverse primers for the 18S region are 5'-GTAGTCATATGCTTGTCTC-3' and 5'-CTTCCGTCAATTCCTTTAAG-3' and are added at 0.4 uM concentration each. PCR is performed with the following protocol: 95 C for 10 min, 35 cycles of 95 C for 15 seconds, 52C for 30 seconds. 72C for 1.5s; and finally 72C for 7 minutes followed by storage at 4 C. All forward primers contained the M13F-20 sequencing primer, and reverse primers included the M13R-27 sequencing primer. PCR products (3 μL) were enzymatically cleaned before cycle sequencing with 1 μL ExoSap-IT and 1 μL Tris EDTA and incubated at 37° C. for 20 min followed by 80° C. for 15 min. Cycle sequencing reactions contained 5 μL cleaned PCR product, 2 μL BigDye Terminator v3.1 Ready Reaction Mix, 1 μL 5× Sequencing Buffer, 1.6 pmol of appropriate sequencing primers designed by one skilled in the art, and water in a final volume of 10 μL. The standard cycle sequencing protocol is 27 cycles of 10 s at 96° C., 5 s at 50° C., 4 min at 60° C., and hold at 4° C. Sequencing cleaning is performed with the BigDye XTerminator Purification Kit as recommended by the manufacturer for 10-μL volumes. The genetic sequence of the resulting 18S and ITS sequences is performed using methods familiar to one with ordinary skill in the art using either Sanger sequencing technology or next-generation sequencing technologies such as but not limited to Illumina.

Preparation of Extracted Nucleic Acids for Metagenomic Characterization by Massively Parallel Sequencing Technologies

[0710] Extracted nucleic acids (DNA or RNA) are purified and prepared by downstream sequencing using standard methods familiar to one with ordinary skill in the art and as described by the sequencing technology's manufactures instructions for library preparation. In short, RNA or DNA are purified using standard purification kits such as but not limited to Qiagen's RNeasy Kit or Promega's Genomic DNA purification kit. For RNA, the RNA is converted to cDNA prior to sequence library construction. Following purification of nucleic acids, RNA is converted to cDNA using reverse transcription technology such as but not limited to Nugen Ovation RNA-Seq System or Illumina Truseq as per the manufacturer's instructions. Extracted DNA or transcribed cDNA are sheared using physical (e.g., Hydroshear), acoustic (e.g., Covaris), or molecular (e.g., Nextera) technologies and then size selected as per the sequencing technologies manufacturer's recommendations. Following size selection, nucleic acids are prepared for sequencing as per the manufacturer's instructions for sample indexing and sequencing adapter ligation using methods familiar to one with ordinary skill in the art of genomic sequencing.

Massively Parallel Sequencing of Target Amplicons from Heterogeneous Samples

[0711] DNA Quantification & Library Construction.

[0712] The cleaned PCR amplification products are quantified using the Quant-iTT PicoGreen® dsDNA Assay Kit (Life Technologies, Grand Island, N.Y.) according to the manufacturer's instructions. Following quantification, the barcoded cleaned PCR products are combined such that each distinct PCR product is at an equimolar ratio to create a prepared Illumina library.

[0713] Nucleic Acid Detection.

[0714] The prepared library is sequenced on Illumina HiSeq or MiSeq sequencers (Illumina, San Diego, Calif.) with cluster generation, template hybridization, isothermal amplification, linearization, blocking and denaturation and hybridization of the sequencing primers performed according to the manufacturer's instructions. 16SV4SeqFw (TATGGTAATTGTGTGCCAGCMGCCGCGGTAA), 16SV4SeqRev (AGTCAGTCAGCCGGACTACHVGGGTWTCTAAT), and 16SV4Index (ATTAGAWACCCBDGTAGTCCGGCTGACTGACT) (IDT, Coralville, Iowa) are used for sequencing. Other sequencing technologies can be used such as but not limited to 454, Pacific Biosciences, Helicos, Ion Torrent, and Nanopore using protocols that are standard to someone skilled in the art of genomic sequencing.

Example 19

Data Analysis, Sequence Annotation and Taxonomic Characterization Primary Read Annotation

[0715] Nucleic acid sequences are analyzed to define taxonomic assignments using sequence similarity and phylogenetic placement methods or a combination of the two strategies. A similar approach is used to annotate protein names, protein function, transcription factor names, and any other classification schema for nucleic acid sequences. Sequence similarity based methods include those familiar to individuals skilled in the art including, but not limited to, BLAST, BLASTx, tBLASTn, tBLASTx, RDP-classifier, DNAclust, and various implementations of these algorithms such as Qiime or Mothur. These methods rely on mapping a sequence read to a reference database and selecting the match with the best score and e-value. Common databases include, but are

not limited to the Human Microbiome Project, NCBI non-redundant database, Greengenes, RDP, and Silva for taxonomic assignments. For functional assignments reads are mapped to various functional databases such as but not limited to COG, KEGG, BioCyc, and MetaCyc. Further functional annotations can be derived from 16S taxonomic annotations using programs such as PICRUST (M. Langille, et al 2013. Nature Biotechnology 31, 814-821). Phylogenetic methods can be used in combination with sequence similarity methods to improve the calling accuracy of an annotation or taxonomic assignment. Here tree topologies and nodal structure are used to refine the resolution of the analysis. In this approach we analyze nucleic acid sequences using one of numerous sequence similarity approaches and leverage phylogenetic methods that are well known to those skilled in the art, including but not limited to maximum likelihood phylogenetic reconstruction (see e.g. Liu K, Linder C R, and Warnow T. 2011. RAxML and FastTree: Comparing Two Methods for Large-Scale Maximum Likelihood Phylogeny Estimation. PLoS ONE 6: e27731. McGuire G, Denham M C, and Balding D J. 2001. Models of sequence evolution for DNA sequences containing gaps. Mol. Biol. Evol 18: 481-490. Wróbel B. 2008. Statistical measures of uncertainty for branches in phylogenetic trees inferred from molecular sequences by using model-based methods. J. Appl. Genet. 49: 49-67.) Sequence reads are placed into a reference phylogeny comprised of appropriate reference sequences. Annotations are made based on the placement of the read in the phylogenetic tree. The certainty or significance of the OTU annotation is defined based on the OTU's sequence similarity to a reference nucleic acid sequence and the proximity of the OTU sequence relative to one or more reference sequences in the phylogeny. As an example, the specificity of a taxonomic assignment is defined with confidence at the level of Family, Genus, Species, or Strain with the confidence determined based on the position of bootstrap supported branches in the reference phylogenetic tree relative to the placement of the OTU sequence being interrogated. Nucleic acid sequences can be assigned functional annotations using the methods described above.

[0716] In some embodiments, microbial clades are assigned using databases including, but not limited to, MetaPhlAn. Microbial diversity is quantified using the Shannon diversity index following closed-reference operational taxonomic unit picking. Phylogenetic abundance comparisons are performed in order to identify biomarkers of GVHD-related mortality using linear discriminant analysis (LDA) effect size (LEfSe) analysis, using a logarithmic LDA cutoff of 2.0.

Clade Assignments

[0717] The ability of 16S-V4 OTU identification to assign an OTU as a specific species depends in part on the resolving power of the 16S-V4 region of the 16S gene for a particular species or group of species. Both the density of available reference 16S sequences for different regions of the tree as well as the inherent variability in the 16S gene between different species will determine the definitiveness of a taxonomic annotation. Given the topological nature of a phylogenetic tree and the fact that tree represents hierarchical relationships of OTUs to one another based on their sequence similarity and an underlying evolutionary model, taxonomic annotations of a read can be rolled up to a higher level using a clade-based assignment procedure (Table 1). Using this approach, clades are defined based on the topology of a phylogenetic tree that is constructed from full-length 16S sequences using maximum likelihood or other phylogenetic models familiar to individuals with ordinary skill in the art of phylogenetics. Clades are constructed to ensure that all OTUs in a given clade are: (i) within a specified number of bootstrap supported nodes from one another (generally, 1-5 bootstraps), and (ii) share a defined percent similarity. e.g., within a 5% genetic similarity (for 16S molecular data typically set to 95%-97% sequence similarity). OTUs that are within the same clade can be distinguished as genetically and phylogenetically distinct from OTUs in a different clade based on 16S-V4 sequence data. OTUs falling within the same clade are evolutionarily closely related and may or may not be distinguishable from one another using 16S-V4 sequence data. The power of clade based analysis is that members of the same clade, due to their evolutionary relatedness, are likely to play similar functional roles in a microbial ecology such as that found in the human gut or vagina. Compositions substituting one species with another from the same clade are likely to have conserved ecological function and therefore are useful in the present invention. Notably in addition to 16S-V4 sequences, clade-based analysis can be used to analyze 18S, ITS, and other genetic sequences.

[0718] Notably, 16S sequences of isolates of a given OTU are phylogenetically placed within their respective clades, sometimes in conflict with the microbiological-based assignment of species and genus that may have preceded 16S-based assignment. Discrepancies between taxonomic assignment based on microbiological characteristics versus genetic sequencing are known to exist from the literature.

[0719] For a given network ecology or functional network ecology one can define a set of OTUs from the network's representative clades.

Metagenomic Read Annotation

[0720] Metagenomic or whole genome shotgun sequence data is annotated as described above, with the additional step that sequences are either clustered or assembled prior to annotation.

[0721] Following sequence characterization as described above, sequence reads are demultiplexed using the indexing (i.e. barcodes). Following demultiplexing sequence reads are either: (i) clustered using a rapid clustering algorithm such as but not limited to UCLUST (http://drive5.com/usearch/manual/uclust_algo.html) or hash methods such VICUNA (Xiao Yang, Patrick Charlebois, Sante Gnerre, Matthew G Coole, Niall J. Lennon, Joshua Z. Levin, James Qu, Elizabeth M. Ryan, Michael C. Zody, and Matthew R. Henn. 2012. De novo assembly of highly diverse viral populations. BMC Genomics 13:475). Following clustering a representative read for each cluster is identified based and analyzed as described above in "Primary Read Annotation". The result of the primary annotation is then applied to all reads in a given cluster. (ii) A second strategy for metagenomic sequence analysis is genome assembly followed by annotation of genomic assemblies using a platform such as but not limited to MetAMOS (T J. Treangen et al. 2013 Geneome Biology 14:R2), HUMAaN (Abubucker S, Segata N, Goll J, Schubert A M, Izard J, Cantarel B L, Rodriguez-Mueller B, Zucker J, Thiagarajan M, Henrissat B, et al. 2012. Metabolic Reconstruction for Metagenomic Data and Its Application to the

Human Microbiome ed. J. A. Eisen. PLoS Computational Biology 8: e1002358) and other methods familiar to one with ordinary skill in the art.

Example 20

OTU Identification Using Microbial Culturing Techniques

[0722] The identity of the bacterial species which grew up from a complex fraction can be determined in multiple ways. First, individual colonies can be picked into liquid media in a 96 well format, grown up and saved as 15% glycerol stocks at −80° C. Aliquots of the cultures can be placed into cell lysis buffer and colony PCR methods can be used to amplify and sequence the 16S rDNA gene (Example 18). Alternatively, colonies may be streaked to purity in several passages on solid media. Well separated colonies are streaked onto the fresh plates of the same kind and incubated for 48-72 hours at 37° C. The process is repeated multiple times in order to ensure purity. Pure cultures can be analyzed by phenotypic- or sequence-based methods, including 16S rDNA amplification and sequencing as described in Example 18. Sequence characterization of pure isolates or mixed communities e.g. plate scrapes and spore fractions can also include whole genome shotgun sequencing. The latter is valuable to determine the presence of genes associated with sporulation, antibiotic resistance, pathogenicity, and virulence. Colonies can also be scraped from plates en masse and sequenced using a massively parallel sequencing method as described in Example 7. such that individual 16S signatures can be identified in a complex mixture. Optionally, the sample can be sequenced prior to germination (if appropriate DNA isolation procedures are used to lsye and release the DNA from spores) in order to compare the diversity of germinable species with the total number of species in a spore sample. As an alternative or complementary approach to 16S analysis, MALDI-TOF-mass spec can also be used for species identification (Barreau M, Pagnier I. La Scola B. 2013. Improving the identification of anaerobes in the clinical microbiology laboratory through MALDI-TOF mass spectrometry. Anaerobe 22: 123-125).

Example 21

Microbiological Strain Identification Approaches

[0723] Pure bacterial isolates can be identified using microbiological methods as described in Wadsworth-KTL Anaerobic Microbiology Manual (Jouseimies-Somer H, Summanen P H. Citron D, Baron E, Wexler H M, Finegold S M. 2002. Wadsworth-KTL Anaerobic Bacteriology Manual), and The Manual of Clinical Microbiology (ASM Press, 10th Edition). These methods rely on phenotypes of strains and include Gram-staining to confirm Gram positive or negative staining behavior of the cell envelope, observance of colony morphologies on solid media, motility, cell morphology observed microscopically at 60× or 100× magnification including the presence of bacterial endospores and flagella. Biochemical tests that discriminate between genera and species are performed using appropriate selective and differential agars and/or commercially available kits for identification of Gram negative and Gram positive bacteria and yeast, for example, RapID tests (Remel) or API tests (bioMerieux). Similar identification tests can also be performed using instrumentation such as the Vitek 2 system (bioMerieux). Phenotypic tests that discriminate between genera and species and strains (for example the ability to use various carbon and nitrogen sources) can also be performed using growth and metabolic activity detection methods, for example the Biolog Microbial identification microplates. The profile of short chain fatty acid production during fermentation of particular carbon sources can also be used as a way to discriminate between species (Wadsworth-KTL Anaerobic Microbiology Manual. Jousimies-Somer, et al 2002). MALDI-TOF-mass spectrometry can also be used for species identification (as reviewed in Anaerobe 22:123).

Example 22

Construction of an In Vitro Assay to Screen for Combinations of Microbes Inhibitory to the Growth of Pathogenic *E. coli*

[0724] The in vitro assay is used to screen for combinations of bacteria inhibitory to the growth of *E. coli* by modifying the media used for growth of the pathogen inoculum. One of several choices of media is used for growth of the pathogen such as Reinforced Clostridial Media (RCM). Brain Heart Infusion Broth (BHI) or Luria Bertani Broth (LB) (also known as Lysogeny Broth). *E. coli* is quantified by using alternative selective media specific for *E. coli* or using qPCR probes specific for the pathogen. For example, aerobic growth on MacConkey lactose medium selects for enteric Gram negatives, including *E. coli*. qPCR is conducted using probes specific for the shiga toxin of pathogenic *E. coli*.

Example 23

Construction of an In Vitro Assay to Screen for Combinations of Microbes Inhibitory to the Growth of Vancomycin-Resistant *Enterococcus* (VRE)

[0725] The in vitro assay is used to screen for combinations of bacteria inhibitory to the growth of Vancomycin-Resistant *Enterococcus* spp. (VRE) by modifying the media used for growth of the pathogen inoculum. Several choices of media are used for growth of the pathogen such as Reinforced Clostridial Media (RCM), Brain Heart Infusion Broth (BHI) or Luria Bertani Broth (LB). VRE is quantified by using alternative selective media specific for VRE or using qPCR probes specific for the pathogen. For example, m-*Enterococcus* agar containing sodium azide is selective for *Enterococcus* spp. and a small number of other species. Probes specific to the van genes conferring vancomycin resistance are used in the qPCR.

Example 24

Testing of Bacterial Composition Against *Salmonella*

[0726] The in vitro assay is used to screen for combinations of bacteria inhibitory to the growth of *Salmonella* spp. by modifying the media used for growth of the pathogen inoculum. Several choices of media are used for growth of the pathogen such as Reinforced Clostridial Media (RCM). Brain Heart Infusion Broth (BHI) or Luria Bertani Broth (LB). *Salmonella* spp. are quantified by using alternative selective media specific for *Salmonella* spp. or using qPCR probes specific for the pathogen. For example, MacConkey agar is used to select for *Salmonella* spp. and the invA gene is tar-

geted with qPCR probes; this gene encodes an invasion protein carried by many pathogenic *Salmonella* spp. and is used in invading eukaryotic cells.

Example 25

Method of Preparing the Bacterial Composition for Administration to a Subject

[0727] Two or more strains that comprise the bacterial composition are independently cultured and mixed together before administration. Both strains are independently be grown at 37° C., pH 7, in a GMM or other animal-products-free medium, pre-reduced with 1 g/L cysteine HCl. After each strain reaches a sufficient biomass, it is preserved for banking by adding 15% glycerol and then frozen at −80° C. in 1 ml cryotubes.

[0728] Each strain is then be cultivated to a concentration of 10^{10} CFU/mL. then concentrated 20-fold by tangential flow microfiltration; the spent medium is exchanged by diafiltering with a preservative medium consisting of 2% gelatin, 100 mM trehalose, and 10 mM sodium phosphate buffer, or other suitable preservative medium. The suspension is freeze-dried to a powder and titrated.

[0729] After drying, the powder is blended with microcrystalline cellulose and magnesium stearate and formulated into a 250 mg gelatin capsule containing 10 mg of lyophilized powder (10^8 to 10^{11} bacteria), 160 mg microcrystalline cellulose, 77.5 mg gelatin, and 2.5 mg magnesium stearate.

[0730] A bacterial composition can be derived by selectively fractionating the desired bacterial OTUs from a raw material such as but not limited to stool. As example we prepared a 10% w/v suspension of human stool material in PBS that is filtered, centrifuged at low speed, and then the supernate containing spores is mixed with absolute ethanol in a 1:1 ratio and vortexed to mix. The suspension is incubated at room temperature for 1 hour. After incubation the suspension is centrifuged at high speed to concentrate spores into a pellet containing a purified spore-containing preparation. The supernate is discarded and the pellet resuspended in an equal mass of glycerol, and the purified spore preparation is placed into capsules and stored at −80 degrees Celsius; this preparation is referred to as an ethanol-treated spore population.

Example 26

Method of Treating a Subject with a Bacterial Composition

[0731] A subject has suffered from recurrent bouts of *C. difficile*. In the most recent acute phase of illness, the subject is treated with an antibiotic sufficient to ameliorate the symptoms of the illness. In order to prevent another relapse of *C. difficile*, the subject is administered one of the present bacterial compositions. Specifically, the subject is administered one of the present bacterial compositions at a dose in the range of $1e10^7$ to $1e10^{12}$ in a lyophilized form, in a gelatin capsule containing 10 mg of lyophilized bacteria and stabilizing components. The subject takes the capsule by mouth and resumes a normal diet after 4, 8, 12, or 24 hours. In another embodiment, the subject may take the capsule by mouth before, during, or immediately after a meal. In a further embodiment, the subject takes the dose daily for a specified period of time.

[0732] Stool is collected before and after treatment. In one embodiment stool is collected at 1 day, 3 days, 1 week, and 1 month after administration. The presence of *C. difficile* is found in the stool before administration of the bacterial composition, but stool collections after administration show reducing (such as at least 50% less, 60%, 70%, 80%, 90%, or 95%) to no detectable levels of *C. difficile*, as measured by qPCR, as described above. ELISA for toxin protein or traditional microbiological identification techniques may also be used.

[0733] As another measure of subject success, a positive response may be defined as absence of diarrhea, which itself is defined as 3 or more loose or watery stools per day for at least 2 consecutive days or 8 or more loose or watery stools in 48 hours, or persisting diarrhea (due to other causes) with repeating (three times) negative stool tests for toxins of *C. difficile*.

[0734] Treatment failure is defined as persisting diarrhea with a positive *C. difficile* toxin stool test or no reduction in levels of *C. difficile*, as measured by qPCR sequencing. ELISA or traditional microbiological identification techniques may also be used.

Example 27

Microbiological Strain Identification Approaches

[0735] Pure bacterial isolates are identified using microbiological methods as described in Wadsworth-KTL Anaerobic Microbiology Manual (Jouseimies-Somer H, Summanen P H, Citron D, Baron E, Wexler H M, Finegold S M. 2002. Wadsworth-KTL Anaerobic Bacteriology Manual), and The Manual of Clinical Microbiology (ASM Press, 10th Edition). These methods rely on phenotypes of strains and include Gram-staining to confirm Gram positive or negative staining behavior of the cell envelope, observance of colony morphologies on solid media, motility, cell morphology observed microscopically at 60× or 100× magnification including the presence of bacterial endospores and flagella. Biochemical tests that discriminate between genera and species are performed using appropriate selective and differential agars and/or commercially available kits for identification of Gram negative and Gram positive bacteria and yeast, for example, RapID tests (Remel) or API tests (bioMerieux). Similar identification tests can also be performed using instrumentation such as the Vitek 2 system (bioMerieux). Phenotypic tests that discriminate between genera and species and strains (for example the ability to use various carbon and nitrogen sources) can also be performed using growth and metabolic activity detection methods, for example the Biolog Microbial identification microplates. The profile of short chain fatty acid production during fermentation of particular carbon sources can also be used as a way to discriminate between species (Wadsworth-KTL Anaerobic Microbiology Manual, Jousimies-Somer, et al 2002). MALDI-TOF-mass spectrometry can also be used for species identification (as reviewed in Anaerobe 22:123).

Example 28

Computational Prediction of Network Ecologies

[0736] Source data comprising a genomic-based characterization of a microbiome of individual samples are used as input computationally delineate network ecologies that would have biological properties that are characteristic of a state of health and could catalyze a shift from a state of microbial dysbiosis to a state of health. Applicants obtained

16S and metagenomic sequence datasets from public data repositories (see e.g. The Human Microbiome Project Consortium. 2012. Structure, function and diversity of the healthy human microbiome. Nature 486: 207-214. Data accessible at URL: hmpdacc.org) and MetaHit Project (Arumugam M, Raes J, Pelletier E, Paslier D L, Yamada T, Mende D R, Fernandes G R, Tap J, Bruls T, Batto J-M, et al. 2011. Enterotypes of the human gut microbiome. Nature 473: 174-180. Data accessible at URL: metahit.eu) for relevant microbiome studies in multiple disease indications including CDAD, Type 2 Diabetes, Ulcerative Colitis, and Irritable Bowel Disease, or generated data sets from samples directly using the methods described in Examples 18 and 19 and further described in the literature (see e.g. Aagaard K, Riehle K, Ma J, Segata N, Mistretta T-A, Coarfa C, Raza S, Rosenbaum S, Van den Veyver I, Milosavljevic A, et al. 2012. A Metagenomic Approach to Characterization of the Vaginal Microbiome Signature in Pregnancy ed. A. J. Ratner. PLoS ONE 7: e36466. Jumpstart Consortium Human Microbiome Project Data Generation Working Group. 2012. Evaluation of 16S rDNA-Based Community Profiling for Human Microbiome Research ed. J. Ravel. PLoS ONE 7: e39315. The Human Microbiome Project Consortium. 2012. Structure, function and diversity of the healthy human microbiome. Nature 486: 207-214.). Nucleic acid sequences are analyzed and taxonomic and phylogenetic assignments of specific OTUs are made using sequence similarity and phylogenetic methods that are well known to those skilled in the art, including but not limited to maximum likelihood phylogenetic reconstruction (see e.g. Liu K, Linder C R, and Warnow T. 2011. RAxML and FastTree: Comparing Two Methods for Large-Scale Maximum Likelihood Phylogeny Estimation. PLoS ONE 6: e27731. McGuire G, Denham M C, and Balding D J. 2001. Models of sequence evolution for DNA sequences containing gaps. Mol. Biol. Evol 18: 481-490. Wróbel B. 2008. Statistical measures of uncertainty for branches in phylogenetic trees inferred from molecular sequences by using model-based methods. J. Appl. Genet. 49: 49-67.) From these taxonomic assignments OTUs and clades in the dataset are defined using the method described in Examples 18 and 19. The certainty of the OTU call is defined based on the OTU's sequence similarity to a reference nucleic acid sequence and the proximity of the OTU sequence relative to one or more reference sequences in the phylogeny. The specificity of an OTU's taxonomic and phlylogenetic assignment determines whether the match is assigned at the level of Family, Genus, Species, or Strain, and the confidence of this assignment is determined based on the position of bootstrap supported branches in the reference phylogenetic tree relative to the placement of the OTU sequence being interrogated. In addition, microbial OTU assignments may be obtained from assignments made in peer-reviewed publications.

[0737] Applicants designated individual subject samples to biologically relevant sample phenotypes such as but not limited to "healthy state," "recurrent *Clostridium difficile* infection," "Crohn's disease," "Insulin Resistance," "Obesity," "Type 2 diabetes," "Ulcerative Colitis". In one embodiment samples are assigned to "health" and "disease" phenotypes. In another embodiment, samples are assigned higher resolution phenotype such as but not limited to: "health:human", "health:mouse", "health:human microbiome project", "health:microbiota donor", "health:microbiota recipient", "disease:microbiota recipient", or "disease:no treatment", "disease:human", or "disease:mouse". In another embodiment, samples where assigned to higher resolution phenotypes, such as but not limited to those defined that characterize phenotypes specific to samples from fecal donors and patients who received a fecal microbial transplant from these donors.

[0738] In another embodiment, other phenotypes that define a category of disease or health that represents the underlying state of the population under study can be used. Applicants then computationally determined the microbial network ecologies for each phenotype using the OTU and clade assignments that comprise the microbial profile for each sample and the algorithms described above in the Section entitled "Method of Determining Network Ecologies."

[0739] Importantly, Network Ecologies that represent a state of health in one disease indication can represent states of health in additional disease states. Additionally, Keystone OTUs found in a network associated with health for different disease indications can overlap. Applicants found that a large number of network ecologies overlapped particularly between those associated with health in the cases of CDAD and Type 2 Diabetes despite the analysis of substantially different genomic data sets for the two diseases.

Example 29

Identification of Network Classes, Keystone OTUs, Clades, and Functional Modalities

Identification of Keystone OTUs, Clades and Functions

[0740] The human body is an ecosystem in which the microbiota and the microbiome play a significant role in the basic healthy function of human systems (e.g. metabolic, immunological, and neurological). The microbiota and resulting microbiome comprise an ecology of microorganisms that co-exist within single subjects interacting with one another and their host (i.e., the mammalian subject) to form a dynamic unit with inherent biodiversity and functional characteristics. Within these networks of interacting microbes (i.e. ecologies), particular members can contribute more significantly than others; as such these members are also found in many different ecologies, and the loss of these microbes from the ecology can have a significant impact on the functional capabilities of the specific ecology. Robert Paine coined the concept "Keystone Species" in 1969 (see Paine R T. 1969. A note on trophic complexity and community stability. The American Naturalist 103: 91-93) to describe the existence of such lynchpin species that are integral to a given ecosystem regardless of their abundance in the ecological community. Paine originally describe the role of the starfish *Pisaster ochraceus* in marine systems and since the concept has been experimentally validated in numerous ecosystems.

[0741] Keystone OTUs, Phylogenetic Clades (a.k.a. Clades), and/or Functions (for example, but not limited to, KEGG Orthology Pathways) are computationally-derived by analysis of network ecologies elucidated from a defined set of samples that share a specific phenotype. Keystone OTUs, Clades and/or Functions are defined as all Nodes within a defined set of networks that meet two or more of the following criteria. Using Criterion 1, the node is frequently observed in networks, and the networks in which the node is observed are found in a large number of individual subjects; the frequency of occurrence of these Nodes in networks and the pervasiveness of the networks in individuals indicates these Nodes

perform an important biological function in many individuals. Using Criterion 2, the node is frequently observed in networks, and the Node is observed contains a large number of edges connecting it to other nodes in the network. These Nodes are thus "super-connectors", meaning that they form a nucleus of a majority of networks and as such have high biological significance with respect to their functional contributions to a given ecology.

[0742] In another embodiment a Keystone Node is defined as one that occurs in a sample phenotype of interest such as but not limited to "health" and simultaneously does not occur in a sample phenotype that is not of interest such as but not limited to "disease." Optionally, a Keystone Node is defined as one that is shown to be significantly different from what is observed using permuted test datasets to measure significance. In another embodiment of Criterion 2 Keystone OTUs, Clades, or Functions can be defined using a hierarchical clustering method that clusters Networks based on their OTU, Clade, or functional pathways. Statistically significant branch points in the hierarchy are defined based on the topological overlap measure; this measure is a highly robust measure of network interconnectedness (Langfelder P, Zhang B, Horvath S. 2008. Defining clusters from a hierarchical cluster tree: the Dynamic Tree Cut package for R. Bioinformatics 24: 719-720.). Once these branch points are defined the Keystones are delineated as OTUs, clades or functional pathways that are found consistently across all networks in all or a subset of the network clusters.

[0743] Importantly, we identify the absence of Keystone OTUs in multiple particular disease states, indicating that bacterial compositions comprised of specific sets of Keystone OTUs are likely to have utility in multiple disease indications.

Example 30

Network Analysis Across Multiple Data Sets and Selection of Target Network Ecologies with Capacity to Sporulate

[0744] One can select Network Ecologies and/or Network Class Ecologies as lead targets by defining networks with a specific biological function or activity such as sporulation. Networks Ecologies or Network Class Ecologies are first selected as described above. In one example, all Network Ecologies or Network Class Ecologies that contain at least one OTU that is capable of forming spores are targeted. In another example, all Network Ecologies or Network Class Ecologies that contain at least one OTU that is capable of forming spores, and that are comprised of at least 50%, 75%, or 100% Keystone OTUs are targeted. Keystone OTUs are selected as described above. OTUs are defined as spore formers using either phenotypic assays (see e.g. Stackebrandt and Hippe. Taxonomy and Systematics. In Clostridia. Biotechnology and Medical Applications.) or genetic assays (see e.g. Abecasis A B, Serrano M, Alves R, Quintais L, Pereira-Leal J B, and Henriques A O. 2013. A genomic signature and the identification of new sporulation genes. J. Bacteriol.; Paredes-Sabja D, Setlow P, and Sarker M R. 2011. Germination of spores of Bacillales and *Clostridiales* species: mechanisms and proteins involved. Trends Microbiol. 19: 85-94).

[0745] Clade membership of bacterial OTUs is based on 16S sequence data. Clades are defined based on the topology of a phylogenetic tree that is constructed from full-length 16S sequences using maximum likelihood methods familiar to individuals with ordinary skill in the art of phylogenetics. Clades are constructed to ensure that all OTUs in a given clade are: (i) within a specified number of bootstrap supported nodes from one another, and (ii) within 5% genetic similarity. OTUs that are within the same clade can be distinguished as genetically and phylogenetically distinct from OTUs in a different clade based on 16S-V4 sequence data, while OTUs falling within the same clade are closely related. OTUs falling within the same clade are evolutionarily closely related and may or may not be distinguishable from one another using 16S-V4 sequence data. Members of the same clade, due to their evolutionary relatedness, play similar functional roles in a microbial ecology such as that found in the human gut. Compositions substituting one species with another from the same clade are likely to have conserved ecological function and therefore are useful in the present invention. All OTUs are denoted as to their putative capacity to form spores and whether they are a Pathogen or Pathobiont (see Definitions for description of "Pathobiont"). NIAID Priority Pathogens are denoted as 'Category-A', 'Category-B', or 'Category-C', and Opportunistic Pathogens are denoted as 'OP'. OTUs that are not pathogenic or for which their ability to exist as a pathogen is unknown are denoted as 'N'. The 'SEQ ID Number' denotes the identifier of the OTU in the Sequence Listing File and 'Public DB Accession' denotes the identifier of the OTU in a public sequence repository. For SEQ ID NOs referenced in Table 1, reference is made to e.g., WO2014/121304, which is incorporated by reference herein in its entirety.

Example 31

Selection of Patients and Method for Specimen Collection

[0746] Paired stool samples and blood specimens are collected and stored weekly over the course of the transplant hospitalization including prior to conditioning, as well as on days 0, 7, 14, 21, 30, 60, and 100. For Chronic GVHD, samples are collected post GVHD at day 105, day 120, day 180.

[0747] Skin, lung, vaginal and oral samples are obtained as well pre- and post-transplant. Intestinal biopsies samples are saved from patients subjected to such analysis. Stool samples from patients are stored at 4° C. for <24 h before eezing at −80° C. GVHD is diagnosed clinically, confirmed pathologically by biopsy whenever possible, and classified according to standard criteria. Patients are evaluated for acute GVHD based on historical consensus criteria as described previously (see Rowlings P A, Przepiorka D, Klein J P, et al. IBMTR Severity Index for grading acute graft-versus-host disease: retrospective comparison with Glucksberg grade. *Br J Haematol.* 1997). Cases of GVHD are further categorized by treatment with or without systemic steroids (prednisone or methylprednisolone, 0.5 mg/kg daily or higher). Cause of death is determined using a standard algorithm where outcomes are prioritized in the following order: 1) primary disease recurrence, 2) graft failure, 3) GVHD, 4) infection, and 5) organ failure. Thus in patients without disease recurrence or graft failure, those who are being treated for GVHD at the time of death are considered to have succumbed to GVHD-related mortality, including those who died from infections.

Example 32

Cross Niche Analysis of Microbiome

[0748] DNA is extracted from samples from various sites—gut, blood, lung, vaginal, oral and skin. Extracted DNA is

subjected to 16S, ITS or 18S sequencing as described elsewhere. Nucleic acid sequences are analyzed to define taxonomic assignments using sequence similarity and phylogenetic placement methods or a combination of the two strategies. These methods map a sequence read to a reference database and selecting the match with the best score and e-value. Common databases include, but are not limited to the Human Microbiome Project, NCBI non-redundant database, Greengenes, RDP, and Silva for taxonomic assignments. Microbial clades are assigned using databases including but not limited to MetaPhlAn. Phylogenetic abundance comparisons are performed using linear discriminant analysis (LDA) effect size (LEfSe) analysis, using a logarithmic LDA cutoff of 2.0. Taxonomic and phylogenetic abundance data from various niches is then subjected to comparative analysis to identify microbes that are unique to each site vs those that overlap between two or more sites.

Example 33

Selection of Microbes to be Used for Mitigating GVHD and Other Immune Based Diseases Based on Microbiome Analysis

[0749] Candidate microbes to be used for mitigating GVHD and other immune based disorder are selected based on microbiome analysis of samples from single or multiple niche. For example, microbes that are highly abundant in patients who do not succumb to GVHD or are alive post bone marrow transplantation are associated with low or no GVHD incidence and survival post GVHD. These microbes could be abundant at a single site such as the gut. Alternatively, these microbes are also abundant at another site in addition such as the skin, lung, vagina and oral or at all of these sites within a diseased subject. Alternatively, microbes are selected based on their abundance at one site such as the gut and not at other sites. These microbes are then tested in in vitro and in vivo models to test their ability to inhibit inappropriate immune responses and reduce inflammation at multiple disease target sites such as but not limited to gut, liver, kidney, lung and skin.

Example 34

Selection of a Metabolically Altered Organism Based on Prebiotic Fermentation

[0750] Bacterial isolates or evolved laboratory strains are inoculated in 25 ml of Versa TREK REDOX 2 broth (Trek Diagnostic Systems) supplemented with 30% sterile-filtered cow rumen fluid and prebiotic of interest incubated under anaerobic conditions for 2 days at 37° C. Following incubation, cultures are centrifuged at 6000 rpm for 10 min. Supernatants, uninoculated medium, or standards of short chain fatty acids (e.g., acetate, propionate, butyrate (Sigma-Aldrich) are injected into a Perkin Elmer Autosystem XL Gas Chromatograph containing a Supelco packed column (Sigma-Aldrich) according to the manufacturer's protocol (Dairy One Cooperative) (Foditsch C et al., 2014. Isolation and Characterization of *Faecalibacterium prausnitzii* from Calves and Piglets. PLoS One. 9(12): e116455). Bacterial isolates are selected with maximal short chain fatty acid (e.g., butyrate) production. Similar kind of analysis is done to access impact of prebiotics on other bacterial metabolite production such as but not limited to secondary bile acids.

Example 35

Mouse Model to Study the Impact of Microbiome in Acute Graft Versus Host Disease

[0751] A number of experimental models for studying acute GVHD exist and involve the transplantation of T-cell-depleted bone marrow supplemented with varying numbers and phenotypic classes of donor lymphocytes (either splenocytes or lymph node T cells) into lethally irradiated recipients. The severity of aGvHD depends on several factors—1) the dose and type of T-cell subsets (i.e. CD4+, CD8+ or TReg cells), 2) Irradiation dose, 3) Genetic disparities (MHC, miHAs), 4) Variation in environmental pathogens between labs and in mice from different suppliers. Allogeneic GVHD mouse models can be MHC-mismatched and miHA-mismatched. The more recently developed xenogeneic GVHD mouse models involve transplantation of human cells into immunodeficient mice. Both these models are extensively in Schroeder and DiPersio, 2011 *Disease Models & Mechanisms.*

[0752] To study the impact of microbiome on acute GVHD using the allogeneic GVHD mouse models, recipient mice such as BALB/c (H2d) or C57BL/6 (H2b) mice are treated with a gut-decontaminating antibiotic cocktail (ampicillin and vancomycin) to mimic microbiota injury that occurs in allo BMT patients. Mice are then exposed to a myeloablative dose of total body irradiation (TBI, 11 Gy) and then transplanted by intravenous injection with bone marrow and purified T cells from fully MHC-mismatched C57/B16 (H2b) or B10.BR mice respectively. Alternatively, xenogeneic GVHD mouse models are utilized where the immunodeficient NOD.scid (IL-2Rγc)−/− (NOG) or NOD.scid (Il2rgmut) (NSG) mice are treated with a gut-decontaminating antibiotic cocktail (ampicillin and vancomycin), transplanted with human PBMCs by I.V. or I.P. injection and subsequently exposed to a myeloablative dose of total body irradiation (2.5 Gy).

Example 36

Murine Model to Study the Impact of Microbiome in Chronic Graft Versus Host Disease

[0753] Current mouse models of cGvHD (Schroeder and DiPersio, 2011) can be broadly divided into sclerodermatous (pro-fibrotic) models, autoantibody-mediated (lupus-like) models and a more recently reported model in which thymic function is defective (Sakoda et al., 2007; Chu and Gress, 2008). Herein is an example with a validated sclerodermatous (pro-fibrotic) models model. Recipient mice BALB/c (H2d) or C57/B16 (H2b) are treated with a gut-decontaminating antibiotic cocktail (ampicillin and vancomycin) to mimic microbiota injury that occurs in allo BMT patients. Mice are then exposed to a myeloablative dose of total body irradiation (700-900 cGy ore 900-1100 cGy respectively) and then transplanted by intravenous injection with bone marrow and purified T cells or splenocytes from B10.D2 (H2c) or LP/J (H2b) mice respectively.

Example 37

Culturing and Banking Bacterial Isolates from Mouse or Human Feces

[0754] Entire stool specimens are collected and homogenized in 1-3 volumes of 0.05% peptone using a sterile stain-

less steel blender with 1-3 volumes of peptone. Approximately 1 gram of the specimen is serially diluted (10-fold) in pre-reduced, anaerobically sterilized (PRAS) dilution blanks (Anaerobe Systems). A separate ~1 gram aliquot is weight, dried in a vacuum over, and re-weighed in order to calculate counts on a dry-weight basis. To select for *Clostridiales* bacteria, including *Blautia* species, 100 μL of the homogenized stool sample dilution series is plated on Brain-Heart Infusion blood agar (SBA, Becton Dickinson) supplemented with 4 pig/mL trimethoprim (Sigma Chemical) and 1 μg/mL sulfamethoxazole (Sigma), *Brucella* Blood Agar (BAP, Anaeobe Systems), CDC ANA blood agar, (BBL Microbiology Systems), and egg yolk agar (EYA, Anaerobe Systems) (Finegold S M, Molitoris D, Song Y, Liu C, Vaisanen M L, Bolte E, McTeague M, Sandler R, Wexler H, Marlowe E M, Collins M D, Lawson P A, Summanen P, Baysallar M, Tomzynski T J, Read E, Johnson E, Rolfe R, Nasir P, Shah H, Haake D A, Manning P, Kaul A, 2002. Gastrointestinal microflora studies in late-onset autism. Clin Infect Dis 1:35). To select for spore-formers, the dilutions may be heated at 70-80 C for 10-20 minutes and plated in the same manner as the non-heated homogenized stool samples. After 5 days of growth at 37 C in an anaerobic chamber, single colonies are selected. The colony purification process is repeated by restreaking select single colonies, growing as described above, and selecting again for single colonies. Single colonies are frozen in 15%-25% glycerol in 1 mL cryotubes and stored at −80° C.

Example 38

Administration of Bacterial Isolates, with or without Prebiotics, to Mitigate Experimental Acute GVHD

[0755] BALB/c (H2d) or C57BL/6 mice in the case of allogeneic models and NOD.scid (IL-2Rγc)−/− (NOG) or NOD.scid (Il2rgmut) (NSG) in the case of xenogeneic models are treated with oral vancomycin and ampicillin. Following decontamination, mice are housed in autoclaved conditions (caging, bedding, water and food) to eliminate nearly all endogenous bacteria present within the flora of mice. Mice are then treated by gavage with a liquid suspension of the cultured bacterial isolate, optionally with one or more prebiotic carbohydrates. Mice are then exposed to a myeloablative dose of total body irradiation and then transplanted by intravenous injection with bone marrow and purified T cells from fully MHC-mismatched C57/B16 (H2b) or B10.BR mice for allogeneic models and human PBMCs for xenogeneic models. Effect on organ pathology, weight and overall survival is measured as described.

Example 39

Administration of Bacterial Isolates, with or without Prebiotics, to Mitigate Experimental Chronic GVHD

[0756] Recipient mice BALB/c (H2d) or C57/B16 (H2b) are treated with a gut-decontaminating antibiotic cocktail (ampicillin and vancomycin). Following decontamination, mice are housed in autoclaved conditions (caging, bedding, water and food) to eliminate nearly all endogenous bacteria present within the flora of mice. Mice are then treated by gavage with a liquid suspension of the cultured bacterial isolate in addition to one or more prebiotic carbohydrates. Mice are then exposed to a myeloablative dose of total body irradiation and then transplanted by intravenous injection with bone marrow and purified T cells or splenocytes from B10.D2 (H2c) or LP/J (H2b) mice respectively. Mice are evaluated for fibrotic changes in the dermis, which can involve the lung, liver and salivary glands beginning day 30 post transplantation.

Example 40

GVHD Clinical and Histological Scoring

[0757] Mice are monitored daily for survival and weekly for GVHD clinical scores (see Cooke, K. R., L. Kobzik, T. R. Martin, J. Brewer, J. Delmonte Jr. J. M. Crawford, and J. L. Ferrara. 1996. An experimental model of idiopathic pneumonia syndrome after bone marrow transplantation: I. The roles of minor H antigens and endotoxin. Blood. 88:3230-3239). Small intestine, large intestine, and liver samples are evaluated histologically for evidence of GVHD and scored as previously described (see Hill, G. R., J. M. Crawford, K. R. Cooke, Y. S. Brinson, L. Pan, and J. L. Ferrara. 1997. Total body irradiation and acute graft-versus-host disease:the role of gastrointestinal damage and inflammatory cytokines. Blood. 90:3204-3213).

Example 41

Measuring Paneth Cell Numbers and Functionality

[0758] The small intestinal lumens of adult mice are rinsed with ice-cold water and segmented. Crypts are eluted by first turning the segments inside out and then shaking them in PBS containing 30 mM EDTA and lacking Ca^{2+} and Mg^{2+}. The eluted villi and crypts are pelleted at 700×g, resuspended in PBS, and transferred to siliconized microfuge tubes using capillary pipettes. The crypts are resuspended in iPIPES buffer (10 mM PIPES (pH 7.4) and 137 mM NaCl) in preparation of exposure to secretory stimuli.

[0759] Crypts are incubated in 30 μl of iPIPES containing 1000 bacterial (*Clostridiales*) CFU per crypt for 30 min at 37° C. Cellular components are pelleted by brief centrifugation, and supernatants transferred to sterile microfuge tubes and stored at −20° C. This method may be scaled up using up to ~3000 crypts in 2 ml iPIPES (plus or minus *Clostridiales* bacteria). Crypts are pelleted and 10 μL of the supernatants are analyzed for bactericidal activity against Clostriales and *Enterococcus* bacteria in liquid culture or on agar plates. Proteins are extracted from the rest of the supernatant as well as the crypts using 30% acetic acid. Total protein extracted from each fraction was resolved by AU-PAGE and subjected to western blot analysis using anti-cryptdin-1 as follows. Proteins from AU-PAGE are transferred to a nitrocellulose membrane. The membrane is then blocked with 5% skim milk, incubated sequentially with anti-rabbit mouse cryptdin-1 (1:500), horseradish peroxidase-conjugated anti-rabbit IgG (1:20,000) and chemiluminescent substrate (SuperSignal, Pierce, Rockland, Ill.), and visualized (Ayabe T, Satchell D P, Wilson C L, Parks W C, Selsted M E, Ouellette A J, 2000. Secretion of microbicidal α-defensins by intestinal Paneth cells in response to bacteria. Nature Immunology 1:113-118).

Example 42

Measuring Intestinal Crypt Regeneration by Organoid Growth

[0760] Organoid formation may be used as a proxy for intestinal crypt regeneration as follows:

[0761] Lgr5-EGFP-IRES-CreERT2 knock-in (B6.129P2-Lgr5tm1(cre/ERT2)Cle/J, JAX mice #008875) and ROSA26-

tdTomato (B6.Cg-Gt(ROSA)26Sortml4(CAG-tdTomato) Hze/J, JAX mice #007914) mice are purchased from the Jackson Laboratory (Bar Harbor, Me., USA) and crossed to produce Lgr5-EGFP-IRES-CreERT2/ROSA26-tdTomato mice (LRT mice). The obtain persistent labeling of Lgr5+ stem cells with tdTomato (as well as tdTomato-labeled progeny of Lgr5+ stem cells), the LRT mice are administered 4-hydroxytamoxifen (4-OHT; Sigma Aldrich) intraperitoneally, once, at 10-20 days old.

[0762] To obtain single crypt cells for in vitro analyses, the LRT mice are sacrificed at 3-5 weeks old, and the duodenum and jejunum (10 cm from the stomach) are harvested and rinsed three times with cold phosphate-buffered saline (PBS−). The intestinal tubes are opened longitudinally and the villi are scraped using a coverslip, then washed three times in cold 1×PBS−. The intestinal tubes are cut into 2-3 mm pieces and suspended and extensively washed in 1×PBS−+2% fetal bovine serum (FBS). Then, the 2-3-mm pieces are treated with 50 mM EDTA/1×PBS− for 30 min at 4° C. on a rocking platform to dissociate the crypts from the intestinal tubes. The dissociated crypts are passed through a 70-μm cell strainer, washed once with 1×PBS−, and treated with TrypLE Express (Life Technologies, Carlsbad, Calif., USA) for 30 min at 37° C. Then, the dissociated cells are passed through a 40-μm strainer and subsequently, through a 20-μm strainer. The strained cells are pelleted, resuspended in 1×PBS−+2% FBS, and used as single crypt cells.

[0763] The isolated single crypt cells are cultured in organoid medium [advanced DMEM/F12 supplemented with 1×GlutaMAX, 10 mM HEPES, 1× penicillin/streptomycin, 1×N2, 1×B27 (all obtained from Life Technologies, Carlsbad, Calif., USA), N-acetylcysteine (Sigma-Aldrich, St Louis, Mo., USA, 1 mM), murine epidermal growth factor (Life Technologies, Carlsbad, Calif., USA, 50 ng/ml), murine Noggin (Peprotech, Rocky Hill, N.J., USA, 100 ng/ml), and murine R-Spondin I (R&D Systems, Minneapolis, Minn., USA, 1 pig/ml)]. During the first two days of culturing 10 μM of Rho kinase inhibitor Y-27632 (Sigma-Aldrich, St Louis, Mo., USA) is added.

[0764] 350 μM of organoid medium is added into wells of 48-well plates, and then single crypt cells are plated to the wells (1×105 cells/10 μl 1×PBS−+2% FBS per well). Matrigel (BD, Franklin Lakes, N.J., USA) is added to a final concentration of 10%. The organoid medium is replenished every day for the first 3 days and every 2-3 days thereafter. The cells are incubated in a humidified CO2 incubator at 37° C. After 12 days, the number of organoids is counted by phase-contrast microscopy with a 4× objective (Yamauchi M, Otsuka K, Kondo H, Hamada N, Tomita M, Takahashi M, Nakasono S, Iwasaki T, Yoshida K, 2014. A novel in vitro survival assay of small intestinal stem cells after exposure to ionizing radiation. J Radiat Res. 55:381-390).

[0765] To investigate organoid growth over time, time-lapse microscopy is performed using a confocal laser microscope (C1si, Nikon, Japan) and images are analyzed using ImageJ software (National Institutes of Health, Bethesda, Md., USA).

Example 43

Measuring Intestinal Crypt Regeneration by Quantitative Real Time PCR

[0766] Alternatively, C57BL/6J mice may be used to study intestinal regeneration using a real time PCR (qPCR) method. Duodenum and jejunum are harvested as described in Example 20 and cut into 1 cm small pieces. The tissue pieces are placed in a FastPrep-24 Lysing Matrix D tubes (MP Biomedicals, Solon, Ohio) filled with 600 μL of RLT lysis buffer (Qiagen, Valencia, Calif.). Next, 6 μL β-mercaptoethanol (Sigma-Aldrich, St. Louis, Mo.) is added to the lysing tubes. And total RNA is isolated from the lysed samples using the Qiagen RNeasy Mini Kit according to the manufacturer's instructions. Complimentary DNA is made using a High Capacity cDNA Reverse Transcription Kit (Applied Biosystems, Foster City, Calif.) according to the manufacturer's instructions. qPCR is performed on cDNA samples in triplicate using an Applied Biosystems StepOne Plus system. Individual probes for Lgr5(Mm00438890_m1), Ascl2 (Mm01268891_g1), Bmi1 (Mm03053308_g1), Olfm4 (Mm01320260_m1), and mTert(Mm01352136_m1) from Applied Biosystems are used and data analyzed using a relative standard curve method normalized to β-actin (Mm00607939_s1; Applied Biosystems). Actively cycling intestinal stem cells are labeled by Lgr5, Ascl2, and Olfm4, whereas slowly cycling (quiescent) intestinal stem cells are labeled by mTert and Bmi1 (Dehmer J J, Garrison A P, Speck K E, Dekaney C M, Van Landeghem L, Sun X, Henning S J, Helmrath M A, 2011. Expansion of intestinal epithelial stem cells during murine development. PLoS One. 6:e27070).

Example 44

Measurement of Transepithelial Electrical Resistance

[0767] The following protocol is preferentially used for monocultures of intestinal epithelial cells but may also be applied to epithelial cells derived from other organs such as the vagina or liver. Monolayers of epithelial cells (e.g., Caco-2) are obtained from the ATCC or from patient biopsy and maintained in Dulbeco's Modified Eagle Medium with 10% fetal bovine serum or RPMI 1640 with 10% fetal bovine serum.

[0768] A monolayer is formed by seeding epithelial cells grown to 80-90% confluency (~10^5 cells/cm2) on transwell plates (Corning) and incubating the plates between at 37° C. and 5% CO2. The cells are incubated for 10 days, during which they are fed with fresh medium (basolaterally and/or apically) every other day. The integrity of the cell layer is assessed by transepithelial electrical resistance (TEER) using Millicell-ERS equipment (Millipore) and a World Precision Instruments probe (WPI according to the manufacturers' instructions.

Example 45

Dye-Based Evaluation of Epithelial Integrity

[0769] Cells from ATCC or patient biopsy are treated as in Example 43. Instead of measuring TEER, the transwell plates are disassembled and each filter well is treated with 75 μL 100 μg/mL of the non-membrane permeable dye Lucifer Yellow (Sigma) in Hank's Buffered Salt Solution (HBSS) buffer, pH 7.4 (Invitrogen). Next, 250 μL of HBSS buffer, pH 7.4 is added to the bottom wells and the transwell plates are reassembled and then incubated for 2 hours with shaking (60 rpm) at room temperature. Lucifer yellow fluorescence is measured using a Cytofluor II fluorometer at an excitation wavelength of 485 nm and an emission wavelength of 530 nm Permeability is calculated based on the percentage of Lucifer

Yellow that leaked from the apical chamber to the basolateral chamber of the transwell plates.

Example 46

Method for Measuring Intestinal Permeability Based on Citrulline Production by Enterocytes

[0770] Recently, it was shown that citrulline appeared to be particularly useful to detect gut damage, as blood concentrations of this amino acid directly reflect functioning small intestinal cell mass (Crenn P, Vahedi K, Lavergne-Slove A, Cynober L, Matuchansky C, Messing B. Plasma citrulline: a marker of enterocyte mass in villous atrophy-associated small bowel disease. Gastroenterology 2003). Blood is collected in heparin from each patient through the central venous catheter before starting therapy and on each Monday, Wednesday and Friday thereafter until discharge. Plasma is prepared and stored at −80 1 C for later analysis. Citrulline concentrations (mM) are measured by a standard procedure for determining amino acid concentrations using high-performance liquid chromatography (Shimadzu, Kyoto, Japan) as described in Herbers et al., 2008. Bacteraemia coincides with low citrulline concentrations after high-dose melphalan in autologous HSCT recipients. Bone Marrow Transplant. 42:345-349.

Example 47

Method for Measuring Levels of Microbes in Distal Organs (Liver, Thymus, Lungs, Kidneys)

[0771] Liver, thymus, lungs, and kidneys from mice that had received transplants are removed aseptically and homogenized in 200 uL sterile saline 0.9%. Then, 100 uL is cultured aerobically on blood agar and deMan-Rogosa-Sharp agar plates (Difco, Detroit, Mich.), blood agar supplemented for anaerobes, chocolate blood agar, MacConkey agar, and Sabouraud agar for 24 hours in room air supplemented with 10% C02; colony-forming units are counted and numbers adjusted to weight. Alternatively, genomic DNA from the bacteria is extracted and 16S rDNA sequencing is performed as described

Example 48

Method for Measuring Effect of Microbes, with or without Prebiotics, on Bacterial Metabolites Such as SCFA Levels

[0772] Short-chain fatty acids (SCFA), which are produced by many bacteria as a byproduct of carbohydrate fermentation. SCFA have been found to be important modulators of the immune system. They are abundantly produced bacteria from the Class Clostridia. To evaluate the effect of administered bacterial composition, optionally with one or more prebiotics, on SCFA, fecal pellets are collected to quantify SCFA levels, particularly acetate, propionate, or butyrate. SCFAs, creatines, and hydroxy-SCFAs are quantified by alkalinizing stool samples, obtaining fingerprints of the metabolic composition of the sample using 1D 1H NMR on a Bruker Avance-600 MHz Spectrometer, and analyzing with supervised multivariate statistical methods using Chenomx NMR Suite software.

Example 49

Administration of Bacterial Metabolites Such as SCFA to Mitigate GVHD

[0773] Sodium acetate (150 mM) is delivered via the drinking water of mice beginning 2 weeks prior to BMT. Mice are then irradiated and transplanted with continued supplementation of sodium acetate. Mice are euthanized to evaluate for pathological evidence of GVHD, as well as to quantify and characterize large intestinal Tregs and alloreactive effector T cells by surface staining or intracellular staining followed by flow cytometry on days 14 and 28.

Example 50

Extraction and Purification of Immunomodulatory Oligosaccharides from Plants

[0774] Store-bought plants are cut, lyophilized, and ground into powder. The powder (~500 grams) is extracted three times with 2 L of ethanol, and the concentrated extract was collected, lyophilized, and resuspended with 1 L of distilled water at 85° C. The water-soluble portion is precipitated by four volumes of ethanol at 4° C. to yield polysaccharides. Peptides are removed from this sample by treating with Pronase (Roche Applied Science). The resulting sample is run over a Bio-Gel P-6 gel filtration column (1.5×90 cm) and eluted with distilled water containing 0.02% sodium azide at a flow rate of 0.5 ml/min. All chromatographic fractions containing carbohydrates are analyzed by a phenol-sulfuric acid method (e.g., Masuko T, Minami A, Iisaki N, Majima T, Nishimura S-I, Lee Y C, 2005. Carbohydrate analysis by a phenol-sulfuric acid method in microplate format. 339:69-72) and quantitated by measuring the optical density at 490 nm (Tsai C-C, Lin C-R, Tsai H-Y, Chen C-J, Li W-T, Yu H-M, Ke Y-Y, Hsieh W-Y, Chang C-Y, Wu C-Y, Chen S-T, Wong C-H, 2013. The Immunologically Active Oligosaccharides Isolated from Wheatgrass Modulate Monocytes via Toll-like Receptor-2 Signaling. 288:17689-17697).

Example 51

Selection of Oligosaccharides to Augment Gut Microbiome

[0775] The ability of bacterial isolates to grow on a panel of simple and complex carbohydrates is evaluated using a phenotypic array whose composition has been previously described previously (Martens E C, Lowe E C, Chiang H, Pudlo N A, Wu M, et al. 2011. Recognition and degradation of plant cell wall polysaccharides by two human gut symbionts. PLoS Biol 9: e1001221). Growth measurements are collected in duplicate over the course of 3 days at 37° C. under anaerobic conditions. A total of three independent experiments are performed for each species tested (n=6 growth profiles/substrate/species). Total growth (A_{tot}) is calculated from each growth curve as the difference between the maximum and minimum optical densities (OD_{600}) observed (i.e., $A_{max}-A_{min}$). Growth rates are calculated as total growth divided by time ($A_{tot}/(t_{max}-t_{min})$), where tmax and tmin correspond to the time-points at which Amax and Amin, respectively, are collected.

Example 52

Administration of Carbohydrates to Mitigate Experimental GVHD

[0776] Carbohydrates such as xylose are delivered via the drinking water of mice beginning 2 weeks prior to BMT. Mice are then irradiated and transplanted with continued supplementation of xylose. Mice are euthanized to evaluate for pathological evidence of GVHD, as well as to quantify and characterize large intestinal Tregs and alloreactive effector T cells by surface staining or intracellular staining followed by flow cytometry on days 14 and 28. This method may be applied monosaccharides, disaccharides, oligosaccharides, polysaccharides, and mixtures thereof.

Example 53

Preventing Graft Versus Host Disease in a Subject

[0777] To determine efficacy in preventing GVHD, subjects undergoing allogeneic hematopoietic stem cell transplantation are selected. GVHD prophylactic regimen is administered on day −1, where day 0 is day of transplantation or day −1 plus day 17. One arm of the study includes the test article, second arm test article plus standard of care and the third arm is standard of care alone. Standard GVHD prophylaxis consists of cyclosporine twice a day starting on day −1 with target trough levels >200 ng/mL in combination with short course of methotrexate (15 mg/sqm on day +1 and 10 mg/sqm on days +3 and +6). Most patients transplanted from unrelated donors received anti-T-cell globulin (ATG Fresenius) at a low dose of 5 mg/kg on days −3 to −1. To estimate the prophylactic and therapeutic effect of test article, the patients are carefully monitored and documented for the presentation of acute and chronic GVHD symptoms, the time of onset, the severity of the symptoms, the responsiveness to treatment, and the occurrence of infections. Stool and blood samples are collected at pretreatment, day 4, day 14, day 28, 3 months, and 6 months.

Example 54

Treating Acute Graft Versus Host Disease in a Subject

[0778] To determine the efficacy of treating acute GVHD, test article is administered to a subject with clinical signs of acute GVHD as described elsewhere. Test article is orally administered daily either alone or in conjunction with standard of care. At the time of test article administration, subjects are at least 10 days post allogeneic hematopoietic cell transplantation, have GI symptoms consistent with Grade II GVHD, and have endoscopic evidence of GVHD. The diagnosis of GVHD is confirmed by biopsy of the intestine (esophagus, stomach, small intestine, or colon) or skin. Stool, blood and other samples are collected prior to administration of test article day −2 and day +1, day +7 and Day +10. To evaluate therapeutic effect of test article, the patients are carefully monitored and documented for the presentation of acute GVHD symptoms, the severity of the symptoms, the responsiveness to treatment, and the occurrence of infections.

Example 55

Treating Chronic Graft Versus Host Disease in a Subject

[0779] Chronic GVHD presents anytime starting day 100 post bone marrow transplantation. Conventional treatment of chronic GVHD requires prolonged periods of systemic immunosuppressive therapy with potent drugs such as corticosteroids and cyclosporine. Agents such as mycophenolate mofetil, rapamycin (sirolimus), imatinib and rituximab are used in patients with steroid-refractory chronic GVHD. To determine the efficacy of treating chronic GVHD, test article is administered to a subject with clinical signs of chronic GVHD as described elsewhere. Test article is orally administered daily either alone or in conjunction standard of care. At the time of test article administration, subjects are at least 100 days post allogeneic hematopoietic cell transplantation, have symptoms consistent with chronic GVHD.

Example 56

Immunomodulation of Autologous BMT Recipients

[0780] Subjects undergoing autologous hematopoietic stem cell transplantation are selected. Test article is administered on day −1, where day 0 is day of transplantation or day −1 plus day 17. Subjects are monitored clinical signs of infections, functionality of organs as well as success of graft uptake or engraftment. Engraftment is measured by assessing graft versus tumor effect. Other outcomes that are measured include neutropenic recovery which is assessed by measurement total blood counts.

Example 57

Prevention Solid Organ Transplant Rejection in a Rat Model

[0781] Recipient LBN rats ranged in weight from 325 to 350 grams. ACI donor weights ranged from 200-250 grams. Test article is administered to rats using oral gavage. The treatment started the day before transplant and the entire treatment period ranged from 12 to 27 days. Control rats received saline. Twenty four hours after test article administration, the heterotopic heart transplant is performed. The hearts are transplanted using a modification of the technique of Ono and Lindsey (J. of Thoracic and Cardiovascular Surgery, 57, 225-229 (1969). The rats are palpated daily and asystole defined the day of rejection.

Example 58

Immunomodulation of Solid Organ Transplant Recipients

[0782] Here is a method of preventing graft rejection in a recipient of a transplanted solid organ, by administering to said mammalian recipient an effective graft rejection preventative amount of test article. Transplanted solid organ may include a kidney, heart, skin, a lung, a liver, a pancreas, an intestine, an endocrine gland, a bladder, or a skeletal muscle. Test article is administered pre-transplant at least 24 hours before transplant and after transplant beginning 24 hours after transplant and then on day 3, day, 5 and day 15. Patients are closely monitored for clinical signs and symptoms of transplant rejection as well as complications such as infections. Stool and blood samples are collected before transplantation, day 3, day 5, day 15 and day 21 and subsequently subjected to microbiome analysis. Immune response is monitored by clinical symptoms as well as biochemical analysis of the serum such as measurement of cytokine levels.

Example 59

Inhibition of Antigen Presenting Cells

[0783] Peripheral blood mononuclear cells (PBMC) are prepared by density gradient centrifugation on Ficoll-Paque (Pharmacia). Aliquots of cells are frozen in 90% FCS with 10% DMSO and stored in liquid nitrogen. After thawing, the cells are ished twice with MSC medium (DMEM with low glucose and 10% FCS) and re-suspended in assay medium (ISCOVE'S with 25 mM Hepes, 1 mM sodium pyruvate, 100 μM non-essential amino acids, 100 U/ml penicillin, 100 μg/ml streptomycin, 0.25 μg/ml amphotericin B, 5.5×10^{-5}M 2-mercaptoethanol (all reagents from GibcoBLR) and 5% human AB serum (Sigma, MLR tested)). To prepare monocyte derived dendritic cells (moDCs), PBMCs are plated and adherent fraction is enriched for a. CD11c+ DCs by CD11c MACS sorting. Microbes or microbes preincubated with prebiotics or microbial metabolites to be tested are incubated with CD11c+moDCs for 4-10 h. Following incubation period, effect of DC maturation is measured by staining and FACS analysis by looking at markers such as CD40, CD80, CD86 PD-L1 and PD-L2. Endocytic capacity is measured by FITC-dextran incubation followed by FACS analysis). Cytokine production e.g. IL-10, IL-4, IL-12 is analyzed by ELISA or intracellular staining. Effect on naïve T cell stimulation is analyzed by co-cultured by the moDCs preincubated with test article with naïve T cells isolated from PBMCs as described. T cell activation status is analyzed by surface staining followed by FACS analysis for CD3, CD4, CD25.

Example 60

Inhibition of Alloreactivation by a Microbial Composition Using Mixed Lymphocyte Reaction (MLR) Assays In Vitro

[0784] Peripheral blood mononuclear cells (PBMC) are prepared by density gradient centrifugation on Ficoll-Paque (Pharmacia). Aliquots of cells are frozen in 90% FCS with 10% DMSO and stored in liquid nitrogen. After thawing, the cells are ished twice with MSC medium (DMEM with low glucose and 10% FCS) and re-suspended in assay medium (ISCOVE'S with 25 mM Hepes, 1 mM sodium pyruvate, 100 μM non-essential amino acids, 100 U/ml penicillin, 100 μg/ml streptomycin, 0.25 μg/ml amphotericin B, 5.5×10^{-5}M 2-mercaptoethanol (all reagents from GibcoBLR) and 5% human AB serum (Sigma, MLR tested)). To prepare the T cell-enriched fraction, PBMCs from donor X are depleted of monocytes and B cells by immunomagnetic negative selection. PBMCs are incubated with mouse anti-human CD19 and CD14 mAbs (no azide/low endotoxin (NA/LE) format) followed by biotin-conjugated goat anti-mouse IgG (multiple adsorption) Ab (all reagents from Pharmingen) and streptavidin microbeads (Miltenyi Biotec). Cells are then separated using a magnetic cell sorter (MACS, Miltenyi Biotec). PBMC from donor Y are X-ray irradiated with 3600 rad (12 min at 70 kV) using Cabinet X ray system (Faxitron X ray, Buffalo Grove, Ill.). To prepare monocyte derived dendritic cells (moDCs), PBMCs are plated and adherent fraction is enriched for a. CD11c+ DCs by CD11c MACS sorting. T cells (15×10^6/dish) from donor X are cultured in 10 cm tissue culture dishes with PBMC/moDCs (15×10^6 cells/dish) from donor Y for 7 days. The cells are incubated at 37° C. in 5% CO_2 atmosphere for 7 days. Various concentrations of microbial composition or microbes pre-incubated with sugars are added to T cells activated in the MLR for 3 days at 37° C. in 5% CO_2 atmosphere. In control cultures activated T cells are cultured without any test agent. At the end of co-culture period, T cells are recovered. CD8 cells are depleted by negative immunomagnetic selection with anti-CD8 MicroBeads (Miltenyi Biotec). Aliquots of cells collected before and after depletion are stained with anti-CD4-PE and anti-CD8-APC antibodies (Caltag) and analyzed by FACS. T cell activation status is analyzed by surface staining followed by FACS analysis for CD3, CD4, CD25. Phenotypic analysis for regulatory T cell differentiation is done by surface staining for CD3, CD4, CD25, CD 127 and Foxp3 intracellular staining followed by FACS analysis. Cytokine Analysis for various cytokines including IL-6, TNF-alpha is done by ELISA or BD™ Cytometric Bead Array. To assess T cell proliferation status cultures are pulsed with [H^3]TdR (Amersham) (5 Ci/mmol, 1 μCi/well) for 18 hours immediately after plating, or incubated for 1, 2, 3 or 4 days and then pulsed with [H^3]TdR) for an additional 18 hours. Cultures are collected using Harvester 96 (Tomtec), filters are analyzed using Microbeta Trilux liquid scintillation and luminescence counter (E.G.& G Wallac). To assess T cell proliferation status cultures are pulsed with [H^3]TdR (Amersham) (5 Ci/mmol, 1 μCi/well) for 18 hours immediately after plating, or incubated for 1, 2, 3 or 4 days and then pulsed with [H^3]TdR) for an additional 18 hours. Cultures are collected using Harvester 96 (Tomtec), filters are analyzed using Microbeta Trilux liquid scintillation and luminescence counter (E.G.& G Wallac). To assess effect on cytotoxic capacity of CD8+ cells, at the end of co-culture period, CD8+ cells are sorted by MACS. CD8+ T cells are then co-incubated with target cells such as hepatocytes and ^{51}Cromium for 4-16 h. After incubation period, level of ^{51}Cromium in supernanat is measured to gauge cytotoxic activity.

Example 61

Inhibition of PHA Induced T Cell Proliferation and T Cell Activation by a Microbial Composition Using Mixed Lymphocyte Reaction (MLR) Assays In Vitro

[0785] 5×10^4 T cells are stimulated with PHA (5 μg/ml) and then test article added at various concentrations. Alternatively, T cells are first incubated with test article and then activated with PHA.T cell activation status is analyzed by surface staining followed by FACS analysis for CD3, CD4, CD25. To assess T cell proliferation status cultures are pulsed with [H^3]TdR (Amersham) (5 Ci/mmol, 1 μCi/well) for 18 hours immediately after plating, or incubated for 1, 2, 3 or 4 days and then pulsed with [H^3]TdR) for an additional 18 hours. Cultures are collected using Harvester 96 (Tomtec), filters are analyzed using Microbeta Trilux liquid scintillation and luminescence counter (E.G.& G Wallac).

Example 62

Culturing and Banking Bacterial Isolates from Mouse or Human Feces

[0786] Entire stool specimens are collected and homogenized in 1-3 volumes of 0.05% peptone using a sterile stainless steel blender with 1-3 volumes of peptone. Approximately 1 gram of the specimen is serially diluted (10-fold) in pre-reduced, anaerobically sterilized (PRAS) dilution blanks (Anaerobe Systems). A separate ~1 gram aliquot is weight,

dried in a vacuum over, and re-weighed in order to calculate counts on a dry-weight basis. To select for *Clostridiales* bacteria, including *Blautia* species, 100 μL of the homogenized stool sample dilution series is plated on Brain-Heart Infusion blood agar (SBA, Becton Dickinson) supplemented with 4 μg/mL trimethoprim (Sigma Chemical) and 1 μg/mL sulfamethoxazole (Sigma), *Brucella* Blood Agar (BAP, Anaeobe Systems), CDC ANA blood agar, (BBL Microbiology Systems), and egg yolk agar (EYA, Anaerobe Systems) (Finegold S M, Molitoris D, Song Y, Liu C, Vaisanen M L, Bolte E, McTeague M, Sandler R, Wexler H, Marlowe E M, Collins M D, Lawson P A, Summanen P, Baysallar M, Tomzynski T J, Read E, Johnson E, Rolfe R, Nasir P, Shah H, Haake D A, Manning P, Kaul A, 2002. Gastrointestinal microflora studies in late-onset autism. Clin Infect Dis 1:35). To select for spore-formers, the dilutions may be heated at 70-80 C for 10-20 minutes and plated in the same manner as the non-heated homogenized stool samples. After 5 days of growth at 37 C in an anaerobic chamber, single colonies are selected. The colony purification process is repeated by restreaking select single colonies, growing as described above, and selecting again for single colonies. Single colonies are frozen in 15%-25% glycerol in 1 mL cryotubes and stored at −80° C.

Example 63

Sampling of Human Vaginal Microflora

[0787] The vaginal microflora were collected in duplicate from the left and right sides of the vaginal sidewall using FLOQSwabs® (Copan Diagnostics, USA) (Jacobson J., et al. 2014. Vaginal microbiome changes with levonorgestrel intrauterine system placement. Contraception. 90(2): 130-135). To control for variables that can alter the vaginal microbiome, samples were collected at the same time of a woman's menstrual cycle (i.e., one week into the menstrual cycle) and patients were tested for pregnancy and for recent sexual activity (using a prostate-specific antigen membrane test).

Example 64

Sampling of Human Lung Microflora

[0788] Bronchoscopy was performed using endotracheal tube (Combicath™. KOL Bio-Medical Instruments, USA). Using a syringe, Normal Saline at 1 mg/kg was lavaged into the right middle lobe of the lung. For adult patients. 2-5 mL of bronchoalveolar lavage fluid (BALF) was collected into a sterile sputum trap. For children ages three and older, 2 mL was collected; I mL was collected from children 1-3 years old; 0.5 mL of BALF was collected from children under the age of one. Within ten minutes of sample collection, the sample was transferred from the sterile sputum trap to a sterile container and frozen and stored at −80° C.

Example 65

Preparation of Bacterial Suspension

[0789] A human microbiome sample from stool, saliva, or tissue is obtained from a healthy, normal subjects or subjects suffering from a particular condition which enriches their microbiome for unique and desirable species. The sample is diluted to produce a 10-50% slurry in saline+glycerol solution (0.9% (w/v) NaCl, 10% (w/w) glycerol) and placed in a filter membrane-containing stomaching bag. The material is then homogenized and removed from the filtered side of the bag producing the bacterial suspension. Alternatively, a blender is used and filtering is performed after the blending. A low speed centrifugation step is used as an alternative to filtering to remove the large, non-bacterial components of the suspension. The bacterial suspension is tittered by producing serial dilutions differing by a log and plating on BBA agar and growing at 37 C in anaerobic conditions. Colonies are considered countable at between 10-400 colonies per plate and triplicates are plated for each dilution. The bacterial suspension is flash frozen and stored at −80 C for future use.

[0790] Isolation of Spore Formers

[0791] To isolate the subpopulation of spore formers, the bacterial slurry is treated with 100% ethanol to generate a 50% ethanol slurry for 1 hr. Alternatively a heat treatment of 50 C for 30 minutes is added to inactivate the bacteria that are not capable of forming spores. The 50% ethanol suspension is then pelleted by centrifugation (13,000 rpm for 5 min) and the pellet is washed with equal 10× volume of saline and 10% glycerol 3 times to remove the excess ethanol. The final spore fraction is snap frozen in liquid nitrogen in a solution of injection grade saline and 10% glycerol for subsequent use and stored at −80 C.

[0792] Alternatively, a 10% w/v suspension of human fecal material in PBS is incubated in a water bath at 80 degrees Celsius for 30 minutes. Glycerol is added to a final concentration of 15% and then the enriched spore containing material is stored at −80 degrees Celsius.

[0793] Alternatively, a 10% w/v suspension of human feces in PBS is prepared to contain a final concentration of 0.5 to 2% Triton X-100. After shaking incubation for 30 minutes at 25 to 37 degrees Celsius, the sample is centrifuged at 1000 g for 5-10 minutes to pellet particulate matter and large cells. The bacterial entities are recovered in the supernatant fraction, where the purified spore population is optionally further treated, such as by thermal treatment and/or ethanol treatment as described above.

Example 66

Determining Titer of Bacteria

[0794] Counts of viable bacteria are determined by performing 10-fold serial dilutions in PBS and plating to *Brucella* Blood Agar Petri plates or other applicable solid media known to one skilled in the art (see. e.g. The Manual of Clinical Microbiology ASM Press, 10th Edition or Atlas, Handbook of Microbiological Media, 4th ed, ASM Press, 2010). Plates are incubated at 37 degrees Celsius for 2 days. Colonies are counted from a dilution plate with 50-400 colonies and used to back-calculate the number of viable bacteria in the population. Visual counts are determined by phase contrast microscopy for further morphological identification.

[0795] Alternatively, optical density measurements of bacteria containing media is used to determine a the concentration of bacteria by comparing to a standard curve of known concentrations of bacteria that have previously measured optical densities in culture.

[0796] Bacteria are also isolated and quantified by cell sorting techniques known to one skilled in the art (e.g. see Nebevon-Caron, G., Stephens, P. J. & Hewitt, C. J. Analysis of bacterial function by multi-color fluorescence flow cytometry and single cell sorting. Journal of Microbiological Methods, 2000). With this technique surface antibodies are raised to specific markers of a desired bacteria and they are incubated,

washed, and imaged via flow cytometry to count bacteria in a complex mixture of other bacteria or tissue.

Example 67

FFAB Culturing and Banking Fungal Isolates

[0797] Microbial samples e.g. fecal sample; skin swab sample, are washed and homogenized in PBS. Samples are then serially diluted and fivefold dilutions are spread-plated in triplicate on Sobour and dextrose agar, potato dextrose agar, malt agar, and yeast peptone dextrose (YPD) agar each supplemented with chloramphenicol (40 μg/ml) and kanamycin (50 μg/ml). Alternatively, cultures can be grown in liquid conditions on Sabouraud Dextrose Broth (SDB; EMD chemicals) at 37° C., 30° C. and 20° C. and subsequently plated to enrich for yeast fractions. Plates are incubated both aerobically and anaerobically for 48 hours at 37° C., 30° C., and 20° C. and subsequent colonies are counted. Random colonies are selected with different morphologies and are re-streaked three times to obtain a pure culture. Cultures can then be grown up in liquid culture as described above, placed in 10% glycerol and stored at −80° C. for banking purposes. A sample of culture can be submitted for genetic analysis by extracting DNA and performing 18S and ITS identification as described herein

Example 68

Measurement of Metabolites with Mass Spectrometry

[0798] To determine the prebiotics in a complex media enabling specific growth, fractionation and mass spectrometry techniques are used to identify prebiotics compounds in media responsible for specific growth. Basically, bacteria are grown in media that has been fractionated by HPLC using standard techniques, and fractions are tested for their ability to promote growth. The fractions that promote growth are further fractionated or metabolites in the media are identified using HPLC-MS techniques described below. Furthermore, any metabolomics on tissues, fresh or spent media, blood, or mammalian excretions are determined using methods described herein. Unbiased methods exist to determine the relative concentration of metabolites in a sample and are known to one skilled in the art. Gas or liquid chromatography combined with mass spectrometry demonstrate the amounts and identities of various metabolites in the aforementioned samples and are further validated by obtaining pure metabolites and running on through the same LC-MS systems.

[0799] Gas Chromatography Mass Spectrometry

[0800] Polar metabolites and fatty acids are extracted using monophasic or biphasic systems of organic solvents and an aqueous sample as previously described (Metallo et al., 2012, Fendt et al., 2013). Derivatization of both polar metabolites and fatty acids has been described previously (Metallo et al., 2012). Briefly, polar metabolites are derivatized to form methoxime-tBDMS derivatives by incubation with 2% methoxylamine hydrochloride (MP Biomedicals) in pyridine (or MOX reagent (Thermo Scientific) followed by addition of N-tert-butyldimethylsilyl-N-methyltrifluoroacetamide (MTBSTFA) with 1% tert-butyldimethylchlorosilane (t-BDMCS) (Regis Technologies). Non-polar fractions, including triacylglycerides and phospholipids are saponified to free fatty acids and esterified to form fatty acid methyl esters either by incubation with 2% H2SO4 in methanol or by using Methyl-8 reagent (Thermo Scientific). Derivatized samples are analysed by GC-MS using a DB-35MS column (30 m×0.25 mm i.d.×0.25 μm, Agilent J&W Scientific) installed in an Agilent 7890A gas chromatograph (GC) interfaced with an Agilent 5975C mass spectrometer (MS). Mass isotopomer distributions are determined by integrating metabolite ion fragments and corrected for natural abundance using algorithms adapted from Fernandez et al. (Fernandez et al., 1996).

[0801] Liquid Chromatography Mass Spectrometry of Polar Metabolites

[0802] After extraction, samples are transferred to a polypropylene vial and samples are analysed using a Q Exactive Benchtop LC-MS/MS (Thermo Fisher Scientific). Chromatographic separation is achieved by injecting 2 uL of sample on a SeQuant ZIC-pHILIC Polymeric column (2.1× 150 mm 5 uM, EMD Millipore). Flow rate is set to 100 uL/min, column compartment is set to 25 C, and autosampler sample tray is set to 4° C. Mobile Phase A consists of 20 mM Ammonium Carbonate, 0.1% Ammonium Hydroxide in 100% Water. Mobile Phase B is 100% Acetonitrile. The mobile phase gradient (% B) is as follows: 0 min 80%, 5 min 80%, 30 min 20%, 31 min 80%, 42 min 80%. All mobile phase is introduced into the Ion Max source equipped with a HESI II probe set with the following parameters: Sheath Gas=40, Aux Gas=15, Sweep Gas=1, Spray Voltage=3.1 kV, Capillary Temperature=275 C, S-lens RF level=40, Heater Temp=350 C. Metabolites are monitored in negative or positive mode using full scan or a targeted selected ion monitoring (tSIM) method. For tSIM methods, raw counts are corrected for quadropole bias by measuring the quadropole bias experimentally in a set of adjacent runs of samples at natural abundance. Quadropole bias is measured for all species by monitoring the measured vs. theoretical m1/m0 ratio at natural abundance of all species with m-1, m0, m1, and m2 centred scans. Quadropole bias-corrected counts are additionally corrected for natural abundance to obtain the final mass isotopomer distribution for each compound in each sample.

Example 69

Selection of Oligosaccharides to Augment Gut Microbiome or the Growth of Administered Microbes

[0803] The ability of bacterial isolates to grow on a panel of simple and complex carbohydrates is evaluated using a phenotypic array whose composition has been previously described previously (Martens E C, Lowe E C. Chiang H, Pudlo N A, Wu M. et al. 2011. Recognition and degradation of plant cell wall polysaccharides by two human gut symbionts. PLoS Biol 9: e1001221). Bacteria isolates are removed from a frozen stock and grown in synthetic minimal media overnight and washed in PBS twice to ensure minimal transfer of residual materials. They are then grown in synthetic minimal media with various prebiotic substrates as specified by the manufacturer. Growth measurements [(optical density at 600 nm (OD_{600})] are collected every 30 min in duplicate over the course of 3 days at 37° C. under anaerobic conditions. A total of three independent experiments are performed for each species tested (n=6 growth profiles/substrate/species). Total growth (A_{tot}) is calculated from each growth curve as the difference between the maximum and minimum optical densities (OD_{600}) observed (i.e., $A_{max}-A_{min}$). Growth rates are calculated as total growth divided by time ($A_{tot}/(t_{max}-t_{min})$).

where tmax and t_{min} correspond to the time-points at which A_{max} and A_{min}, respectively, were collected.

[0804] This may be followed by a step to ensure that the selected oligosaccharide(s) promote the growth of the healthy-state gut microbiota and/or the microbe(s) comprising a therapeutic composition without augmenting the growth of microbes associated with an autoimmune or inflammatory disease state. By testing oligosaccharides against a panel of bacteria (individually or in groups) overrepresented in a selected autoimmune or inflammatory condition, a prebiotic that selectively allows enhanced growth of healthy-state bacteria over disease-state bacteria is selected.

Example 70

Validating Selective Prebiotics Enhance the Growth of Bacteria in the Blood of Mammalian Subjects

[0805] Four cohorts of 8, 6-8 week old Balb/c wildtype male mice acquired and fed a normal diet. One cohort is injected with 100 ul of 1E4 CFU/ml of the bacterial composition containing 100 ul 0.1 mg/ml prebiotic mixture, the second cohort is injected with 100 ul of 1E4 CFU/ml of the bacterial composition alone, the third is injected with 100 ul 0.1 mg/ml of a prebiotic mixture and the final cohort serves as a vehicle control cohort injected with vehicle via tail vein. The mice cohorts are then readily bleed at 1 hr, 2 hrs 4 hrs 6 hrs 12 hrs and 24 hrs after the initial administration. At 24 hours gross necropsy is performed and the organs including the lymph nodes, lungs, liver, pancreas, colon, kidneys, esophagus, mammary glands, prostate, bladder, and blood samples are assessed for the amount of the administered bacteria by qPCR primers designed for the bacteria injected. The samples are normalized to the vehicle control and the biodistribution of the bacteria is assessed demonstrating the ability of the prebiotic to alter the distribution of the administered bacteria when compared with the bacteria administered alone. Additional the experiment is repeated with oral administration of the bacteria at 1E10 CFU/ml and prebiotic mixture administered at 10 mg/ml via gavage. The prebiotic mixture demonstrates the ability to both enhance the level of the bacteria observed in blood and other organs including the lungs, kidneys, liver, colon, pancreas,

[0806] 16s analysis is further performed to assess the effects on cohorts of bacteria not present in bacterial composition administered. Comparing the combined bacteria and prebiotic composition to the other cohorts shows the enhanced growth observed in a mammalian subject. The blood is also submitted for metabolomics with the pure prebiotic composition administered as a control to demonstrate appropriate utilization and production of specific bacterial metabolites not present in compositions containing the combination of bacteria and prebiotic.

Example 71

Selection of Immunomodulatory Carbohydrates or Fungal Species

[0807] A carbohydrate library is selected based on production by bacteria associated with a healthy microbiome or bacteria associated with a disease state including but not limited to Type 1 Diabetes. Graft-Versus-Host Disease, Crohn's Disease, Celiac Disease, and Irritable Bowel Syndrome. In some embodiments, the carbohydrates are functionalized with an amine linker at the reducing end of the sugar and dissolved in phosphate buffer (50 mM NaH_2PO_4. pH 8.5) at a concentration of 1 mM. In other embodiments, the carbohydrates are functionalized with a thiol linker at the reducing end of the sugar and dissolved in PBS (pH 7.4: including an equimolar amount of tris(2-carboxyethyl)phosphine hydrochloride (Thermo Scientific) at a concentration of 1 mM. The compounds are robotically printed in triplicates using a piezoelectric spotting device (S3, Scienion) onto epoxy functionalized microarray slides (sciChip Epoxy, Scienion) in 60% relative humidity, at 23° C. The slides are placed in a humidified chamber for 18 hours and then stored in an anhydrous environment.

[0808] Prior to using the microarray, the slides are washed three times with water, incubated with 100 mM ethanolamine in 50 mM NaH_2PO_4 buffer (pH 9) at 50° C. for 1 hour, rinsed again three times with water, and finally dried by centrifugation. The microarray slides are blocked with blocking buffer (10 mM HEPES, 1 mM $CaCl_2$, 1 mM $MgCl_2$, 2% BSA) at room temperature for 1 hour and washed three times with lectin buffer (10 mM HEPES, 1 mM $CaCl_2$, 1 mM $MgCl_2$) for 5 min. 1 μg of C-type lectin receptor-binding protein sample, diluted in lectin buffer supplemented with 0.01% Tween 20. is applied and the slides are incubated for 1 hour at room temperature. The arrays are washed three times with lectin buffer for 5 min and monoclonal mouse anti-human IgG1-AlexaFluor 488 (Invitrogen, Carlsbad, Calif.) is applied at a 1:100 dilution in lectin buffer with 0.5% BSA at room temperature for 1 hour. The slides are then washed twice with lectin buffer and once with distilled water, spun at 1000 rpm for 5 min, and scanned with a Genepix scanner 7 (Molecular Devices, Sunnyvale, Calif., USA). Binding affinities are determined by measuring the mean fluorescent intensities (MFI) using Genepix Pro 7 (Molecular Devices, Sunnyvale, Calif., USA) (Maglinao M, Eriksson M, Schlegel M K, Zimmermann S, Johannssen T, Gotze S, Seeberger P H, Lepenies B, 2014. A platform to screen for C-type lectin receptor-binding carbohydrates and their potential for cell-specific targeting and immune modulation, Journal of Controlled Release, 175:36-42). Ligands for C-type lectin receptors are often fungal in origin, and thus in addition to being a selection mechanism for carbohydrates, this method also serves as a selection mechanism for immunomodulatory fungal species.

Example 72

Co-Culture of Bacteria Plus Prebiotic and Host-Cells and Analysis of Host Cell Cytokine Response

[0809] The following work is done in the presence and absence (as a control) of one or more selected prebiotic carbohydrates. This assay may be used to test or confirm the ability of a prebiotic-bacterium pair to elicit an immunomodulatory response such that the production or release of proinflammatory cytokines decreases and/or the production or release of anti-inflammatory cytokines increases, may be used to evaluate the difference in cytokine response in the presence or absence of a prebiotic mixture, and/or may be used to evaluate an array of prebiotic candidates. Clostridales bacteria are obtained from the ATCC or purified from a human donor and cultured in brain-heart infusion broth at 37° C. The bacteria are harvested by centrifugation (3000 g, 15 minutes) after 24 hours of stationary growth. To test the effects of spores on human intestinal cells and/or human peripheral blood mononuclear cells (huPBMC), bacteria are first heat killed (95° C., 30 minutes) before the centrifugation

step. Bacteria (or spores) are washed three times with 1×PBS (pH 7.2, Gibco BRL) and subsequently diluted to obtain final cell densities of 10^6 and 10^7 colony forming units (cfu)/ml in RPMI 1640 medium (Gibco BRL).

[0810] Human enterocyte-like CaCO-2 cells (passage 60-65) are seeded at a density of 2.5×10^5 cells/ml on 25 mm cell culture inserts (0.4 μm nucleopore size; Becton Dickinson). The inserts are placed into six well tissue culture plates (Nunc) and cultured 18-22 days at 37° C./10% CO_2 in DMEM (glutamine, high glucose; Amimed) supplemented with 20% decomplemented fetal calf serum (56° C., 30 minutes; Amimed), 1% MEM non-essential amino acids (Gibco BRL), 10 μg/ml gentamycin (Gibco BRL), and 0.1% penicillin/streptomycin (10 000 IU/ml/10 000 UG/ml; Gibco BRL). The cell culture medium is changed every second day until the cells are fully differentiated. Transepithelial electrical resistance (TEER) is determined continuously in confluent CaCO-2 monolayers using a MultiCell-ERS voltmeter/ohmmeter or as described in Example 44.

[0811] Tissue culture inserts covered with CaCO-2 cell monolayers are washed twice with prewarmed RPMI 1640 medium and transferred to six well tissue culture plates. 2 mL culture medium is added to the apical and basolateral compartments of the transwell cell culture system.

[0812] Next, the apical surface of CaCO-2 monolayers is challenged by addition of 10^6 or 10^7 cfu/ml of *Clostridiales* bacteria or spores, in the absence of gentamicin. After four hours, gentamicin is added (at 150 μg/mL) to stop bacterial growth and metabolite secretion. CaCO-2 cells are stimulated with the bacteria or spores for 6-36 hours in a 37° C., 10% CO_2 incubator. Then the CaCO-2 cells are collected, washed once with cold 1×PBS (pH 7.2), and lysed in denaturation solution for RNA extraction (Micro RNA Isolation Kit, Stratagene). Cellular lysates are stored at −20° C. and cell culture supernatants are collected from the apical compartment and frozen at −20° C. The immune response of CaCO-2 cells is monitored by analysis of cytokine gene transcription (TNF-α, IL-8, monocyte chemoattracting protein 1 (MCP-1), TGF-β, IL-12, IFN-γ, IL-4, IL-10) using a reverse transcription-polymerase chain reaction (RT-PCR) technique and determination of cytokine secretion in cell culture supernatants using an ELISA (Haller D, Bode C, Hammes W P, Pfeifer A M A, Schiffrin E J, Blum S, 2000. Non-pathogenic bacteria elicit a differential cytokine response by intestinal epithelial cell/leucocyte co-cultures. Gut. 47:79-97).

Example 73

Analysis of Microbially-Produced Short Chain Fatty Acids and Lactic Acid

[0813] Microbes may be selected for administration to a patient based on its fermentation products. Microbes may be selected for their ability to produce immunosuppressive short chain fatty acids such as propionate (priopionic acid) and/or butyrate (butyric acid). Such analysis is also used to pair microbes with a prebiotic carbohydrate such that the prebiotic carbohydrate is a substrate for the production of the desired immunosuppressive fermentation products.

[0814] 5 M stock solutions of standards [formic acid (FA). acetic acid (AA), propionic acid (PA), butyric acid (BA), valeric acid, iso-caproic acid, D/L-lactic acid (D/L-LA), 2-ethyl-butyric acid and pimelic acid (Sigma Aldrich)] are made up in HPLC-grade water (VWR). A 0.2M succinic acid (SA) internal standard is prepared in HPLC-grade water with NaOH (Sigma Aldrich) to promote dissolution. Combined working solutions (WS. containing FA, AA, PA, BA and LA) of 0.5 M and 0.05 M are prepared by diluting the stock solution appropriately with HPLC-grade water. Standard solutions of 0.1 M in water/methanol (50/50. v/v) are prepared for valeric acid. iso-caproic acid, 2-ethyl-butyric acid and pimelic acid.

[0815] Microbes are purchased or purified from human donors or patients as described in Examples 18 and 36 and are grown in M2GSC medium. The M2GSC medium is at pH 6 and contains, per 100 mL: 30 mL of rumen fluid. 1 g of casitone, 0.25 of yeast extract, 0.2 g of glucose, 0.2 g of cellobiose, 0.2 g of soluble starch. 0.045 g of K_2HPO_4, 0.045 g of KH_2PO_4, 0.09 g of $(NH_4)_2SO_4$, 0.09 g of NaCl, 0.009 g of $MgSO_4.7H_2O$, 0.009 g of $CaCl_2$, 0.1 mg of resazurin, 0.4 g of $NaHCO_3$ and 0.1 g of cystein hydrochloride.

[0816] For analysis of microbially-produced short chain fatty acids, 1 mL supernatant from the microbial cultures is placed in a pyrex extraction tube. 50 μL of the SA stock solution is added as an internal standard to each standard sample or experimental sample. The samples are vortexed and equilibrated at room temperature for 5 minutes. Then, 100 μL of concentrated HCl (VWR) is added, followed by vortexing for 15 seconds. The samples are extracted for 20 min by gently rolling using 5 mL of diethylether (VWR). After centrifugation (5 min, 3500 rpm), the supernatant is transferred to another pyrex extraction tube and 500 μL of a 1 M solution of NaOH is added. The samples are extracted again for 20 min, followed by a centrifugation step. The aqueous phase is transferred to an autosampler vial and 100 μL of concentrated HCl is added. After vortexing, a 10 μL aliquot is injected onto the HPLC-UV apparatus, which comprises a P4000 gradient pump with vacuum degassing, an AS3000 autosampler (10° C.), an UV6000 detector, and a SN4000 module (Thermo Separations Products, Thermo Scientific).

[0817] Chromatographic separation is performed as described in De Baere S., Eeckhaut V., Steppe M., De Maesschalck C., De Backer P., Van Immerseel F., Croubels S., 2013. Development of a HPLC-UV method for the quantitative determination of four short-chain fatty acids and lactic acid produced by intestinal bacteria during in vitro fermentation. Journal of Pharmaceutical and Biomedical Analysis. 80:107-115.

Example 74

Method of Preparing the Microbial and Prebiotic Composition for Administration to a Patient

[0818] One strain of bacteria or fungi is independently cultured and mixed together with a selected prebiotic carbohydrate before administration. The strain is grown at 37° C. pH 7, in a GMM or other animal-products-free medium. pre-reduced with 3 g/L cysteine YHCl. After each strain reaches a sufficient biomass, it is preserved for banking by adding 15% glycerol and then frozen at −80° C. in 1 mL cryotubes. The strain is then cultivated to a concentration of 10 CFU/mL. then concentrated 20-fold by tangential flow microfiltration. The spent medium is exchanged by diafiltering with a preservative medium consisting of 2% gelatin, 100 mM trehalose, and 10 mM sodium phosphate buffer, or other suitable preservative medium. The suspension is freeze-dried to a powder and titrated.

[0819] After drying, the powder is blended with microcrystalline cellulose and magnesium stearate and formulated into a 250 mg gelatin capsule containing 10 mg of lyophilized powder (10^8 to 10^{11} bacteria), 160 mg microcrystalline cellulose, 77.5 mg gelatin, and 2.5 mg magnesium stearate, and the prebiotic mixture. The prebiotic mixture is in powder form and is mixed with the microbial composition in a ratio of prebiotic:microbe of about 3:1, 2:1, 1:1, 1:2, 1:3, 1:5, 1:10, 1:15, 1:20, 1:25, 1:30, 1:35, 1:40, 1:45, 1:50, 1:55, 1:60, 1:70, 1:80, 1:90, 1:100. or 1:500.

Example 75

A Rat Model for Radiation- and Chemotherapy-Induced Mucositis

[0820] Eighteen female Wistar rats of 150-200 grams, aged 14-16 weeks, may be obtained from the Central Animal Research Facility, Manipal University, Manipal (License No. 94/1999 CPCSEA). The rats are housed in polycarbonate cages and were provided free access to standard rat food and filtered water. After one week adaptation to the environment, rats are subjected to chemotherapy by orally administering busulfan (Sigma-Aldrich Co. LLC, St. Louis, Mo. USA) at 6 mg/kg for four days. To administer infrared radiation to the rats. the tail flick apparatus (model 37360, Ugo Basile Srl, Comerio, Va., Italy) is used. The rats are anesthetized with light ether and the dorsal surface of the tongue is exposed to IR radiation of intensity 40 mV/cm^2 for 5 second on the first and fourth days of treatment with busulfan (Patel A, Rajesh S, Chandrashekar V M, Rathnam S. Shah K, Rao C M, Nandakumar K, 2013. A rat model against chemotherapy plus radiation-induced mucositis. Saudi Pharmaceutical Journal. 21:399-403).

Example 76

A Mouse Model for Bone Marrow Transplantation

[0821] Female C57BL/6 and B6D2F1 mice are purchased from the Jackson Laboratory (Bar Harbor, Me., USA). Bone marrow is harvested from the femurs and tibias of 12-20 week old mice. Before receiving transplantation, B6D2F1 mice are given 14 Gy total body irradiation (^{137}Cs source). Irradiation is done twice, three hours apart. 5×10^6 bone marrow cells are supplemented with 2×10^6 nylon-wool nonadherent splenetic T cells from C57BL/6 mice and resuspended in Leibovitz's L15 medium (Life Technologies Inc., New York USA) and transplanted by tail vein infusion (0.25 mL) into B6D2F1 mice (Cooke K R, Gerbitz A, Crawford J M, Teshmia T. Hill G R, Tesolin A. Rossignol D P, Ferrara J L M, 2001. LPS antagonism reduces graft-versus-host disease and preserves graft-versus-host leukemia after experimental bone marrow transplantation. The Journal of Clinical Investigation. 107: 1581-1589).

Example 77

A Mouse Model for Studying Gut Microbiome in Graft Versus Host Disease

[0822] Blood from healthy human donors is collected in a tube containing sodium heparin. The blood is diluted in an equal volume of Ca^{2+}- and Mg^{2+}-free phosphate buffered saline with 2% v/v fetal bovine serum and centrifuged at room temperate at 200×g for 10 minutes. The white "buffy coat" layer is removed to yield human peripheral mononuclear cells (huPBMCs), washed five times in RPMI 1640, and diluted (2×10^6 cells/mL) in RPMI 1640 with decomplemented 20% human AB serum (56° C., 30 minutes, Sigma) and 150 μg/mL gentamicin.

[0823] At 4- to 5 weeks old, the Rag2$^{-/-}\gamma c^{-/-}$ mice (purchased from Taconic) are pretreated with liposome-clodronate (VU Medisch Centrum) and sublethally irradiated (1 Gy/6 g). then transplanted intraperitoneally with 3.0×10^7 huPBMCs. After 4 weeks, these humanized mice sublethally irradiated and, one day later, are injected intravenously with 1.0×10^7 allogeneic huPBMCs (1 Gy/6 g). The transplanted mice are monitored daily for GVHD symptoms including weight loss, temperature changes, and diarrhea. (Zheng J, Liu Y, Liu U, Liu M, Xiang Z, Lam K-T, Lewis D B, Lau Y-L, Tu W, 2013. Human CD8$^+$ Regulatory T Cells Inhibit GVHD and Preserve General Immunity in Humanized Mice Sci Transl Med 5:168ra9.)

Example 78

Detection of Bacteria in Antigen-Presenting Cells

[0824] The following methods may be applied to assess the persistence of dysbiotic or disease-associated bacteria. Optionally, these methods may be applied to assess immunomodulatory behavior of bacteria administered to a patient or of bacteria associated with the patient's natural "healthy" microbiome.

[0825] Dendritic cells (DCs) are isolated from bone marrow or blood according to standard methods or kit protocols (e.g., Inaba K, Swiggard W J, Steinman R M, Romani N, Schuler G, 2001. Isolation of dendritic cells. Current Protocols in Immunology. Chapter 3:Unit3.7) or are obtained from the ATCC.

[0826] GFP-expressing *Clostridiales* bacteria are made using the pGLO™ Bacterial Transformation Kit (BioRad, USA) according to the manufacturer's instructions.

[0827] To evaluate bacterial entrance into and/or presence in DCs, 250,000 DCs are seeded on a round cover slip in complete RPMI-1640 medium and are then infected with GFP-expressing *Clostridiales* bacteria. After 1 hour of infection, the cells are washed twice with ice-cold PBS. To kill extracellular bacteria, the cells are incubated in complete RPMI-1640 medium supplemented with 50 μg/ml gentamicin for 2-3 hours. Cells are fixed and permeabilized for 10 min at −20° C. with 100% methanol and blocked for 1 hour with PBS plus 3% bovine serum albumin. After incubation, the cover slips is washed three times, mounted on microscope slides and analyzed on a confocal microscope (e.g., a fluoview FV100 Olympus confocal microscope). The number of cells containing intracellular bacteria are counted and normalized to the total number of cells in the field. Z-stack analysis (using 0.5 μm steps) is used to discern intracellular bacteria from extracellular bacteria (Bueno S M, Wozniak A, Leiva E D, Riquelme S A, Carrefio U J, Hardt W D, Riedel C A, Kalergis A M, 2010. *Salmonella* pathogenicity island 1 differentially modulates bacterial entry to dendritic and nonphagocytic cells. Immunology. 130:273-87). To detect bacteria outside of dendritic cells, confocal microscopy may be performed in which immunospecific antibioties to the GFP-expressing bacteria are visualized.

[0828] Additionally or alternatively, gentamicin protection assays are used to evaluate bacterial survival inside DCs. Overnight cultures of Clostriadles bacteria are subcultured

until they reached an OD600 of 0.5-0.7 and are then washed and resuspended in ice-cold PBS. The DCs are infected with bacteria a multiplicity of infection (MOI) equal to 25 for 1 hour. The DCs are washed and extracellular bacteria are killed by incubating the DCs for 2 hours with 50 μg/ml gentamicin (Sigma-Aldrich). To recover intracellular bacteria, 10,000 live cells are counted and lysed for 15 min with 0.1% Triton-X-100 in PBS. The lysed cells are seeded on Luria-Bertani agar plates and incubated for 12-16 hours at 37° C. to count intracellular bacteria as colony-forming units (CFUs). Data from gentamicin protection assays are normalized as the percentage of recovered CFUs relative to the maximum amount obtained in each experiment (defined as 100%) (Bueno S M, Wozniak A, Leiva E D, Riquelme S A, Carrefio U J, Hardt W D, Riedel C A, Kalergis A M, 2010. *Salmonella* pathogenicity island 1 differentially modulates bacterial entry to dendritic and non-phagocytic cells. Immunology. 130:273-87). The methods described above may also be performed in substantially the same manner, using macrophages (obtained from the ATCC) in place of DCs.

Example 79

Detection of Bacteria in MLN, PLN and Spleen

[0829] Radiolabeled bacteria may be detected in organs and serve as an indicator of bacterial translocation in an animal model.

[0830] To prepare radiolabeled bacteria, the following steps are repeated three times: A bacterial sample (e.g., *Escherichia coli* ATCC-10536) is obtained from the ATCC and grown overnight in an appropriate medium (e.g., trypticasein agar). The next day, the strain is transferred to a tube containing 10 mL of sterile saline solution. The bacterial concentration is adjusted to 11% of transmittance in a spectrophotometer at 580 nm, corresponding to a CFU/mL of approximately 10^8. Two mL of the bacterial suspension is incubated in tubes containing 1 mL of stannous chloride solution (580 μM, pH 7.0) at 37° C. for 10 minutes. After incubation, 37.0-55.5 MBq of ^{99m}Tc obtained by elution from the sterile ^{99}Mo/^{99m}Tc generator (IPEN/Brazil) is added, and the sample is incubated for 10 minutes at 37° C. The tubes are centrifuged at 3000 g for 25 minutes.

[0831] Once repeated three times, the radioactivity of the supernatant and precipitate is measured using a dose calibrator (CRC-25R Dose Calibrator; Capintec, Ramsey, N.J.), and the labeling efficiency is calculated by dividing the cpm of the precipitate by the total cpm (precipitate plus supernatant) and multiplying by 100%.

[0832] Adult Swiss male mice are fed standard chow. If the experiment calls for the assessment of a treatment (e.g., supplementation with citrulline, microbial composition, and/or an immunomodulatory or prebiotic carbohydrate), the mice fed standard chow plus treatment are compared with mice only fed standard chow. The mice are administered 0.1 mL of a suspension containing 1.8 MBq of the ^{99m}Tc-labeled bacteria (10^7 CFU/mL), by gavage. One to two days later, the animals were euthanized, and the mesenteric lymph nodes (MLNs), popliteal lymph notes (PLNs), and spleen are removed, weighed, and placed in tubes. Incorporated radioactivity is assessed using a counter with an NaI (Tl) crystal (ANSR; Abbott, Chicago, Ill.) and normalized to the organ's weight (Batista M A, Nicoli J R, Martins Fdos S, Machado J A, Arantes R M, Quinino I E, Correia M I, Cardoso V N, 2012. Pretreatment with citrulline improves gut barrier after intestinal obstruction in mice. JPEN J Parenter Enteral Nutr. 36:69-76).

Example 80

Measuring Intestinal Integrity by Zonulin ELISA

[0833] Age-matched male diabetes-prone and diabetes-resistant rats are anesthetized with ketamine and killed at increasing ages (20, 50, 75, and >100 days) by exsanguination. The rat abdominal wall is opened, small intestinal loops are isolated, and intraluminal lavage is performed by instillation of 0.5 ml of PBS into the proximal small intestine followed by aspiration. The aspirate is stored at −80° C. until a zonulin ELISA is performed as follows. Plastic microtiter plates (Costar. Cambridge, Mass.) are coated with polyclonal rabbit, zonulin-specific anti-Zot antibodies (dilution 1:100) overnight at 4° C. and are then blocked by incubation with 0.05% PBS-Tween 20 for 15 min at room temperature. A standard curve is made by serial dilution of zonulin (0.78-50 ng/ml) in 0.05% PBS-Tween 20. Equal amounts of the standards and experimental samples are aliquotted into the microtiter plate wells and incubated for 1 hour at room temperature. Unbound zonulin is removed by washing, and the wells are incubated by agitation with biotinylated anti-Zot antibodies for 1 hour at room temperature. A color reaction is developed by adding 100 μl of Extra-Avidin (Sigma) diluted 1:20,000 in 0.1 M Tris.HCl, 1 mM $MgCl_2$, 1% BSA, pH 7.3, for 15 min. followed by incubation with 100 μl of a 1 mg/ml of p-nitrophenyl-phosphate substrate (Sigma) solution. Absorbance at 405 nm is read after 30 min (Watts T. Berti I, Sapone A. Gerarduzzi T. Not T. Zielke R. and Fasano A, 2005. Role of the intestinal tight junction modular zonulin in the pathogenesis of type I diabetes in BB diabetic-prone rats. PNAS. 102:2916-2921).

Example 81

Measuring Intestinal Integrity by Western Blot of Tight Junction Proteins

[0834] Intestinal integrity may also be evaluated by measuring tight junction protein levels by Western blot. In this case, primary antibodies for occluding and zona occludins-1 (Grand Island, N.Y.), primary antibodies for claudin-1 and claudin-2 (Santa Cruz Biotechnology, CA), and secondary antibodies (fluorescein-conjugated goat anti-mouse and goat anti-rabbit from Santa Cruz Biotechnology, CA) are used. One centimeter sections of mid-jujunal intestine are harvested from an appropriate animal model (e.g., rat or mouse) and immediately homogenized in 1 mL ice-cold RIPA-buffer (50 mM TRIS-HCl, pH 7.4, 150 mM NaCl, 1 mM DTT, 0.5 mM EDTA, 1.0% NP40, 0.5% sodium deoxycholate, 0.1% SDS, 2 mM phenylmethylsulfonyl fluoride, 20 μg/ml aprotinin, 2 μg/ml leupeptin and 2 mM sodium orthovanadate). Tissue lysates are sonicated, incubated on ice for 20 min and centrifuged at 4° C., and the resulting supernatants are collected for immunoprecipitation. The protein concentration of the supernatants is measured using the techniques known to one skilled in the art, including but not limited to a Bradford assay. The samples are boiled for 5 min and then 2 μg of protein from each sample is loaded into the lanes of a 10% acrylamide gel. Following electrophoresis, the proteins are transferred onto nitrocellulose filters, which are then incubated with primary antibodies directed against occludin,

zona-occludin-1, claudin-1, and/or claudin-2 overnight at 4° C. The filters are then washed with 1×TBST and incubated with secondary antibodies conjugated with horseradish peroxidase (HRP) for one hour at room temperature. Immunocomplexes for each of the tight junction proteins are then detected by chemiluminescence (Alaish S M, Smith A D, Timmons J, Greenspon J, Eyvazzadeh D, Murphy E, Shea-Donahue T, Cirimotich S, Mongodin E, Zhao A, Fasano A, Nataro J P, Cross A, 2013. Gut microbiota, tight junction protein expression, intestinal resistance, bacterial translocation and mortality following cholestasis depend on the genetic background of the host. Gut Microbes. 4:292-305).

Example 82

Measurement of Intestinal Permeability in a Mouse Model for Alcoholism

[0835] Eight-week-old male C57BL/6N mice are fed a modified Lieber-DeCarli liquid diet containing ethanol (35% of total calories) or containing no ethanol for one week and then gradually increasing amounts of ethanol (to a maximum of 35% total calories) over the course of 3-4 days. After eight weeks of ethanol feeding, the mice are fasted overnight, anesthetized intraperitonially with sodium-pentobarbital (nembutal, 80 mg/kg), and whole intestinal samples are collected and weighed. The freshly isolated intestinal segments (duodenum, jejunum, ileum) are placed in Krebs-Henseleit bicarbonate buffer and then used for ex vivo intestinal permeability assay as follows. One end of the gut segment is ligated with suture, and 200 μl of fluorescent dextran-FITC (FD-4; M.W. 4,000, 40 mg/ml) is injected into the lumen using a gavage needle. The other end of the gut segment is ligated to form a gut sac. The gut sac is rinse in Krebs-Henseleit bicarbonate buffer and placed in 4 ml of fresh buffer, then incubated at 37° C. for 20 minutes. The FD-4 that penetrated from the lumen into the buffer is measured with a spectrofluorometer using an excitation wave length of 485 nm and an emission wave length of 530 nm (Kirpich I A, Feng W, Wang Y, Lie Y, Barker D F, Barve S S, McClain C J, 2011. The Type of Dietary Fat Modulates Intestinal Tight Junction Integrity, Gut Permeability, and Hepatic Toll-Like Receptor Expression in a Mouse Model of Alcoholic Liver Disease. Alcoholism: Clinical and Experimental Research. 36:835-846).

Example 83

Detection of Bacteria in Distal Organs

[0836] A fragment from a liver or spleen biopsy 15 minutes after reperfusion is moved to a sterile tube containing thioglycolate and the immediately cultured on a medium including but not limited to blood agar, blood agar supplemented for anaerobes. chocolate blood agar, MacConkey agar. and Sabouraud agar. Bacteria are purified as described (Example 18) or using other medium as described in Example 36 and 16S rDNA sequencing is performed as described (Examples 7, 31, 62-65).

Example 84

Distal Effects of Microbiota

[0837] It has been It has been determined that the presence of certain probiotics in the microbiome plays a role in the therapeutic effectiveness of certain immunomodulatory cancer therapies, including anti-PD-1 and anti-CTLA-4 antibodies. In particular, it has been found that the addition of certain bacteria to the gut of a subject enhances the activity of these checkpoint inhibitors, resulting in increased anti-tumor T cell responses and inhibition of tumor growth (See Vétizou, et al. *Science, Nov.* 5, 2015, science.aad1329 and Sivan et al. *Science, Nov.* 5, 2015, science.aac4255).

[0838] In particular, it has been shown that oral administration of *Bifidobacterium* or *Bacteroides* probiotics, but not *Lactobacillus*, increases the responsiveness to checkpoint inhibitor therapy in cancer (Sivan et al., Vetizou et al). Anti-PD-1 and anti-CTLA-4 antibody therapies relieve a block, or checkpoint, that otherwise limits anti-tumor immunity. Checkpoint inhibition by these antibodies results in an increase in anti-tumor T cell immune responses, and more effective killing of cancer cells. Tumors have also been shown to be surrounded by microbiomes that are different from the microbiome in normal adjacent tissues, as a result of the interaction between the immune system and the cancer. The observation that addition of certain bacteria to the gut leads to an effect on the immune system and on the growth of tumors at a distal site suggests a concomitant impact on the tumor microbiome at these distal site(s).

[0839] In order for the immune cells induced by the combination of a checkpoint inhibitor and certain gut bacteria to have an effect, the cells must travel to the tumor site, altering both the immune and tumor environments, which will alter the tumor microbiome as well. Thus, the presence of bacteria introduced in the gut leads to an alteration in the microbiome of tumors at a distal site. The above studies support the distal effects of microbials, and the role of certain bacteria in the effectiveness of certain cancer therapies.

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TABLE 1

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Eubacterium saburreum	858	AB525414	clade_178	Y	N
Eubacterium sp. oral clone IR009	866	AY349376	clade_178	Y	N
Lachnospiraceae bacterium ICM62	1061	HQ616401	clade_178	Y	N
Lachnospiraceae bacterium MSX33	1062	HQ616384	clade_178	Y	N
Lachnospiraceae bacterium oral taxon 107	1063	ADDS01000069	clade_178	Y	N
Alicyclobacillus acidocaldarius	122	NR_074721	clade_179	Y	N
Clostridium baratii	555	NR_029229	clade_223	Y	N
Clostridium colicanis	576	FJ957863	clade_223	Y	N
Clostridium paraputrificum	611	AB536771	clade_223	Y	N
Clostridium sardiniense	621	NR_041006	clade_223	Y	N
Eubacterium budayi	837	NR_024682	clade_223	Y	N
Eubacterium moniliforme	851	HF558373	clade_223	Y	N
Eubacterium multiforme	852	NR_024683	clade_223	Y	N
Eubacterium nitritogenes	853	NR_024684	clade_223	Y	N
Anoxybacillus flavithermus	173	NR_074667	clade_238	Y	N
Bacillus aerophilus	196	NR_042339	clade_238	Y	N
Bacillus aestuarii	197	GQ980243	clade_238	Y	N
Bacillus amyloliquefaciens	199	NR_075005	clade_238	Y	N
Bacillus anthracis	200	AAEN01000020	clade_238	Y	Category-A
Bacillus atrophaeus	201	NR_075016	clade_238	Y	OP
Bacillus badius	202	NR_036893	clade_238	Y	OP
Bacillus cereus	203	ABDJ01000015	clade_238	Y	OP
Bacillus circulans	204	AB271747	clade_238	Y	OP
Bacillus firmus	207	NR_025842	clade_238	Y	OP
Bacillus flexus	208	NR_024691	clade_238	Y	OP
Bacillus fordii	209	NR_025786	clade_238	Y	OP
Bacillus halmapalus	211	NR_026144	clade_238	Y	OP
Bacillus herbersteinensis	213	NR_042286	clade_238	Y	OP
Bacillus idriensis	215	NR_043268	clade_238	Y	OP
Bacillus lentus	216	NR_040792	clade_238	Y	OP
Bacillus licheniformis	217	NC_006270	clade_238	Y	OP
Bacillus megaterium	218	GU252124	clade_238	Y	OP
Bacillus nealsonii	219	NR_044546	clade_238	Y	OP
Bacillus niabensis	220	NR_043334	clade_238	Y	OP
Bacillus niacini	221	NR_024695	clade_238	Y	OP
Bacillus pocheonensis	222	NR_041377	clade_238	Y	OP
Bacillus pumilus	223	NR_074977	clade_238	Y	OP
Bacillus safensis	224	JQ624766	clade_238	Y	OP
Bacillus simplex	225	NR_042136	clade_238	Y	OP
Bacillus sonorensis	226	NR_025130	clade_238	Y	OP
Bacillus sp. 10403023 MM10403188	227	CAET01000089	clade_238	Y	OP
Bacillus sp. 2_A_57_CT2	230	ACWD01000095	clade_238	Y	OP
Bacillus sp. 2008724126	228	GU252108	clade_238	Y	OP
Bacillus sp. 2008724139	229	GU252111	clade_238	Y	OP
Bacillus sp. 7_16AIA	231	FN397518	clade_238	Y	OP
Bacillus sp. AP8	233	JX101689	clade_238	Y	OP
Bacillus sp. B27(2008)	234	EU362173	clade_238	Y	OP
Bacillus sp. BT1B_CT2	235	ACWC01000034	clade_238	Y	OP
Bacillus sp. GB1.1	236	FJ897765	clade_238	Y	OP
Bacillus sp. GB9	237	FJ897766	clade_238	Y	OP
Bacillus sp. HU19.1	238	FJ897769	clade_238	Y	OP
Bacillus sp. HU29	239	FJ897771	clade_238	Y	OP
Bacillus sp. HU33.1	240	FJ897772	clade_238	Y	OP
Bacillus sp. JC6	241	JF824800	clade_238	Y	OP
Bacillus sp. oral taxon F79	248	HM099654	clade_238	Y	OP
Bacillus sp. SRC_DSF1	243	GU797283	clade_238	Y	OP
Bacillus sp. SRC_DSF10	242	GU797292	clade_238	Y	OP
Bacillus sp. SRC_DSF2	244	GU797284	clade_238	Y	OP
Bacillus sp. SRC_DSF6	245	GU797288	clade_238	Y	OP
Bacillus sp. tc09	249	HQ844242	clade_238	Y	OP
Bacillus sp. zh168	250	FJ851424	clade_238	Y	OP
Bacillus sphaericus	251	DQ286318	clade_238	Y	OP
Bacillus sporothermodurans	252	NR_026010	clade_238	Y	OP
Bacillus subtilis	253	EU627588	clade_238	Y	OP
Bacillus thermoamylovorans	254	NR_029151	clade_238	Y	OP
Bacillus thuringiensis	255	NC_008600	clade_238	Y	OP
Bacillus weihenstephanensis	256	NR_074926	clade_238	Y	OP
Geobacillus kaustophilus	933	NR_074989	clade_238	Y	N
Geobacillus stearothermophilus	936	NR_040794	clade_238	Y	N
Geobacillus thermodenitrificans	938	NR_074976	clade_238	Y	N
Geobacillus thermoglucosidasius	939	NR_043022	clade_238	Y	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Lysinibacillus sphaericus	1193	NR_074883	clade_238	Y	N
Clostridiales sp. SS3_4	543	AY305316	clade_246	Y	N
Clostridium beijerinckii	557	NR_074434	clade_252	Y	N
Clostridium botulinum	560	NC_010723	clade_252	Y	Category-A
Clostridium butyricum	561	ABDT01000017	clade_252	Y	N
Clostridium chauvoei	568	EU106372	clade_252	Y	N
Clostridium favososporum	582	X76749	clade_252	Y	N
Clostridium histolyticum	592	HF558362	clade_252	Y	N
Clostridium isatidis	597	NR_026347	clade_252	Y	N
Clostridium limosum	602	FR870444	clade_252	Y	N
Clostridium sartagoforme	622	NR_026490	clade_252	Y	N
Clostridium septicum	624	NR_026020	clade_252	Y	N
Clostridium sp. 7_2_43FAA	626	ACDK01000101	clade_252	Y	N
Clostridium sporogenes	645	ABKW02000003	clade_252	Y	N
Clostridium tertium	653	Y18174	clade_252	Y	N
Clostridium carnis	564	NR_044716	clade_253	Y	N
Clostridium celatum	565	X77844	clade_253	Y	N
Clostridium disporicum	579	NR_026491	clade_253	Y	N
Clostridium gasigenes	585	NR_024945	clade_253	Y	N
Clostridium quinii	616	NR_026149	clade_253	Y	N
Clostridium hylemonae	593	AB023973	clade_260	Y	N
Clostridium scindens	623	AF262238	clade_260	Y	N
Lachnospiraceae bacterium 5_1_57FAA	1054	ACTR0100002	clade_260	Y	N
Clostridium glycyrrhizinilyticum	588	AB233029	clade_262	Y	N
Clostridium nexile	607	X73443	clade_262	Y	N
Coprococcus comes	674	ABVR01000038	clade_262	Y	N
Lachnospiraceae bacterium 1_1_57FAA	1048	ACTM01000065	clade_262	Y	N
Lachnospiraceae bacterium 1_4_56FAA	1049	ACTN01000028	clade_262	Y	N
Lachnospiraceae bacterium 8_1_57FAA	1057	ACWQ01000079	clade_262	Y	N
Ruminococcus lactaris	1663	ABOU02000049	clade_262	Y	N
Ruminococcus torques	1670	AAVP02000002	clade_262	Y	N
Paenibacillus lautus	1397	NR_040882	clade_270	Y	N
Paenibacillus polymyxa	1399	NR_037006	clade_270	Y	N
Paenibacillus sp. HGF5	1402	AEXS01000095	clade_270	Y	N
Paenibacillus sp. HGF7	1403	AFDH01000147	clade_270	Y	N
Eubacterium sp. oral clone JI012	868	AY349379	clade_298	Y	N
Alicyclobacillus contaminans	124	NR_041475	clade_301	Y	N
Alicyclobacillus herbarius	126	NR_024753	clade_301	Y	N
Alicyclobacillus pomorum	127	NR_024801	clade_301	Y	N
Blautia coccoides	373	AB571656	clade_309	Y	N
Blautia glucerasea	374	AB588023	clade_309	Y	N
Blautia glucerasei	375	AB439724	clade_309	Y	N
Blautia hansenii	376	ABYU02000037	clade_309	Y	N
Blautia luti	378	AB691576	clade_309	Y	N
Blautia producta	379	AB600998	clade_309	Y	N
Blautia schinkii	380	NR_026312	clade_309	Y	N
Blautia sp. M25	381	HM626178	clade_309	Y	N
Blautia stercoris	382	HM626177	clade_309	Y	N
Blautia wexlerae	383	EF036467	clade_309	Y	N
Bryantella formatexigens	439	ACCL02000018	clade_309	Y	N
Clostridium coccoides	573	EF025906	clade_309	Y	N
Eubacterium cellulosolvens	839	AY178842	clade_309	Y	N
Lachnospiraceae bacterium 6_1_63FAA	1056	ACTV01000014	clade_309	Y	N
Ruminococcus hansenii	1662	M59114	clade_309	Y	N
Ruminococcus obeum	1664	AY169419	clade_309	Y	N
Ruminococcus sp. 5_1_39BFAA	1666	ACII01000172	clade_309	Y	N
Ruminococcus sp. K_1	1669	AB222208	clade_309	Y	N
Syntrophococcus sucromutans	1911	NR_036869	clade_309	Y	N
Bacillus alcalophilus	198	X76436	clade_327	Y	N
Bacillus clausii	205	FN397477	clade_327	Y	OP
Bacillus gelatini	210	NR_025595	clade_327	Y	OP
Bacillus halodurans	212	AY144582	clade_327	Y	OP
Bacillus sp. oral taxon F26	246	HM099642	clade_327	Y	OP
Clostridium innocuum	595	M23732	clade_351	Y	N
Clostridium sp. HGF2	628	AENW01000022	clade_351	Y	N
Clostridium perfringens	612	ABDW01000023	clade_353	Y	Category-B
Sarcina ventriculi	1687	NR_026146	clade_353	Y	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Clostridium bartlettii	556	ABEZ02000012	clade_354	Y	N
Clostridium bifermentans	558	X73437	clade_354	Y	N
Clostridium ghonii	586	AB542933	clade_354	Y	N
Clostridium glycolicum	587	FJ384385	clade_354	Y	N
Clostridium mayombei	605	FR733682	clade_354	Y	N
Clostridium sordellii	625	AB448946	clade_354	Y	N
Clostridium sp. MT4 E	635	FJ159523	clade_354	Y	N
Eubacterium tenue	872	M59118	clade_354	Y	N
Clostridium argentinense	553	NR_029232	clade_355	Y	N
Clostridium sp. JC122	630	CAEV01000127	clade_355	Y	N
Clostridium sp. NMBHI_1	636	JN093130	clade_355	Y	N
Clostridium subterminale	650	NR_041795	clade_355	Y	N
Clostridium sulfidigenes	651	NR_044161	clade_355	Y	N
Dorea formicigenerans	773	AAXA02000006	clade_360	Y	N
Dorea longicatena	774	AJ132842	clade_360	Y	N
Lachnospiraceae bacterium 2_1_46FAA	1050	ADLB01000035	clade_360	Y	N
Lachnospiraceae bacterium 2_1_58FAA	1051	ACTO01000052	clade_360	Y	N
Lachnospiraceae bacterium 4_1_37FAA	1053	ADCR01000030	clade_360	Y	N
Lachnospiraceae bacterium 9_1_43BFAA	1058	ACTX01000023	clade_360	Y	N
Ruminococcus gnavus	1661	X94967	clade_360	Y	N
Ruminococcus sp. ID8	1668	AY960564	clade_360	Y	N
Blautia hydrogenotrophica	377	ACBZ01000217	clade_368	Y	N
Lactonifactor longoviformis	1147	DQ100449	clade_368	Y	N
Robinsoniella peoriensis	1633	AF445258	clade_368	Y	N
Eubacterium infirmum	849	U13039	clade_384	Y	N
Eubacterium sp. WAL 14571	864	FJ687606	clade_384	Y	N
Erysipelotrichaceae bacterium 5_2_54FAA	823	ACZW01000054	clade_385	Y	N
Eubacterium biforme	835	ABYT01000002	clade_385	Y	N
Eubacterium cylindroides	842	FP929041	clade_385	Y	N
Eubacterium dolichum	844	L34682	clade_385	Y	N
Eubacterium sp. 3_1_31	861	ACTL01000045	clade_385	Y	N
Eubacterium tortuosum	873	NR_044648	clade_385	Y	N
Bulleidia extructa	441	ADFR01000011	clade_388	Y	N
Solobacterium moorei	1739	AECQ01000039	clade_388	Y	N
Coprococcus catus	673	EU266552	clade_393	Y	N
Lachnospiraceae bacterium oral taxon F15	1064	HM099641	clade_393	Y	N
Clostridium cochlearium	574	NR_044717	clade_395	Y	N
Clostridium malenominatum	604	FR749893	clade_395	Y	N
Clostridium tetani	654	NC_004557	clade_395	Y	N
Acetivibrio ethanolgignens	6	FR749897	clade_396	Y	N
Anaerosporobacter mobilis	161	NR_042953	clade_396	Y	N
Bacteroides pectinophilus	288	ABVQ01000036	clade_396	Y	N
Clostridium aminovalericum	551	NR_029245	clade_396	Y	N
Clostridium phytofermentans	613	NR_074652	clade_396	Y	N
Eubacterium hallii	848	L34621	clade_396	Y	N
Eubacterium xylanophilum	875	L34628	clade_396	Y	N
Ruminococcus callidus	1658	NR_029160	clade_406	Y	N
Ruminococcus champanellensis	1659	FP929052	clade_406	Y	N
Ruminococcus sp. 18P13	1665	AJ515913	clade_406	Y	N
Ruminococcus sp. 9SE51	1667	FM954974	clade_406	Y	N
Anaerostipes caccae	162	ABAX03000023	clade_408	Y	N
Anaerostipes sp. 3_2_56FAA	163	ACWB01000002	clade_408	Y	N
Clostridiales bacterium 1_7_47FAA	541	ABQR01000074	clade_408	Y	N
Clostridiales sp. SM4_1	542	FP929060	clade_408	Y	N
Clostridiales sp. SSC_2	544	FP929061	clade_408	Y	N
Clostridium aerotolerans	546	X76163	clade_408	Y	N
Clostridium aldenense	547	NR_043680	clade_408	Y	N
Clostridium algidixylanolyticum	550	NR_028726	clade_408	Y	N
Clostridium amygdalinum	552	AY353957	clade_408	Y	N
Clostridium asparagiforme	554	ACCJ01000522	clade_408	Y	N
Clostridium bolteae	559	ABCC02000039	clade_408	Y	N
Clostridium celerecrescens	566	JQ246092	clade_408	Y	N
Clostridium citroniae	569	ADLJ01000059	clade_408	Y	N
Clostridium clostridiiformes	571	M59089	clade_408	Y	N
Clostridium clostridioforme	572	NR_044715	clade_408	Y	N
Clostridium hathewayi	590	AY552788	clade_408	Y	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Clostridium indolis	594	AF028351	clade_408	Y	N
Clostridium lavalense	600	EF564277	clade_408	Y	N
Clostridium saccharolyticum	620	CP002109	clade_408	Y	N
Clostridium sp. M62_1	633	ACFX02000046	clade_408	Y	N
Clostridium sp. SS2_1	638	ABGC03000041	clade_408	Y	N
Clostridium sphenoides	643	X73449	clade_408	Y	N
Clostridium symbiosum	652	ADLQ01000114	clade_408	Y	N
Clostridium xylanolyticum	658	NR_037068	clade_408	Y	N
Eubacterium hadrum	847	FR749933	clade_408	Y	N
Lachnospiraceae bacterium 3_1_57FAA_CT1	1052	ACTP01000124	clade_408	Y	N
Lachnospiraceae bacterium 5_1_63FAA	1055	ACTS01000081	clade_408	Y	N
Lachnospiraceae bacterium A4	1059	DQ789118	clade_408	Y	N
Lachnospiraceae bacterium DJF VP30	1060	EU728771	clade_408	Y	N
Lachnospiraceae genomosp. C1	1065	AY278618	clade_408	Y	N
Clostridium difficile	578	NC_013315	clade_409	Y	OP
Eubacterium sp. AS15b	862	HQ616364	clade_428	Y	N
Eubacterium sp. OBRC9	863	HQ616354	clade_428	Y	N
Eubacterium sp. oral clone OH3A	871	AY947497	clade_428	Y	N
Eubacterium yurii	876	AEES01000073	clade_428	Y	N
Clostridium acetobutylicum	545	NR_074511	clade_430	Y	N
Clostridium algidicarnis	549	NR_041746	clade_430	Y	N
Clostridium cadaveris	562	AB542932	clade_430	Y	N
Clostridium carboxidivorans	563	FR733710	clade_430	Y	N
Clostridium estertheticum	580	NR_042153	clade_430	Y	N
Clostridium fallax	581	NR_044714	clade_430	Y	N
Clostridium felsineum	583	AF270502	clade_430	Y	N
Clostridium frigidicarnis	584	NR_024919	clade_430	Y	N
Clostridium kluyveri	598	NR_074165	clade_430	Y	N
Clostridium magnum	603	X77835	clade_430	Y	N
Clostridium putrefaciens	615	NR_024995	clade_430	Y	N
Clostridium sp. HPB_46	629	AY862516	clade_430	Y	N
Clostridium tyrobutyricum	656	NR_044718	clade_430	Y	N
Sutterella parvirubra	1899	AB300989	clade_432	Y	N
Acetanaerobacterium elongatum	4	NR_042930	clade_439	Y	N
Clostridium cellulosi	567	NR_044624	clade_439	Y	N
Ethanoligenens harbinense	832	AY675965	clade_439	Y	N
Eubacterium rectale	856	FP929042	clade_444	Y	N
Eubacterium sp. oral clone GI038	865	AY349374	clade_444	Y	N
Lachnobacterium bovis	1045	GU324407	clade_444	Y	N
Roseburia cecicola	1634	GU233441	clade_444	Y	N
Roseburia faecalis	1635	AY804149	clade_444	Y	N
Roseburia faecis	1636	AY305310	clade_444	Y	N
Roseburia hominis	1637	AJ270482	clade_444	Y	N
Roseburia intestinalis	1638	FP929050	clade_444	Y	N
Roseburia inulinivorans	1639	AJ270473	clade_444	Y	N
Brevibacillus brevis	410	NR_041524	clade_448	Y	N
Brevibacillus laterosporus	414	NR_037005	clade_448	Y	N
Bacillus coagulans	206	DQ297928	clade_451	Y	OP
Sporolactobacillus inulinus	1752	NR_040962	clade_451	Y	N
Kocuria palustris	1041	EU333884	clade_453	Y	N
Nocardia farcinica	1353	NC_006361	clade_455	Y	N
Bacillus sp. oral taxon F28	247	HM099650	clade_456	Y	OP
Catenibacterium mitsuokai	495	AB030224	clade_469	Y	N
Clostridium sp. TM_40	640	AB249652	clade_469	Y	N
Coprobacillus cateniformis	670	AB030218	clade_469	Y	N
Coprobacillus sp. 29_1	671	ADKX01000057	clade_469	Y	N
Clostridium rectum	618	NR_029271	clade_470	Y	N
Eubacterium nodatum	854	U13041	clade_476	Y	N
Eubacterium saphenum	859	NR_026031	clade_476	Y	N
Eubacterium sp. oral clone JH012	867	AY349373	clade_476	Y	N
Eubacterium sp. oral clone JS001	870	AY349378	clade_476	Y	N
Faecalibacterium prausnitzii	880	ACOP02000011	clade_478	Y	N
Gemmiger formicilis	932	GU562446	clade_478	Y	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Subdoligranulum variabile	1896	AJ518869	clade_478	Y	N
Clostridiaceae bacterium JC13	532	JF824807	clade_479	Y	N
Clostridium sp. MLG055	634	AF304435	clade_479	Y	N
Erysipelotrichaceae bacterium 3_1_53	822	ACTJ01000113	clade_479	Y	N
Clostridium cocleatum	575	NR_026495	clade_481	Y	N
Clostridium ramosum	617	M23731	clade_481	Y	N
Clostridium saccharogumia	619	DQ100445	clade_481	Y	N
Clostridium spiroforme	644	X73441	clade_481	Y	N
Coprobacillus sp. D7	672	ACDT01000199	clade_481	Y	N
Clostridiales bacterium SY8519	535	AB477431	clade_482	Y	N
Clostridium sp. SY8519	639	AP012212	clade_482	Y	N
Eubacterium ramulus	855	AJ011522	clade_482	Y	N
Erysipelothrix inopinata	819	NR_025594	clade_485	Y	N
Erysipelothrix rhusiopathiae	820	ACLK01000021	clade_485	Y	N
Erysipelothrix tonsillarum	821	NR_040871	clade_485	Y	N
Holdemania filiformis	1004	Y11466	clade_485	Y	N
Mollicutes bacterium pACH93	1258	AY297808	clade_485	Y	N
Coxiella burnetii	736	CP000890	clade_486	Y	Category-B
Clostridium hiranonis	591	AB023970	clade_487	Y	N
Clostridium irregulare	596	NR_029249	clade_487	Y	N
Clostridium orbiscindens	609	Y18187	clade_494	Y	N
Clostridium sp. NML 04A032	637	EU815224	clade_494	Y	N
Flavonifractor plautii	886	AY724678	clade_494	Y	N
Pseudoflavonifractor capillosus	1591	AY136666	clade_494	Y	N
Ruminococcaceae bacterium D16	1655	ADDX01000083	clade_494	Y	N
Acetivibrio cellulolyticus	5	NR_025917	clade_495	Y	N
Clostridium aldrichii	548	NR_026099	clade_495	Y	N
Clostridium clariflavum	570	NR_041235	clade_495	Y	N
Clostridium stercorarium	647	NR_025100	clade_495	Y	N
Clostridium straminisolvens	649	NR_024829	clade_495	Y	N
Clostridium thermocellum	655	NR_074629	clade_495	Y	N
Fusobacterium nucleatum	901	ADVK01000034	clade_497	Y	N
Eubacterium barkeri	834	NR_044661	clade_512	Y	N
Eubacterium callanderi	838	NR_026330	clade_512	Y	N
Eubacterium limosum	850	CP002273	clade_512	Y	N
Anaerotruncus colihominis	164	ABGD02000021	clade_516	Y	N
Clostridium methylpentosum	606	ACEC01000059	clade_516	Y	N
Clostridium sp. YIT 12070	642	AB491208	clade_516	Y	N
Hydrogenoanaerobacterium saccharovorans	1005	NR_044425	clade_516	Y	N
Ruminococcus albus	1656	AY445600	clade_516	Y	N
Ruminococcus flavefaciens	1660	NR_025931	clade_516	Y	N
Clostridium haemolyticum	589	NR_024749	clade_517	Y	N
Clostridium novyi	608	NR_074343	clade_517	Y	N
Clostridium sp. LMG 16094	632	X95274	clade_517	Y	N
Eubacterium ventriosum	874	L34421	clade_519	Y	N
Bacteroides galacturonicus	280	DQ497994	clade_522	Y	N
Eubacterium eligens	845	CP001104	clade_522	Y	N
Lachnospira multipara	1046	FR733699	clade_522	Y	N
Lachnospira pectinoschiza	1047	L14675	clade_522	Y	N
Lactobacillus rogosae	1114	GU269544	clade_522	Y	N
Bacillus horti	214	NR_036860	clade_527	Y	OP
Bacillus sp. 9_3AIA	232	FN397519	clade_527	Y	OP
Eubacterium brachy	836	U13038	clade_533	Y	N
Filifactor alocis	881	CP002390	clade_533	Y	N
Filifactor villosus	882	NR_041928	clade_533	Y	N
Clostridium leptum	601	AJ305238	clade_537	Y	N
Clostridium sp. YIT 12069	641	AB491207	clade_537	Y	N
Clostridium sporosphaeroides	646	NR_044835	clade_537	Y	N
Eubacterium coprostanoligenes	841	HM037995	clade_537	Y	N
Ruminococcus bromii	1657	EU266549	clade_537	Y	N
Eubacterium siraeum	860	ABCA03000054	clade_538	Y	N
Clostridium viride	657	NR_026204	clade_540	Y	N
Oscillibacter sp. G2	1386	HM626173	clade_540	Y	N
Oscillibacter valericigenes	1387	NR_074793	clade_540	Y	N
Oscillospira guilliermondii	1388	AB040495	clade_540	Y	N
Butyrivibrio crossotus	455	ABWN01000012	clade_543	Y	N
Clostridium sp. L2_50	631	AAYW02000018	clade_543	Y	N
Coprococcus eutactus	675	EF031543	clade_543	Y	N
Coprococcus sp. ART55_1	676	AY350746	clade_543	Y	N
Eubacterium ruminantium	857	NR_024661	clade_543	Y	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Collinsella aerofaciens	659	AAVN02000007	clade_553	Y	N
Alkaliphilus metalliredigenes	137	AY137848	clade_554	Y	N
Alkaliphilus oremlandii	138	NR_043674	clade_554	Y	N
Clostridium sticklandii	648	L04167	clade_554	Y	N
Turicibacter sanguinis	1965	AF349724	clade_555	Y	N
Fulvimonas sp. NML 060897	892	EF589680	clade_557	Y	N
Desulfitobacterium frappieri	753	AJ276701	clade_560	Y	N
Desulfitobacterium hafniense	754	NR_074996	clade_560	Y	N
Desulfotomaculum nigrificans	756	NR_044832	clade_560	Y	N
Lutispora thermophila	1191	NR_041236	clade_564	Y	N
Brachyspira pilosicoli	405	NR_075069	clade_565	Y	N
Eggerthella lenta	778	AF292375	clade_566	Y	N
Streptomyces albus	1888	AJ697941	clade_566	Y	N
Chlamydiales bacterium NS11	505	JN606074	clade_567	Y	N
Anaerofustis stercorihominis	159	ABIL02000005	clade_570	Y	N
Butyricicoccus pullicaecorum	453	HH793440	clade_572	Y	N
Eubacterium desmolans	843	NR_044644	clade_572	Y	N
Papillibacter cinnamivorans	1415	NR_025025	clade_572	Y	N
Sporobacter termitidis	1751	NR_044972	clade_572	Y	N
Deferribacteres sp. oral clone JV006	744	AY349371	clade_575	Y	N
Clostridium colinum	577	NR_026151	clade_576	Y	N
Clostridium lactatifermentans	599	NR_025651	clade_576	Y	N
Clostridium piliforme	614	D14639	clade_576	Y	N
Saccharomonospora viridis	1671	X54286	clade_579	Y	N
Thermobifida fusca	1921	NC_007333	clade_579	Y	N
Leptospira licerasiae	1164	EF612284	clade_585	Y	OP
Moorella thermoacetica	1259	NR_075001	clade_590	Y	N
Thermoanaerobacter pseudethanolicus	1920	CP000924	clade_590	Y	N
Flexistipes sinusarabici	888	NR_074881	clade_591	Y	N
Gloeobacter violaceus	942	NR_074282	clade_596	Y	N
Eubacterium sp. oral clone JN088	869	AY349377	clade_90	Y	N
Clostridium oroticum	610	FR749922	clade_96	Y	N
Clostridium sp. D5	627	ADBG01000142	clade_96	Y	N
Eubacterium contortum	840	FR749946	clade_96	Y	N
Eubacterium fissicatena	846	FR749935	clade_96	Y	N
Corynebacterium coyleae	692	X96497	clade_100	N	N
Corynebacterium mucifaciens	711	NR_026396	clade_100	N	N
Corynebacterium ureicelerivorans	733	AM397636	clade_100	N	N
Corynebacterium appendicis	684	NR_028951	clade_102	N	N
Corynebacterium genitalium	698	ACLJ01000031	clade_102	N	N
Corynebacterium glaucum	699	NR_028971	clade_102	N	N
Corynebacterium imitans	703	AF537597	clade_102	N	N
Corynebacterium riegelii	719	EU848548	clade_102	N	N
Corynebacterium sp. L_2012475	723	HE575405	clade_102	N	N
Corynebacterium sp. NML 93_0481	724	GU238409	clade_102	N	N
Corynebacterium sundsvallense	728	Y09655	clade_102	N	N
Corynebacterium tuscaniae	730	AY677186	clade_102	N	N
Prevotella maculosa	1504	AGEK01000035	clade_104	N	N
Prevotella oris	1513	ADDV01000091	clade_104	N	N
Prevotella salivae	1517	AB108826	clade_104	N	N
Prevotella sp. ICM55	1521	HQ616399	clade_104	N	N
Prevotella sp. oral clone AA020	1528	AY005057	clade_104	N	N
Prevotella sp. oral clone GI032	1538	AY349396	clade_104	N	N
Prevotella sp. oral taxon G70	1558	GU432179	clade_104	N	N
Prevotella corporis	1491	L16465	clade_105	N	N
Bacteroides sp. 4_1_36	312	ACTC01000133	clade_110	N	N
Bacteroides sp. AR20	315	AF139524	clade_110	N	N
Bacteroides sp. D20	319	ACPT01000052	clade_110	N	N
Bacteroides sp. F_4	322	AB470322	clade_110	N	N
Bacteroides uniformis	329	AB050110	clade_110	N	N
Prevotella nanceiensis	1510	JN867228	clade_127	N	N
Prevotella sp. oral taxon 299	1548	ACWZ01000026	clade_127	N	N
Prevotella bergensis	1485	ACKS01000100	clade_128	N	N
Prevotella buccalis	1489	JN867261	clade_129	N	N
Prevotella timonensis	1564	ADEF01000012	clade_129	N	N
Prevotella oralis	1512	AEPE01000021	clade_130	N	N
Prevotella sp. SEQ072	1525	JN867238	clade_130	N	N
Leuconostoc carnosum	1177	NR_040811	clade_135	N	N
Leuconostoc gasicomitatum	1179	FN822744	clade_135	N	N
Leuconostoc inhae	1180	NR_025204	clade_135	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Leuconostoc kimchii	1181	NR_075014	clade_135	N	N
Edwardsiella tarda	777	CP002154	clade_139	N	N
Photorhabdus asymbiotica	1466	Z76752	clade_139	N	N
Psychrobacter arcticus	1607	CP000082	clade_141	N	N
Psychrobacter cibarius	1608	HQ698586	clade_141	N	N
Psychrobacter cryohalolentis	1609	CP000323	clade_141	N	N
Psychrobacter faecalis	1610	HQ698566	clade_141	N	N
Psychrobacter nivimaris	1611	HQ698587	clade_141	N	N
Psychrobacter pulmonis	1612	HQ698582	clade_141	N	N
Pseudomonas aeruginosa	1592	AABQ07000001	clade_154	N	N
Pseudomonas sp. 2_1_26	1600	ACWU01000257	clade_154	N	N
Corynebacterium confusum	691	Y15886	clade_158	N	N
Corynebacterium propinquum	712	NR_037038	clade_158	N	N
Corynebacterium pseudodiphtheriticum	713	X84258	clade_158	N	N
Bartonella bacilliformis	338	NC_008783	clade_159	N	N
Bartonella grahamii	339	CP001562	clade_159	N	N
Bartonella henselae	340	NC_005956	clade_159	N	N
Bartonella quintana	341	BX897700	clade_159	N	N
Bartonella tamiae	342	EF672728	clade_159	N	N
Bartonella washoensis	343	FJ719017	clade_159	N	N
Brucella abortus	430	ACBJ01000075	clade_159	N	Category-B
Brucella canis	431	NR_044652	clade_159	N	Category-B
Brucella ceti	432	ACJD01000006	clade_159	N	Category-B
Brucella melitensis	433	AE009462	clade_159	N	Category-B
Brucella microti	434	NR_042549	clade_159	N	Category-B
Brucella ovis	435	NC_009504	clade_159	N	Category-B
Brucella sp. 83_13	436	ACBQ01000040	clade_159	N	Category-B
Brucella sp. BO1	437	EU053207	clade_159	N	Category-B
Brucella suis	438	ACBK01000034	clade_159	N	Category-B
Ochrobactrum anthropi	1360	NC_009667	clade_159	N	N
Ochrobactrum intermedium	1361	ACQA01000001	clade_159	N	N
Ochrobactrum pseudintermedium	1362	DQ365921	clade_159	N	N
Prevotella genomosp. C2	1496	AY278625	clade_164	N	N
Prevotella multisaccharivorax	1509	AFJE01000016	clade_164	N	N
Prevotella sp. oral clone IDR_CEC_0055	1543	AY550997	clade_164	N	N
Prevotella sp. oral taxon 292	1547	GQ422735	clade_164	N	N
Prevotella sp. oral taxon 300	1549	GU409549	clade_164	N	N
Prevotella marshii	1505	AEEI01000070	clade_166	N	N
Prevotella sp. oral clone IK053	1544	AY349401	clade_166	N	N
Prevotella sp. oral taxon 781	1554	GQ422744	clade_166	N	N
Prevotella stercorea	1562	AB244774	clade_166	N	N
Prevotella brevis	1487	NR_041954	clade_167	N	N
Prevotella ruminicola	1516	CP002006	clade_167	N	N
Prevotella sp. sp24	1560	AB003384	clade_167	N	N
Prevotella sp. sp34	1561	AB003385	clade_167	N	N
Prevotella albensis	1483	NR_025300	clade_168	N	N
Prevotella copri	1490	ACBX02000014	clade_168	N	N
Prevotella oulorum	1514	L16472	clade_168	N	N
Prevotella sp. BI_42	1518	AJ581354	clade_168	N	N
Prevotella sp. oral clone P4PB_83 P2	1546	AY207050	clade_168	N	N
Prevotella sp. oral taxon G60	1557	GU432133	clade_168	N	N
Prevotella amnii	1484	AB547670	clade_169	N	N
Bacteroides caccae	268	EU136686	clade_170	N	N
Bacteroides finegoldii	277	AB222699	clade_170	N	N
Bacteroides intestinalis	283	ABJL02000006	clade_171	N	N
Bacteroides sp. XB44A	326	AM230649	clade_171	N	N
Bifidobacteriaceae genomosp. C1	345	AY278612	clade_172	N	N
Bifidobacterium adolescentis	346	AAXD02000018	clade_172	N	N
Bifidobacterium angulatum	347	ABYS02000004	clade_172	N	N
Bifidobacterium animalis	348	CP001606	clade_172	N	N
Bifidobacterium breve	350	CP002743	clade_172	N	N
Bifidobacterium catenulatum	351	ABXY01000019	clade_172	N	N
Bifidobacterium dentium	352	CP001750	clade_172	N	OP
Bifidobacterium gallicum	353	ABXB03000004	clade_172	N	N
Bifidobacterium infantis	354	AY151398	clade_172	N	N
Bifidobacterium kashiwanohense	355	AB491757	clade_172	N	N
Bifidobacterium longum	356	ABQQ01000041	clade_172	N	N
Bifidobacterium pseudocatenulatum	357	ABXX02000002	clade_172	N	N
Bifidobacterium pseudolongum	358	NR_043442	clade_172	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Bifidobacterium scardovii	359	AJ307005	clade_172	N	N
Bifidobacterium sp. HM2	360	AB425276	clade_172	N	N
Bifidobacterium sp. HMLN12	361	JF519685	clade_172	N	N
Bifidobacterium sp. M45	362	HM626176	clade_172	N	N
Bifidobacterium sp. MSX5B	363	HQ616382	clade_172	N	N
Bifidobacterium sp. TM_7	364	AB218972	clade_172	N	N
Bifidobacterium thermophilum	365	DQ340557	clade_172	N	N
Leuconostoc citreum	1178	AM157444	clade_175	N	N
Leuconostoc lactis	1182	NR_040823	clade_175	N	N
Alicyclobacillus acidoterrestris	123	NR_040844	clade_179	N	N
Alicyclobacillus cycloheptanicus	125	NR_024754	clade_179	N	N
Acinetobacter baumannii	27	ACYQ01000014	clade_181	N	N
Acinetobacter calcoaceticus	28	AM157426	clade_181	N	N
Acinetobacter genomosp. C1	29	AY278636	clade_181	N	N
Acinetobacter haemolyticus	30	ADMT01000017	clade_181	N	N
Acinetobacter johnsonii	31	ACPL01000162	clade_181	N	N
Acinetobacter junii	32	ACPM01000135	clade_181	N	N
Acinetobacter lwoffii	33	ACPN01000204	clade_181	N	N
Acinetobacter parvus	34	AIEB01000124	clade_181	N	N
Acinetobacter schindleri	36	NR_025412	clade_181	N	N
Acinetobacter sp. 56A1	37	GQ178049	clade_181	N	N
Acinetobacter sp. CIP 101934	38	JQ638573	clade_181	N	N
Acinetobacter sp. CIP 102143	39	JQ638578	clade_181	N	N
Acinetobacter sp. M16_22	41	HM366447	clade_181	N	N
Acinetobacter sp. RUH2624	42	ACQF01000094	clade_181	N	N
Acinetobacter sp. SH024	43	ADCH01000068	clade_181	N	N
Lactobacillus jensenii	1092	ACQD01000066	clade_182	N	N
Alcaligenes faecalis	119	AB680368	clade_183	N	N
Alcaligenes sp. CO14	120	DQ643040	clade_183	N	N
Alcaligenes sp. S3	121	HQ262549	clade_183	N	N
Oligella ureolytica	1366	NR_041998	clade_183	N	N
Oligella urethralis	1367	NR_041753	clade_183	N	N
Eikenella corrodens	784	ACEA01000028	clade_185	N	N
Kingella denitrificans	1019	AEWV01000047	clade_185	N	N
Kingella genomosp. P1 oral cone MB2_C20	1020	DQ003616	clade_185	N	N
Kingella kingae	1021	AFHS01000073	clade_185	N	N
Kingella oralis	1022	ACJW02000005	clade_185	N	N
Kingella sp. oral clone ID059	1023	AY349381	clade_185	N	N
Neisseria elongata	1330	ADBF01000003	clade_185	N	N
Neisseria genomosp. P2 oral clone MB5_P15	1332	DQ003630	clade_185	N	N
Neisseria sp. oral clone JC012	1345	AY349388	clade_185	N	N
Neisseria sp. SMC_A9199	1342	FJ763637	clade_185	N	N
Simonsiella muelleri	1731	ADCY01000105	clade_185	N	N
Corynebacterium glucuronolyticum	700	ABYP01000081	clade_193	N	N
Corynebacterium pyruviciproducens	716	FJ185225	clade_193	N	N
Rothia aeria	1649	DQ673320	clade_194	N	N
Rothia dentocariosa	1650	ADDW01000024	clade_194	N	N
Rothia sp. oral taxon 188	1653	GU470892	clade_194	N	N
Corynebacterium accolens	681	ACGD01000048	clade_195	N	N
Corynebacterium macginleyi	707	AB359393	clade_195	N	N
Corynebacterium pseudogenitalium	714	ABYQ01000237	clade_195	N	N
Corynebacterium tuberculostearicum	729	ACVP01000009	clade_195	N	N
Lactobacillus casei	1074	CP000423	clade_198	N	N
Lactobacillus paracasei	1106	ABQV01000067	clade_198	N	N
Lactobacillus zeae	1143	NR_037122	clade_198	N	N
Prevotella dentalis	1492	AB547678	clade_205	N	N
Prevotella sp. oral clone ASCG10	1529	AY923148	clade_206	N	N
Prevotella sp. oral clone HF050	1541	AY349399	clade_206	N	N
Prevotella sp. oral clone ID019	1542	AY349400	clade_206	N	N
Prevotella sp. oral clone IK062	1545	AY349402	clade_206	N	N
Prevotella genomosp. P9 oral clone MB7_G16	1499	DQ003633	clade_207	N	N
Prevotella sp. oral clone AU069	1531	AY005062	clade_207	N	N
Prevotella sp. oral clone CY006	1532	AY005063	clade_207	N	N
Prevotella sp. oral clone FL019	1534	AY349392	clade_207	N	N
Actinomyces genomosp. C1	56	AY278610	clade_212	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Actinomyces genomosp. C2	57	AY278611	clade_212	N	N
Actinomyces genomosp. P1 oral clone MB6_C03	58	DQ003632	clade_212	N	N
Actinomyces georgiae	59	GU561319	clade_212	N	N
Actinomyces israelii	60	AF479270	clade_212	N	N
Actinomyces massiliensis	61	AB545934	clade_212	N	N
Actinomyces meyeri	62	GU561321	clade_212	N	N
Actinomyces odontolyticus	66	ACYT01000123	clade_212	N	N
Actinomyces orihominis	68	AJ575186	clade_212	N	N
Actinomyces sp. CCUG 37290	71	AJ234058	clade_212	N	N
Actinomyces sp. ICM34	75	HQ616391	clade_212	N	N
Actinomyces sp. ICM41	76	HQ616392	clade_212	N	N
Actinomyces sp. ICM47	77	HQ616395	clade_212	N	N
Actinomyces sp. ICM54	78	HQ616398	clade_212	N	N
Actinomyces sp. oral clone IP081	87	AY349366	clade_212	N	N
Actinomyces sp. oral taxon 178	91	AEUH01000060	clade_212	N	N
Actinomyces sp. oral taxon 180	92	AEPP01000041	clade_212	N	N
Actinomyces sp. TeJ5	80	GU561315	clade_212	N	N
Haematobacter sp. BC14248	968	GU396991	clade_213	N	N
Paracoccus denitrificans	1424	CP000490	clade_213	N	N
Paracoccus marcusii	1425	NR_044922	clade_213	N	N
Grimontia hollisae	967	ADAQ01000013	clade_216	N	N
Shewanella putrefaciens	1723	CP002457	clade_216	N	N
Afipia genomosp. 4	111	EU117385	clade_217	N	N
Rhodopseudomonas palustris	1626	CP000301	clade_217	N	N
Methylobacterium extorquens	1223	NC_010172	clade_218	N	N
Methylobacterium podarium	1224	AY468363	clade_218	N	N
Methylobacterium radiotolerans	1225	GU294320	clade_218	N	N
Methylobacterium sp. 1sub	1226	AY468371	clade_218	N	N
Methylobacterium sp. MM4	1227	AY468370	clade_218	N	N
Achromobacter denitrificans	18	NR_042021	clade_224	N	N
Achromobacter piechaudii	19	ADMS01000149	clade_224	N	N
Achromobacter xylosoxidans	20	ACRC01000072	clade_224	N	N
Bordetella bronchiseptica	384	NR_025949	clade_224	N	OP
Bordetella holmesii	385	AB683187	clade_224	N	OP
Bordetella parapertussis	386	NR_025950	clade_224	N	OP
Bordetella pertussis	387	BX640418	clade_224	N	OP
Microbacterium chocolatum	1230	NR_037045	clade_225	N	N
Microbacterium flavescens	1231	EU714363	clade_225	N	N
Microbacterium lacticum	1233	EU714351	clade_225	N	N
Microbacterium oleivorans	1234	EU714381	clade_225	N	N
Microbacterium oxydans	1235	EU714348	clade_225	N	N
Microbacterium paraoxydans	1236	AJ491806	clade_225	N	N
Microbacterium phyllosphaerae	1237	EU714359	clade_225	N	N
Microbacterium schleiferi	1238	NR_044936	clade_225	N	N
Microbacterium sp. 768	1239	EU714378	clade_225	N	N
Microbacterium sp. oral strain C24KA	1240	AF287752	clade_225	N	N
Microbacterium testaceum	1241	EU714365	clade_225	N	N
Corynebacterium atypicum	686	NR_025540	clade_229	N	N
Corynebacterium mastitidis	708	AB359395	clade_229	N	N
Corynebacterium sp. NML 97_0186	725	GU238411	clade_229	N	N
Mycobacterium elephantis	1275	AF385898	clade_237	N	OP
Mycobacterium paraterrae	1288	EU919229	clade_237	N	OP
Mycobacterium phlei	1289	GU142920	clade_237	N	OP
Mycobacterium sp. 1776	1293	EU703152	clade_237	N	N
Mycobacterium sp. 1781	1294	EU703147	clade_237	N	N
Mycobacterium sp. AQ1GA4	1297	HM210417	clade_237	N	N
Mycobacterium sp. GN_10546	1299	FJ497243	clade_237	N	N
Mycobacterium sp. GN_10827	1300	FJ497247	clade_237	N	N
Mycobacterium sp. GN_11124	1301	FJ652846	clade_237	N	N
Mycobacterium sp. GN_9188	1302	FJ497240	clade_237	N	N
Mycobacterium sp. GR_2007_210	1303	FJ555538	clade_237	N	N
Anoxybacillus contaminans	172	NR_029006	clade_238	N	N
Bacillus aeolius	195	NR_025557	clade_238	N	N
Brevibacterium frigoritolerans	422	NR_042639	clade_238	N	N
Geobacillus sp. E263	934	DQ647387	clade_238	N	N
Geobacillus sp. WCH70	935	CP001638	clade_238	N	N
Geobacillus thermocatenulatus	937	NR_043020	clade_238	N	N
Geobacillus thermoleovorans	940	NR_074931	clade_238	N	N
Lysinibacillus fusiformis	1192	FN397522	clade_238	N	N
Planomicrobium koreense	1468	NR_025011	clade_238	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Sporosarcina newyorkensis	1754	AFPZ01000142	clade_238	N	N
Sporosarcina sp. 2681	1755	GU994081	clade_238	N	N
Ureibacillus composti	1968	NR_043746	clade_238	N	N
Ureibacillus suwonensis	1969	NR_043232	clade_238	N	N
Ureibacillus terrenus	1970	NR_025394	clade_238	N	N
Ureibacillus thermophilus	1971	NR_043747	clade_238	N	N
Ureibacillus thermosphaericus	1972	NR_040961	clade_238	N	N
Prevotella micans	1507	AGWK01000061	clade_239	N	N
Prevotella sp. oral clone DA058	1533	AY005065	clade_239	N	N
Prevotella sp. SEQ053	1523	JN867222	clade_239	N	N
Treponema socranskii	1937	NR_024868	clade_240	N	OP
Treponema sp. 6:H:D15A_4	1938	AY005083	clade_240	N	N
Treponema sp. oral taxon 265	1953	GU408850	clade_240	N	N
Treponema sp. oral taxon G85	1958	GU432215	clade_240	N	N
Porphyromonas endodontalis	1472	ACNN01000021	clade_241	N	N
Porphyromonas sp. oral clone BB134	1478	AY005068	clade_241	N	N
Porphyromonas sp. oral clone F016	1479	AY005069	clade_241	N	N
Porphyromonas sp. oral clone P2PB_52 P1	1480	AY207054	clade_241	N	N
Porphyromonas sp. oral clone P4GB_100 P2	1481	AY207057	clade_241	N	N
Acidovorax sp. 98_63833	26	AY258065	clade_245	N	N
Comamonadaceae bacterium NML000135	663	JN585335	clade_245	N	N
Comamonadaceae bacterium NML790751	664	JN585331	clade_245	N	N
Comamonadaceae bacterium NML910035	665	JN585332	clade_245	N	N
Comamonadaceae bacterium NML910036	666	JN585333	clade_245	N	N
Comamonas sp. NSP5	668	AB076850	clade_245	N	N
Delftia acidovorans	748	CP000884	clade_245	N	N
Xenophilus aerolatus	2018	JN585329	clade_245	N	N
Oribacterium sp. oral taxon 078	1380	ACIQ02000009	clade_246	N	N
Oribacterium sp. oral taxon 102	1381	GQ422713	clade_246	N	N
Weissella cibaria	2007	NR_036924	clade_247	N	N
Weissella confusa	2008	NR_040816	clade_247	N	N
Weissella hellenica	2009	AB680902	clade_247	N	N
Weissella kandleri	2010	NR_044659	clade_247	N	N
Weissella koreensis	2011	NR_075058	clade_247	N	N
Weissella paramesenteroides	2012	ACKU01000017	clade_247	N	N
Weissella sp. KLDS 7.0701	2013	EU600924	clade_247	N	N
Mobiluncus curtisii	1251	AEPZ01000013	clade_249	N	N
Enhydrobacter aerosaccus	785	ACYI01000081	clade_256	N	N
Moraxella osloensis	1262	JN175341	clade_256	N	N
Moraxella sp. GM2	1264	JF837191	clade_256	N	N
Brevibacterium casei	420	JF951998	clade_257	N	N
Brevibacterium epidermidis	421	NR_029262	clade_257	N	N
Brevibacterium sanguinis	426	NR_028016	clade_257	N	N
Brevibacterium sp. H15	427	AB177640	clade_257	N	N
Acinetobacter radioresistens	35	ACVR01000010	clade_261	N	N
Lactobacillus alimentarius	1068	NR_044701	clade_263	N	N
Lactobacillus farciminis	1082	NR_044707	clade_263	N	N
Lactobacillus kimchii	1097	NR_025045	clade_263	N	N
Lactobacillus nodensis	1101	NR_041629	clade_263	N	N
Lactobacillus tucceti	1138	NR_042194	clade_263	N	N
Pseudomonas mendocina	1595	AAUL01000021	clade_265	N	N
Pseudomonas pseudoalcaligenes	1598	NR_037000	clade_265	N	N
Pseudomonas sp. NP522b	1602	EU723211	clade_265	N	N
Pseudomonas stutzeri	1603	AM905854	clade_265	N	N
Paenibacillus barcinonensis	1390	NR_042272	clade_270	N	N
Paenibacillus barengoltzii	1391	NR_042756	clade_270	N	N
Paenibacillus chibensis	1392	NR_040885	clade_270	N	N
Paenibacillus cookii	1393	NR_025372	clade_270	N	N
Paenibacillus durus	1394	NR_037017	clade_270	N	N
Paenibacillus glucanolyticus	1395	D78470	clade_270	N	N
Paenibacillus lactis	1396	NR_025739	clade_270	N	N
Paenibacillus pabuli	1398	NR_040853	clade_270	N	N
Paenibacillus popilliae	1400	NR_040888	clade_270	N	N
Paenibacillus sp. CIP 101062	1401	HM212646	clade_270	N	N
Paenibacillus sp. JC66	1404	JF824808	clade_270	N	N
Paenibacillus sp. R_27413	1405	HE586333	clade_270	N	N
Paenibacillus sp. R_27422	1406	HE586338	clade_270	N	N
Paenibacillus timonensis	1408	NR_042844	clade_270	N	N
Rothia mucilaginosa	1651	ACVO01000020	clade_271	N	N
Rothia nasimurium	1652	NR_025310	clade_271	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Prevotella sp. oral taxon 302	1550	ACZK01000043	clade_280	N	N
Prevotella sp. oral taxon F68	1556	HM099652	clade_280	N	N
Prevotella tannerae	1563	ACIJ02000018	clade_280	N	N
Prevotellaceae bacterium P4P_62 P1	1566	AY207061	clade_280	N	N
Porphyromonas asaccharolytica	1471	AENO01000048	clade_281	N	N
Porphyromonas gingivalis	1473	AE015924	clade_281	N	N
Porphyromonas macacae	1475	NR_025908	clade_281	N	N
Porphyromonas sp. UQD 301	1477	EU012301	clade_281	N	N
Porphyromonas uenonis	1482	ACLR01000152	clade_281	N	N
Leptotrichia buccalis	1165	CP001685	clade_282	N	N
Leptotrichia hofstadii	1168	ACVB02000032	clade_282	N	N
Leptotrichia sp. oral clone HE012	1173	AY349386	clade_282	N	N
Leptotrichia sp. oral taxon223	1176	GU408547	clade_282	N	N
Bacteroides fluxus	278	AFBN01000029	clade_285	N	N
Bacteroides helcogenes	281	CP002352	clade_285	N	N
Parabacteroides johnsonii	1419	ABYH01000014	clade_286	N	N
Parabacteroides merdae	1420	EU136685	clade_286	N	N
Treponema denticola	1926	ADEC01000002	clade_288	N	OP
Treponema genomosp. P5 oral clone MB3_P23	1929	DQ003624	clade_288	N	N
Treponema putidum	1935	AJ543428	clade_288	N	OP
Treponema sp. oral clone P2PB_53 P3	1942	AY207055	clade_288	N	N
Treponema sp. oral taxon 247	1949	GU408748	clade_288	N	N
Treponema sp. oral taxon 250	1950	GU408776	clade_288	N	N
Treponema sp. oral taxon 251	1951	GU408781	clade_288	N	N
Anaerococcus hydrogenalis	144	ABXA01000039	clade_289	N	N
Anaerococcus sp. 8404299	148	HM587318	clade_289	N	N
Anaerococcus sp. gpac215	156	AM176540	clade_289	N	N
Anaerococcus vaginalis	158	ACXU01000016	clade_289	N	N
Propionibacterium acidipropionici	1569	NC_019395	clade_290	N	N
Propionibacterium avidum	1571	AJ003055	clade_290	N	N
Propionibacterium granulosum	1573	FJ785716	clade_290	N	N
Propionibacterium jensenii	1574	NR_042269	clade_290	N	N
Propionibacterium propionicum	1575	NR_025277	clade_290	N	N
Propionibacterium sp. H456	1577	AB177643	clade_290	N	N
Propionibacterium thoenii	1581	NR_042270	clade_290	N	N
Bifidobacterium bifidum	349	ABQP01000027	clade_293	N	N
Leuconostoc mesenteroides	1183	ACKV01000113	clade_295	N	N
Leuconostoc pseudomesenteroides	1184	NR_040814	clade_295	N	N
Johnsonella ignava	1016	X87152	clade_298	N	N
Propionibacterium acnes	1570	ADJM01000010	clade_299	N	N
Propionibacterium sp. 434_HC2	1576	AFIL01000035	clade_299	N	N
Propionibacterium sp. LG	1578	AY354921	clade_299	N	N
Propionibacterium sp. S555a	1579	AB264622	clade_299	N	N
Alicyclobacillus sp. CCUG 53762	128	HE613268	clade_301	N	N
Actinomyces cardiffensis	53	GU470888	clade_303	N	N
Actinomyces funkei	55	HQ906497	clade_303	N	N
Actinomyces sp. HKU31	74	HQ335393	clade_303	N	N
Actinomyces sp. oral taxon C55	94	HM099646	clade_303	N	N
Kerstersia gyiorum	1018	NR_025669	clade_307	N	N
Pigmentiphaga daeguensis	1467	JN585327	clade_307	N	N
Aeromonas allosaccharophila	104	S39232	clade_308	N	N
Aeromonas enteropelogenes	105	X71121	clade_308	N	N
Aeromonas hydrophila	106	NC_008570	clade_308	N	N
Aeromonas jandaei	107	X60413	clade_308	N	N
Aeromonas salmonicida	108	NC_009348	clade_308	N	N
Aeromonas trota	109	X60415	clade_308	N	N
Aeromonas veronii	110	NR_044845	clade_308	N	N
Marvinbryantia formatexigens	1196	AJ505973	clade_309	N	N
Rhodobacter sp. oral taxon C30	1620	HM099648	clade_310	N	N
Rhodobacter sphaeroides	1621	CP000144	clade_310	N	N
Lactobacillus antri	1071	ACLL01000037	clade_313	N	N
Lactobacillus coleohominis	1076	ACOH01000030	clade_313	N	N
Lactobacillus fermentum	1083	CP002033	clade_313	N	N
Lactobacillus gastricus	1085	AICN01000060	clade_313	N	N
Lactobacillus mucosae	1099	FR693800	clade_313	N	N
Lactobacillus oris	1103	AEKL01000077	clade_313	N	N
Lactobacillus pontis	1111	HM218420	clade_313	N	N
Lactobacillus reuteri	1112	ACGW02000012	clade_313	N	N
Lactobacillus sp. KLDS 1.0707	1127	EU600911	clade_313	N	N
Lactobacillus sp. KLDS 1.0709	1128	EU600913	clade_313	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Lactobacillus sp. KLDS 1.0711	1129	EU600915	clade_313	N	N
Lactobacillus sp. KLDS 1.0713	1131	EU600917	clade_313	N	N
Lactobacillus sp. KLDS 1.0716	1132	EU600921	clade_313	N	N
Lactobacillus sp. KLDS 1.0718	1133	EU600922	clade_313	N	N
Lactobacillus sp. oral taxon 052	1137	GQ422710	clade_313	N	N
Lactobacillus vaginalis	1140	ACGV01000168	clade_313	N	N
Brevibacterium aurantiacum	419	NR_044854	clade_314	N	N
Brevibacterium linens	423	AJ315491	clade_314	N	N
Lactobacillus pentosus	1108	JN813103	clade_315	N	N
Lactobacillus plantarum	1110	ACGZ02000033	clade_315	N	N
Lactobacillus sp. KLDS 1.0702	1123	EU600906	clade_315	N	N
Lactobacillus sp. KLDS 1.0703	1124	EU600907	clade_315	N	N
Lactobacillus sp. KLDS 1.0704	1125	EU600908	clade_315	N	N
Lactobacillus sp. KLDS 1.0705	1126	EU600909	clade_315	N	N
Agrobacterium radiobacter	115	CP000628	clade_316	N	N
Agrobacterium tumefaciens	116	AJ389893	clade_316	N	N
Corynebacterium argentoratense	685	EF463055	clade_317	N	N
Corynebacterium diphtheriae	693	NC_002935	clade_317	N	OP
Corynebacterium pseudotuberculosis	715	NR_037070	clade_317	N	N
Corynebacterium renale	717	NR_037069	clade_317	N	N
Corynebacterium ulcerans	731	NR_074467	clade_317	N	N
Aurantimonas coralicida	191	AY065627	clade_318	N	N
Aureimonas altamirensis	192	FN658986	clade_318	N	N
Lactobacillus acidipiscis	1066	NR_024718	clade_320	N	N
Lactobacillus salivarius	1117	AEBA01000145	clade_320	N	N
Lactobacillus sp. KLDS 1.0719	1134	EU600923	clade_320	N	N
Lactobacillus buchneri	1073	ACGH01000101	clade_321	N	N
Lactobacillus genomosp. C1	1086	AY278619	clade_321	N	N
Lactobacillus genomosp. C2	1087	AY278620	clade_321	N	N
Lactobacillus hilgardii	1089	ACGP01000200	clade_321	N	N
Lactobacillus kefiri	1096	NR_042230	clade_321	N	N
Lactobacillus parabuchneri	1105	NR_041294	clade_321	N	N
Lactobacillus parakefiri	1107	NR_029039	clade_321	N	N
Lactobacillus curvatus	1079	NR_042437	clade_322	N	N
Lactobacillus sakei	1116	DQ989236	clade_322	N	N
Aneurinibacillus aneurinilyticus	167	AB101592	clade_323	N	N
Aneurinibacillus danicus	168	NR_028657	clade_323	N	N
Aneurinibacillus migulanus	169	NR_036799	clade_323	N	N
Aneurinibacillus terranovensis	170	NR_042271	clade_323	N	N
Staphylococcus aureus	1757	CP002643	clade_325	N	Category-B
Staphylococcus auricularis	1758	JQ624774	clade_325	N	N
Staphylococcus capitis	1759	ACFR01000029	clade_325	N	N
Staphylococcus caprae	1760	ACRH01000033	clade_325	N	N
Staphylococcus carnosus	1761	NR_075003	clade_325	N	N
Staphylococcus cohnii	1762	JN175375	clade_325	N	N
Staphylococcus condimenti	1763	NR_029345	clade_325	N	N
Staphylococcus epidermidis	1764	ACHE01000056	clade_325	N	N
Staphylococcus equorum	1765	NR_027520	clade_325	N	N
Staphylococcus haemolyticus	1767	NC_007168	clade_325	N	N
Staphylococcus hominis	1768	AM157418	clade_325	N	N
Staphylococcus lugdunensis	1769	AEQA01000024	clade_325	N	N
Staphylococcus pasteuri	1770	FJ189773	clade_325	N	N
Staphylococcus pseudintermedius	1771	CP002439	clade_325	N	N
Staphylococcus saccharolyticus	1772	NR_029158	clade_325	N	N
Staphylococcus saprophyticus	1773	NC_007350	clade_325	N	N
Staphylococcus sp. clone bottae7	1777	AF467424	clade_325	N	N
Staphylococcus sp. H292	1775	AB177642	clade_325	N	N
Staphylococcus sp. H780	1776	AB177644	clade_325	N	N
Staphylococcus succinus	1778	NR_028667	clade_325	N	N
Staphylococcus warneri	1780	ACPZ01000009	clade_325	N	N
Staphylococcus xylosus	1781	AY395016	clade_325	N	N
Cardiobacterium hominis	490	ACKY01000036	clade_326	N	N
Cardiobacterium valvarum	491	NR_028847	clade_326	N	N
Pseudomonas fluorescens	1593	AY622220	clade_326	N	N
Pseudomonas gessardii	1594	FJ943496	clade_326	N	N
Pseudomonas monteilii	1596	NR_024910	clade_326	N	N
Pseudomonas poae	1597	GU188951	clade_326	N	N
Pseudomonas putida	1599	AF094741	clade_326	N	N
Pseudomonas sp. G1229	1601	DQ910482	clade_326	N	N
Pseudomonas tolaasii	1604	AF320988	clade_326	N	N
Pseudomonas viridiflava	1605	NR_042764	clade_326	N	N
Listeria grayi	1185	ACCR02000003	clade_328	N	OP

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Listeria innocua	1186	JF967625	clade_328	N	N
Listeria ivanovii	1187	X56151	clade_328	N	N
Listeria monocytogenes	1188	CP002003	clade_328	N	Category-B
Listeria welshimeri	1189	AM263198	clade_328	N	OP
Capnocytophaga sp. oral clone ASCH05	484	AY923149	clade_333	N	N
Capnocytophaga sputigena	489	ABZV01000054	clade_333	N	N
Leptotrichia genomosp. C1	1166	AY278621	clade_334	N	N
Leptotrichia shahii	1169	AY029806	clade_334	N	N
Leptotrichia sp. neutropenicPatient	1170	AF189244	clade_334	N	N
Leptotrichia sp. oral clone GT018	1171	AY349384	clade_334	N	N
Leptotrichia sp. oral clone GT020	1172	AY349385	clade_334	N	N
Bacteroides sp. 20_3	296	ACRQ01000064	clade_335	N	N
Bacteroides sp. 3_1_19	307	ADCJ01000062	clade_335	N	N
Bacteroides sp. 3_2_5	311	ACIB01000079	clade_335	N	N
Parabacteroides distasonis	1416	CP000140	clade_335	N	N
Parabacteroides goldsteinii	1417	AY974070	clade_335	N	N
Parabacteroides gordonii	1418	AB470344	clade_335	N	N
Parabacteroides sp. D13	1421	ACPW01000017	clade_335	N	N
Capnocytophaga genomosp. C1	477	AY278613	clade_336	N	N
Capnocytophaga ochracea	480	AEOH01000054	clade_336	N	N
Capnocytophaga sp. GEJ8	481	GU561335	clade_336	N	N
Capnocytophaga sp. oral strain A47ROY	486	AY005077	clade_336	N	N
Capnocytophaga sp. S1b	482	U42009	clade_336	N	N
Paraprevotella clara	1426	AFFY01000068	clade_336	N	N
Bacteroides heparinolyticus	282	JN867284	clade_338	N	N
Prevotella heparinolytica	1500	GQ422742	clade_338	N	N
Treponema genomosp. P4 oral clone MB2_G19	1928	DQ003618	clade_339	N	N
Treponema genomosp. P6 oral clone MB4_G11	1930	DQ003625	clade_339	N	N
Treponema sp. oral taxon 254	1952	GU408803	clade_339	N	N
Treponema sp. oral taxon 508	1956	GU413616	clade_339	N	N
Treponema sp. oral taxon 518	1957	GU413640	clade_339	N	N
Chlamydia muridarum	502	AE002160	clade_341	N	OP
Chlamydia trachomatis	504	U68443	clade_341	N	OP
Chlamydia psittaci	503	NR_036864	clade_342	N	Category-B
Chlamydophila pneumoniae	509	NC_002179	clade_342	N	OP
Chlamydophila psittaci	510	D85712	clade_342	N	OP
Anaerococcus octavius	146	NR_026360	clade_343	N	N
Anaerococcus sp. 8405254	149	HM587319	clade_343	N	N
Anaerococcus sp. 9401487	150	HM587322	clade_343	N	N
Anaerococcus sp. 9403502	151	HM587325	clade_343	N	N
Gardnerella vaginalis	923	CP001849	clade_344	N	N
Campylobacter lari	466	CP000932	clade_346	N	OP
Anaerobiospirillum succiniciproducens	142	NR_026075	clade_347	N	N
Anaerobiospirillum thomasii	143	AJ420985	clade_347	N	N
Ruminobacter amylophilus	1654	NR_026450	clade_347	N	N
Succinatimonas hippei	1897	AEVO01000027	clade_347	N	N
Actinomyces europaeus	54	NR_026363	clade_348	N	N
Actinomyces sp. oral clone GU009	82	AY349361	clade_348	N	N
Moraxella catarrhalis	1260	CP002005	clade_349	N	N
Moraxella lincolnii	1261	FR822735	clade_349	N	N
Moraxella sp. 16285	1263	JF682466	clade_349	N	N
Psychrobacter sp. 13983	1613	HM212668	clade_349	N	N
Actinobaculum massiliae	49	AF487679	clade_350	N	N
Actinobaculum schaalii	50	AY957507	clade_350	N	N
Actinobaculum sp. BM#101342	51	AY282578	clade_350	N	N
Actinobaculum sp. P2P_19 P1	52	AY207066	clade_350	N	N
Actinomyces sp. oral clone IO076	84	AY349363	clade_350	N	N
Actinomyces sp. oral taxon 848	93	ACUY01000072	clade_350	N	N
Actinomyces neuii	65	X71862	clade_352	N	N
Mobiluncus mulieris	1252	ACKW01000035	clade_352	N	N
Blastomonas natatoria	372	NR_040824	clade_356	N	N
Novosphingobium aromaticivorans	1357	AAAV03000008	clade_356	N	N
Sphingomonas sp. oral clone FI012	1745	AY349411	clade_356	N	N
Sphingopyxis alaskensis	1749	CP000356	clade_356	N	N
Oxalobacter formigenes	1389	ACDQ01000020	clade_357	N	N
Veillonella atypica	1974	AEDS01000059	clade_358	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Veillonella dispar	1975	ACIK02000021	clade_358	N	N
Veillonella genomosp. P1 oral clone MB5_P17	1976	DQ003631	clade_358	N	N
Veillonella parvula	1978	ADFU01000009	clade_358	N	N
Veillonella sp. 3_1_44	1979	ADCV01000019	clade_358	N	N
Veillonella sp. 6_1_27	1980	ADCW01000016	clade_358	N	N
Veillonella sp. ACP1	1981	HQ616359	clade_358	N	N
Veillonella sp. AS16	1982	HQ616365	clade_358	N	N
Veillonella sp. BS32b	1983	HQ616368	clade_358	N	N
Veillonella sp. ICM51a	1984	HQ616396	clade_358	N	N
Veillonella sp. MSA12	1985	HQ616381	clade_358	N	N
Veillonella sp. NVG 100cf	1986	EF108443	clade_358	N	N
Veillonella sp. OK11	1987	JN695650	clade_358	N	N
Veillonella sp. oral clone ASCG01	1990	AY923144	clade_358	N	N
Veillonella sp. oral clone ASCG02	1991	AY953257	clade_358	N	N
Veillonella sp. oral clone OH1A	1992	AY947495	clade_358	N	N
Veillonella sp. oral taxon 158	1993	AENU01000007	clade_358	N	N
Kocuria marina	1040	GQ260086	clade_365	N	N
Kocuria rhizophila	1042	AY030315	clade_365	N	N
Kocuria rosea	1043	X87756	clade_365	N	N
Kocuria varians	1044	AF542074	clade_365	N	N
Clostridiaceae bacterium END_2	531	EF451053	clade_368	N	N
Micrococcus antarcticus	1242	NR_025285	clade_371	N	N
Micrococcus luteus	1243	NR_075062	clade_371	N	N
Micrococcus lylae	1244	NR_026200	clade_371	N	N
Micrococcus sp. 185	1245	EU714334	clade_371	N	N
Lactobacillus brevis	1072	EU194349	clade_372	N	N
Lactobacillus parabrevis	1104	NR_042456	clade_372	N	N
Pediococcus acidilactici	1436	ACXB01000026	clade_372	N	N
Pediococcus pentosaceus	1437	NR_075052	clade_372	N	N
Lactobacillus dextrinicus	1081	NR_036861	clade_373	N	N
Lactobacillus perolens	1109	NR_029360	clade_373	N	N
Lactobacillus rhamnosus	1113	ABWJ01000068	clade_373	N	N
Lactobacillus saniviri	1118	AB602569	clade_373	N	N
Lactobacillus sp. BT6	1121	HQ616370	clade_373	N	N
Mycobacterium mageritense	1282	FR798914	clade_374	N	OP
Mycobacterium neoaurum	1286	AF268445	clade_374	N	OP
Mycobacterium smegmatis	1291	CP000480	clade_374	N	OP
Mycobacterium sp. HE5	1304	AJ012738	clade_374	N	N
Dysgonomonas gadei	775	ADLV01000001	clade_377	N	N
Dysgonomonas mossii	776	ADLW01000023	clade_377	N	N
Porphyromonas levii	1474	NR_025907	clade_377	N	N
Porphyromonas somerae	1476	AB547667	clade_377	N	N
Bacteroides barnesiae	267	NR_041446	clade_378	N	N
Bacteroides coprocola	272	ABIY02000050	clade_378	N	N
Bacteroides coprophilus	273	ACBW01000012	clade_378	N	N
Bacteroides dorei	274	ABWZ01000093	clade_378	N	N
Bacteroides massiliensis	284	AB200226	clade_378	N	N
Bacteroides plebeius	289	AB200218	clade_378	N	N
Bacteroides sp. 3_1_33FAA	309	ACPS01000085	clade_378	N	N
Bacteroides sp. 3_1_40A	310	ACRT01000136	clade_378	N	N
Bacteroides sp. 4_3_47FAA	313	ACDR02000029	clade_378	N	N
Bacteroides sp. 9_1_42FAA	314	ACAA01000096	clade_378	N	N
Bacteroides sp. NB_8	323	AB117565	clade_378	N	N
Bacteroides vulgatus	331	CP000139	clade_378	N	N
Bacteroides ovatus	287	ACWH01000036	clade_38	N	N
Bacteroides sp. 1_1_30	294	ADCL01000128	clade_38	N	N
Bacteroides sp. 2_1_22	297	ACPQ01000117	clade_38	N	N
Bacteroides sp. 2_2_4	299	ABZZ01000168	clade_38	N	N
Bacteroides sp. 3_1_23	308	ACRS01000081	clade_38	N	N
Bacteroides sp. D1	318	ACAB02000030	clade_38	N	N
Bacteroides sp. D2	321	ACGA01000077	clade_38	N	N
Bacteroides sp. D22	320	ADCK01000151	clade_38	N	N
Bacteroides xylanisolvens	332	ADKP01000087	clade_38	N	N
Treponema lecithinolyticum	1931	NR_026247	clade_380	N	OP
Treponema parvum	1933	AF302937	clade_380	N	OP
Treponema sp. oral clone JU025	1940	AY349417	clade_380	N	N
Treponema sp. oral taxon 270	1954	GQ422733	clade_380	N	N
Parascardovia denticolens	1428	ADEB01000020	clade_381	N	N
Scardovia inopinata	1688	AB029087	clade_381	N	N
Scardovia wiggsiae	1689	AY278626	clade_381	N	N
Clostridiales bacterium 9400853	533	HM587320	clade_384	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Mogibacterium diversum	1254	NR_027191	clade_384	N	N
Mogibacterium neglectum	1255	NR_027203	clade_384	N	N
Mogibacterium pumilum	1256	NR_028608	clade_384	N	N
Mogibacterium timidum	1257	Z36296	clade_384	N	N
Borrelia burgdorferi	389	ABGI01000001	clade_386	N	OP
Borrelia garinii	392	ABJV01000001	clade_386	N	OP
Borrelia sp. NE49	397	AJ224142	clade_386	N	OP
Caldimonas manganoxidans	457	NR_040787	clade_387	N	N
Comamonadaceae bacterium oral taxon F47	667	HM099651	clade_387	N	N
Lautropia mirabilis	1149	AEQP01000026	clade_387	N	N
Lautropia sp. oral clone AP009	1150	AY005030	clade_387	N	N
Peptoniphilus asaccharolyticus	1441	D14145	clade_389	N	N
Peptoniphilus duerdenii	1442	EU526290	clade_389	N	N
Peptoniphilus harei	1443	NR_026358	clade_389	N	N
Peptoniphilus indolicus	1444	AY153431	clade_389	N	N
Peptoniphilus lacrimalis	1446	ADDO01000050	clade_389	N	N
Peptoniphilus sp. gpac077	1450	AM176527	clade_389	N	N
Peptoniphilus sp. JC140	1447	JF824803	clade_389	N	N
Peptoniphilus sp. oral taxon 386	1452	ADCS01000031	clade_389	N	N
Peptoniphilus sp. oral taxon 836	1453	AEAA01000090	clade_389	N	N
Peptostreptococcaceae bacterium ph1	1454	JN837495	clade_389	N	N
Dialister pneumosintes	765	HM596297	clade_390	N	N
Dialister sp. oral taxon 502	767	GQ422739	clade_390	N	N
Cupriavidus metallidurans	741	GU230889	clade_391	N	N
Herbaspirillum seropedicae	1001	CP002039	clade_391	N	N
Herbaspirillum sp. JC206	1002	JN657219	clade_391	N	N
Janthinobacterium sp. SY12	1015	EF455530	clade_391	N	N
Massilia sp. CCUG 43427A	1197	FR773700	clade_391	N	N
Ralstonia pickettii	1615	NC_010682	clade_391	N	N
Ralstonia sp. 5_7_47FAA	1616	ACUF01000076	clade_391	N	N
Francisella novicida	889	ABSS01000002	clade_392	N	N
Francisella philomiragia	890	AY928394	clade_392	N	N
Francisella tularensis	891	ABAZ01000082	clade_392	N	Category-A
Ignatzschineria indica	1009	HQ823562	clade_392	N	N
Ignatzschineria sp. NML 95_0260	1010	HQ823559	clade_392	N	N
Streptococcus mutans	1814	AP010655	clade_394	N	N
Lactobacillus gasseri	1084	ACOZ01000018	clade_398	N	N
Lactobacillus hominis	1090	FR681902	clade_398	N	N
Lactobacillus iners	1091	AEKJ01000002	clade_398	N	N
Lactobacillus johnsonii	1093	AE017198	clade_398	N	N
Lactobacillus senioris	1119	AB602570	clade_398	N	N
Lactobacillus sp. oral clone HT002	1135	AY349382	clade_398	N	N
Weissella beninensis	2006	EU439435	clade_398	N	N
Sphingomonas echinoides	1744	NR_024700	clade_399	N	N
Sphingomonas sp. oral taxon A09	1747	HM099639	clade_399	N	N
Sphingomonas sp. oral taxon F71	1748	HM099645	clade_399	N	N
Zymomonas mobilis	2032	NR_074274	clade_399	N	N
Arcanobacterium haemolyticum	174	NR_025347	clade_400	N	N
Arcanobacterium pyogenes	175	GU585578	clade_400	N	N
Trueperella pyogenes	1962	NR_044858	clade_400	N	N
Lactococcus garvieae	1144	AF061005	clade_401	N	N
Lactococcus lactis	1145	CP002365	clade_401	N	N
Brevibacterium mcbrellneri	424	ADNU01000076	clade_402	N	N
Brevibacterium paucivorans	425	EU086796	clade_402	N	N
Brevibacterium sp. JC43	428	JF824806	clade_402	N	N
Selenomonas artemidis	1692	HM596274	clade_403	N	N
Selenomonas sp. FOBRC9	1704	HQ616378	clade_403	N	N
Selenomonas sp. oral taxon 137	1715	AENV01000007	clade_403	N	N
Desmospora activa	751	AM940019	clade_404	N	N
Desmospora sp. 8437	752	AFHT01000143	clade_404	N	N
Paenibacillus sp. oral taxon F45	1407	HM099647	clade_404	N	N
Corynebacterium ammoniagenes	682	ADNS01000011	clade_405	N	N
Corynebacterium aurimucosum	687	ACLH01000041	clade_405	N	N
Corynebacterium bovis	688	AF537590	clade_405	N	N
Corynebacterium canis	689	GQ871934	clade_405	N	N
Corynebacterium casei	690	NR_025101	clade_405	N	N
Corynebacterium durum	694	Z97069	clade_405	N	N
Corynebacterium efficiens	695	ACLI01000121	clade_405	N	N
Corynebacterium falsenii	696	Y13024	clade_405	N	N
Corynebacterium flavescens	697	NR_037040	clade_405	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Corynebacterium glutamicum	701	BA000036	clade_405	N	N
Corynebacterium jeikeium	704	ACYW01000001	clade_405	N	OP
Corynebacterium kroppenstedtii	705	NR_026380	clade_405	N	N
Corynebacterium lipophiloflavum	706	ACHJ01000075	clade_405	N	N
Corynebacterium matruchotii	709	ACSH02000003	clade_405	N	N
Corynebacterium minutissimum	710	X82064	clade_405	N	N
Corynebacterium resistens	718	ADGN01000058	clade_405	N	N
Corynebacterium simulans	720	AF537604	clade_405	N	N
Corynebacterium singulare	721	NR_026394	clade_405	N	N
Corynebacterium sp. 1 ex sheep	722	Y13427	clade_405	N	N
Corynebacterium sp. NML 99_0018	726	GU238413	clade_405	N	N
Corynebacterium striatum	727	ACGE01000001	clade_405	N	OP
Corynebacterium urealyticum	732	X81913	clade_405	N	OP
Corynebacterium variabile	734	NR_025314	clade_405	N	N
Aerococcus sanguinicola	98	AY837833	clade_407	N	N
Aerococcus urinae	99	CP002512	clade_407	N	N
Aerococcus urinaeequi	100	NR_043443	clade_407	N	N
Aerococcus viridans	101	ADNT01000041	clade_407	N	N
Fusobacterium naviforme	898	HQ223106	clade_408	N	N
Moryella indoligenes	1268	AF527773	clade_408	N	N
Selenomonas genomosp. P5	1697	AY341820	clade_410	N	N
Selenomonas sp. oral clone IQ048	1710	AY349408	clade_410	N	N
Selenomonas sputigena	1717	ACKP02000033	clade_410	N	N
Hyphomicrobium sulfonivorans	1007	AY468372	clade_411	N	N
Methylocella silvestris	1228	NR_074237	clade_411	N	N
Legionella pneumophila	1153	NC_002942	clade_412	N	OP
Lactobacillus coryniformis	1077	NR_044705	clade_413	N	N
Arthrobacter agilis	178	NR_026198	clade_414	N	N
Arthrobacter arilaitensis	179	NR_074608	clade_414	N	N
Arthrobacter bergerei	180	NR_025612	clade_414	N	N
Arthrobacter globiformis	181	NR_026187	clade_414	N	N
Arthrobacter nicotianae	182	NR_026190	clade_414	N	N
Mycobacterium abscessus	1269	AGQU01000002	clade_418	N	OP
Mycobacterium chelonae	1273	AB548610	clade_418	N	OP
Bacteroides salanitronis	291	CP002530	clade_419	N	N
Paraprevotella xylaniphila	1427	AFBR01000011	clade_419	N	N
Barnesiella intestinihominis	336	AB370251	clade_420	N	N
Barnesiella viscericola	337	NR_041508	clade_420	N	N
Parabacteroides sp. NS31_3	1422	JN029805	clade_420	N	N
Porphyromonadaceae bacterium NML 060648	1470	EF184292	clade_420	N	N
Tannerella forsythia	1913	CP003191	clade_420	N	N
Tannerella sp. 6_1_58FAA_CT1	1914	ACWX01000068	clade_420	N	N
Mycoplasma amphoriforme	1311	AY531656	clade_421	N	N
Mycoplasma genitalium	1317	L43967	clade_421	N	N
Mycoplasma pneumoniae	1322	NC_000912	clade_421	N	N
Mycoplasma penetrans	1321	NC_004432	clade_422	N	N
Ureaplasma parvum	1966	AE002127	clade_422	N	N
Ureaplasma urealyticum	1967	AAYN01000002	clade_422	N	N
Treponema genomosp. P1	1927	AY341822	clade_425	N	N
Treponema sp. oral taxon 228	1943	GU408580	clade_425	N	N
Treponema sp. oral taxon 230	1944	GU408603	clade_425	N	N
Treponema sp. oral taxon 231	1945	GU408631	clade_425	N	N
Treponema sp. oral taxon 232	1946	GU408646	clade_425	N	N
Treponema sp. oral taxon 235	1947	GU408673	clade_425	N	N
Treponema sp. ovine footrot	1959	AJ010951	clade_425	N	N
Treponema vincentii	1960	ACYH01000036	clade_425	N	OP
Burkholderiales bacterium 1_1_47	452	ADCQ01000066	clade_432	N	OP
Parasutterella excrementihominis	1429	AFBP01000029	clade_432	N	N
Parasutterella secunda	1430	AB491209	clade_432	N	N
Sutterella morbirenis	1898	AJ832129	clade_432	N	N
Sutterella sanguinus	1900	AJ748647	clade_432	N	N
Sutterella sp. YIT 12072	1901	AB491210	clade_432	N	N
Sutterella stercoricanis	1902	NR_025600	clade_432	N	N
Sutterella wadsworthensis	1903	ADMF01000048	clade_432	N	N
Propionibacterium freudenreichii	1572	NR_036972	clade_433	N	N
Propionibacterium sp. oral taxon 192	1580	GQ422728	clade_433	N	N
Tessaracoccus sp. oral taxon F04	1917	HM099640	clade_433	N	N
Peptoniphilus ivorii	1445	Y07840	clade_434	N	N
Peptoniphilus sp. gpac007	1448	AM176517	clade_434	N	N
Peptoniphilus sp. gpac018A	1449	AM176519	clade_434	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Peptoniphilus sp. gpac148	1451	AM176535	clade_434	N	N
Flexispira rappini	887	AY126479	clade_436	N	N
Helicobacter bilis	993	ACDN01000023	clade_436	N	N
Helicobacter cinaedi	995	ABQT01000054	clade_436	N	N
Helicobacter sp. None	998	U44756	clade_436	N	N
Brevundimonas subvibrioides	429	CP002102	clade_438	N	N
Hyphomonas neptunium	1008	NR_074092	clade_438	N	N
Phenylobacterium zucineum	1465	AY628697	clade_438	N	N
Streptococcus downei	1793	AEKN01000002	clade_441	N	N
Streptococcus sp. SHV515	1848	Y07601	clade_441	N	N
Acinetobacter sp. CIP 53.82	40	JQ638584	clade_443	N	N
Halomonas elongata	990	NR_074782	clade_443	N	N
Halomonas johnsoniae	991	FR775979	clade_443	N	N
Butyrivibrio fibrisolvens	456	U41172	clade_444	N	N
Roseburia sp. 11SE37	1640	FM954975	clade_444	N	N
Roseburia sp. 11SE38	1641	FM954976	clade_444	N	N
Shuttleworthia satelles	1728	ACIP02000004	clade_444	N	N
Shuttleworthia sp. MSX8B	1729	HQ616383	clade_444	N	N
Shuttleworthia sp. oral taxon G69	1730	GU432167	clade_444	N	N
Bdellovibrio sp. MPA	344	AY294215	clade_445	N	N
Desulfobulbus sp. oral clone CH031	755	AY005036	clade_445	N	N
Desulfovibrio desulfuricans	757	DQ092636	clade_445	N	N
Desulfovibrio fairfieldensis	758	U42221	clade_445	N	N
Desulfovibrio piger	759	AF192152	clade_445	N	N
Desulfovibrio sp. 3_1_syn3	760	ADDR01000239	clade_445	N	N
Geobacter bemidjiensis	941	CP001124	clade_445	N	N
Brachybacterium alimentarium	401	NR_026269	clade_446	N	N
Brachybacterium conglomeratum	402	AB537169	clade_446	N	N
Brachybacterium tyrofermentans	403	NR_026272	clade_446	N	N
Dermabacter hominis	749	FJ263375	clade_446	N	N
Aneurinibacillus thermoaerophilus	171	NR_029303	clade_448	N	N
Brevibacillus agri	409	NR_040983	clade_448	N	N
Brevibacillus centrosporus	411	NR_043414	clade_448	N	N
Brevibacillus choshinensis	412	NR_040980	clade_448	N	N
Brevibacillus invocatus	413	NR_041836	clade_448	N	N
Brevibacillus parabrevis	415	NR_040981	clade_448	N	N
Brevibacillus reuszeri	416	NR_040982	clade_448	N	N
Brevibacillus sp. phR	417	JN837488	clade_448	N	N
Brevibacillus thermoruber	418	NR_026514	clade_448	N	N
Lactobacillus murinus	1100	NR_042231	clade_449	N	N
Lactobacillus oeni	1102	NR_043095	clade_449	N	N
Lactobacillus ruminis	1115	ACGS02000043	clade_449	N	N
Lactobacillus vini	1141	NR_042196	clade_449	N	N
Gemella haemolysans	924	ACDZ02000012	clade_450	N	N
Gemella morbillorum	925	NR_025904	clade_450	N	N
Gemella morbillorum	926	ACRX01000010	clade_450	N	N
Gemella sanguinis	927	ACRY01000057	clade_450	N	N
Gemella sp. oral clone ASCE02	929	AY923133	clade_450	N	N
Gemella sp. oral clone ASCF04	930	AY923139	clade_450	N	N
Gemella sp. oral clone ASCF12	931	AY923143	clade_450	N	N
Gemella sp. WAL 1945J	928	EU427463	clade_450	N	N
Sporolactobacillus nakayamae	1753	NR_042247	clade_451	N	N
Gluconacetobacter entanii	945	NR_028909	clade_452	N	N
Gluconacetobacter europaeus	946	NR_026513	clade_452	N	N
Gluconacetobacter hansenii	947	NR_026133	clade_452	N	N
Gluconacetobacter oboediens	949	NR_041295	clade_452	N	N
Gluconacetobacter xylinus	950	NR_074338	clade_452	N	N
Auritibacter ignavus	193	FN554542	clade_453	N	N
Dermacoccus sp. Ellin185	750	AEIQ01000090	clade_453	N	N
Janibacter limosus	1013	NR_026362	clade_453	N	N
Janibacter melonis	1014	EF063716	clade_453	N	N
Acetobacter aceti	7	NR_026121	clade_454	N	N
Acetobacter fabarum	8	NR_042678	clade_454	N	N
Acetobacter lovaniensis	9	NR_040832	clade_454	N	N
Acetobacter malorum	10	NR_025513	clade_454	N	N
Acetobacter orientalis	11	NR_028625	clade_454	N	N
Acetobacter pasteurianus	12	NR_026107	clade_454	N	N
Acetobacter pomorum	13	NR_042112	clade_454	N	N
Acetobacter syzygii	14	NR_040868	clade_454	N	N
Acetobacter tropicalis	15	NR_036881	clade_454	N	N
Gluconacetobacter azotocaptans	943	NR_028767	clade_454	N	N
Gluconacetobacter diazotrophicus	944	NR_074292	clade_454	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Gluconacetobacter johannae	948	NR_024959	clade_454	N	N
Nocardia brasiliensis	1351	AIHV01000038	clade_455	N	N
Nocardia cyriacigeorgica	1352	HQ009486	clade_455	N	N
Nocardia puris	1354	NR_028994	clade_455	N	N
Nocardia sp. 01_Je_025	1355	GU574059	clade_455	N	N
Rhodococcus equi	1623	ADNW01000058	clade_455	N	N
Oceanobacillus caeni	1358	NR_041533	clade_456	N	N
Oceanobacillus sp. Ndiop	1359	CAER01000083	clade_456	N	N
Ornithinibacillus bavariensis	1384	NR_044923	clade_456	N	N
Ornithinibacillus sp. 7_10AIA	1385	FN397526	clade_456	N	N
Virgibacillus proomii	2005	NR_025308	clade_456	N	N
Corynebacterium amycolatum	683	ABZU01000033	clade_457	N	OP
Corynebacterium hansenii	702	AM946639	clade_457	N	N
Corynebacterium xerosis	735	FN179330	clade_457	N	OP
Staphylococcaceae bacterium NML 92_0017	1756	AY841362	clade_458	N	N
Staphylococcus fleurettii	1766	NR_041326	clade_458	N	N
Staphylococcus sciuri	1774	NR_025520	clade_458	N	N
Staphylococcus vitulinus	1779	NR_024670	clade_458	N	N
Stenotrophomonas maltophilia	1782	AAVZ01000005	clade_459	N	N
Stenotrophomonas sp. FG_6	1783	EF017810	clade_459	N	N
Mycobacterium africanum	1270	AF480605	clade_46	N	OP
Mycobacterium alsiensis	1271	AJ938169	clade_46	N	OP
Mycobacterium avium	1272	CP000479	clade_46	N	OP
Mycobacterium colombiense	1274	AM062764	clade_46	N	OP
Mycobacterium gordonae	1276	GU142930	clade_46	N	OP
Mycobacterium intracellulare	1277	GQ153276	clade_46	N	OP
Mycobacterium kansasii	1278	AF480601	clade_46	N	OP
Mycobacterium lacus	1279	NR_025175	clade_46	N	OP
Mycobacterium leprae	1280	FM211192	clade_46	N	OP
Mycobacterium lepromatosis	1281	EU203590	clade_46	N	OP
Mycobacterium mantenii	1283	FJ042897	clade_46	N	OP
Mycobacterium marinum	1284	NC_010612	clade_46	N	OP
Mycobacterium microti	1285	NR_025234	clade_46	N	OP
Mycobacterium parascrofulaceum	1287	ADNV01000350	clade_46	N	OP
Mycobacterium seoulense	1290	DQ536403	clade_46	N	OP
Mycobacterium sp. 1761	1292	EU703150	clade_46	N	N
Mycobacterium sp. 1791	1295	EU703148	clade_46	N	N
Mycobacterium sp. 1797	1296	EU703149	clade_46	N	N
Mycobacterium sp. B10_07.09.0206	1298	HQ174245	clade_46	N	N
Mycobacterium sp. NLA001000736	1305	HM627011	clade_46	N	N
Mycobacterium sp. W	1306	DQ437715	clade_46	N	N
Mycobacterium tuberculosis	1307	CP001658	clade_46	N	Category-C
Mycobacterium ulcerans	1308	AB548725	clade_46	N	OP
Mycobacterium vulneris	1309	EU834055	clade_46	N	OP
Xanthomonas campestris	2016	EF101975	clade_461	N	N
Xanthomonas sp. kmd_489	2017	EU723184	clade_461	N	N
Dietzia natronolimnaea	769	GQ870426	clade_462	N	N
Dietzia sp. BBDP51	770	DQ337512	clade_462	N	N
Dietzia sp. CA149	771	GQ870422	clade_462	N	N
Dietzia timorensis	772	GQ870424	clade_462	N	N
Gordonia bronchialis	951	NR_027594	clade_463	N	N
Gordonia polyisoprenivorans	952	DQ385609	clade_463	N	N
Gordonia sp. KTR9	953	DQ068383	clade_463	N	N
Gordonia sputi	954	FJ536304	clade_463	N	N
Gordonia terrae	955	GQ848239	clade_463	N	N
Leptotrichia goodfellowii	1167	ADAD01000110	clade_465	N	N
Leptotrichia sp. oral clone IK040	1174	AY349387	clade_465	N	N
Leptotrichia sp. oral clone P2PB_51 P1	1175	AY207053	clade_465	N	N
Bacteroidales genomosp. P7 oral clone MB3_P19	264	DQ003623	clade_466	N	N
Butyricimonas virosa	454	AB443949	clade_466	N	N
Odoribacter laneus	1363	AB490805	clade_466	N	N
Odoribacter splanchnicus	1364	CP002544	clade_466	N	N
Capnocytophaga gingivalis	478	ACLQ01000011	clade_467	N	N
Capnocytophaga granulosa	479	X97248	clade_467	N	N
Capnocytophaga sp. oral clone AH015	483	AY005074	clade_467	N	N
Capnocytophaga sp. oral strain S3	487	AY005073	clade_467	N	N
Capnocytophaga sp. oral taxon 338	488	AEXX01000050	clade_467	N	N
Capnocytophaga canimorsus	476	CP002113	clade_468	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Capnocytophaga sp. oral clone ID062	485	AY349368	clade_468	N	N
Lactobacillus catenaformis	1075	M23729	clade_469	N	N
Lactobacillus vitulinus	1142	NR_041305	clade_469	N	N
Cetobacterium somerae	501	AJ438155	clade_470	N	N
Fusobacterium gonidiaformans	896	ACET01000043	clade_470	N	N
Fusobacterium mortiferum	897	ACDB02000034	clade_470	N	N
Fusobacterium necrogenes	899	X55408	clade_470	N	N
Fusobacterium necrophorum	900	AM905356	clade_470	N	N
Fusobacterium sp. 12_1B	905	AGWJ01000070	clade_470	N	N
Fusobacterium sp. 3_1_5R	911	ACDD01000078	clade_470	N	N
Fusobacterium sp. D12	918	ACDG02000036	clade_470	N	N
Fusobacterium ulcerans	921	ACDH01000090	clade_470	N	N
Fusobacterium varium	922	ACIE01000009	clade_470	N	N
Mycoplasma arthritidis	1312	NC_011025	clade_473	N	N
Mycoplasma faucium	1314	NR_024983	clade_473	N	N
Mycoplasma hominis	1318	AF443616	clade_473	N	N
Mycoplasma orale	1319	AY796060	clade_473	N	N
Mycoplasma salivarium	1324	M24661	clade_473	N	N
Mitsuokella jalaludinii	1247	NR_028840	clade_474	N	N
Mitsuokella multacida	1248	ABWK02000005	clade_474	N	N
Mitsuokella sp. oral taxon 521	1249	GU413658	clade_474	N	N
Mitsuokella sp. oral taxon G68	1250	GU432166	clade_474	N	N
Selenomonas genomosp. C1	1695	AY278627	clade_474	N	N
Selenomonas genomosp. P8 oral clone MB5_P06	1700	DQ003628	clade_474	N	N
Selenomonas ruminantium	1703	NR_075026	clade_474	N	N
Veillonellaceae bacterium oral taxon 131	1994	GU402916	clade_474	N	N
Alloscardovia omnicolens	139	NR_042583	clade_475	N	N
Alloscardovia sp. OB7196	140	AB425070	clade_475	N	N
Bifidobacterium urinalis	366	AJ278695	clade_475	N	N
Prevotella loescheii	1503	JN867231	clade_48	N	N
Prevotella sp. oral clone ASCG12	1530	DQ272511	clade_48	N	N
Prevotella sp. oral clone GU027	1540	AY349398	clade_48	N	N
Prevotella sp. oral taxon 472	1553	ACZS01000106	clade_48	N	N
Selenomonas dianae	1693	GQ422719	clade_480	N	N
Selenomonas flueggei	1694	AF287803	clade_480	N	N
Selenomonas genomosp. C2	1696	AY278628	clade_480	N	N
Selenomonas genomosp. P6 oral clone MB3_C41	1698	DQ003636	clade_480	N	N
Selenomonas genomosp. P7 oral clone MB5_C08	1699	DQ003627	clade_480	N	N
Selenomonas infelix	1701	AF287802	clade_480	N	N
Selenomonas noxia	1702	GU470909	clade_480	N	N
Selenomonas sp. oral clone FT050	1705	AY349403	clade_480	N	N
Selenomonas sp. oral clone GI064	1706	AY349404	clade_480	N	N
Selenomonas sp. oral clone GT010	1707	AY349405	clade_480	N	N
Selenomonas sp. oral clone HU051	1708	AY349406	clade_480	N	N
Selenomonas sp. oral clone IK004	1709	AY349407	clade_480	N	N
Selenomonas sp. oral clone JI021	1711	AY349409	clade_480	N	N
Selenomonas sp. oral clone JS031	1712	AY349410	clade_480	N	N
Selenomonas sp. oral clone OH4A	1713	AY947498	clade_480	N	N
Selenomonas sp. oral clone P2PA_80 P4	1714	AY207052	clade_480	N	N
Selenomonas sp. oral taxon 149	1716	AEEJ01000007	clade_480	N	N
Veillonellaceae bacterium oral taxon 155	1995	GU470897	clade_480	N	N
Agrococcus jenensis	117	NR_026275	clade_484	N	N
Microbacterium gubbeenense	1232	NR_025098	clade_484	N	N
Pseudoclavibacter sp. Timone	1590	FJ375951	clade_484	N	N
Tropheryma whipplei	1961	BX251412	clade_484	N	N
Zimmermannella bifida	2031	AB012592	clade_484	N	N
Legionella hackeliae	1151	M36028	clade_486	N	OP
Legionella longbeachae	1152	M36029	clade_486	N	OP
Legionella sp. D3923	1154	JN380999	clade_486	N	OP
Legionella sp. D4088	1155	JN381012	clade_486	N	OP
Legionella sp. H63	1156	JF831047	clade_486	N	OP
Legionella sp. NML 93L054	1157	GU062706	clade_486	N	OP
Legionella steelei	1158	HQ398202	clade_486	N	OP
Tatlockia micdadei	1915	M36032	clade_486	N	N
Helicobacter pullorum	996	ABQU01000097	clade_489	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Acetobacteraceae bacterium AT_5844	16	AGEZ01000040	clade_490	N	N
Roseomonas cervicalis	1643	ADVL01000363	clade_490	N	N
Roseomonas mucosa	1644	NR_028857	clade_490	N	N
Roseomonas sp. NML94_0193	1645	AF533357	clade_490	N	N
Roseomonas sp. NML97_0121	1646	AF533359	clade_490	N	N
Roseomonas sp. NML98_0009	1647	AF533358	clade_490	N	N
Roseomonas sp. NML98_0157	1648	AF533360	clade_490	N	N
Rickettsia akari	1627	CP000847	clade_492	N	OP
Rickettsia conorii	1628	AE008647	clade_492	N	OP
Rickettsia prowazekii	1629	M21789	clade_492	N	Category-B
Rickettsia rickettsii	1630	NC_010263	clade_492	N	OP
Rickettsia slovaca	1631	L36224	clade_492	N	OP
Rickettsia typhi	1632	AE017197	clade_492	N	OP
Anaeroglobus geminatus	160	AGCJ01000054	clade_493	N	N
Megasphaera genomosp. C1	1201	AY278622	clade_493	N	N
Megasphaera micronuciformis	1203	AECS01000020	clade_493	N	N
Clostridiales genomosp. BVAB3	540	CP001850	clade_495	N	N
Tsukamurella paurometabola	1963	X80628	clade_496	N	N
Tsukamurella tyrosinosolvens	1964	AB478958	clade_496	N	N
Abiotrophia para_adiacens	2	AB022027	clade_497	N	N
Carnobacterium divergens	492	NR_044706	clade_497	N	N
Carnobacterium maltaromaticum	493	NC_019425	clade_497	N	N
Enterococcus avium	800	AF133535	clade_497	N	N
Enterococcus caccae	801	AY943820	clade_497	N	N
Enterococcus casseliflavus	802	AEWT01000047	clade_497	N	N
Enterococcus durans	803	AJ276354	clade_497	N	N
Enterococcus faecalis	804	AE016830	clade_497	N	N
Enterococcus faecium	805	AM157434	clade_497	N	N
Enterococcus gallinarum	806	AB269767	clade_497	N	N
Enterococcus gilvus	807	AY033814	clade_497	N	N
Enterococcus hawaiiensis	808	AY321377	clade_497	N	N
Enterococcus hirae	809	AF061011	clade_497	N	N
Enterococcus italicus	810	AEPV01000109	clade_497	N	N
Enterococcus mundtii	811	NR_024906	clade_497	N	N
Enterococcus raffinosus	812	FN600541	clade_497	N	N
Enterococcus sp. BV2CASA2	813	JN809766	clade_497	N	N
Enterococcus sp. CCRI_16620	814	GU457263	clade_497	N	N
Enterococcus sp. F95	815	FJ463817	clade_497	N	N
Enterococcus sp. RfL6	816	AJ133478	clade_497	N	N
Enterococcus thailandicus	817	AY321376	clade_497	N	N
Fusobacterium canifelinum	893	AY162222	clade_497	N	N
Fusobacterium genomosp. C1	894	AY278616	clade_497	N	N
Fusobacterium genomosp. C2	895	AY278617	clade_497	N	N
Fusobacterium periodonticum	902	ACJY01000002	clade_497	N	N
Fusobacterium sp. 1_1_41FAA	906	ADGG01000053	clade_497	N	N
Fusobacterium sp. 11_3_2	904	ACUO01000052	clade_497	N	N
Fusobacterium sp. 2_1_31	907	ACDC02000018	clade_497	N	N
Fusobacterium sp. 3_1_27	908	ADGF01000045	clade_497	N	N
Fusobacterium sp. 3_1_33	909	ACQE01000178	clade_497	N	N
Fusobacterium sp. 3_1_36A2	910	ACPU01000044	clade_497	N	N
Fusobacterium sp. AC18	912	HQ616357	clade_497	N	N
Fusobacterium sp. ACB2	913	HQ616358	clade_497	N	N
Fusobacterium sp. AS2	914	HQ616361	clade_497	N	N
Fusobacterium sp. CM1	915	HQ616371	clade_497	N	N
Fusobacterium sp. CM21	916	HQ616375	clade_497	N	N
Fusobacterium sp. CM22	917	HQ616376	clade_497	N	N
Fusobacterium sp. oral clone ASCF06	919	AY923141	clade_497	N	N
Fusobacterium sp. oral clone ASCF11	920	AY953256	clade_497	N	N
Granulicatella adiacens	959	ACKZ01000002	clade_497	N	N
Granulicatella elegans	960	AB252689	clade_497	N	N
Granulicatella paradiacens	961	AY879298	clade_497	N	N
Granulicatella sp. oral clone ASC02	963	AY923126	clade_497	N	N
Granulicatella sp. oral clone ASCA05	964	DQ341469	clade_497	N	N
Granulicatella sp. oral clone ASCB09	965	AY953251	clade_497	N	N
Granulicatella sp. oral clone ASCG05	966	AY923146	clade_497	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Tetragenococcus halophilus	1918	NR_075020	clade_497	N	N
Tetragenococcus koreensis	1919	NR_043113	clade_497	N	N
Vagococcus fluvialis	1973	NR_026489	clade_497	N	N
Chryseobacterium anthropi	514	AM982793	clade_498	N	N
Chryseobacterium gleum	515	ACKQ02000003	clade_498	N	N
Chryseobacterium hominis	516	NR_042517	clade_498	N	N
Treponema refringens	1936	AF426101	clade_499	N	OP
Treponema sp. oral clone JU031	1941	AY349416	clade_499	N	N
Treponema sp. oral taxon 239	1948	GU408738	clade_499	N	N
Treponema sp. oral taxon 271	1955	GU408871	clade_499	N	N
Alistipes finegoldii	129	NR_043064	clade_500	N	N
Alistipes onderdonkii	131	NR_043318	clade_500	N	N
Alistipes putredinis	132	ABFK02000017	clade_500	N	N
Alistipes shahii	133	FP929032	clade_500	N	N
Alistipes sp. HGB5	134	AENZ01000082	clade_500	N	N
Alistipes sp. JC50	135	JF824804	clade_500	N	N
Alistipes sp. RMA 9912	136	GQ140629	clade_500	N	N
Mycoplasma agalactiae	1310	AF010477	clade_501	N	N
Mycoplasma bovoculi	1313	NR_025987	clade_501	N	N
Mycoplasma fermentans	1315	CP002458	clade_501	N	N
Mycoplasma flocculare	1316	X62699	clade_501	N	N
Mycoplasma ovipneumoniae	1320	NR_025989	clade_501	N	N
Arcobacter butzleri	176	AEPT01000071	clade_502	N	N
Arcobacter cryaerophilus	177	NR_025905	clade_502	N	N
Campylobacter curvus	461	NC_009715	clade_502	N	OP
Campylobacter rectus	467	ACFU01000050	clade_502	N	OP
Campylobacter showae	468	ACVQ01000030	clade_502	N	OP
Campylobacter sp. FOBRC14	469	HQ616379	clade_502	N	OP
Campylobacter sp. FOBRC15	470	HQ616380	clade_502	N	OP
Campylobacter sp. oral clone BB120	471	AY005038	clade_502	N	OP
Campylobacter sputorum	472	NR_044839	clade_502	N	OP
Bacteroides ureolyticus	330	GQ167666	clade_504	N	N
Campylobacter gracilis	463	ACYG01000026	clade_504	N	OP
Campylobacter hominis	464	NC_009714	clade_504	N	OP
Dialister invisus	762	ACIM02000001	clade_506	N	N
Dialister micraerophilus	763	AFBB01000028	clade_506	N	N
Dialister microaerophilus	764	AENT01000008	clade_506	N	N
Dialister propionicifaciens	766	NR_043231	clade_506	N	N
Dialister succinatiphilus	768	AB370249	clade_506	N	N
Megasphaera elsdenii	1200	AY038996	clade_506	N	N
Megasphaera genomosp. type_1	1202	ADGP01000010	clade_506	N	N
Megasphaera sp. BLPYG_07	1204	HM990964	clade_506	N	N
Megasphaera sp. UPII 199_6	1205	AFIJ01000040	clade_506	N	N
Chromobacterium violaceum	513	NC_005085	clade_507	N	N
Laribacter hongkongensis	1148	CP001154	clade_507	N	N
Methylophilus sp. ECd5	1229	AY436794	clade_507	N	N
Finegoldia magna	883	ACHM02000001	clade_509	N	N
Parvimonas micra	1431	AB729072	clade_509	N	N
Parvimonas sp. oral taxon 110	1432	AFII01000002	clade_509	N	N
Peptostreptococcus micros	1456	AM176538	clade_509	N	N
Peptostreptococcus sp. oral clone FJ023	1460	AY349390	clade_509	N	N
Peptostreptococcus sp. P4P_31 P3	1458	AY207059	clade_509	N	N
Helicobacter pylori	997	CP000012	clade_510	N	OP
Anaplasma marginale	165	ABOR01000019	clade_511	N	N
Anaplasma phagocytophilum	166	NC_007797	clade_511	N	N
Ehrlichia chaffeensis	783	AAIF01000035	clade_511	N	OP
Neorickettsia risticii	1349	CP001431	clade_511	N	N
Neorickettsia sennetsu	1350	NC_007798	clade_511	N	N
Pseudoramibacter alactolyticus	1606	AB036759	clade_512	N	N
Veillonella montpellierensis	1977	AF473836	clade_513	N	N
Veillonella sp. oral clone ASCA08	1988	AY923118	clade_513	N	N
Veillonella sp. oral clone ASCB03	1989	AY923122	clade_513	N	N
Inquilinus limosus	1012	NR_029046	clade_514	N	N
Sphingomonas sp. oral clone FZ016	1746	AY349412	clade_514	N	N
Anaerococcus lactolyticus	145	ABYO01000217	clade_515	N	N
Anaerococcus prevotii	147	CP001708	clade_515	N	N
Anaerococcus sp. gpac104	152	AM176528	clade_515	N	N
Anaerococcus sp. gpac126	153	AM176530	clade_515	N	N
Anaerococcus sp. gpac155	154	AM176536	clade_515	N	N
Anaerococcus sp. gpac199	155	AM176539	clade_515	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Anaerococcus tetradius	157	ACGC01000107	clade_515	N	N
Bacteroides coagulans	271	AB547639	clade_515	N	N
Clostridiales bacterium 9403326	534	HM587324	clade_515	N	N
Clostridiales bacterium ph2	539	JN837487	clade_515	N	N
Peptostreptococcus sp. 9succ1	1457	X90471	clade_515	N	N
Peptostreptococcus sp. oral clone AP24	1459	AB175072	clade_515	N	N
Tissierella praeacuta	1924	NR_044860	clade_515	N	N
Helicobacter canadensis	994	ABQS01000108	clade_518	N	N
Peptostreptococcus anaerobius	1455	AY326462	clade_520	N	N
Peptostreptococcus stomatis	1461	ADGQ01000048	clade_520	N	N
Bilophila wadsworthia	367	ADCP01000166	clade_521	N	N
Desulfovibrio vulgaris	761	NR_074897	clade_521	N	N
Actinomyces nasicola	64	AJ508455	clade_523	N	N
Cellulosimicrobium funkei	500	AY501364	clade_523	N	N
Lactococcus raffinolactis	1146	NR_044359	clade_524	N	N
Bacteroidales genomosp. P1	258	AY341819	clade_529	N	N
Bacteroidales genomosp. P2 oral clone MB1_G13	259	DQ003613	clade_529	N	N
Bacteroidales genomosp. P3 oral clone MB1_G34	260	DQ003615	clade_529	N	N
Bacteroidales genomosp. P4 oral clone MB2_G17	261	DQ003617	clade_529	N	N
Bacteroidales genomosp. P5 oral clone MB2_P04	262	DQ003619	clade_529	N	N
Bacteroidales genomosp. P6 oral clone MB3_C19	263	DQ003634	clade_529	N	N
Bacteroidales genomosp. P8 oral clone MB4_G15	265	DQ003626	clade_529	N	N
Bacteroidetes bacterium oral taxon D27	333	HM099638	clade_530	N	N
Bacteroidetes bacterium oral taxon F31	334	HM099643	clade_530	N	N
Bacteroidetes bacterium oral taxon F44	335	HM099649	clade_530	N	N
Flavobacterium sp. NF2_1	885	FJ195988	clade_530	N	N
Myroides odoratimimus	1326	NR_042354	clade_530	N	N
Myroides sp. MY15	1327	GU253339	clade_530	N	N
Chlamydiales bacterium NS16	507	JN606076	clade_531	N	N
Chlamydophila pecorum	508	D88317	clade_531	N	OP
Parachlamydia sp. UWE25	1423	BX908798	clade_531	N	N
Fusobacterium russii	903	NR_044687	clade_532	N	N
Streptobacillus moniliformis	1784	NR_027615	clade_532	N	N
Eubacteriaceae bacterium P4P_50 P4	833	AY207060	clade_533	N	N
Abiotrophia defectiva	1	ACIN02000016	clade_534	N	N
Abiotrophia sp. oral clone P4PA_155 P1	3	AY207063	clade_534	N	N
Catonella genomosp. P1 oral clone MB5_P12	496	DQ003629	clade_534	N	N
Catonella morbi	497	ACIL02000016	clade_534	N	N
Catonella sp. oral clone FL037	498	AY349369	clade_534	N	N
Eremococcus coleocola	818	AENN01000008	clade_534	N	N
Facklamia hominis	879	Y10772	clade_534	N	N
Granulicatella sp. M658_99_3	962	AJ271861	clade_534	N	N
Campylobacter coli	459	AAFL01000004	clade_535	N	OP
Campylobacter concisus	460	CP000792	clade_535	N	OP
Campylobacter fetus	462	ACLG01001177	clade_535	N	OP
Campylobacter jejuni	465	AL139074	clade_535	N	Category-B
Campylobacter upsaliensis	473	AEPU01000040	clade_535	N	OP
Atopobium minutum	183	HM007583	clade_539	N	N
Atopobium parvulum	184	CP001721	clade_539	N	N
Atopobium rimae	185	ACFE01000007	clade_539	N	N
Atopobium sp. BS2	186	HQ616367	clade_539	N	N
Atopobium sp. F0209	187	EU592966	clade_539	N	N
Atopobium sp. ICM42b10	188	HQ616393	clade_539	N	N
Atopobium sp. ICM57	189	HQ616400	clade_539	N	N
Atopobium vaginae	190	AEDQ01000024	clade_539	N	N
Coriobacteriaceae bacterium BV3Ac1	677	JN809768	clade_539	N	N
Actinomyces naeslundii	63	X81062	clade_54	N	N
Actinomyces oricola	67	NR_025559	clade_54	N	N
Actinomyces oris	69	BABV01000070	clade_54	N	N
Actinomyces sp. 7400942	70	EU484334	clade_54	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Actinomyces sp. ChDC B197	72	AF543275	clade_54	N	N
Actinomyces sp. GEJ15	73	GU561313	clade_54	N	N
Actinomyces sp. M2231_94_1	79	AJ234063	clade_54	N	N
Actinomyces sp. oral clone GU067	83	AY349362	clade_54	N	N
Actinomyces sp. oral clone IO077	85	AY349364	clade_54	N	N
Actinomyces sp. oral clone IP073	86	AY349365	clade_54	N	N
Actinomyces sp. oral clone JA063	88	AY349367	clade_54	N	N
Actinomyces sp. oral taxon 170	89	AFBL01000010	clade_54	N	N
Actinomyces sp. oral taxon 171	90	AECW01000034	clade_54	N	N
Actinomyces urogenitalis	95	ACFH01000038	clade_54	N	N
Actinomyces viscosus	96	ACRE01000096	clade_54	N	N
Orientia tsutsugamushi	1383	AP008981	clade_541	N	OP
Megamonas funiformis	1198	AB300988	clade_542	N	N
Megamonas hypermegale	1199	AJ420107	clade_542	N	N
Aeromicrobium marinum	102	NR_025681	clade_544	N	N
Aeromicrobium sp. JC14	103	JF824798	clade_544	N	N
Luteococcus sanguinis	1190	NR_025507	clade_544	N	N
Propionibacteriaceae bacterium NML 02_0265	1568	EF599122	clade_544	N	N
Rhodococcus corynebacterioides	1622	X80615	clade_546	N	N
Rhodococcus erythropolis	1624	ACNO01000030	clade_546	N	N
Rhodococcus fascians	1625	NR_037021	clade_546	N	N
Segniliparus rotundus	1690	CP001958	clade_546	N	N
Segniliparus rugosus	1691	ACZI01000025	clade_546	N	N
Exiguobacterium acetylicum	878	FJ970034	clade_547	N	N
Macrococcus caseolyticus	1194	NR_074941	clade_547	N	N
Streptomyces sp. 1 AIP_2009	1890	FJ176782	clade_548	N	N
Streptomyces sp. SD 524	1892	EU544234	clade_548	N	N
Streptomyces sp. SD 528	1893	EU544233	clade_548	N	N
Streptomyces thermoviolaceus	1895	NR_027616	clade_548	N	N
Borrelia afzelii	388	ABCU01000001	clade_549	N	OP
Borrelia crocidurae	390	DQ057990	clade_549	N	OP
Borrelia duttonii	391	NC_011229	clade_549	N	OP
Borrelia hermsii	393	AY597657	clade_549	N	OP
Borrelia hispanica	394	DQ057988	clade_549	N	OP
Borrelia persica	395	HM161645	clade_549	N	OP
Borrelia recurrentis	396	AF107367	clade_549	N	OP
Borrelia spielmanii	398	ABKB01000002	clade_549	N	OP
Borrelia turicatae	399	NC_008710	clade_549	N	OP
Borrelia valaisiana	400	ABCY01000002	clade_549	N	OP
Providencia alcalifaciens	1586	ABXW01000071	clade_55	N	N
Providencia rettgeri	1587	AM040492	clade_55	N	N
Providencia rustigianii	1588	AM040489	clade_55	N	N
Providencia stuartii	1589	AF008581	clade_55	N	N
Treponema pallidum	1932	CP001752	clade_550	N	OP
Treponema phagedenis	1934	AEFH01000172	clade_550	N	N
Treponema sp. clone DDKL_4	1939	Y08894	clade_550	N	N
Acholeplasma laidlawii	17	NR_074448	clade_551	N	N
Mycoplasma putrefaciens	1323	U26055	clade_551	N	N
Mycoplasmataceae genomosp. P1 oral clone MB1_G23	1325	DQ003614	clade_551	N	N
Spiroplasma insolitum	1750	NR_025705	clade_551	N	N
Collinsella intestinalis	660	ABXH02000037	clade_553	N	N
Collinsella stercoris	661	ABXJ01000150	clade_553	N	N
Collinsella tanakaei	662	AB490807	clade_553	N	N
Caminicella sporogenes	458	NR_025485	clade_554	N	N
Acidaminococcus fermentans	21	CP001859	clade_556	N	N
Acidaminococcus intestini	22	CP003058	clade_556	N	N
Acidaminococcus sp. D21	23	ACGB01000071	clade_556	N	N
Phascolarctobacterium faecium	1462	NR_026111	clade_556	N	N
Phascolarctobacterium sp. YIT 12068	1463	AB490812	clade_556	N	N
Phascolarctobacterium succinatutens	1464	AB490811	clade_556	N	N
Acidithiobacillus ferrivorans	25	NR_074660	clade_557	N	N
Xanthomonadaceae bacterium NML 03_0222	2015	EU313791	clade_557	N	N
Catabacter hongkongensis	494	AB671763	clade_558	N	N
Christensenella minuta	512	AB490809	clade_558	N	N
Clostridiales bacterium oral clone P4PA_66 P1	536	AY207065	clade_558	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Clostridiales bacterium oral taxon 093	537	GQ422712	clade__558	N	N
Heliobacterium modesticaldum	1000	NR__074517	clade__560	N	N
Alistipes indistinctus	130	AB490804	clade__561	N	N
Bacteroidales bacterium ph8	257	JN837494	clade__561	N	N
Candidatus Sulcia muelleri	475	CP002163	clade__561	N	N
Cytophaga xylanolytica	742	FR733683	clade__561	N	N
Flavobacteriaceae genomosp. C1	884	AY278614	clade__561	N	N
Gramella forsetii	958	NR__074707	clade__561	N	N
Sphingobacterium faecium	1740	NR__025537	clade__562	N	N
Sphingobacterium mizutaii	1741	JF708889	clade__562	N	N
Sphingobacterium multivorum	1742	NR__040953	clade__562	N	N
Sphingobacterium spiritivorum	1743	ACHA02000013	clade__562	N	N
Jonquetella anthropi	1017	ACOO02000004	clade__563	N	N
Pyramidobacter piscolens	1614	AY207056	clade__563	N	N
Synergistes genomosp. C1	1904	AY278615	clade__563	N	N
Synergistes sp. RMA 14551	1905	DQ412722	clade__563	N	N
Synergistetes bacterium ADV897	1906	GQ258968	clade__563	N	N
Candidatus Arthromitus sp. SFB__mouse__Yit	474	NR__074460	clade__564	N	N
Gracilibacter thermotolerans	957	NR__043559	clade__564	N	N
Brachyspira aalborgi	404	FM178386	clade__565	N	N
Brachyspira sp. HIS3	406	FM178387	clade__565	N	N
Brachyspira sp. HIS4	407	FM178388	clade__565	N	N
Brachyspira sp. HIS5	408	FM178389	clade__565	N	N
Adlercreutzia equolifaciens	97	AB306661	clade__566	N	N
Coriobacteriaceae bacterium JC110	678	CAEM01000062	clade__566	N	N
Coriobacteriaceae bacterium phI	679	JN837493	clade__566	N	N
Cryptobacterium curtum	740	GQ422741	clade__566	N	N
Eggerthella sinensis	779	AY321958	clade__566	N	N
Eggerthella sp. 1__3__56FAA	780	ACWN01000099	clade__566	N	N
Eggerthella sp. HGA1	781	AEXR01000021	clade__566	N	N
Eggerthella sp. YY7918	782	AP012211	clade__566	N	N
Gordonibacter pamelaeae	680	AM886059	clade__566	N	N
Gordonibacter pamelaeae	956	FP929047	clade__566	N	N
Slackia equolifaciens	1732	EU377663	clade__566	N	N
Slackia exigua	1733	ACUX01000029	clade__566	N	N
Slackia faecicanis	1734	NR__042220	clade__566	N	N
Slackia heliotrinireducens	1735	NR__074439	clade__566	N	N
Slackia isoflavoniconvertens	1736	AB566418	clade__566	N	N
Slackia piriformis	1737	AB490806	clade__566	N	N
Slackia sp. NATTS	1738	AB505075	clade__566	N	N
Chlamydiales bacterium NS13	506	JN606075	clade__567	N	N
Victivallaceae bacterium NML 080035	2003	FJ394915	clade__567	N	N
Victivallis vadensis	2004	ABDE02000010	clade__567	N	N
Streptomyces griseus	1889	NR__074787	clade__573	N	N
Streptomyces sp. SD 511	1891	EU544231	clade__573	N	N
Streptomyces sp. SD 534	1894	EU544232	clade__573	N	N
Cloacibacillus evryensis	530	GQ258966	clade__575	N	N
Deferribacteres sp. oral clone JV001	743	AY349370	clade__575	N	N
Deferribacteres sp. oral clone JV023	745	AY349372	clade__575	N	N
Synergistetes bacterium LBVCM1157	1907	GQ258969	clade__575	N	N
Synergistetes bacterium oral taxon 362	1909	GU410752	clade__575	N	N
Synergistetes bacterium oral taxon D48	1910	GU430992	clade__575	N	N
Peptococcus sp. oral clone JM048	1439	AY349389	clade__576	N	N
Helicobacter winghamensis	999	ACDO01000013	clade__577	N	N
Wolinella succinogenes	2014	BX571657	clade__577	N	N
Olsenella genomosp. C1	1368	AY278623	clade__578	N	N
Olsenella profusa	1369	FN178466	clade__578	N	N
Olsenella sp. F0004	1370	EU592964	clade__578	N	N
Olsenella sp. oral taxon 809	1371	ACVE01000002	clade__578	N	N
Olsenella uli	1372	CP002106	clade__578	N	N
Nocardiopsis dassonvillei	1356	CP002041	clade__579	N	N
Peptococcus niger	1438	NR__029221	clade__580	N	N
Peptococcus sp. oral taxon 167	1440	GQ422727	clade__580	N	N
Akkermansia muciniphila	118	CP001071	clade__583	N	N
Opitutus terrae	1373	NR__074978	clade__583	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Clostridiales bacterium oral taxon F32	538	HM099644	clade_584	N	N
Leptospira borgpetersenii	1161	NC_008508	clade_585	N	OP
Leptospira broomii	1162	NR_043200	clade_585	N	OP
Leptospira interrogans	1163	NC_005823	clade_585	N	OP
Methanobrevibacter gottschalkii	1213	NR_044789	clade_587	N	N
Methanobrevibacter millerae	1214	NR_042785	clade_587	N	N
Methanobrevibacter oralis	1216	HE654003	clade_587	N	N
Methanobrevibacter thaueri	1219	NR_044787	clade_587	N	N
Methanobrevibacter smithii	1218	ABYV02000002	clade_588	N	N
Deinococcus radiodurans	746	AE000513	clade_589	N	N
Deinococcus sp. R_43890	747	FR682752	clade_589	N	N
Thermus aquaticus	1923	NR_025900	clade_589	N	N
Actinomyces sp. c109	81	AB167239	clade_590	N	N
Syntrophomonadaceae genomosp. P1	1912	AY341821	clade_590	N	N
Anaerobaculum hydrogeniformans	141	ACJX02000009	clade_591	N	N
Microcystis aeruginosa	1246	NC_010296	clade_592	N	N
Prochlorococcus marinus	1567	CP000551	clade_592	N	N
Methanobrevibacter acididurans	1208	NR_028779	clade_593	N	N
Methanobrevibacter arboriphilus	1209	NR_042783	clade_593	N	N
Methanobrevibacter curvatus	1210	NR_044796	clade_593	N	N
Methanobrevibacter cuticularis	1211	NR_044776	clade_593	N	N
Methanobrevibacter filiformis	1212	NR_044801	clade_593	N	N
Methanobrevibacter woesei	1220	NR_044788	clade_593	N	N
Roseiflexus castenholzii	1642	CP000804	clade_594	N	N
Methanobrevibacter olleyae	1215	NR_043024	clade_595	N	N
Methanobrevibacter ruminantium	1217	NR_042784	clade_595	N	N
Methanobrevibacter wolinii	1221	NR_044790	clade_595	N	N
Methanosphaera stadtmanae	1222	AY196684	clade_595	N	N
Chloroflexi genomosp. P1	511	AY331414	clade_596	N	N
Halorubrum lipolyticum	992	AB477978	clade_597	N	N
Methanobacterium formicicum	1207	NR_025028	clade_597	N	N
Acidilobus saccharovorans	24	AY350586	clade_598	N	N
Hyperthermus butylicus	1006	CP000493	clade_598	N	N
Ignicoccus islandicus	1011	X99562	clade_598	N	N
Metallosphaera sedula	1206	D26491	clade_598	N	N
Thermofilum pendens	1922	X14835	clade_598	N	N
Prevotella melaninogenica	1506	CP002122	clade_6	N	N
Prevotella sp. ICM1	1520	HQ616385	clade_6	N	N
Prevotella sp. oral clone FU048	1535	AY349393	clade_6	N	N
Prevotella sp. oral clone GI030	1537	AY349395	clade_6	N	N
Prevotella sp. SEQ116	1526	JN867246	clade_6	N	N
Streptococcus anginosus	1787	AECT01000011	clade_60	N	N
Streptococcus milleri	1812	X81023	clade_60	N	N
Streptococcus sp. 16362	1829	JN590019	clade_60	N	N
Streptococcus sp. 69130	1832	X78825	clade_60	N	N
Streptococcus sp. AC15	1833	HQ616356	clade_60	N	N
Streptococcus sp. CM7	1839	HQ616373	clade_60	N	N
Streptococcus sp. OBRC6	1847	HQ616352	clade_60	N	N
Burkholderia ambifaria	442	AAUZ01000009	clade_61	N	OP
Burkholderia cenocepacia	443	AAHI01000060	clade_61	N	OP
Burkholderia cepacia	444	NR_041719	clade_61	N	OP
Burkholderia mallei	445	CP000547	clade_61	N	Category-B
Burkholderia multivorans	446	NC_010086	clade_61	N	OP
Burkholderia oklahomensis	447	DQ108388	clade_61	N	OP
Burkholderia pseudomallei	448	CP001408	clade_61	N	Category-B
Burkholderia rhizoxinica	449	HQ005410	clade_61	N	OP
Burkholderia sp. 383	450	CP000151	clade_61	N	OP
Burkholderia xenovorans	451	U86373	clade_61	N	OP
Prevotella buccae	1488	ACRB01000001	clade_62	N	N
Prevotella genomosp. P8 oral clone MB3_P13	1498	DQ003622	clade_62	N	N
Prevotella sp. oral clone FW035	1536	AY349394	clade_62	N	N
Prevotella bivia	1486	ADFO01000096	clade_63	N	N
Prevotella disiens	1494	AEDO01000026	clade_64	N	N
Bacteroides faecis	276	GQ496624	clade_65	N	N
Bacteroides fragilis	279	AP006841	clade_65	N	N
Bacteroides nordii	285	NR_043017	clade_65	N	N
Bacteroides salyersiae	292	EU136690	clade_65	N	N
Bacteroides sp. 1_1_14	293	ACRP01000155	clade_65	N	N
Bacteroides sp. 1_1_6	295	ACIC01000215	clade_65	N	N
Bacteroides sp. 2_1_56FAA	298	ACWI01000065	clade_65	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Bacteroides sp. AR29	316	AF139525	clade_65	N	N
Bacteroides sp. B2	317	EU722733	clade_65	N	N
Bacteroides thetaiotaomicron	328	NR_074277	clade_65	N	N
Actinobacillus minor	45	ACFT01000025	clade_69	N	N
Haemophilus parasuis	978	GU226366	clade_69	N	N
Vibrio cholerae	1996	AAUR01000095	clade_71	N	Category-B
Vibrio fluvialis	1997	X76335	clade_71	N	Category-B
Vibrio furnissii	1998	CP002377	clade_71	N	Category-B
Vibrio mimicus	1999	ADAF01000001	clade_71	N	Category-B
Vibrio parahaemolyticus	2000	AAWQ01000116	clade_71	N	Category-B
Vibrio sp. RC341	2001	ACZT01000024	clade_71	N	Category-B
Vibrio vulnificus	2002	AE016796	clade_71	N	Category-B
Lactobacillus acidophilus	1067	CP000033	clade_72	N	N
Lactobacillus amylolyticus	1069	ADNY01000006	clade_72	N	N
Lactobacillus amylovorus	1070	CP002338	clade_72	N	N
Lactobacillus crispatus	1078	ACOG01000151	clade_72	N	N
Lactobacillus delbrueckii	1080	CP002341	clade_72	N	N
Lactobacillus helveticus	1088	ACLM01000202	clade_72	N	N
Lactobacillus kalixensis	1094	NR_029083	clade_72	N	N
Lactobacillus kefiranofaciens	1095	NR_042440	clade_72	N	N
Lactobacillus leichmannii	1098	JX986966	clade_72	N	N
Lactobacillus sp. 66c	1120	FR681900	clade_72	N	N
Lactobacillus sp. KLDS 1.0701	1122	EU600905	clade_72	N	N
Lactobacillus sp. KLDS 1.0712	1130	EU600916	clade_72	N	N
Lactobacillus sp. oral clone HT070	1136	AY349383	clade_72	N	N
Lactobacillus ultunensis	1139	ACGU01000081	clade_72	N	N
Prevotella intermedia	1502	AF414829	clade_81	N	N
Prevotella nigrescens	1511	AFPX01000069	clade_81	N	N
Prevotella pallens	1515	AFPY01000135	clade_81	N	N
Prevotella sp. oral taxon 310	1551	GQ422737	clade_81	N	N
Prevotella genomosp. C1	1495	AY278624	clade_82	N	N
Prevotella sp. CM38	1519	HQ610181	clade_82	N	N
Prevotella sp. oral taxon 317	1552	ACQH01000158	clade_82	N	N
Prevotella sp. SG12	1527	GU561343	clade_82	N	N
Prevotella denticola	1493	CP002589	clade_83	N	N
Prevotella genomosp. P7 oral clone MB2_P31	1497	DQ003620	clade_83	N	N
Prevotella histicola	1501	JN867315	clade_83	N	N
Prevotella multiformis	1508	AEWX01000054	clade_83	N	N
Prevotella sp. JCM 6330	1522	AB547699	clade_83	N	N
Prevotella sp. oral clone GI059	1539	AY349397	clade_83	N	N
Prevotella sp. oral taxon 782	1555	GQ422745	clade_83	N	N
Prevotella sp. oral taxon G71	1559	GU432180	clade_83	N	N
Prevotella sp. SEQ065	1524	JN867234	clade_83	N	N
Prevotella veroralis	1565	ACVA01000027	clade_83	N	N
Bacteroides acidifaciens	266	NR_028607	clade_85	N	N
Bacteroides cellulosilyticus	269	ACCH01000108	clade_85	N	N
Bacteroides clarus	270	AFBM01000011	clade_85	N	N
Bacteroides eggerthii	275	ACWG01000065	clade_85	N	N
Bacteroides oleiciplenus	286	AB547644	clade_85	N	N
Bacteroides pyogenes	290	NR_041280	clade_85	N	N
Bacteroides sp. 315_5	300	FJ848547	clade_85	N	N
Bacteroides sp. 31SF15	301	AJ583248	clade_85	N	N
Bacteroides sp. 31SF18	302	AJ583249	clade_85	N	N
Bacteroides sp. 35AE31	303	AJ583244	clade_85	N	N
Bacteroides sp. 35AE37	304	AJ583245	clade_85	N	N
Bacteroides sp. 35BE34	305	AJ583246	clade_85	N	N
Bacteroides sp. 35BE35	306	AJ583247	clade_85	N	N
Bacteroides sp. WH2	324	AY895180	clade_85	N	N
Bacteroides sp. XB12B	325	AM230648	clade_85	N	N
Bacteroides stercoris	327	ABFZ02000022	clade_85	N	N
Actinobacillus pleuropneumoniae	46	NR_074857	clade_88	N	N
Actinobacillus ureae	48	AEVG01000167	clade_88	N	N
Haemophilus aegyptius	969	AFBC01000053	clade_88	N	N
Haemophilus ducreyi	970	AE017143	clade_88	N	OP
Haemophilus haemolyticus	973	JN175335	clade_88	N	N
Haemophilus influenzae	974	AADP01000001	clade_88	N	OP
Haemophilus parahaemolyticus	975	GU561425	clade_88	N	N
Haemophilus parainfluenzae	976	AEWU01000024	clade_88	N	N
Haemophilus paraphrophaemolyticus	977	M75076	clade_88	N	N
Haemophilus somnus	979	NC_008309	clade_88	N	N
Haemophilus sp. 70334	980	HQ680854	clade_88	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Haemophilus sp. HK445	981	FJ685624	clade_88	N	N
Haemophilus sp. oral clone ASCA07	982	AY923117	clade_88	N	N
Haemophilus sp. oral clone ASCG06	983	AY923147	clade_88	N	N
Haemophilus sp. oral clone BJ021	984	AY005034	clade_88	N	N
Haemophilus sp. oral clone BJ095	985	AY005033	clade_88	N	N
Haemophilus sp. oral taxon 851	987	AGRK01000004	clade_88	N	N
Haemophilus sputorum	988	AFNK01000005	clade_88	N	N
Histophilus somni	1003	AF549387	clade_88	N	N
Mannheimia haemolytica	1195	ACZX01000102	clade_88	N	N
Pasteurella bettyae	1433	L06088	clade_88	N	N
Moellerella wisconsensis	1253	JN175344	clade_89	N	N
Morganella morganii	1265	AJ301681	clade_89	N	N
Morganella sp. JB_T16	1266	AJ781005	clade_89	N	N
Proteus mirabilis	1582	ACLE01000013	clade_89	N	N
Proteus penneri	1583	ABVP01000020	clade_89	N	N
Proteus sp. HS7514	1584	DQ512963	clade_89	N	N
Proteus vulgaris	1585	AJ233425	clade_89	N	N
Oribacterium sinus	1374	ACKX01000142	clade_90	N	N
Oribacterium sp. ACB1	1375	HM120210	clade_90	N	N
Oribacterium sp. ACB7	1376	HM120211	clade_90	N	N
Oribacterium sp. CM 12	1377	HQ616374	clade_90	N	N
Oribacterium sp. ICM51	1378	HQ616397	clade_90	N	N
Oribacterium sp. OBRC12	1379	HQ616355	clade_90	N	N
Oribacterium sp. oral taxon 108	1382	AFIH01000001	clade_90	N	N
Actinobacillus actinomycetemcomitans	44	AY362885	clade_92	N	N
Actinobacillus succinogenes	47	CP000746	clade_92	N	N
Aggregatibacter actinomycetemcomitans	112	CP001733	clade_92	N	N
Aggregatibacter aphrophilus	113	CP001607	clade_92	N	N
Aggregatibacter segnis	114	AEPS01000017	clade_92	N	N
Averyella dalhousiensis	194	DQ481464	clade_92	N	N
Bisgaard Taxon	368	AY683487	clade_92	N	N
Bisgaard Taxon	369	AY683489	clade_92	N	N
Bisgaard Taxon	370	AY683491	clade_92	N	N
Bisgaard Taxon	371	AY683492	clade_92	N	N
Buchnera aphidicola	440	NR_074609	clade_92	N	N
Cedecea davisae	499	AF493976	clade_92	N	N
Citrobacter amalonaticus	517	FR870441	clade_92	N	N
Citrobacter braakii	518	NR_028687	clade_92	N	N
Citrobacter farmeri	519	AF025371	clade_92	N	N
Citrobacter freundii	520	NR_028894	clade_92	N	N
Citrobacter gillenii	521	AF025367	clade_92	N	N
Citrobacter koseri	522	NC_009792	clade_92	N	N
Citrobacter murliniae	523	AF025369	clade_92	N	N
Citrobacter rodentium	524	NR_074903	clade_92	N	N
Citrobacter sedlakii	525	AF025364	clade_92	N	N
Citrobacter sp. 30_2	526	ACDJ01000053	clade_92	N	N
Citrobacter sp. KMSI_3	527	GQ468398	clade_92	N	N
Citrobacter werkmanii	528	AF025373	clade_92	N	N
Citrobacter youngae	529	ABWL02000011	clade_92	N	N
Cronobacter malonaticus	737	GU122174	clade_92	N	N
Cronobacter sakazakii	738	NC_009778	clade_92	N	N
Cronobacter turicensis	739	FN543093	clade_92	N	N
Enterobacter aerogenes	786	AJ251468	clade_92	N	N
Enterobacter asburiae	787	NR_024640	clade_92	N	N
Enterobacter cancerogenus	788	Z96078	clade_92	N	N
Enterobacter cloacae	789	FP929040	clade_92	N	N
Enterobacter cowanii	790	NR_025566	clade_92	N	N
Enterobacter hormaechei	791	AFHR01000079	clade_92	N	N
Enterobacter sp. 247BMC	792	HQ122932	clade_92	N	N
Enterobacter sp. 638	793	NR_074777	clade_92	N	N
Enterobacter sp. JC163	794	JN657217	clade_92	N	N
Enterobacter sp. SCSS	795	HM007811	clade_92	N	N
Enterobacter sp. TSE38	796	HM156134	clade_92	N	N
Enterobacteriaceae bacterium 9_2_54FAA	797	ADCU01000033	clade_92	N	N
Enterobacteriaceae bacterium CF01Ent_1	798	AJ489826	clade_92	N	N
Enterobacteriaceae bacterium Smarlab 3302238	799	AY538694	clade_92	N	N
Escherichia albertii	824	ABKX01000012	clade_92	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Escherichia coli	825	NC_008563	clade_92	N	Category-B
Escherichia fergusonii	826	CU928158	clade_92	N	N
Escherichia hermannii	827	HQ407266	clade_92	N	N
Escherichia sp. 1_1_43	828	ACID01000033	clade_92	N	N
Escherichia sp. 4_1_40B	829	ACDM02000056	clade_92	N	N
Escherichia sp. B4	830	EU722735	clade_92	N	N
Escherichia vulneris	831	NR_041927	clade_92	N	N
Ewingella americana	877	JN175329	clade_92	N	N
Haemophilus genomosp. P2 oral clone MB3_C24	971	DQ003621	clade_92	N	N
Haemophilus genomosp. P3 oral clone MB3_C38	972	DQ003635	clade_92	N	N
Haemophilus sp. oral clone JM053	986	AY349380	clade_92	N	N
Hafnia alvei	989	DQ412565	clade_92	N	N
Klebsiella oxytoca	1024	AY292871	clade_92	N	OP
Klebsiella pneumoniae	1025	CP000647	clade_92	N	OP
Klebsiella sp. AS10	1026	HQ616362	clade_92	N	N
Klebsiella sp. Co9935	1027	DQ068764	clade_92	N	N
Klebsiella sp. enrichment culture clone SRC_DSD25	1036	HM195210	clade_92	N	N
Klebsiella sp. OBRC7	1028	HQ616353	clade_92	N	N
Klebsiella sp. SP_BA	1029	FJ999767	clade_92	N	N
Klebsiella sp. SRC_DSD1	1033	GU797254	clade_92	N	N
Klebsiella sp. SRC_DSD11	1030	GU797263	clade_92	N	N
Klebsiella sp. SRC_DSD12	1031	GU797264	clade_92	N	N
Klebsiella sp. SRC_DSD15	1032	GU797267	clade_92	N	N
Klebsiella sp. SRC_DSD2	1034	GU797253	clade_92	N	N
Klebsiella sp. SRC_DSD6	1035	GU797258	clade_92	N	N
Klebsiella variicola	1037	CP001891	clade_92	N	N
Kluyvera ascorbata	1038	NR_028677	clade_92	N	N
Kluyvera cryocrescens	1039	NR_028803	clade_92	N	N
Leminorella grimontii	1159	AJ233421	clade_92	N	N
Leminorella richardii	1160	HF558368	clade_92	N	N
Pantoea agglomerans	1409	AY335552	clade_92	N	N
Pantoea ananatis	1410	CP001875	clade_92	N	N
Pantoea brenneri	1411	EU216735	clade_92	N	N
Pantoea citrea	1412	EF688008	clade_92	N	N
Pantoea conspicua	1413	EU216737	clade_92	N	N
Pantoea septica	1414	EU216734	clade_92	N	N
Pasteurella dagmatis	1434	ACZR01000003	clade_92	N	N
Pasteurella multocida	1435	NC_002663	clade_92	N	N
Plesiomonas shigelloides	1469	X60418	clade_92	N	N
Raoultella ornithinolytica	1617	AB364958	clade_92	N	N
Raoultella planticola	1618	AF129443	clade_92	N	N
Raoultella terrigena	1619	NR_037085	clade_92	N	N
Salmonella bongori	1683	NR_041699	clade_92	N	Category-B
Salmonella enterica	1672	NC_011149	clade_92	N	Category-B
Salmonella enterica	1673	NC_011205	clade_92	N	Category-B
Salmonella enterica	1674	DQ344532	clade_92	N	Category-B
Salmonella enterica	1675	ABEH02000004	clade_92	N	Category-B
Salmonella enterica	1676	ABAK02000001	clade_92	N	Category-B
Salmonella enterica	1677	NC_011080	clade_92	N	Category-B
Salmonella enterica	1678	EU118094	clade_92	N	Category-B
Salmonella enterica	1679	NC_011094	clade_92	N	Category-B
Salmonella enterica	1680	AE014613	clade_92	N	Category-B
Salmonella enterica	1682	ABFH02000001	clade_92	N	Category-B
Salmonella enterica	1684	ABEM01000001	clade_92	N	Category-B
Salmonella enterica	1685	ABAM02000001	clade_92	N	Category-B
Salmonella typhimurium	1681	DQ344533	clade_92	N	Category-B
Salmonella typhimurium	1686	AF170176	clade_92	N	Category-B
Serratia fonticola	1718	NR_025339	clade_92	N	N
Serratia liquefaciens	1719	NR_042062	clade_92	N	N
Serratia marcescens	1720	GU826157	clade_92	N	N
Serratia odorifera	1721	ADBY01000001	clade_92	N	N
Serratia proteamaculans	1722	AAUN01000015	clade_92	N	N
Shigella boydii	1724	AAKA01000007	clade_92	N	Category-B
Shigella dysenteriae	1725	NC_007606	clade_92	N	Category-B
Shigella flexneri	1726	AE005674	clade_92	N	Category-B
Shigella sonnei	1727	NC_007384	clade_92	N	Category-B
Tatumella ptyseos	1916	NR_025342	clade_92	N	N
Trabulsiella guamensis	1925	AY373830	clade_92	N	N
Yersinia aldovae	2019	AJ871363	clade_92	N	OP

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Yersinia aleksiciae	2020	AJ627597	clade_92	N	OP
Yersinia bercovieri	2021	AF366377	clade_92	N	OP
Yersinia enterocolitica	2022	FR729477	clade_92	N	Category-B
Yersinia frederiksenii	2023	AF366379	clade_92	N	OP
Yersinia intermedia	2024	AF366380	clade_92	N	OP
Yersinia kristensenii	2025	ACCA01000078	clade_92	N	OP
Yersinia mollaretii	2026	NR_027546	clade_92	N	OP
Yersinia pestis	2027	AE013632	clade_92	N	Category-A
Yersinia pseudotuberculosis	2028	NC_009708	clade_92	N	OP
Yersinia rohdei	2029	ACCD01000071	clade_92	N	OP
Yokenella regensburgei	2030	AB273739	clade_92	N	N
Conchiformibius kuhniae	669	NR_041821	clade_94	N	N
Morococcus cerebrosus	1267	JN175352	clade_94	N	N
Neisseria bacilliformis	1328	AFAY01000058	clade_94	N	N
Neisseria cinerea	1329	ACDY01000037	clade_94	N	N
Neisseria flavescens	1331	ACQV01000025	clade_94	N	N
Neisseria gonorrhoeae	1333	CP002440	clade_94	N	OP
Neisseria lactamica	1334	ACEQ01000095	clade_94	N	N
Neisseria macacae	1335	AFQE01000146	clade_94	N	N
Neisseria meningitidis	1336	NC_003112	clade_94	N	OP
Neisseria mucosa	1337	ACDX01000110	clade_94	N	N
Neisseria pharyngis	1338	AJ239281	clade_94	N	N
Neisseria polysaccharea	1339	ADBE01000137	clade_94	N	N
Neisseria sicca	1340	ACKO02000016	clade_94	N	N
Neisseria sp. KEM232	1341	GQ203291	clade_94	N	N
Neisseria sp. oral clone AP132	1344	AY005027	clade_94	N	N
Neisseria sp. oral strain B33KA	1346	AY005028	clade_94	N	N
Neisseria sp. oral taxon 014	1347	ADEA01000039	clade_94	N	N
Neisseria sp. TM10_1	1343	DQ279352	clade_94	N	N
Neisseria subflava	1348	ACEO01000067	clade_94	N	N
Okadaella gastrococcus	1365	HQ699465	clade_98	N	N
Streptococcus agalactiae	1785	AAJO01000130	clade_98	N	N
Streptococcus alactolyticus	1786	NR_041781	clade_98	N	N
Streptococcus australis	1788	AEQR01000024	clade_98	N	N
Streptococcus bovis	1789	AEEL01000030	clade_98	N	N
Streptococcus canis	1790	AJ413203	clade_98	N	N
Streptococcus constellatus	1791	AY277942	clade_98	N	N
Streptococcus cristatus	1792	AEVC01000028	clade_98	N	N
Streptococcus dysgalactiae	1794	AP010935	clade_98	N	N
Streptococcus equi	1795	CP001129	clade_98	N	N
Streptococcus equinus	1796	AEVB01000043	clade_98	N	N
Streptococcus gallolyticus	1797	FR824043	clade_98	N	N
Streptococcus genomosp. C1	1798	AY278629	clade_98	N	N
Streptococcus genomosp. C2	1799	AY278630	clade_98	N	N
Streptococcus genomosp. C3	1800	AY278631	clade_98	N	N
Streptococcus genomosp. C4	1801	AY278632	clade_98	N	N
Streptococcus genomosp. C5	1802	AY278633	clade_98	N	N
Streptococcus genomosp. C6	1803	AY278634	clade_98	N	N
Streptococcus genomosp. C7	1804	AY278635	clade_98	N	N
Streptococcus genomosp. C8	1805	AY278609	clade_98	N	N
Streptococcus gordonii	1806	NC_009785	clade_98	N	N
Streptococcus infantarius	1807	ABJK02000017	clade_98	N	N
Streptococcus infantis	1808	AFNN01000024	clade_98	N	N
Streptococcus intermedius	1809	NR_028736	clade_98	N	N
Streptococcus lutetiensis	1810	NR_037096	clade_98	N	N
Streptococcus massiliensis	1811	AY769997	clade_98	N	N
Streptococcus mitis	1813	AM157420	clade_98	N	N
Streptococcus oligofermentans	1815	AY099095	clade_98	N	N
Streptococcus oralis	1816	ADMV01000001	clade_98	N	N
Streptococcus parasanguinis	1817	AEKM01000012	clade_98	N	N
Streptococcus pasteurianus	1818	AP012054	clade_98	N	N
Streptococcus peroris	1819	AEVF01000016	clade_98	N	N
Streptococcus pneumoniae	1820	AE008537	clade_98	N	N
Streptococcus porcinus	1821	EF121439	clade_98	N	N
Streptococcus pseudopneumoniae	1822	FJ827123	clade_98	N	N
Streptococcus pseudoporcinus	1823	AENS01000003	clade_98	N	N
Streptococcus pyogenes	1824	AE006496	clade_98	N	OP
Streptococcus ratti	1825	X58304	clade_98	N	N
Streptococcus sanguinis	1827	NR_074974	clade_98	N	N
Streptococcus sinensis	1828	AF432857	clade_98	N	N
Streptococcus sp. 2_1_36FAA	1831	ACOI01000028	clade_98	N	N
Streptococcus sp. 2285_97	1830	AJ131965	clade_98	N	N

TABLE 1-continued

See, e.g., WO2014/121304

OTU	SEQ ID Number	Public DB Accession	Clade	Spore Former	Pathogen Status
Streptococcus sp. ACS2	1834	HQ616360	clade_98	N	N
Streptococcus sp. AS20	1835	HQ616366	clade_98	N	N
Streptococcus sp. BS35a	1836	HQ616369	clade_98	N	N
Streptococcus sp. C150	1837	ACRI01000045	clade_98	N	N
Streptococcus sp. CM6	1838	HQ616372	clade_98	N	N
Streptococcus sp. ICM10	1840	HQ616389	clade_98	N	N
Streptococcus sp. ICM12	1841	HQ616390	clade_98	N	N
Streptococcus sp. ICM2	1842	HQ616386	clade_98	N	N
Streptococcus sp. ICM4	1844	HQ616387	clade_98	N	N
Streptococcus sp. ICM45	1843	HQ616394	clade_98	N	N
Streptococcus sp. M143	1845	ACRK01000025	clade_98	N	N
Streptococcus sp. M334	1846	ACRL01000052	clade_98	N	N
Streptococcus sp. oral clone ASB02	1849	AY923121	clade_98	N	N
Streptococcus sp. oral clone ASCA03	1850	DQ272504	clade_98	N	N
Streptococcus sp. oral clone ASCA04	1851	AY923116	clade_98	N	N
Streptococcus sp. oral clone ASCA09	1852	AY923119	clade_98	N	N
Streptococcus sp. oral clone ASCB04	1853	AY923123	clade_98	N	N
Streptococcus sp. oral clone ASCB06	1854	AY923124	clade_98	N	N
Streptococcus sp. oral clone ASCC04	1855	AY923127	clade_98	N	N
Streptococcus sp. oral clone ASCC05	1856	AY923128	clade_98	N	N
Streptococcus sp. oral clone ASCC12	1857	DQ272507	clade_98	N	N
Streptococcus sp. oral clone ASCD01	1858	AY923129	clade_98	N	N
Streptococcus sp. oral clone ASCD09	1859	AY923130	clade_98	N	N
Streptococcus sp. oral clone ASCD10	1860	DQ272509	clade_98	N	N
Streptococcus sp. oral clone ASCE03	1861	AY923134	clade_98	N	N
Streptococcus sp. oral clone ASCE04	1862	AY953253	clade_98	N	N
Streptococcus sp. oral clone ASCE05	1863	DQ272510	clade_98	N	N
Streptococcus sp. oral clone ASCE06	1864	AY923135	clade_98	N	N
Streptococcus sp. oral clone ASCE09	1865	AY923136	clade_98	N	N
Streptococcus sp. oral clone ASCE10	1866	AY923137	clade_98	N	N
Streptococcus sp. oral clone ASCE12	1867	AY923138	clade_98	N	N
Streptococcus sp. oral clone ASCF05	1868	AY923140	clade_98	N	N
Streptococcus sp. oral clone ASCF07	1869	AY953255	clade_98	N	N
Streptococcus sp. oral clone ASCF09	1870	AY923142	clade_98	N	N
Streptococcus sp. oral clone ASCG04	1871	AY923145	clade_98	N	N
Streptococcus sp. oral clone BW009	1872	AY005042	clade_98	N	N
Streptococcus sp. oral clone CH016	1873	AY005044	clade_98	N	N
Streptococcus sp. oral clone GK051	1874	AY349413	clade_98	N	N
Streptococcus sp. oral clone GM006	1875	AY349414	clade_98	N	N
Streptococcus sp. oral clone P2PA_41 P2	1876	AY207051	clade_98	N	N
Streptococcus sp. oral clone P4PA_30 P4	1877	AY207064	clade_98	N	N
Streptococcus sp. oral taxon 071	1878	AEEP01000019	clade_98	N	N
Streptococcus sp. oral taxon G59	1879	GU432132	clade_98	N	N
Streptococcus sp. oral taxon G62	1880	GU432146	clade_98	N	N
Streptococcus sp. oral taxon G63	1881	GU432150	clade_98	N	N
Streptococcus suis	1882	FM252032	clade_98	N	N
Streptococcus thermophilus	1883	CP000419	clade_98	N	N
Streptococcus salivarius	1826	AGBV01000001	clade_98	N	N
Streptococcus uberis	1884	HQ391900	clade_98	N	N
Streptococcus urinalis	1885	DQ303194	clade_98	N	N
Streptococcus vestibularis	1886	AEKO01000008	clade_98	N	N
Streptococcus viridans	1887	AF076036	clade_98	N	N
Synergistetes bacterium oral clone 03 5 D05	1908	GU227192	clade_98	N	N

TABLE 1A

Exemplary Immunomodulatory Bacterial Species
Alkaliphilus metalliredigens
Ammonifex degensii
Anaerofustis stercorihominis
Anaerostipes caccae
Anaerotruncus colihominis
Bacillus amyloliquefaciens
Bacillus anthracis
Bacillus cellulosilyticus

TABLE 1A-continued

Exemplary Immunomodulatory Bacterial Species
Bacillus cereus
Bacillus clausii
Bacillus coagulans
Bacillus cytotoxicus
Bacillus halodurans
Bacillus licheniformis
Bacillus pumilus
Bacillus subtilis

TABLE 1A-continued

Exemplary Immunomodulatory Bacterial Species
Bacillus thuringiensis
Bacillus weihenstephanensis
Blautia (*Ruminococcus*) *hansenii*
Blautia (*Ruminococcus*) *obeum*
Brevibacillus brevis
Bryantella formatexigens
Caldicellulosiruptor saccharolyticus
Candidatus Desulforudis audaxviator
Carboxydibrachium pacificum
Carboxydothermus hydrogenoformans
Clostridium acetobutylicum
Clostridium asparagiforme
Clostridium bartlettii
Clostridium beijerinckii
Clostridium bolteae
Clostridium botulinum A str. ATCC 19397
Clostridium botulinum B str. Eklund 17B
Clostridium butyricum pathogenic E4 str. BoNT BL5262
Clostridium carboxidivorans
Clostridium cellulolyticum
Clostridium cellulovorans
Clostridium difficile
Clostridium (*Hungatella*) *hathewayi*
Clostridium hylemonae
Clostridium kluyveri
Clostridium leptum
Clostridium methylpentosum
Clostridium (*Tyzzerella*) *nexile*
Clostridium novyi NT
Clostridium papyrosolvens
Clostridium perfringens
Clostridium phytofermentans ISDg
Clostridium scindens
Clostridium sp. 7_2_43FAA
Clostridium sporogenes
Clostridium tetani
Clostridium thermocellum
Coprococcus comes
Desulfotomaculum reducens
Dorea longicatena
Eubacterium eligens
Eubacterium hallii
Eubacterium rectale
Eubacterium ventriosum
Faecalibacterium prausnitzii
Geobacillus kaustophilus
Geobacillus sp. G11MC16
Geobacillus thermodenitrificans
Heliobacterium modesticaldum
Lysinibacillus sphaericus
Oceanobacillus iheyensis
Paenibacillus sp. JDR-2
Pelotomaculum thermopropionicum
Roseburia intestinalis
Ruminococcus bromii
Ruminococcus gnavus
Ruminococcus torques
Subdoligranulum variabile
Symbiobacterium thermophilum
Thermoanaerobacter italicus
Thermoanaerobacter tengcongensis
Thermoanaerobacterium thermosaccharolyticum
Thermosinus carboxydivorans

TABLE 1B

Exemplary Bacteria Useful in the Present Invention
Acidaminococcus intestini
Acinetobacter baumannii
Acinetobacter lwoffii
Akkermansia muciniphila

TABLE 1B-continued

Exemplary Bacteria Useful in the Present Invention
Alistipes putredinis
Alistipes shahii
Anaerostipes hadrus
Anaerotruncus colihominis
Bacteroides caccae
Bacteroides cellulosilyticus
Bacteroides dorei
Bacteroides eggerthii
Bacteroides finegoldii
Bacteroides fragilis
Bacteroides massiliensis
Bacteroides ovatus
Bacteroides salanitronis
Bacteroides salyersiae
Bacteroides sp. 1_1_6
Bacteroides sp. 3_1_23
Bacteroides sp. D20
Bacteroides thetaiotaomicron
Bacteroides uniformis
Bacteroides vulgatus
Bifidobacterium adolescentis
Bifidobacterium bifidum
Bifidobacterium breve
Bifidobacterium faecale
Bifidobacterium kashiwanohense
Bifidobacterium longum subsp. *longum*
Bifidobacterium pseudocatenulatum
Bifidobacterium stercoris
Blautia (*Ruminococcus*) *coccoides*
Blautia faecis
Blautia glucerasea
Blautia (*Ruminococcus*) *hansenii*
Blautia hydrogenotrophica (*Ruminococcus hydrogenotrophicus*)
Blautia (*Ruminococcus*) *luti*
Blautia (*Ruminococcus*) *obeum*
Blautia producta (*Ruminococcus productus*)
Blautia (*Ruminococcus*) *schinkii*
Blautia stercoris
Blautia uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1)
Blautia uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1)
Blautia uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1)
Blautia uncultured bacterium clone S1-5 (GenBank: GQ898099.1)
Blautia uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2)
Blautia wexlerae
Candidatus Arthromitus sp. SFB-mouse-Yit
Catenibacterium mitsuokai
Clostridiaceae bacterium (*Dielma fastidiosa*) JC13
Clostridiales bacterium 1_7_47FAA
Clostridium asparagiforme
Clostridium bolteae
Clostridium clostridioforme
Clostridium glycyrrhizinilyticum
Clostridium (*Hungatella*) *hathewayi*
Clostridium histolyticum
Clostridium indolis
Clostridium leptum
Clostridium (*Tyzzerella*) *nexile*
Clostridium perfringens
Clostridium (*Erysipelatoclostridium*) *ramosum*
Clostridium scindens
Clostridium sp. 14774
Clostridium sp. 7_3_54FAA
Clostridium sp. HGF2
Clostridium symbiosum
Collinsella aerofaciens
Collinsella intestinalis
Coprobacillus sp. D7
Coprococcus catus
Coprococcus comes
Dorea formicigenerans
Dorea longicatena

TABLE 1B-continued

Exemplary Bacteria Useful in the Present Invention
Enterococcus faecalis
Enterococcus faecium
Erysipelotrichaceae bacterium 3_1_53
Escherichia coli
Escherichia coli S88
Eubacterium eligens
Eubacterium fissicatena
Eubacterium ramulus
Eubacterium rectale
Faecalibacterium prausnitzii
Flavonifractor plautii
Fusobacterium mortiferum
Fusobacterium nucleatum
Holdemania filiformis
Hydrogenoanaerobacterium saccharovorans
Klebsiella oxytoca
Lachnospiraceae bacterium 3_1_57FAA_CT1
Lachnospiraceae bacterium 7_1_58FAA
Lachnospiraceae bacterium 5_1_57FAA
Lactobacillus casei
Lactobacillus rhamnosus
Lactobacillus ruminis
Lactococcus casei
Odoribacter splanchnicus
Oscillibacter valericigenes
Parabacteroides gordonii
Parabacteroides johnsonii
Parabacteroides merdae
Pediococcus acidilactici
Peptostreptococcus asaccharolyticus
Propionibacterium granulosum
Roseburia intestinalis
Roseburia inulinivorans
Ruminococcus faecis
Ruminococcus gnavus
Ruminococcus sp. ID8
Ruminococcus torques
Slackia piriformis
Staphylococcus epidermidis
Staphylococcus saprophyticus
Streptococcus cristatus
Streptococcus dysgalactiae subsp. *equisimilis*
Streptococcus infantis
Streptococcus oralis
Streptococcus sanguinis
Streptococcus viridans
Streptococcus thermophilus
Veillonella dispar

TABLE 1C

Exemplary Bacteria Useful in the Present Invention
Anaerotruncus colihominis strain 13
Blautia producta strain 6
Clostridium bolteae strain 7
Clostridiaceae bacterium JC13 strain 8
Clostridiales bacterium 1_7_47FAA strain 28
Clostridium sp. 7_3_54FAA strain 16
Clostridium asparagiforme strain 15
Clostridium clostridioforme
Clostridium (*Hungatella*) *hathewayi* strain 4
Clostridium indolis strain 9
Clostridium (*Erysipelatoclostridium*) *ramosum* strain 18
Clostridium scindens strain 26
Clostridium sp. 14774 strain 1
Eubacterium fissicatena strain 21
Hydrogenoanaerobacterium saccharovorans
Lachnospiraceae bacterium 3_1_57FAA strain 27
Lachnospiraceae bacterium 3_1_57FAA strain 29

TABLE 1C-continued

Exemplary Bacteria Useful in the Present Invention
Lachnospiraceae bacterium 7_1_58FAA strain 3
Oscillibacter valericigenes
Ruminococcus sp. ID8 strain 14

TABLE 1D

Exemplary Bacteria Useful in the Present Invention
Bacteroides caccae
Bacteroides eggerthii
Bacteroides ovatus
Bacteroides sp. 1_1_6
Bacteroides sp. 3_1_23
Bacteroides sp. D20
Bacteroides vulgatus
Bifidobacterium adolescentis
Bifidobacterium pseudocatenulatum
Blautia (*Ruminococcus*) *obeum*
Blautia producta (*Ruminococcus productus*)
Blautia (*Ruminococcus*) *schinkii*
Clostridium (*Hungatella*) *hathewayi*
Clostridium (*Tyzzerella*) *nexile*
Clostridium sp. HGF2
Clostridium symbiosum
Collinsella aerofaciens
Coprobacillus sp. D7
Coprococcus catus
Coprococcus comes
Dorea formicigenerans
Dorea longicatena
Enterococcus faecalis
Erysipelotrichaceae bacterium 3_1_53
Escherichia coli
Escherichia coli S88
Eubacterium eligens
Eubacterium rectale
Faecalibacterium prausnitzii
Lachnospiraceae bacterium 5_1_57FAA
Odoribacter splanchnicus
Parabacteroides merdae
Roseburia intestinalis
Ruminococcus torques
Streptococcus thermophilus

TABLE 1E

Exemplary Bacteria Useful in the Present Invention
Akkermansia muciniphila
Enterococcus faecalis
Klebsiella oxytoca
Lactobacillus rhamnosus
Staphylococcus epidermidis
Streptococcus viridans
Veillonella dispar

TABLE 1F

Exemplary Bacteria Useful in the Present Invention
Acinetobacter baumannii
Acinetobacter lwoffii
Akkermansia muciniphila
Alistipes shahii
Anaerotruncus colihominis
Bacteroides caccae
Bacteroides dorei
Bacteroides eggerthii

TABLE 1F-continued

Exemplary Bacteria Useful in the Present Invention
Bacteroides finegoldii
Bacteroides fragilis
Bacteroides massiliensis
Bacteroides ovatus
Bacteroides salanitronis
Bacteroides sp. 1_1_6
Bacteroides sp. 3_1_23
Bacteroides sp. D20
Bacteroides thetaiotaomicron
Bacteroides uniformis
Bacteroides vulgatus
Bifidobacterium adolescentis
Bifidobacterium breve
Bifidobacterium pseudocatenulatum
Blautia (*Ruminococcus*) *coccoides*
Blautia faecis
Blautia glucerasea
Blautia (*Ruminococcus*) *hansenii*
Blautia hydrogenotrophica (*Ruminococcus hydrogenotrophicus*)
Blautia (*Ruminococcus*) *luti*
Blautia (*Ruminococcus*) *obeum*
Blautia producta (*Ruminococcus productus*)
Blautia (*Ruminococcus*) *schinkii*
Blautia stercoris
Blautia wexlerae
Candidatus Arthromitus sp. SFB-mouse-Yit
Clostridiaceae bacterium (*Dielma fastidiosa*) JC13
Clostridiales bacterium 1_7_47FAA
Clostridium asparagiforme
Clostridium bolteae
Clostridium clostridioforme
Clostridium (*Hungatella*) *hathewayi*
Clostridium histolyticum
Clostridium indolis
Clostridium leptum
Clostridium (*Tyzzerella*) *nexile*
Clostridium perfringens
Clostridium (*Erysipelatoclostridium*) *ramosum*
Clostridium scindens
Clostridium sp. 14774

TABLE 1F-continued

Exemplary Bacteria Useful in the Present Invention
Clostridium sp. 7_3_54FAA
Clostridium sp. HGF2
Clostridium symbiosum
Collinsella aerofaciens
Coprobacillus sp. D7
Coprococcus catus
Coprococcus comes
Dorea formicigenerans
Dorea longicatena
Enterococcus faecium
Erysipelotrichaceae bacterium 3_1_53
Escherichia coli
Escherichia coli S88
Eubacterium eligens
Eubacterium fissicatena
Eubacterium rectale
Faecalibacterium prausnitzii
Fusobacterium mortiferum
Fusobacterium nucleatum
Hydrogenoanaerobacterium saccharovorans
Lachnospiraceae bacterium 3_1_57FAA_CT1
Lachnospiraceae bacterium 7_1_58FAA
Lachnospiraceae bacterium 5_1_57FAA
Lactobacillus casei
Lactococcus casei
Odoribacter splanchnicus
Oscillibacter valericigenes
Parabacteroides johnsonii
Parabacteroides merdae
Pediococcus acidilactici
Peptostreptococcus asaccharolyticus
Propionibacterium granulosum
Roseburia intestinalis
Ruminococcus gnavus
Ruminococcus sp. ID8
Ruminococcus torques
Staphylococcus saprophyticus
Streptococcus thermophilus

TABLE 2A

Species identified as germinable and sporulatable by colony picking

OTU	BBA	GAM + FOS/inulin	M2GSC	Sweet B + FOS/Inulin	Sweet GAM	Total
Blautia producta	1					1
Clostridium bartlettii	4		1			5
Clostridium bolteae	2			5	1	8
Clostridium botulinum				5		5
Clostridium butyricum	37	43	8	1	33	122
Clostridium celatum	4				1	5
Clostridium clostridioforme	1				1	2
Clostridium disporicum	26	26	22	33	50	157
Clostridium glycolicum	4	9	14			27
Clostridium mayombei	2	2				4
Clostridium paraputrificum	8	8	33	16	6	71
Clostridium sordellii			14			14
Clostridium sp. 7_2_43FAA		1				1
Clostridium symbiosum	3					3
Clostridium tertium		1		1		2
(blank)		2		31		33
Totals	92	92	92	92	92	460

TABLE 2B

Species identified as germinable by 16S colony pick approach
Clostridium_paraputrificum
Clostridium_disporicum
Clostridium_glycolicum
Clostridium_bartlettii
Clostridium_butyricum
Ruminococcus_bromii
Lachnospiraceae_bacterium_2_1_58FAA
Eubacterium_hadrum
Turicibacter_sanguinis
Lachnospiraceae_bacterium_oral_taxon_F15
Clostridium_perfringens
Clostridium_bifermentans
Roseburia_sp_11SE37
Clostridium_quinii
Ruminococcus_lactaris
Clostridium_botulinum
Clostridium_tyrobutyricum
Blautia_hansenii
Clostridium_kluyveri
Clostridium_sp_JC122
Clostridium_hylemonae
Clostridium_celatum
Clostridium_straminisolvens
Clostridium_orbiscindens
Roseburia_cecicola
Eubacterium_tenue
Clostridium_sp_7_2_43FAA
Lachnospiraceae_bacterium_4_1_37FAA
Eubacterium_rectale
Clostridium_viride
Ruminococcus_sp_K_1
Clostridium_symbiosum
Ruminococcus_torques
Clostridium_algidicarnis

TABLE 2C

Species identified as sporulatable by 16S NGS approach
Clostridium_paraputrificum
Clostridium_bartlettii
Lachnospiraceae_bacterium_2_1_58FAA
Clostridium_disporicum
Ruminococcus_bromii
Eubacterium_hadrum
Clostridium_butyricum
Roseburia_sp_11SE37
Clostridium_perfringens
Clostridium_glycolicum
Clostridium_hylemonae
Clostridium_orbiscindens
Ruminococcus_lactaris
Clostridium_symbiosum
Lachnospiraceae_bacterium_oral_taxon_F15

TABLE 2C-continued

Species identified as sporulatable by 16S NGS approach
Blautia_hansenii
Turicibacter_sanguinis
Clostridium_straminisolvens
Clostridium_botulinum
Lachnospiraceae_bacterium_4_1_37FAA
Roseburia_cecicola
Ruminococcus_sp_K_1
Clostridium_bifermentans
Eubacterium_rectale
Clostridium_quinii
Clostridium_viride
Clostridium_kluyveri
Clostridium_tyrobutyricum
Oscillibacter_sp_G2
Clostridium_sp_JC122
Lachnospiraceae_bacterium_3_1_57FAA
Clostridium_aldenense
Ruminococcus_torques
Clostridium_sp_7_2_43FAA
Clostridium_celatum
Eubacterium_sp_WAL_14571
Eubacterium_tenue
Lachnospiraceae_bacterium_5_1_57FAA
Clostridium_clostridioforme
Clostridium_sp_YIT_12070
Blautia_sp_M25
Anaerostipes_caccae
Roseburia_inulinivorans
Clostridium_sp_D5
Clostridium_asparagiforme
Coprobacillus_sp_D7
Clostridium_sp_HGF2
Clostridium_citroniae
Clostridium_difficile
Oscillibacter_valericigenes
Clostridium_algidicarnis

TABLE 3

Criteria for stages of acute GVHD

ORGAN	
Skin	<25% 25-50% >50% or Generalized (maculopapular rash generalised erythroderma with extent, % of body erythroderma bullous formation surface area) or desquamation
Liver	34-50 51-102 103-255 >255 (bilirubin mmol L) [2-3] [3-6] [6-15] [>15] [bilirubin mg/dL] ø) (or AST 150-750 U/L)
Gut	>30 mL kg or >60 mL/kg or >90 mL/kg or >2000 mL/day or (daily diarrhea >500 mL (2) >1000 mL >1500 mL severe abdominal volume) pain with or without ileus

TABLE 4

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG0022	Pyruvate/2-oxoglutarate/acetoin dehydrogenase complex, dehydrogenase (E1) component	C
COG0039	Malate/lactate dehydrogenase	C
COG0045	Succinyl-CoA synthetase, beta subunit	C
COG0055	FoF1-type ATP synthase, beta subunit	C
COG0056	FoF1-type ATP synthase, alpha subunit	C
COG0074	Succinyl-CoA synthetase, alpha subunit	C
COG0114	Fumarate hydratase class II	C
COG0224	FoF1-type ATP synthase, gamma subunit	C
COG0240	Glycerol-3-phosphate dehydrogenase	C

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG0243	Anaerobic selenocysteine-containing dehydrogenase	C
COG0247	Fe—S oxidoreductase	C
COG0277	FAD/FMN-containing dehydrogenase	C
COG0280	Phosphotransacetylase	C
COG0281	Malic enzyme	C
COG0282	Acetate kinase	C
COG0348	Polyferredoxin	C
COG0355	FoF1-type ATP synthase, epsilon subunit	C
COG0356	FoF1-type ATP synthase, membrane subunit a	C
COG0371	Glycerol dehydrogenase or related enzyme, iron-containing ADH family	C
COG0372	Citrate synthase	C
COG0374	Ni, Fe-hydrogenase I large subunit	C
COG0377	NADH: ubiquinone oxidoreductase 20 kD subunit (chhain B) or related Fe—S oxidoreductase	C
COG0426	Flavorubredoxin	C
COG0427	Acyl-CoA hydrolase	C
COG0431	NAD(P)H-dependent FMN reductase	C
COG0435	Glutathionyl-hydroquinone reductase	C
COG0437	Fe—S-cluster-containing dehydrogenase component	C
COG0479	Succinate dehydrogenase/fumarate reductase, Fe—S protein subunit	C
COG0508	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide acyltransferase (E2) component	C
COG0538	Isocitrate dehydrogenase	C
COG0546	Phosphoglycolate phosphatase, HAD superfamily	C
COG0554	Glycerol kinase	C
COG0567	2-oxoglutarate dehydrogenase complex, dehydrogenase (E1) component, and related enzymes	C
COG0578	Glycerol-3-phosphate dehydrogenase	C
COG0633	Ferredoxin	C
COG0636	FoF1-type ATP synthase, membrane subunit c/Archaeal/vacuolar-type H+-ATPase, subunit K	C
COG0644	Dehydrogenase (flavoprotein)	C
COG0649	NADH: ubiquinone oxidoreductase 49 kD subunit (chain D)	C
COG0650	Formate hydrogenlyase subunit 4	C
COG0655	Multimeric flavodoxin WrbA	C
COG0674	Pyruvate: ferredoxin oxidoreductase or related 2-oxoacid: ferredoxin oxidoreductase, alpha subunit	C
COG0680	Ni, Fe-hydrogenase maturation factor	C
COG0711	FoF1-type ATP synthase, membrane subunit b or b'	C
COG0712	FoF1-type ATP synthase, delta subunit	C
COG0713	NADH: ubiquinone oxidoreductase subunit 11 or 4L (chain K)	C
COG0716	Flavodoxin	C
COG0723	Rieske Fe—S protein	C
COG0778	Nitroreductase	C
COG0838	NADH: ubiquinone oxidoreductase subunit 3 (chain A)	C
COG0839	NADH: ubiquinone oxidoreductase subunit 6 (chain J)	C
COG0843	Heme/copper-type cytochrome/quinol oxidase, subunit 1	C
COG0852	NADH: ubiquinone oxidoreductase 27 kD subunit (chain C)	C
COG1005	NADH: ubiquinone oxidoreductase subunit 1 (chain H)	C
COG1007	NADH: ubiquinone oxidoreductase subunit 2 (chain N)	C
COG1008	NADH: ubiquinone oxidoreductase subunit 4 (chain M)	C
COG1012	Acyl-CoA reductase or other NAD-dependent aldehyde dehydrogenase	C
COG1013	Pyruvate: ferredoxin oxidoreductase or related 2-oxoacid: ferredoxin oxidoreductase, beta subunit	C
COG1014	Pyruvate: ferredoxin oxidoreductase or related 2-oxoacid: ferredoxin oxidoreductase, gamma subunit	C
COG1017	Hemoglobin-like flavoprotein	C
COG1018	Ferredoxin-NADP reductase	C
COG1029	Formylmethanofuran dehydrogenase subunit B	C
COG1034	NADH dehydrogenase/NADH: ubiquinone oxidoreductase 75 kD subunit (chain G)	C
COG1035	Coenzyme F420-reducing hydrogenase, beta subunit	C
COG1036	Archaeal flavoprotein	C
COG1038	Pyruvate carboxylase	C
COG1042	Acyl-CoA synthetase (NDP forming)	C
COG1048	Aconitase A	C
COG1049	Aconitase B	C
COG1053	Succinate dehydrogenase/fumarate reductase, flavoprotein subunit	C
COG1071	TPP-dependent pyruvate or acetoin dehydrogenase subunit alpha	C

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG1139	L-lactate utilization protein LutB, contains a ferredoxin-type domain	C
COG1141	Ferredoxin	C
COG1142	Fe—S-cluster-containing hydrogenase component 2	C
COG1143	Formate hydrogenlyase subunit 6/NADH: ubiquinone oxidoreductase 23 kD subunit (chain I)	C
COG1144	Pyruvate: ferredoxin oxidoreductase or related 2-oxoacid: ferredoxin oxidoreductase, delta subunit	C
COG1145	Ferredoxin	C
COG1148	Heterodisulfide reductase, subunit A (polyferredoxin)	C
COG1150	Heterodisulfide reductase, subunit C	C
COG1152	CO dehydrogenase/acetyl-CoA synthase alpha subunit	C
COG1153	Formylmethanofuran dehydrogenase subunit D	C
COG1155	Archaeal/vacuolar-type H+-ATPase catalytic subunit A/Vma1	C
COG1156	Archaeal/vacuolar-type H+-ATPase subunit B/Vma2	C
COG1182	FMN-dependent NADH-azoreductase	C
COG1229	Formylmethanofuran dehydrogenase subunit A	C
COG1249	Pyruvate/2-oxoglutarate dehydrogenase complex, dihydrolipoamide dehydrogenase (E3) component or related enzyme	C
COG1251	NAD(P)H-nitrite reductase, large subunit	C
COG1252	NADH dehydrogenase, FAD-containing subunit	C
COG1254	Acylphosphatase	C
COG1269	Archaeal/vacuolar-type H+-ATPase subunit I/STV1	C
COG1271	Cytochrome bd-type quinol oxidase, subunit 1	C
COG1274	Phosphoenolpyruvate carboxykinase, GTP-dependent	C
COG1282	NAD/NADP transhydrogenase beta subunit	C
COG1290	Cytochrome b subunit of the bc complex	C
COG1294	Cytochrome bd-type quinol oxidase, subunit 2	C
COG1301	Na+/H+-dicarboxylate symporter	C
COG1319	CO or xanthine dehydrogenase, FAD-binding subunit	C
COG1347	Na+-transporting NADH: ubiquinone oxidoreductase, subunit NqrD	C
COG1359	Quinol monooxygenase YgiN	C
COG1390	Archaeal/vacuolar-type H+-ATPase subunit E/Vma4	C
COG1394	Archaeal/vacuolar-type H+-ATPase subunit D/Vma8	C
COG1436	Archaeal/vacuolar-type H+-ATPase subunit F/Vma7	C
COG1454	Alcohol dehydrogenase, class IV	C
COG1456	CO dehydrogenase/acetyl-CoA synthase gamma subunit (corrinoid Fe—S protein)	C
COG1526	Formate dehydrogenase assembly factor FdhD	C
COG1527	Archaeal/vacuolar-type H+-ATPase subunit C/Vma6	C
COG1529	CO or xanthine dehydrogenase, Mo-binding subunit	C
COG1556	L-lactate utilization protein LutC, contains LUD domain	C
COG1584	Succinate-acetate transporter protein	C
COG1592	Rubrerythrin	C
COG1614	CO dehydrogenase/acetyl-CoA synthase beta subunit	C
COG1620	L-lactate permease	C
COG1622	Heme/copper-type cytochrome/quinol oxidase, subunit 2	C
COG1625	Fe—S oxidoreductase, related to NifB/MoaA family	C
COG1679	Predicted aconitase	C
COG1726	Na+-transporting NADH: ubiquinone oxidoreductase, subunit NqrA	C
COG1740	Ni, Fe-hydrogenase I small subunit	C
COG1757	Na+/H+ antiporter NhaC	C
COG1773	Rubredoxin	C
COG1795	Formaldehyde-activating enzyme nesessary for methanogenesis	C
COG1805	Na+-transporting NADH: ubiquinone oxidoreductase, subunit NqrB	C
COG1838	Tartrate dehydratase beta subunit/Fumarate hydratase class I, C-terminal domain	C
COG1845	Heme/copper-type cytochrome/quinol oxidase, subunit 3	C
COG1853	NADH-FMN oxidoreductase RutF, flavin reductase (DIM6/NTAB) family	C
COG1866	Phosphoenolpyruvate carboxykinase, ATP-dependent	C
COG1880	CO dehydrogenase/acetyl-CoA synthase epsilon subunit	C
COG1882	Pyruvate-formate lyase	C
COG1883	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, beta subunit	C
COG1894	NADH: ubiquinone oxidoreductase, NADH-binding 51 kD subunit (chain F)	C
COG1902	2,4-dienoyl-CoA reductase or related NADH-dependent reductase, Old Yellow Enzyme (OYE) family	C

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG1905	NADH: ubiquinone oxidoreductase 24 kD subunit (chain E)	C
COG1908	Coenzyme F420-reducing hydrogenase, delta subunit	C
COG1927	F420-dependent methylenetetrahydromethanopterin dehydrogenase	C
COG1941	Coenzyme F420-reducing hydrogenase, gamma subunit	C
COG1951	Tartrate dehydratase alpha subunit/Fumarate hydratase class I, N-terminal domain	C
COG1969	Ni, Fe-hydrogenase I cytochrome b subunit	C
COG1979	Alcohol dehydrogenase YqhD, Fe-dependent ADH family	C
COG2009	Succinate dehydrogenase/fumarate reductase, cytochrome b subunit	C
COG2010	Cytochrome c, mono- and diheme variants	C
COG2025	Electron transfer flavoprotein, alpha subunit	C
COG2033	Desulfoferrodoxin, superoxide reductase-like (SORL) domain	C
COG2037	Formylmethanofuran: tetrahydromethanopterin formyltransferase	C
COG2041	Periplasmic DMSO/TMAO reductase YedYZ, molybdopterin-dependent catalytic subunit	C
COG2048	Heterodisulfide reductase, subunit B	C
COG2055	Malate/lactate/ureidoglycolate dehydrogenase, LDH2 family	C
COG2069	CO dehydrogenase/acetyl-CoA synthase delta subunit (corrinoid Fe—S protein)	C
COG2080	Aerobic-type carbon monoxide dehydrogenase, small subunit, CoxS/CutS family	C
COG2086	Electron transfer flavoprotein, alpha and beta subunits	C
COG2142	Succinate dehydrogenase, hydrophobic anchor subunit	C
COG2191	Formylmethanofuran dehydrogenase subunit E	C
COG2209	Na+-transporting NADH: ubiquinone oxidoreductase, subunit NqrE	C
COG2210	Peroxiredoxin family protein	C
COG2218	Formylmethanofuran dehydrogenase subunit C	C
COG2224	Isocitrate lyase	C
COG2225	Malate synthase	C
COG2326	Polyphosphate kinase 2, PPK2 family	C
COG2352	Phosphoenolpyruvate carboxylase	C
COG2414	Aldehyde: ferredoxin oxidoreductase	C
COG2421	Acetamidase/formamidase	C
COG2440	Ferredoxin-like protein FixX	C
COG2609	Pyruvate dehydrogenase complex, dehydrogenase (E1) component	C
COG2717	Periplasmic DMSO/TMAO reductase YedYZ, heme-binding membrane subunit	C
COG2811	Archaeal/vacuolar-type H+-ATPase subunit H	C
COG2828	2-Methylaconitate cis-trans-isomerase PrpF (2-methyl citrate pathway)	C
COG2838	Monomeric isocitrate dehydrogenase	C
COG2851	Mg2+/citrate symporter	C
COG2857	Cytochrome c1	C
COG2863	Cytochrome c553	C
COG2864	Cytochrome b subunit of formate dehydrogenase	C
COG2869	Na+-transporting NADH: ubiquinone oxidoreductase, subunit NqrC	C
COG2871	Na+-transporting NADH: ubiquinone oxidoreductase, subunit NqrF	C
COG2878	Na+-translocating ferredoxin: NAD+ oxidoreductase RNF, RnfB subunit	C
COG2993	Cbb3-type cytochrome oxidase, cytochrome c subunit	C
COG3005	Tetraheme cytochrome c subunit of nitrate or TMAO reductase	C
COG3029	Fumarate reductase subunit C	C
COG3038	Cytochrome b561	C
COG3051	Citrate lyase, alpha subunit	C
COG3052	Citrate lyase, gamma subunit	C
COG3053	Citrate lyase synthetase	C
COG3069	C4-dicarboxylate transporter	C
COG3080	Fumarate reductase subunit D	C
COG3125	Heme/copper-type cytochrome/quinol oxidase, subunit 4	C
COG3181	Tripartite-type tricarboxylate transporter, receptor component TctC	C
COG3202	ATP/ADP translocase	C
COG3241	Azurin	C
COG3245	Cytochrome c5	C
COG3258	Cytochrome c	C
COG3259	Coenzyme F420-reducing hydrogenase, alpha subunit	C
COG3260	Ni, Fe-hydrogenase III small subunit	C

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG3261	Ni, Fe-hydrogenase III large subunit	C
COG3262	Ni, Fe-hydrogenase III component G	C
COG3278	Cbb3-type cytochrome oxidase, subunit 1	C
COG3288	NAD/NADP transhydrogenase alpha subunit	C
COG3302	DMSO reductase anchor subunit	C
COG3312	FoF1-type ATP synthase assembly protein I	C
COG3411	(2Fe—2S) ferredoxin	C
COG3426	Butyrate kinase	C
COG3427	Carbon monoxide dehydrogenase subunit G	C
COG3474	Cytochrome c2	C
COG3493	Na+/citrate or Na+/malate symporter	C
COG3630	Na+-transporting methylmalonyl-CoA/oxaloacetate decarboxylase, gamma subunit	C
COG3658	Cytochrome b	C
COG3761	NADH: ubiquinone oxidoreductase 17.2 kD subunit	C
COG3783	Soluble cytochrome b562	C
COG3794	Plastocyanin	C
COG3808	Na+ or H+-translocating membrane pyrophosphatase	C
COG3909	Cytochrome c556	C
COG3978	Acetolactate synthase small subunit, contains ACT domain	C
COG4036	Energy-converting hydrogenase Eha subunit G	C
COG4037	Energy-converting hydrogenase Eha subunit F	C
COG4038	Energy-converting hydrogenase Eha subunit E	C
COG4039	Energy-converting hydrogenase Eha subunit C	C
COG4041	Energy-converting hydrogenase Eha subunit B	C
COG4042	Energy-converting hydrogenase Eha subunit A	C
COG4074	5,10-methenyltetrahydromethanopterin hydrogenase	C
COG4078	Energy-converting hydrogenase Eha subunit H	C
COG4106	Trans-aconitate methyltransferase	C
COG4147	Na+(or H+)/acetate symporter ActP	C
COG4221	NADP-dependent 3-hydroxy acid dehydrogenase YdfG	C
COG4231	TPP-dependent indolepyruvate ferredoxin oxidoreductase, alpha subunit	C
COG4237	Hydrogenase-4 membrane subunit HyfE	C
COG4459	Periplasmic nitrate reductase system, NapE component	C
COG4624	Iron only hydrogenase large subunit, C-terminal domain	C
COG4654	Cytochrome c551/c552	C
COG4656	Na+-translocating ferredoxin: NAD+ oxidoreductase RNF, RnfC subunit	C
COG4657	Na+-translocating ferredoxin: NAD+ oxidoreductase RNF, RnfA subunit	C
COG4658	Na+-translocating ferredoxin: NAD+ oxidoreductase RNF, RnfD subunit	C
COG4659	Na+-translocating ferredoxin: NAD+ oxidoreductase RNF, RnfG subunit	C
COG4660	Na+-translocating ferredoxin: NAD+ oxidoreductase RNF, RnfE subunit	C
COG4736	Cbb3-type cytochrome oxidase, subunit 3	C
COG4802	Ferredoxin-thioredoxin reductase, catalytic subunit	C
COG5012	Methanogenic corrinoid protein MtbC1	C
COG5016	Pyruvate/oxaloacetate carboxyltransferase	C
COG0021	Transketolase	G
COG0033	Phosphoglucomutase	G
COG0036	Pentose-5-phosphate-3-epimerase	G
COG0057	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase	G
COG0058	Glucan phosphorylase	G
COG0120	Ribose 5-phosphate isomerase	G
COG0126	3-phosphoglycerate kinase	G
COG0148	Enolase	G
COG0149	Triosephosphate isomerase	G
COG0153	Galactokinase	G
COG0158	Fructose-1,6-bisphosphatase	G
COG0166	Glucose-6-phosphate isomerase	G
COG0176	Transaldolase	G
COG0191	Fructose/tagatose bisphosphate aldolase	G
COG0205	6-phosphofructokinase	G
COG0235	Ribulose-5-phosphate 4-epimerase/Fuculose-1-phosphate aldolase	G
COG0246	Mannitol-1-phosphate/altronate dehydrogenases	G
COG0269	3-keto-L-gulonate-6-phosphate decarboxylase	G
COG0279	Phosphoheptose isomerase	G
COG0296	1,4-alpha-glucan branching enzyme	G

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG0297	Glycogen synthase	G
COG0362	6-phosphogluconate dehydrogenase	G
COG0363	6-phosphogluconolactonase/Glucosamine-6-phosphate isomerase/deaminase	G
COG0364	Glucose-6-phosphate 1-dehydrogenase	G
COG0366	Glycosidase	G
COG0380	Trehalose-6-phosphate synthase	G
COG0383	Alpha-mannosidase	G
COG0395	ABC-type glycerol-3-phosphate transport system, permease component	G
COG0406	Broad specificity phosphatase PhoE	G
COG0448	ADP-glucose pyrophosphorylase	G
COG0469	Pyruvate kinase	G
COG0471	Di- and tricarboxylate transporter	G
COG0483	Archaeal fructose-1,6-bisphosphatase or related enzyme of inositol monophosphatase family	G
COG0524	Sugar or nucleoside kinase, ribokinase family	G
COG0574	Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	G
COG0579	L-2-hydroxyglutarate oxidase LhgO	G
COG0580	Glycerol uptake facilitator and related aquaporins (Major Intrinsic Protein Family)	G
COG0588	Phosphoglycerate mutase (BPG-dependent)	G
COG0662	Mannose-6-phosphate isomerase, cupin superfamily	G
COG0676	D-hexose-6-phosphate mutarotase	G
COG0696	Phosphoglycerate mutase (BPG-independent, AlkP superfamily)	G
COG0698	Ribose 5-phosphate isomerase RpiB	G
COG0738	Fucose permease	G
COG0800	2-keto-3-deoxy-6-phosphogluconate aldolase	G
COG0837	Glucokinase	G
COG1015	Phosphopentomutase	G
COG1023	6-phosphogluconate dehydrogenase (decarboxylating)	G
COG1064	D-arabinose 1-dehydrogenase, Zn-dependent alcohol dehydrogenase family	G
COG1069	Ribulose kinase	G
COG1070	Sugar (pentulose or hexulose) kinase	G
COG1080	Phosphoenolpyruvate-protein kinase (PTS system EI component in bacteria)	G
COG1082	Sugar phosphate isomerase/epimerase	G
COG1085	Galactose-1-phosphate uridylyltransferase	G
COG1105	Fructose-1-phosphate kinase or kinase (PfkB)	G
COG1109	Phosphomannomutase	G
COG1129	ABC-type sugar transport system, ATPase component	G
COG1172	Ribose/xylose/arabinose/galactoside ABC-type transport system, permease component	G
COG1175	ABC-type sugar transport system, permease component	G
COG1216	Glycosyltransferase, GT2 family	G
COG1263	Phosphotransferase system IIC components, glucose/maltose/N-acetylglucosamine-specific	G
COG1264	Phosphotransferase system IIB components	G
COG1299	Phosphotransferase system, fructose-specific IIC component	G
COG1312	D-mannonate dehydratase	G
COG1440	Phosphotransferase system cellobiose-specific component IIB	G
COG1445	Phosphotransferase system fructose-specific component IIB	G
COG1447	Phosphotransferase system cellobiose-specific component IIA	G
COG1449	Alpha-amylase/alpha-mannosidase, GH57 family	G
COG1455	Phosphotransferase system cellobiose-specific component IIC	G
COG1472	Periplasmic beta-glucosidase and related glycosidases	G
COG1482	Mannose-6-phosphate isomerase, class I	G
COG1486	Alpha-galactosidase/6-phospho-beta-glucosidase, family 4 of glycosyl hydrolase	G
COG1494	Fructose-1,6-bisphosphatase/sedoheptulose 1,7-bisphosphatase or related protein	G
COG1501	Alpha-glucosidase, glycosyl hydrolase family GH31	G
COG1523	Pullulanase/glycogen debranching enzyme	G
COG1543	Predicted glycosyl hydrolase, contains GH57 and DUF1957 domains	G
COG1554	Trehalose and maltose hydrolase (possible phosphorylase)	G
COG1593	TRAP-type C4-dicarboxylate transport system, large permease component	G
COG1621	Sucrose-6-phosphate hydrolase SacC, GH32 family	G
COG1626	Neutral trehalase	G
COG1638	TRAP-type C4-dicarboxylate transport system, periplasmic component	G

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG1640	4-alpha-glucanotransferase	G
COG1653	ABC-type glycerol-3-phosphate transport system, periplasmic component	G
COG1803	Methylglyoxal synthase	G
COG1819	UDP: flavonoid glycosyltransferase YjiC, YdhE family	G
COG1820	N-acetylglucosamine-6-phosphate deacetylase	G
COG1830	Fructose-bisphosphate aldolase class Ia, DhnA family	G
COG1850	Ribulose 1,5-bisphosphate carboxylase, large subunit, or a RuBisCO-like protein	G
COG1869	D-ribose pyranose/furanose isomerase RbsD	G
COG1874	Beta-galactosidase GanA	G
COG1877	Trehalose-6-phosphatase	G
COG1879	ABC-type sugar transport system, periplasmic component, contains N-terminal xre family HTH domain	G
COG1892	Phosphoenolpyruvate carboxylase	G
COG1904	Glucuronate isomerase	G
COG1929	Glycerate kinase	G
COG1980	Archaeal fructose 1,6-bisphosphatase	G
COG2017	Galactose mutarotase or related enzyme	G
COG2074	2-phosphoglycerate kinase	G
COG2079	2-methylcitrate dehydratase PrpD	G
COG2115	Xylose isomerase	G
COG2120	N-acetylglucosaminyl deacetylase, LmbE family	G
COG2133	Glucose/arabinose dehydrogenase, beta-propeller fold	G
COG2140	Oxalate decarboxylase/archaeal phosphoglucose isomerase, cupin superfamily	G
COG2152	Predicted glycosyl hydrolase, GH43/DUF377 family	G
COG2160	L-arabinose isomerase	G
COG2182	Maltose-binding periplasmic protein MalE	G
COG2190	Phosphotransferase system IIA component	G
COG2211	Na+/melibiose symporter or related transporter	G
COG2213	Phosphotransferase system, mannitol-specific IIBC component	G
COG2220	L-ascorbate metabolism protein UlaG, beta-lactamase superfamily	G
COG2271	Sugar phosphate permease	G
COG2273	Beta-glucanase, GH16 family	G
COG2301	Citrate lyase beta subunit	G
COG2342	Endo alpha-1,4 polygalactosaminidase, GH114 family (was erroneously annotated as Cys-tRNA synthetase)	G
COG2376	Dihydroxyacetone kinase	G
COG2379	Glycerate-2-kinase	G
COG2407	L-fucose isomerase or related protein	G
COG2513	2-Methylisocitrate lyase and related enzymes, PEP mutase family	G
COG2704	Anaerobic C4-dicarboxylate transporter	G
COG2706	6-phosphogluconolactonase, cycloisomerase 2 family	G
COG2721	Altronate dehydratase	G
COG2723	Beta-glucosidase/6-phospho-beta-glucosidase/beta-galactosidase	G
COG2730	Aryl-phospho-beta-D-glucosidase BglC, GH1 family	G
COG2731	Beta-galactosidase, beta subunit	G
COG2814	Predicted arabinose efflux permease, MFS family	G
COG2861	Uncharacterized conserved protein YibQ, putative polysaccharide deacetylase 2 family	G
COG2893	Phosphotransferase system, mannose/fructose-specific component IIA	G
COG2942	Mannose or cellobiose epimerase, N-acyl-D-glucosamine 2-epimerase family	G
COG2971	BadF-type ATPase, related to human N-acetylglucosamine kinase	G
COG3001	Fructosamine-3-kinase	G
COG3010	Putative N-acetylmannosamine-6-phosphate epimerase	G
COG3037	Ascorbate-specific PTS system EIIC-type component UlaA	G
COG3090	TRAP-type C4-dicarboxylate transport system, small permease component	G
COG3250	Beta-galactosidase/beta-glucuronidase	G
COG3265	Gluconate kinase	G
COG3280	Maltooligosyltrehalose synthase	G
COG3281	Predicted trehalose synthase	G
COG3325	Chitinase, GH18 family	G
COG3345	Alpha-galactosidase	G
COG3347	Rhamnose utilisation protein RhaD, predicted bifunctional aldolase and dehydrogenase	G
COG3386	Sugar lactone lactonase YvrE	G

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG3387	Glucoamylase (glucan-1,4-alpha-glucosidase), GH15 family	G
COG3405	Endo-1,4-beta-D-glucanase Y	G
COG3408	Glycogen debranching enzyme (alpha-1,6-glucosidase)	G
COG3414	Phosphotransferase system, galactitol-specific IIB component	G
COG3429	Glucose-6-phosphate dehydrogenase assembly protein OpcA, contains a peptidoglycan-binding domain	G
COG3444	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIB	G
COG3459	Cellobiose phosphorylase	G
COG3469	Chitinase	G
COG3507	Beta-xylosidase	G
COG3525	N-acetyl-beta-hexosaminidase	G
COG3534	Alpha-L-arabinofuranosidase	G
COG3537	Putative alpha-1,2-mannosidase	G
COG3588	Fructose-bisphosphate aldolase class 1	G
COG3594	Fucose 4-O-acetylase or related acetyltransferase	G
COG3622	Hydroxypyruvate isomerase	G
COG3623	L-ribulose-5-phosphate 3-epimerase UlaE	G
COG3635	2,3-bisphosphoglycerate-independent phosphoglycerate mutase, archeal type	G
COG3661	Alpha-glucuronidase	G
COG3664	Beta-xylosidase	G
COG3669	Alpha-L-fucosidase	G
COG3684	Tagatose-1,6-bisphosphate aldolase	G
COG3693	Endo-1,4-beta-xylanase, GH35 family	G
COG3709	Ribose 1,5-bisphosphokinase PhnN	G
COG3715	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IIC	G
COG3716	Phosphotransferase system, mannose/fructose/N-acetylgalactosamine-specific component IID	G
COG3717	5-keto 4-deoxyuronate isomerase	G
COG3718	5-deoxy-D-glucuronate isomerase	G
COG3730	Phosphotransferase system sorbitol-specific component IIC	G
COG3731	Phosphotransferase system sorbitol-specific component IIA	G
COG3732	Phosphotransferase system sorbitol-specific component IIBC	G
COG3734	2-keto-3-deoxy-galactonokinase	G
COG3769	Predicted mannosyl-3-phosphoglycerate phosphatase, HAD superfamily	G
COG3775	Phosphotransferase system, galactitol-specific IIC component	G
COG3822	D-lyxose ketol-isomerase	G
COG3833	ABC-type maltose transport system, permease component	G
COG3836	2-keto-3-deoxy-L-rhamnonate aldolase RhmA	G
COG3839	ABC-type sugar transport system, ATPase component	G
COG3855	Fructose-1,6-bisphosphatase	G
COG3866	Pectate lyase	G
COG3867	Arabinogalactan endo-1,4-beta-galactosidase	G
COG3892	Myo-inositol catabolism protein IolC	G
COG3934	Endo-1,4-beta-mannosidase	G
COG3936	Membrane-bound acyltransferase YfiQ, involved in biofilm formation	G
COG3940	Beta-xylosidase, GH43 family	G
COG3954	Phosphoribulokinase	G
COG3957	Phosphoketolase	G
COG3958	Transketolase, C-terminal subunit	G
COG3959	Transketolase, N-terminal subunit	G
COG3962	TPP-dependent trihydroxycyclohexane-1,2-dione (THcHDO) dehydratase, myo-inositol metabolism	G
COG3979	Chitodextrinase	G
COG4124	Beta-mannanase	G
COG4130	Predicted sugar epimerase, xylose isomerase-like family	G
COG4154	L-fucose mutarotase/ribose pyranase, RbsD/FucU family	G
COG4193	Beta-N-acetylglucosaminidase	G
COG4209	ABC-type polysaccharide transport system, permease component	G
COG4211	ABC-type glucose/galactose transport system, permease component	G
COG4213	ABC-type xylose transport system, periplasmic component	G
COG4214	ABC-type xylose transport system, permease component	G
COG4225	Rhamnogalacturonyl hydrolase YesR	G
COG4284	UDP-N-acetylglucosamine pyrophosphorylase	G
COG4451	Ribulose bisphosphate carboxylase small subunit	G

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG4468	Galactose-1-phosphate uridylyltransferase	G
COG4573	Tagatose-1,6-bisphosphate aldolase non-catalytic subunit AgaZ/GatZ	G
COG4580	Maltoporin (phage lambda and maltose receptor)	G
COG4632	Exopolysaccharide biosynthesis protein related to N-acetylglucosamine-1-phosphodiester alpha-N-acety . . .	G
COG4668	Mannitol/fructose-specific phosphotransferase system, IIA domain	G
COG4724	Endo-beta-N-acetylglucosaminidase D	G
COG4806	L-rhamnose isomerase	G
COG4809	Archaeal ADP-dependent phosphofructokinase/glucokinase	G
COG4813	Trehalose utilization protein	G
COG4833	Predicted alpha-1,6-mannanase, GH76 family	G
COG4975	Glucose uptake protein GlcU	G
COG4993	Glucose dehydrogenase	G
COG5017	UDP-N-acetylglucosamine transferase subunit ALG13	G
COG5026	Hexokinase	G
COG5263	Glucan-binding domain (YG repeat)	G
COG0002	N-acetyl-gamma-glutamylphosphate reductase	E
COG0006	Xaa-Pro aminopeptidase	E
COG0010	Arginase family enzyme	E
COG0014	Gamma-glutamyl phosphate reductase	E
COG0019	Diaminopimelate decarboxylase	E
COG0031	Cysteine synthase	E
COG0040	ATP phosphoribosyltransferase	E
COG0065	Homoaconitase/3-isopropylmalate dehydratase large subunit	E
COG0066	3-isopropylmalate dehydratase small subunit	E
COG0067	Glutamate synthase domain 1	E
COG0069	Glutamate synthase domain 2	E
COG0070	Glutamate synthase domain 3	E
COG0076	Glutamate or tyrosine decarboxylase or a related PLP-dependent protein	E
COG0077	Prephenate dehydratase	E
COG0078	Ornithine carbamoyltransferase	E
COG0079	Histidinol-phosphate/aromatic aminotransferase or cobyric acid decarboxylase	E
COG0082	Chorismate synthase	E
COG0083	Homoserine kinase	E
COG0106	Phosphoribosylformimino-5-aminoimidazole carboxamide ribonucleotide (ProFAR) isomerase	E
COG0107	Imidazole glycerol phosphate synthase subunit HisF	E
COG0112	Glycine/serine hydroxymethyltransferase	E
COG0118	Imidazoleglycerol phosphate synthase glutamine amidotransferase subunit HisH	E
COG0119	Isopropylmalate/homocitrate/citramalate synthases	E
COG0128	5-enolpyruvylshikimate-3-phosphate synthase	E
COG0131	Imidazoleglycerol phosphate dehydratase HisB	E
COG0133	Tryptophan synthase beta chain	E
COG0134	Indole-3-glycerol phosphate synthase	E
COG0135	Phosphoribosylanthranilate isomerase	E
COG0136	Aspartate-semialdehyde dehydrogenase	E
COG0137	Argininosuccinate synthase	E
COG0139	Phosphoribosyl-AMP cyclohydrolase	E
COG0140	Phosphoribosyl-ATP pyrophosphohydrolase	E
COG0141	Histidinol dehydrogenase	E
COG0159	Tryptophan synthase alpha chain	E
COG0160	4-aminobutyrate aminotransferase or related aminotransferase	E
COG0165	Argininosuccinate lyase	E
COG0169	Shikimate 5-dehydrogenase	E
COG0174	Glutamine synthetase	E
COG0182	Methylthioribose-1-phosphate isomerase (methionine salvage pathway), a paralog of eIF-2B alpha subunit	E
COG0241	Histidinol phosphatase or a related phosphatase	E
COG0253	Diaminopimelate epimerase	E
COG0260	Leucyl aminopeptidase	E
COG0263	Glutamate 5-kinase	E
COG0287	Prephenate dehydrogenase	E
COG0289	Dihydrodipicolinate reductase	E
COG0308	Aminopeptidase N	E
COG0334	Glutamate dehydrogenase/leucine dehydrogenase	E
COG0337	3-dehydroquinate synthetase	E
COG0339	Zn-dependent oligopeptidase	E
COG0345	Pyrroline-5-carboxylate reductase	E

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG0367	Asparagine synthetase B (glutamine-hydrolyzing)	E
COG0403	Glycine cleavage system protein P (pyridoxal-binding), N-terminal domain	E
COG0404	Glycine cleavage system T protein (aminomethyltransferase)	E
COG0405	Gamma-glutamyltranspeptidase	E
COG0410	ABC-type branched-chain amino acid transport system, ATPase component	E
COG0411	ABC-type branched-chain amino acid transport system, ATPase component	E
COG0421	Spermidine synthase	E
COG0436	Aspartate/methionine/tyrosine aminotransferase	E
COG0440	Acetolactate synthase, small subunit	E
COG0460	Homoserine dehydrogenase	E
COG0498	Threonine synthase	E
COG0506	Proline dehydrogenase	E
COG0509	Glycine cleavage system H protein (lipoate-binding)	E
COG0520	Selenocysteine lyase/Cysteine desulfurase	E
COG0527	Aspartokinase	E
COG0531	Amino acid transporter	E
COG0547	Anthranilate phosphoribosyltransferase	E
COG0548	Acetylglutamate kinase	E
COG0549	Carbamate kinase	E
COG0559	Branched-chain amino acid ABC-type transport system, permease component	E
COG0560	Phosphoserine phosphatase	E
COG0591	Na+/proline symporter	E
COG0620	Methionine synthase II (cobalamin-independent)	E
COG0624	Acetylornithine deacetylase/Succinyl-diaminopimelate desuccinylase or related deacylase	E
COG0626	Cystathionine beta-lyase/cystathionine gamma-synthase	E
COG0646	Methionine synthase I (cobalamin-dependent), methyltransferase domain	E
COG0665	Glycine/D-amino acid oxidase (deaminating)	E
COG0683	ABC-type branched-chain amino acid transport system, periplasmic component	E
COG0685	5,10-methylenetetrahydrofolate reductase	E
COG0686	Alanine dehydrogenase	E
COG0687	Spermidine/putrescine-binding periplasmic protein	E
COG0703	Shikimate kinase	E
COG0709	Selenophosphate synthase	E
COG0710	3-dehydroquinate dehydratase	E
COG0722	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	E
COG0747	ABC-type transport system, periplasmic component	E
COG0754	Glutathionylspermidine synthase	E
COG0757	3-dehydroquinate dehydratase	E
COG0765	ABC-type amino acid transport system, permease component	E
COG0786	Na+/glutamate symporter	E
COG0804	Urease alpha subunit	E
COG0814	Amino acid permease	E
COG0831	Urease gamma subunit	E
COG0832	Urease beta subunit	E
COG0833	Amino acid permease	E
COG1003	Glycine cleavage system protein P (pyridoxal-binding), C-terminal domain	E
COG1027	Aspartate ammonia-lyase	E
COG1045	Serine acetyltransferase	E
COG1104	Cysteine sulfinate desulfinase/cysteine desulfurase or related enzyme	E
COG1113	L-asparagine transporter and related permeases	E
COG1114	Branched-chain amino acid permeases	E
COG1115	Na+/alanine symporter	E
COG1125	ABC-type proline/glycine betaine transport system, ATPase component	E
COG1126	ABC-type polar amino acid transport system, ATPase component	E
COG1135	ABC-type methionine transport system, ATPase component	E
COG1164	Oligoendopeptidase F	E
COG1166	Arginine decarboxylase (spermidine biosynthesis)	E
COG1171	Threonine dehydratase	E
COG1174	ABC-type proline/glycine betaine transport system, permease component	E
COG1176	ABC-type spermidine/putrescine transport system, permease component I	E

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG1177	ABC-type spermidine/putrescine transport system, permease component II	E
COG1231	Monoamine oxidase	E
COG1246	N-acetylglutamate synthase or related acetyltransferase, GNAT family	E
COG1247	L-amino acid N-acyltransferase YncA	E
COG1279	Arginine exporter protein ArgO	E
COG1280	Threonine/homoserine/homoserine lactone efflux protein	E
COG1296	Predicted branched-chain amino acid permease (azaleucine resistance)	E
COG1350	Predicted alternative tryptophan synthase beta-subunit (paralog of TrpB)	E
COG1362	Aspartyl aminopeptidase	E
COG1364	N-acetylglutamate synthase (N-acetylornithine aminotransferase)	E
COG1410	Methionine synthase I, cobalamin-binding domain	E
COG1446	Isoaspartyl peptidase or L-asparaginase, Ntn-hydrolase superfamily	E
COG1448	Aspartate/tyrosine/aromatic aminotransferase	E
COG1465	3-dehydroquinate synthase, class II	E
COG1505	Prolyl oligopeptidase PreP, S9A serine peptidase family	E
COG1506	Dipeptidyl aminopeptidase/acylaminoacyl peptidase	E
COG1509	L-lysine 2,3-aminomutase (EF-P beta-lysylation pathway)	E
COG1586	S-adenosylmethionine decarboxylase or arginine decarboxylase	E
COG1605	Chorismate mutase	E
COG1685	Archaeal shikimate kinase	E
COG1687	Branched-chain amino acid transport protein AzlD	E
COG1748	Saccharopine dehydrogenase, NADP-dependent	E
COG1760	L-serine deaminase	E
COG1770	Protease II	E
COG1791	Acireductone dioxygenase (methionine salvage), cupin superfamily	E
COG1823	L-cystine uptake protein TcyP, sodium: dicarboxylate symporter family	E
COG1834	N-Dimethylarginine dimethylaminohydrolase	E
COG1878	Kynurenine formamidase	E
COG1897	Homoserine trans-succinylase	E
COG1945	Pyruvoyl-dependent arginine decarboxylase (PvlArgDC)	E
COG1982	Arginine/lysine/ornithine decarboxylase	E
COG1984	Allophanate hydrolase subunit 2	E
COG2008	Threonine aldolase	E
COG2011	ABC-type methionine transport system, permease component	E
COG2021	Homoserine acetyltransferase	E
COG2040	Homocysteine/selenocysteine methylase (S-methylmethionine-dependent)	E
COG2049	Allophanate hydrolase subunit 1	E
COG2056	Predicted histidine transporter YuiF, NhaC family	E
COG2066	Glutaminase	E
COG2071	Gamma-glutamyl-gamma-aminobutyrate hydrolase PuuD (putrescine degradation), contains GATase1-like domain	E
COG2095	Small neutral amino acid transporter SnatA, MarC family	E
COG2113	ABC-type proline/glycine betaine transport system, periplasmic component	E
COG2171	Tetrahydrodipicolinate N-succinyltransferase	E
COG2195	Di- or tripeptidase	E
COG2235	Arginine deiminase	E
COG2309	Leucyl aminopeptidase (aminopeptidase T)	E
COG2317	Zn-dependent carboxypeptidase, M32 family	E
COG2355	Zn-dependent dipeptidase, microsomal dipeptidase homolog	E
COG2362	D-aminopeptidase	E
COG2423	Ornithine cyclodeaminase/archaeal alanine dehydrogenase, mu-crystallin family	E
COG2502	Asparagine synthetase A	E
COG2515	1-aminocyclopropane-1-carboxylate deaminase/D-cysteine desulfhydrase, PLP-dependent ACC family	E
COG2716	Glycine cleavage system regulatory protein	E
COG2755	Lysophospholipase L1 or related esterase	E
COG2856	Zn-dependent peptidase ImmA, M78 family	E
COG2873	O-acetylhomoserine/O-acetylserine sulfhydrylase, pyridoxal phosphate-dependent	E
COG2876	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase	E
COG2902	NAD-specific glutamate dehydrogenase	E
COG2939	Carboxypeptidase C (cathepsin A)	E

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG2957	Agmatine/peptidylarginine deiminase	E
COG2981	Uncharacterized protein involved in cysteine biosynthesis	E
COG2986	Histidine ammonia-lyase	E
COG2987	Urocanate hydratase	E
COG2988	Succinylglutamate desuccinylase	E
COG3033	Tryptophanase	E
COG3048	D-serine dehydratase	E
COG3075	Anaerobic glycerol-3-phosphate dehydrogenase	E
COG3104	Dipeptide/tripeptide permease	E
COG3138	Arginine/ornithine N-succinyltransferase beta subunit	E
COG3186	Phenylalanine-4-hydroxylase	E
COG3192	Ethanolamine transporter EutH, required for ethanolamine utilization at low pH	E
COG3200	3-deoxy-D-arabino-heptulosonate 7-phosphate (DAHP) synthase, class II	E
COG3232	5-carboxymethyl-2-hydroxymuconate isomerase	E
COG3340	Peptidase E	E
COG3404	Formiminotetrahydrofolate cyclodeaminase	E
COG3457	Predicted amino acid racemase	E
COG3483	Tryptophan 2,3-dioxygenase (vermilion)	E
COG3579	Aminopeptidase C	E
COG3591	V8-like Glu-specific endopeptidase	E
COG3616	D-serine deaminase, pyridoxal phosphate-dependent	E
COG3633	Na+/serine symporter	E
COG3643	Glutamate formiminotransferase	E
COG3681	L-cysteine desulfidase	E
COG3705	ATP phosphoribosyltransferase regulatory subunit HisZ	E
COG3724	Succinylarginine dihydrolase	E
COG3741	N-formylglutamate amidohydrolase	E
COG3799	Methylaspartate ammonia-lyase	E
COG3842	ABC-type Fe3+/spermidine/putrescine transport systems, ATPase components	E
COG3844	Kynureninase	E
COG3931	Predicted N-formylglutamate amidohydrolase	E
COG3938	Proline racemase	E
COG3968	Glutamine synthetase type III	E
COG3977	Alanine-alpha-ketoisovalerate (or valine-pyruvate) aminotransferase	E
COG4091	Predicted homoserine dehydrogenase, contains C-terminal SAF domain	E
COG4126	Asp/Glu/hydantoin racemase	E
COG4160	ABC-type arginine/histidine transport system, permease component	E
COG4161	ABC-type arginine transport system, ATPase component	E
COG4166	ABC-type oligopeptide transport system, periplasmic component	E
COG4175	ABC-type proline/glycine betaine transport system, ATPase component	E
COG4176	ABC-type proline/glycine betaine transport system, permease component	E
COG4177	ABC-type branched-chain amino acid transport system, permease component	E
COG4187	Arginine utilization protein RocB	E
COG4215	ABC-type arginine transport system, permease component	E
COG4229	Enolase-phosphatase E1 involved in merthionine salvage	E
COG4230	Delta 1-pyrroline-5-carboxylate dehydrogenase	E
COG4302	Ethanolamine ammonia-lyase, small subunit	E
COG4303	Ethanolamine ammonia-lyase, large subunit	E
COG4311	Sarcosine oxidase delta subunit	E
COG4359	2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase (methionine salvage)	E
COG4392	Branched-chain amino acid transport protein	E
COG4401	Chorismate mutase	E
COG4413	Urea transporter	E
COG4448	L-asparaginase II	E
COG4583	Sarcosine oxidase gamma subunit	E
COG4597	ABC-type amino acid transport system, permease component	E
COG4598	ABC-type histidine transport system, ATPase component	E
COG4608	ABC-type oligopeptide transport system, ATPase component	E
COG4690	Dipeptidase	E
COG4766	Ethanolamine utilization protein EutQ, cupin superfamily (function unknown)	E
COG4810	Ethanolamine utilization protein EutS, ethanolamine utilization microcompartment shell protein	E

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG4812	Ethanolamine utilization cobalamin adenosyltransferase	E
COG4816	Ethanolamine utilization protein EutL, ethanolamine utilization microcompartment shell protein	E
COG4819	Ethanolamine utilization protein EutA, possible chaperonin protecting lyase from inhibition	E
COG4820	Ethanolamine utilization protein EutJ, possible chaperonin	E
COG4857	5-Methylthioribose kinase, methionine salvage pathway	E
COG4865	Glutamate mutase epsilon subunit	E
COG4917	Ethanolamine utilization protein EutP, contains a P-loop NTPase domain	E
COG4992	Acetylornithine/succinyldiaminopimelate/putrescine aminotransferase	E
COG5006	Threonine/homoserine efflux transporter RhtA	E
COG0020	Undecaprenyl pyrophosphate synthase	I
COG0183	Acetyl-CoA acetyltransferase	I
COG0204	1-acyl-sn-glycerol-3-phosphate acyltransferase	I
COG0245	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	I
COG0331	Malonyl CoA-acyl carrier protein transacylase	I
COG0332	3-oxoacyl-[acyl-carrier-protein] synthase III	I
COG0344	Phospholipid biosynthesis protein PlsY, probable glycerol-3-phosphate acyltransferase	I
COG0365	Acyl-coenzyme A synthetase/AMP-(fatty) acid ligase	I
COG0416	Fatty acid/phospholipid biosynthesis enzyme	I
COG0439	Biotin carboxylase	I
COG0446	NADPH-dependent 2,4-dienoyl-CoA reductase, sulfur reductase, or a related oxidoreductase	I
COG0558	Phosphatidylglycerophosphate synthase	I
COG0575	CDP-diglyceride synthetase	I
COG0584	Glycerophosphoryl diester phosphodiesterase	I
COG0623	Enoyl-[acyl-carrier-protein] reductase (NADH)	I
COG0657	Acetyl esterase/lipase	I
COG0671	Membrane-associated phospholipid phosphatase	I
COG0688	Phosphatidylserine decarboxylase	I
COG0736	Phosphopantetheinyl transferase (holo-ACP synthase)	I
COG0743	1-deoxy-D-xylulose 5-phosphate reductoisomerase	I
COG0761	4-Hydroxy-3-methylbut-2-enyl diphosphate reductase IspH	I
COG0764	3-hydroxymyristoyl/3-hydroxydecanoyl-(acyl carrier protein) dehydratase	I
COG0777	Acetyl-CoA carboxylase beta subunit	I
COG0818	Diacylglycerol kinase	I
COG0821	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase IspG/GcpE	I
COG0824	Acyl-CoA thioesterase FadM	I
COG0825	Acetyl-CoA carboxylase alpha subunit	I
COG1022	Long-chain acyl-CoA synthetase (AMP-forming)	I
COG1024	Enoyl-CoA hydratase/carnithine racemase	I
COG1075	Triacylglycerol esterase/lipase EstA, alpha/beta hydrolase fold	I
COG1133	ABC-type long-chain fatty acid transport system, fused permease and ATPase components	I
COG1183	Phosphatidylserine synthase	I
COG1211	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	I
COG1213	Choline kinase	I
COG1250	3-hydroxyacyl-CoA dehydrogenase	I
COG1257	Hydroxymethylglutaryl-CoA reductase	I
COG1260	Myo-inositol-1-phosphate synthase	I
COG1267	Phosphatidylglycerophosphatase A	I
COG1307	Fatty acid-binding protein DegV (function unknown)	I
COG1398	Fatty-acid desaturase	I
COG1443	Isopentenyldiphosphate isomerase	I
COG1502	Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthase or related enzyme	I
COG1560	Lauroyl/myristoyl acyltransferase	I
COG1562	Phytoene/squalene synthetase	I
COG1577	Mevalonate kinase	I
COG1607	Acyl-CoA hydrolase	I
COG1608	Isopentenyl phosphate kinase	I
COG1646	Heptaprenylglyceryl phosphate synthase	I
COG1657	Squalene cyclase	I
COG1788	Acyl CoA: acetate/3-ketoacid CoA transferase, alpha subunit	I
COG1804	Crotonobetainyl-CoA: carnitine CoA-transferase CaiB and related acyl-CoA transferases	I

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG1884	Methylmalonyl-CoA mutase, N-terminal domain/subunit	I
COG1924	Activator of 2-hydroxyglutaryl-CoA dehydratase (HSP70-class ATPase domain)	I
COG1946	Acyl-CoA thioesterase	I
COG1947	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	I
COG1960	Acyl-CoA dehydrogenase related to the alkylation response protein AidB	I
COG1968	Undecaprenyl pyrophosphate phosphatase UppP	I
COG2030	Acyl dehydratase	I
COG2031	Short chain fatty acids transporter	I
COG2057	Acyl CoA: acetate/3-ketoacid CoA transferase, beta subunit	I
COG2067	Long-chain fatty acid transport protein	I
COG2084	3-hydroxyisobutyrate dehydrogenase or related beta-hydroxyacid dehydrogenase	I
COG2134	CDP-diacylglycerol pyrophosphatase	I
COG2185	Methylmalonyl-CoA mutase, C-terminal domain/subunit (cobalamin-binding)	I
COG2230	Cyclopropane fatty-acyl-phospholipid synthase and related methyltransferases	I
COG2246	Putative flippase GtrA (transmembrane translocase of bactoprenol-linked glucose)	I
COG2267	Lysophospholipase, alpha-beta hydrolase superfamily	I
COG2272	Carboxylesterase type B	I
COG2854	ABC-type transporter Mla maintaining outer membrane lipid asymmetry, periplasmic MlaC component	I
COG2930	Lipid-binding SYLF domain	I
COG2937	Glycerol-3-phosphate O-acyltransferase	I
COG3000	Sterol desaturase/sphingolipid hydroxylase, fatty acid hydroxylase superfamily	I
COG3007	Trans-2-enoyl-CoA reductase	I
COG3124	Acyl carrier protein phosphodiesterase	I
COG3154	Predicted lipid carrier protein YhbT, SCP2 domain	I
COG3239	Fatty acid desaturase	I
COG3243	Poly(3-hydroxyalkanoate) synthetase	I
COG3255	Putative sterol carrier protein	I
COG3356	Predicted membrane-associated lipid hydrolase, neutral ceramidase superfamily	I
COG3407	Mevalonate pyrophosphate decarboxylase	I
COG3425	3-hydroxy-3-methylglutaryl CoA synthase	I
COG3475	Phosphorylcholine metabolism protein LicD	I
COG3675	Predicted lipase	I
COG3777	Hydroxyacyl-ACP dehydratase HTD2, hotdog domain	I
COG3882	Predicted enzyme involved in methoxymalonyl-ACP biosynthesis	I
COG3884	Acyl-ACP thioesterase	I
COG3963	Phospholipid N-methyltransferase	I
COG4247	3-phytase (myo-inositol-hexaphosphate 3-phosphohydrolase)	I
COG4281	Acyl-CoA-binding protein	I
COG4395	Predicted lipid-binding transport protein, Tim44 family	I
COG4553	Poly-beta-hydroxyalkanoate depolymerase	I
COG4667	Predicted phospholipase, patatin/cPLA2 family	I
COG4670	Acyl CoA: acetate/3-ketoacid CoA transferase	I
COG4706	Predicted 3-hydroxylacyl-ACP dehydratase, HotDog domain	I
COG4770	Acetyl/propionyl-CoA carboxylase, alpha subunit	I
COG4781	Membrane-anchored glycerophosphoryl diester phosphodiesterase (GDPDase), membrane domain	I
COG4799	Acetyl-CoA carboxylase, carboxyltransferase component	I
COG4850	Phosphatidate phosphatase APP1	I
COG4981	Enoyl reductase domain of yeast-type FAS1	I
COG4982	3-oxoacyl-ACP reductase domain of yeast-type FAS1	I
COG5083	Phosphatidate phosphatase PAH1, contains Lipin and LNS2 domains. can be involved in plasmid maintenance	I
COG0473	Isocitrate/isopropylmalate dehydrogenase	CE
COG0604	NADPH: quinone reductase or related Zn-dependent oxidoreductase	CR
COG0129	Dihydroxyacid dehydratase/phosphogluconate dehydratase	EG
COG1363	Putative aminopeptidase FrvX	EG
COG0493	NADPH-dependent glutamate synthase beta chain or related oxidoreductase	ER
COG1063	Threonine dehydrogenase or related Zn-dependent dehydrogenase	ER
COG1168	Bifunctional PLP-dependent enzyme with beta-cystathionase and maltose regulon repressor activities	ER

TABLE 4-continued

COGs for Identifying Prebiotic Activities

COG ID	COG NAME	COG CATEGORY
COG1387	Histidinol phosphatase or related hydrolase of the PHP family	ER
COG3185	4-hydroxyphenylpyruvate dioxygenase and related hemolysins	ER
COG0347	Nitrogen regulatory protein PII	TE
COG0834	ABC-type amino acid transport/signal transduction system, periplasmic component/domain	ET
COG4677	Pectin methylesterase and related acyl-CoA thioesterases	GI
COG0637	Beta-phosphoglucomutase or related phosphatase, HAD superfamily	GR
COG2610	H+/gluconate symporter or related permease	GR
COG1489	DNA-binding protein, stimulates sugar fermentation	GT
COG1762	Phosphotransferase system mannitol/fructose-specific IIA domain (Ntr-type)	GT
COG1925	Phosphotransferase system, HPr and related phosphotransfer proteins	TG
COG3925	N-terminal domain of the phosphotransferase system fructose-specific component IIB	GT
COG4945	Carbohydrate-binding DOMON domain	GT
COG1597	Diacylglycerol kinase family enzyme	IR
COG2303	Choline dehydrogenase or related flavoprotein	IR
COG3240	Phospholipase/lecithinase/hemolysin	IR

TABLE 5

List of species enriched in alive GHVD patients:

Lactobacillus gasseri
Lactobacillus fermentum
Lactobacillus reuteri
Enterococcus faecalis
Enterococcus durans
Enterococcus villorum
Lactobacillus plantarum
Pediococcus acidilactici
Staphylococcus pasteuri
Staphylococcus cohnii
Streptococcus sanguinis
Streptococcus sinensis
Streptococcus mitis
Streptococcus sp. SCA22
Streptococcus sp. CR-3145
Streptococcus anginosus
Streptococcus mutans
Coprobacillus cateniformis
Clostridium saccharogumia
Eubacterium dolichum DSM 3991
Clostridium sp. PPf35E6
Clostridium sordelli ATCC 9714
Ruminococcus torques
Ruminococcus gnavus
Clostridium clostridioforme
Ruminococcus obeum
Blautia producta
Clostridium sp. ID5
Megasphaera micronuciformis
Veillonella parvula
Clostridium methylpentosum
Clostridium islandicum
Faecalibacterium prausnitzii
Bacteroides uniformmis
Bacteroides thetaiotaomicron
Bacteroides acidifaciens
Bacteroides ovatus
Bacteroides fragilis
Parabacteroides distasonis
Propionibacteirum propionicum
Actinomycs hyovaginalis
Rothia mucilaginosa
Rothia aeria

TABLE 5-continued

List of species enriched in alive GHVD patients:

Bifidobacterium breve
Scardovia inopinata
Eggerthella lenta

TABLE 6

Anaerobic bacterial species tested for carbon source usage (Biolog plates)

Species purchased:	Species Freshly Isolated:
R. gnavus (EPV1)	*Blautia luti* BlnIX (EPV114)
E. rectale (EPV2)	*Blautia luti* ELU (EPV54)
B. luti (EPV3)	*Ruminococcus gnavus* (EPV102)
B. wexlerae (EPV5)	*Blautia faecis* (EPV78)
C. leptum (EPV6)	*Ruminococcus torques* (EPV76)
B. faecis (EPV15)	*Blautia wexlerae* SJTU1416 (EPV52)
B. obeum (EPV20)	*Blautia* WAL14507 (EPV64)
B. producta (EPV21)	Uncultured bacterium SJTU1416 (EPV51)
B. coccoides (EPV22)	Uncultured bacterium GQ8980099 (EPV47)
B. hydrogenotrophica (EPV23)	*Eubacterium rectale* (EPV35)
B. hansenii (EPV24)	

TABLE 7

Exemplary Prebiotics/Carbon Sources

Chemical	MoA
L-Arabinose	C-Source, carbohydrate
N-Acetyl-D-Glucosamine	C-Source, carbohydrate
D-Saccharic acid	C-Source, carboxylic acid
Succinic acid	C-Source, carboxylic acid
D-Galactose	C-Source, carbohydrate
L-Aspartic acid	C-Source, amino acid
L-Proline	C-Source, amino acid
D-Alanine	C-Source, amino acid
D-Trehalose	C-Source, carbohydrate
D-Mannose	C-Source, carbohydrate
Dulcitol	C-Source, carbohydrate

TABLE 7-continued

Exemplary Prebiotics/Carbon Sources

Chemical	MoA
D-Serine	C-Source, amino acid
D-Sorbitol	C-Source, carbohydrate
Glycerol	C-Source, carbohydrate
L-Fucose	C-Source, carbohydrate
D-Glucuronic acid	C-Source, carboxylic acid
D-Gluconic acid	C-Source, carboxylic acid
DL-a-Glycerol Phosphate	C-Source, carbohydrate
D-Xylose	C-Source, carbohydrate
L-Lactic acid	C-Source, carboxylic acid
Formic acid	C-Source, carboxylic acid
D-Mannitol	C-Source, carbohydrate
L-Glutamic acid	C-Source, amino acid
D-Glucose-6-Phosphate	C-Source, carbohydrate
D-Galactonic acid-g-Lactone	C-Source, carboxylic acid
DL-Malic acid	C-Source, carboxylic acid
D-Ribose	C-Source, carbohydrate
Tween 20	C-Source, fatty acid
L-Rhamnose	C-Source, carbohydrate
D-Fructose	C-Source, carbohydrate
Acetic acid	C-Source, carboxylic acid
a-D-Glucose	C-Source, carbohydrate
Maltose	C-Source, carbohydrate
D-Melibiose	C-Source, carbohydrate
Thymidine	C-Source, carbohydrate
L-Asparagine	C-Source, amino acid
D-Aspartic acid	C-Source, amino acid
D-Glucosaminic acid	C-Source, carboxylic acid
1,2-Propanediol	C-Source, alcohol
Tween 40	C-Source, fatty acid
a-Ketoglutaric acid	C-Source, carboxylic acid
a-Ketobutyric acid	C-Source, carboxylic acid
a-Methyl-D-Galactoside	C-Source, carbohydrate
a-D-Lactose	C-Source, carbohydrate
Lactulose	C-Source, carbohydrate
Sucrose	C-Source, carbohydrate
Uridine	C-Source, carbohydrate
L-Glutamine	C-Source, amino acid
m-Tartaric acid	C-Source, carboxylic acid
D-Glucose-1-Phosphate	C-Source, carbohydrate
D-Fructose-6-Phosphate	C-Source, carbohydrate
Tween 80	C-Source, fatty acid
a-Hydroxyglutaric acid-g-Lactone	C-Source, carboxylic acid
a-Hydroxybutyric acid	C-Source, carboxylic acid
b-Methyl-D-Glucoside	C-Source, carbohydrate
Adonitol	C-Source, carbohydrate
Maltotriose	C-Source, carbohydrate
2'-Deoxyadenosine	C-Source, carbohydrate
Adenosine	C-Source, carbohydrate
Gly-Asp	C-Source, amino acid
Citric acid	C-Source, carboxylic acid
m-Inositol	C-Source, carbohydrate
D-Threonine	C-Source, amino acid
Fumaric acid	C-Source, carboxylic acid
Bromosuccinic acid	C-Source, carboxylic acid
Propionic acid	C-Source, carboxylic acid
Mucic acid	C-Source, carboxylic acid
Glycolic acid	C-Source, carboxylic acid
Glyoxylic acid	C-Source, carboxylic acid
D-Cellobiose	C-Source, carbohydrate
Inosine	C-Source, carbohydrate
Gly-Glu	C-Source, amino acid
Tricarballylic acid	C-Source, carboxylic acid
L-Serine	C-Source, amino acid
L-Threonine	C-Source, amino acid
L-Alanine	C-Source, amino acid
Ala-Gly	C-Source, amino acid
Acetoacetic acid	C-Source, carboxylic acid
N-Acetyl-D-Mannosamine	C-Source, carbohydrate
Mono-Methylsuccinate	C-Source, carboxylic acid
Methylpyruvate	C-Source, ester
D-Malic acid	C-Source, carboxylic acid
L-Malic acid	C-Source, carboxylic acid
Gly-Pro	C-Source, amino acid

TABLE 7-continued

Exemplary Prebiotics/Carbon Sources

Chemical	MoA
p-Hydroxyphenyl Acetic acid	C-Source, carboxylic acid
m-Hydroxyphenyl Acetic acid	C-Source, carboxylic acid
Tyramine	C-Source, amine
D-Psicose	C-Source, carbohydrate
L-Lyxose	C-Source, carbohydrate
Glucuronamide	C-Source, amide
Pyruvic acid	C-Source, carboxylic acid
L-Galactonic acid-g-Lactone	C-Source, carboxylic acid
D-Galacturonic acid	C-Source, carboxylic acid
Phenylethylamine	C-Source, amine
2-Aminoethanol	C-Source, alcohol
Negative Control	C-Source, negative control
Chondroitin Sulfate C	C-Source, polymer
a-Cyclodextrin	C-Source, polymer
b-Cyclodextrin	C-Source, polymer
g-Cyclodextrin	C-Source, polymer
Dextrin	C-Source, polymer
Gelatin	C-Source, polymer
Glycogen	C-Source, polymer
Inulin	C-Source, polymer
Laminarin	C-Source, polymer
Mannan	C-Source, polymer
Pectin	C-Source, polymer
N-Acetyl-D-Galactosamine	C-Source, carbohydrate
N-Acetyl-Neuraminic acid	C-Source, carboxylic acid
b-D-Allose	C-Source, carbohydrate
Amygdalin	C-Source, carbohydrate
D-Arabinose	C-Source, carbohydrate
D-Arabitol	C-Source, carbohydrate
L-Arabitol	C-Source, carbohydrate
Arbutin	C-Source, carbohydrate
2-Deoxy-D-Ribose	C-Source, carbohydrate
i-Erythritol	C-Source, carbohydrate
D-Fucose	C-Source, carbohydrate
3-O-b-D-Galactopyranosyl-D-Arabinose	C-Source, carbohydrate
Gentiobiose	C-Source, carbohydrate
L-Glucose	C-Source, carbohydrate
D-Lactitol	C-Source, carbohydrate
D-Melezitose	C-Source, carbohydrate
Maltitol	C-Source, carbohydrate
a-Methyl-D-Glucoside	C-Source, carbohydrate
b-Methyl-D-Galactoside	C-Source, carbohydrate
3-Methylglucose	C-Source, carbohydrate
b-Methyl-D-Glucuronic acid	C-Source, carboxylic acid
a-Methyl-D-Mannoside	C-Source, carbohydrate
b-Methyl-D-Xyloside	C-Source, carbohydrate
Palatinose	C-Source, carbohydrate
D-Raffinose	C-Source, carbohydrate
Salicin	C-Source, carbohydrate
Sedoheptulosan	C-Source, carbohydrate
L-Sorbose	C-Source, carbohydrate
Stachyose	C-Source, carbohydrate
D-Tagatose	C-Source, carbohydrate
Turanose	C-Source, carbohydrate
Xylitol	C-Source, carbohydrate
N-Acetyl-D-Glucosaminitol	C-Source, carbohydrate
g-Amino-N-Butyric acid	C-Source, carboxylic acid
d-Amino Valeric acid	C-Source, carboxylic acid
Butyric acid	C-Source, carboxylic acid
Capric acid	C-Source, carboxylic acid
Caproic acid	C-Source, carboxylic acid
Citraconic acid	C-Source, carboxylic acid
Citramalic acid	C-Source, carboxylic acid
D-Glucosamine	C-Source, carbohydrate
2-Hydroxybenzoic acid	C-Source, carboxylic acid
4-Hydroxybenzoic acid	C-Source, carboxylic acid
b-Hydroxybutyric acid	C-Source, carboxylic acid
g-Hydroxybutyric acid	C-Source, carboxylic acid
a-Keto-Valeric acid	C-Source, carboxylic acid
Itaconic acid	C-Source, carboxylic acid
5-Keto-D-Gluconic acid	C-Source, carboxylic acid
D-Lactic acid Methyl Ester	C-Source, ester
Malonic acid	C-Source, carboxylic acid

TABLE 7-continued

Exemplary Prebiotics/Carbon Sources

Chemical	MoA
Melibionic acid	C-Source, carbohydrate
Oxalic acid	C-Source, carboxylic acid
Oxalomalic acid	C-Source, carboxylic acid
Quinic acid	C-Source, carboxylic acid
D-Ribono-1,4-Lactone	C-Source, carboxylic acid
Sebacic acid	C-Source, carboxylic acid
Sorbic acid	C-Source, carboxylic acid
Succinamic acid	C-Source, carboxylic acid
D-Tartaric acid	C-Source, carboxylic acid
L-Tartaric acid	C-Source, carboxylic acid
Acetamide	C-Source, amide
L-Alaninamide	C-Source, amide
N-Acetyl-L-Glutamic acid	C-Source, amino acid
L-Arginine	C-Source, amino acid
Glycine	C-Source, amino acid
L-Histidine	C-Source, amino acid
L-Homoserine	C-Source, amino acid
Hydroxy-L-Proline	C-Source, amino acid

TABLE 7-continued

Exemplary Prebiotics/Carbon Sources

Chemical	MoA
L-Isoleucine	C-Source, amino acid
L-Leucine	C-Source, amino acid
L-Lysine	C-Source, amino acid
L-Methionine	C-Source, amino acid
L-Ornithine	C-Source, amino acid
L-Phenylalanine	C-Source, amino acid
L-Pyroglutamic acid	C-Source, amino acid
L-Valine	C-Source, amino acid
D,L-Carnitine	C-Source, carboxylic acid
sec-Butylamine	C-Source, amine
D,L-Octopamine	C-Source, amine
Putrescine	C-Source, amine
Dihydroxyacetone	C-Source, alcohol
2,3-Butanediol	C-Source, alcohol
2,3-Butanedione	C-Source, alcohol
3-Hydroxy-2-butanone	C-Source, alcohol

TABLE 8

Bacterial Species Detected at Low Frequency in Vaginal Samples from Vancomycin-Treated Mice

Site	Group	Taxonomy	Mean abundance day 6 (out of 10,000)	Median abundance day 6 (out of 10,000)
vaginal	Vancomycin	KF008552.1.1432 D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Enterobacteriales; D_4_Enterobacteriaceae; D_5_Klebsiella; D_6_Klebsiella pneumoniae	0.291242675	0.024255713
vaginal	Vancomycin	AB740357.1.1462 D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Enterobacteriales; D_4_Enterobacteriaceae; D_5_Pantoea; D_6_Pantoea sp. NCCP-532	1.436524722	0
vaginal	Vancomycin	DQ799428.1.1372 D_0_Bacteria; D_1_Verrucomicrobia; D_2_Verrucomicrobiae; D_3_Verrucomicrobiales; D_4_Verrucomicrobiaceae; D_5_Akkermansia; D_6_uncultured bacterium	0.348310693	0
vaginal	Vancomycin	JX094996.1.1390 D_0_Bacteria; D_1_Firmicutes; D_2_Clostridia; D_3_Clostridiales; D_4_Lachnospiraceae; D_5_Blautia; D_6_uncultured bacterium	0.348310693	0
vaginal	Vancomycin	EU459716.1.1286 D_0_Bacteria; D_1_Firmicutes; D_2_Clostridia; D_3_Clostridiales; D_4_Lachnospiraceae; D_5_uncultured; D_6_uncultured bacterium	0.348310693	0
vaginal	Vancomycin	EU457230.1.1391 D_0_Bacteria; D_1_Firmicutes;	0.696621386	0

TABLE 8-continued

Bacterial Species Detected at Low Frequency in Vaginal Samples from Vancomycin-Treated Mice

Site	Group	Taxonomy	Mean abundance day 6 (out of 10,000)	Median abundance day 6 (out of 10,000)
		D_2_Clostridia; D_3_Clostridiales; D_4_Lachnospiraceae; D_5_Incertae Sedis; D_6_uncultured bacterium		
vaginal	Vancomycin	EU459317.1.1373	0.348310693	0
		D_0_Bacteria; D_1_Firmicutes; D_2_Clostridia; D_3_Clostridiales; D_4_Clostridiaceae 1; D_5_Clostridium sensu stricto 1; D_6_uncultured bacterium		
vaginal	Vancomycin	HM817954.1.1353	0.348310693	0
		D_0_Bacteria; D_1_Firmicutes; D_2_Clostridia; D_3_Clostridiales; D_4_Lachnospiraceae; D_5_Roseburia; D_6_uncultured bacterium		
vaginal	Vancomycin	GQ134873.1.1373	0.348310693	0
		D_0_Bacteria; D_1_Firmicutes; D_2_Clostridia; D_3_Clostridiales; D_4_Clostridiaceae 1; D_5_Clostridium sensu stricto 1; D_6_uncultured bacterium		
vaginal	Vancomycin	FJ879074.1.1494	0.348310693	0
		D_0_Bacteria; D_1_Firmicutes; D_2_Clostridia; D_3_Clostridiales; D_4_Lachnospiraceae; D_5_uncultured; D_6_uncultured bacterium		
vaginal	Vancomycin	EU774816.1.1381	0.348310693	0
		D_0_Bacteria; D_1_Firmicutes; D_2_Clostridia; D_3_Clostridiales; D_4_Clostridiaceae 1; D_5_Clostridium sensu stricto 1; D_6_uncultured bacterium		
vaginal	Vancomycin	EU775614.1.1398	0.417063419	0
		D_0_Bacteria; D_1_Proteobacteria; D_2_Gammaproteobacteria; D_3_Enterobacteriales; D_4_Enterobacteriaceae; D_5_Enterobacter; D_6_uncultured bacterium		

[0849] Unless otherwise indicated, all numbers expressing quantities of ingredients, reaction conditions, and so forth used in the specification, including claims, are to be understood as being modified in all instances by the term "about." Accordingly, unless otherwise indicated to the contrary, the numerical parameters are approximations and may vary depending upon the desired properties sought to be obtained. At the very least, and not as an attempt to limit the application of the doctrine of equivalents to the scope of the claims, each numerical parameter should be construed in light of the number of significant digits and ordinary rounding approaches.

[0850] Unless otherwise indicated, the term "at least" preceding a series of elements is to be understood to refer to every element in the series.

[0851] While the invention has been particularly shown and described with reference to a preferred embodiment and various alternate embodiments, it will be understood by persons skilled in the relevant art that various changes in form and details can be made therein without departing from the spirit and scope of the invention.

[0852] All references, issued patents and patent applications cited within the body of the instant specification are hereby incorporated by reference in their entirety, for all purposes.

[0853] The foregoing description of the embodiments of the invention has been presented for the purpose of illustration; it is not intended to be exhaustive or to limit the invention to the precise forms disclosed. Persons skilled in the relevant art can appreciate that many modifications and variations are possible in light of the above disclosure.

[0854] Finally, the language used in the specification has been principally selected for readability and instructional purposes, and it may not have been selected to delineate or circumscribe the inventive subject matter. It is therefore intended that the scope of the invention be limited not by this detailed description, but rather by any claims that issue on an application based hereon. Accordingly, the disclosure of the embodiments of the invention is intended to be illustrative, but not limiting, of the scope of the invention, which is set forth in the following claims.

SEQUENCE LISTING

The patent application contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US20160235792A1). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

1. A method of increasing the duration of survival of a subject receiving a bone marrow transplant, comprising administering to the subject a probiotic composition comprising an isolated, human-derived bacterial population, such that the duration of survival of the subject is increased.

2. The method of claim **1**, wherein administration of the probiotic composition reduces the likelihood that the subject will develop sepsis following the bone marrow transplant.

3. The method of claim **1**, wherein administration of the probiotic composition reduces the likelihood that the subject will develop graft versus host disease (GVHD) following the bone marrow transplant.

4. A method of increasing the duration of survival of a subject receiving a bone marrow transplant, comprising:

administering to the subject a probiotic composition comprising an isolated bacterial population and a pharmaceutically acceptable excipient, wherein the probiotic composition reduces intestinal permeability in the subject; and

administering to the subject a prebiotic that enhances the activity of the bacterial population,

such that the duration of survival of the subject is increased.

5. A method of preventing graft versus host disease (GVHD) in a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated, human-derived bacterial population, such that GVHD is prevented.

6. The method of claim **5**, wherein the subject is receiving a hematopoietic stem cell transplant.

7. The method of claim **5**, wherein the subject is receiving a bone marrow transplant.

8. The method of claim **5**, wherein the subject is receiving a solid organ transplant.

9. The method of claim **8**, wherein the solid organ transplant is selected from the group consisting of a kidney transplant, a heart transplant, a lung transplant, a skin transplant, a liver transplant, a pancreas transplant, an intestinal transplant, an endocrine gland transplant, a bladder transplant, and a skeletal muscle transplant.

10. A method of reducing inflammation in the gastrointestinal tract of a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated, anti-inflammatory bacterial population, such that inflammation in the gastrointestinal tract of the subject receiving the transplant is reduced.

11. A method of reducing intestinal permeability in a subject receiving a transplant, comprising administering to the subject a probiotic composition comprising an isolated bacterial population, such that the intestinal permeability of the subject receiving the transplant is reduced.

12. A pharmaceutical composition comprising an isolated anti-inflammatory bacterial population capable of decreasing secretion of a pro-inflammatory cytokine and/or increasing secretion of an anti-inflammatory cytokine by human peripheral blood mononuclear cells (PBMCs), and a pharmaceutically acceptable excipient.

13. The pharmaceutical composition of claim **12**, further comprising a prebiotic.

14. The method or of claim **1**, wherein the bacterial population comprises an isolated population of bacteria selected from the group consisting of *Acidaminococcus intestine, Acinetobacter baumannii, Acinetobacter lwoffii, Akkermansia muciniphila, Alistipes putredinis, Alistipes shahii, Anaerostipes hadrus, Anaerotruncus colihominis, Bacteroides caccae, Bacteroides cellulosilyticus, Bacteroides dorei, Bacteroides eggerthii, Bacteroides finegoldii, Bacteroides fragilis, Bacteroides massiliensis, Bacteroides ovatus, Bacteroides salanitronis, Bacteroides salyersiae, Bacteroides* sp, 1_1_6, *Bacteroides* sp, 3_1_23, *Bacteroides* sp, D20, *Bacteroides thetaiotaomicron, Bacteroides uniformis, Bacteroides vulgatus, Bifidobacterium adolescentis, Bifidobacterium bifidum, Bifidobacterium breve, Bifidobacterium faecale, Bifidobacterium kashiwanohense, Bifidobacterium longum* subsp, *longum, Bifidobacterium pseudocatenulatum, Bifidobacterium stercoris, Blautia* (*Ruminococcus*) *coccoides, Blautia faecis, Blautia glucerasea, Blautia* (*Ruminococcus*) *hansenii, Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*), *Blautia* (*Ruminococcus*) *luti, Blautia* (*Ruminococcus*) *obeum, Blautia producta* (*Ruminococcus productus*), *Blautia* (*Ruminococcus*) *schinkii, Blautia stercoris, Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1), *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1), *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank:

EF404657.1), *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ0898099.1), *Blautia* uncultured PAC000178_s (www.ezbiocloud.neteztaxon/hierarchy?m=browse&k=PAC000178&d=2), *Blautia wexlerae, Candidatus Arthromitus* sp. SFB-mouse-Yit, *Catenibacterium mitsuokai, Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13, *Clostridiales* bacterium 1_7_47FAA, *Clostridium asparagiforme, Clostridium bolteae, Clostridium clostridioforme, Clostridium glycyrrhizinilyticum, Clostridium* (*Hungatella*) *hathewayi, Clostridium histolyticum, Clostridium indolis, Clostridium leptum, Clostridium* (*Tyzzerella*) *nexile, Clostridium perfringens, Clostridium* (*Erysipelatoclostridium*) *ramosum, Clostridium scindens, Clostridium* sp. 14774, *Clostridium* sp. 7_3_54FAA, *Clostridium* sp. HGF2, *Clostridium symbiosum, Collinsella aerofaciens, Collinsella intestinalis, Coprobacillus* sp. D7, *Coprococcus catus, Coprococcus comes, Dorea formicigenerans, Dorea longicatena, Enterococcus faecalis, Enterococcus faecium, Erysipelotrichaceae* bacterium 3_1_53, *Escherichia coli, Escherichia coli* 588, *Eubacterium eligens, Eubacterium fissicatena, Eubacterium ramulus, Eubacterium rectale, Faecalibacterium prausnitzii, Flavonifractor plautii, Fusobacterium mortiferum, Fusobacterium nucleatum, Holdemania filiformis, Hydrogenoanaerobacterium saccharovorans, Klebsiella oxytoca, Lachnospiraceae* bacterium 3_1_57FAA_CT1, *Lachnospiraceae* bacterium 7_1_58FAA, *Lachnospiraceae* bacterium 5_1_57FAA, *Lactobacillus casei, Lactobacillus rhamnosus, Lactobacillus ruminis, Lactococcus casei, Odoribacter splanchnicus, Oscillibacter valericigenes, Parabacteroides gordonii, Parabacteroides johnsonii, Parabacteroides merdae, Pediococcus acidilactici, Peptostreptococcus asaccharolyticus, Propionibacterium granulosum, Roseburia intestinalis, Roseburia inulinivorans, Ruminococcus faecis, Ruminococcus gnavus, Ruminococcus* sp. ID8, *Ruminococcus torques, Slackia piriformis, Staphylococcus epidermidis, Staphylococcus saprophyticus, Streptococcus cristatus, Streptococcus dysgalactiae* subsp, *equisimilis, Streptococcus infantis, Streptococcus oralis, Streptococcus sanguinis, Streptococcus viridans, Streptococcus thermophiles, Veillonella dispar*, and combinations thereof.

15-136. (canceled)

137. The method of claim **4**, wherein the bacterial population comprises an isolated population of bacteria selected from the group consisting of *Acidaminococcus intestine, Acinetobacter baumannii, Acinetobacter lwoffii, Akkermansia muciniphila, Alistipes putredinis, Alistipes shahii, Anaerostipes hadrus, Anaerotruncus colihominis, Bacteroides caccae, Bacteroides cellulosilyticus, Bacteroides dorei, Bacteroides eggerthii, Bacteroides finegoldii, Bacteroides fragilis, Bacteroides massiliensis, Bacteroides ovatus, Bacteroides salanitronis, Bacteroides salyersiae, Bacteroides* sp. 1_1_6, *Bacteroides* sp. 3_1_23, *Bacteroides* sp. D20, *Bacteroides thetaiotaomicron, Bacteroides uniformis, Bacteroides vulgatus, Bifidobacterium adolescentis, Bifidobacterium bifidum, Bifidobacterium breve, Bifidobacterium faecale, Bifidobacterium kashiwanohense, Bifidobacterium longum* subsp. *longum, Bifidobacterium pseudocatenulatum, Bifidobacterium stercoris, Blautia* (*Ruminococcus*) *coccoides, Blautia faecis, Blautia glucerasea, Blautia* (*Ruminococcus*) *hansenii, Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*), *Blautia* (*Ruminococcus*) *luti, Blautia* (*Ruminococcus*) *obeum, Blautia producta* (*Ruminococcus productus*), *Blautia* (*Ruminococcus*) *schinkii, Blautia stercoris, Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1), *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1), *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1), *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1), *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2), *Blautia wexlerae, Candidatus Arthromitus* sp. SFB-mouse-Yit, *Catenibacterium mitsuokai, Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13, *Clostridiales* bacterium 1_7_47FAA, *Clostridium asparagiforme, Clostridium bolteae, Clostridium clostridioforme, Clostridium glycyrrhizinilyticum, Clostridium* (*Hungatella*) *hathewayi, Clostridium histolyticum, Clostridium indolis, Clostridium leptum, Clostridium* (*Tyzzerella*) *nexile, Clostridium perfringens, Clostridium* (*Erysipelatoclostridium*) *ramosum, Clostridium scindens, Clostridium* sp. 14774, *Clostridium* sp. 7_3_54FAA, *Clostridium* sp. HGF2, *Clostridium symbiosum, Collinsella aerofaciens, Collinsella intestinalis, Coprobacillus* sp. D7, *Coprococcus catus, Coprococcus comes, Dorea formicigenerans, Dorea longicatena, Enterococcus faecalis, Enterococcus faecium, Erysipelotrichaceae* bacterium 3_1_53, *Escherichia coli, Escherichia coli* S88, *Eubacterium eligens, Eubacterium fissicatena, Eubacterium ramulus, Eubacterium rectale, Faecalibacterium prausnitzii, Flavonifractor plautii, Fusobacterium mortiferum, Fusobacterium nucleatum, Holdemania filiformis, Hydrogenoanaerobacterium saccharovorans, Klebsiella oxytoca, Lachnospiraceae* bacterium 3_1_57FAA_CT1, *Lachnospiraceae* bacterium 7_1_58FAA, *Lachnospiraceae* bacterium 5_1_57FAA, *Lactobacillus casei, Lactobacillus rhamnosus, Lactobacillus ruminis, Lactococcus casei, Odoribacter splanchnicus, Oscillibacter valericigenes, Parabacteroides gordonii, Parabacteroides johnsonii, Parabacteroides merdae, Pediococcus acidilactici, Peptostreptococcus asaccharolyticus, Propionibacterium granulosum, Roseburia intestinalis, Roseburia inulinivorans, Ruminococcus faecis, Ruminococcus gnavus, Ruminococcus* sp. ID8, *Ruminococcus torques, Slackia piriformis, Staphylococcus epidermidis, Staphylococcus saprophyticus, Streptococcus cristatus, Streptococcus dysgalactiae* subsp. *equisimilis, Streptococcus infantis, Streptococcus oralis, Streptococcus sanguinis, Streptococcus viridans, Streptococcus thermophiles, Veillonella dispar*, and combinations thereof.

138. The method of claim **5**, wherein the bacterial population comprises an isolated population of bacteria selected from the group consisting of *Acidaminococcus intestine, Acinetobacter baumannii, Acinetobacter lwoffii, Akkermansia muciniphila, Alistipes putredinis, Alistipes shahii, Anaerostipes hadrus, Anaerotruncus colihominis, Bacteroides caccae, Bacteroides cellulosilyticus, Bacteroides dorei, Bacteroides eggerthii, Bacteroides finegoldii, Bacteroides fragilis, Bacteroides massiliensis, Bacteroides ovatus, Bacteroides salanitronis, Bacteroides salyersiae, Bacteroides* sp. 1_1_6, *Bacteroides* sp. 3_1_23, *Bacteroides* sp. D20, *Bacteroides thetaiotaomicron, Bacteroides uniformis, Bacteroides vulgatus, Bifidobacterium adolescentis, Bifidobacterium bifidum, Bifidobacterium breve, Bifidobacterium faecale, Bifidobacterium kashiwanohense, Bifidobacterium longum* subsp. *longum, Bifidobacterium pseudocatenulatum, Bifidobacterium stercoris, Blautia* (*Ruminococcus*) *coccoides, Blautia faecis, Blautia glucerasea, Blautia* (*Ruminococcus*) *hansenii, Blautia hydrogenotrophica* (*Ruminococcus*

hydrogenotrophicus), *Blautia* (*Ruminococcus*) *luti, Blautia* (*Ruminococcus*) *obeum, Blautia producta* (*Ruminococcus productus*), *Blautia* (*Ruminococcus*) *schinkii, Blautia stercoris, Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1), *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1), *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1), *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1), *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2), *Blautia wexlerae, Candidatus Arthromitus* sp. SFB-mouse-Yit, *Catenibacterium mitsuokai, Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13, *Clostridiales* bacterium 1_7_47FAA, *Clostridium asparagiforme, Clostridium bolteae, Clostridium clostridioforme, Clostridium glycyrrhizinilyticum, Clostridium* (*Hungatella*) *hathewayi, Clostridium histolyticum, Clostridium indolis, Clostridium leptum, Clostridium* (*Tyzzerella*) *nexile, Clostridium perfringens, Clostridium* (*Erysipelatoclostridium*) *ramosum, Clostridium scindens, Clostridium* sp. 14774, *Clostridium* sp. 7_3_54FAA, *Clostridium* sp. HGF2, *Clostridium symbiosum, Collinsella aerofaciens, Collinsella intestinalis, Coprobacillus* sp. D7, *Coprococcus catus, Coprococcus comes, Dorea formicigenerans, Dorea longicatena, Enterococcus faecalis, Enterococcus faecium, Erysipelotrichaceae* bacterium 3_1_53, *Escherichia coli, Escherichia coli* S88, *Eubacterium eligens, Eubacterium fissicatena, Eubacterium ramulus, Eubacterium rectale, Faecalibacterium prausnitzii, Flavonifractor plautii, Fusobacterium mortiferum, Fusobacterium nucleatum, Holdemania filiformis, Hydrogenoanaerobacterium saccharovorans, Klebsiella oxytoca, Lachnospiraceae* bacterium 3_1_57FAA_CT1, *Lachnospiraceae* bacterium 7_1_58FAA, *Lachnospiraceae* bacterium 5_1_57FAA, *Lactobacillus casei, Lactobacillus rhamnosus, Lactobacillus ruminis, Lactococcus casei, Odoribacter splanchnicus, Oscillibacter valericigenes, Parabacteroides gordonii, Parabacteroides johnsonii, Parabacteroides merdae, Pediococcus acidilactici, Peptostreptococcus asaccharolyticus, Propionibacterium granulosum, Roseburia intestinalis, Roseburia inulinivorans, Ruminococcus faecis, Ruminococcus gnavus, Ruminococcus* sp. ID8, *Ruminococcus torques, Slackia piriformis, Staphylococcus epidermidis, Staphylococcus saprophyticus, Streptococcus cristatus, Streptococcus dysgalactiae* subsp. *equisimilis, Streptococcus infantis, Streptococcus oralis, Streptococcus sanguinis, Streptococcus viridans, Streptococcus thermophiles, Veillonella dispar*, and combinations thereof.

139. The method of claim **10**, wherein the bacterial population comprises an isolated population of bacteria selected from the group consisting of *Acidaminococcus intestine, Acinetobacter baumannii, Acinetobacter lwoffii, Akkermansia muciniphila, Alistipes putredinis, Alistipes shahii, Anaerostipes hadrus, Anaerotruncus colihominis, Bacteroides caccae, Bacteroides cellulosilyticus, Bacteroides dorei, Bacteroides eggerthii, Bacteroides finegoldii, Bacteroides fragilis, Bacteroides massiliensis, Bacteroides ovatus, Bacteroides salanitronis, Bacteroides salyersiae, Bacteroides* sp. 1_1_6, *Bacteroides* sp. 3_1_23, *Bacteroides* sp. D20, *Bacteroides thetaiotaomicron, Bacteroides uniformis, Bacteroides vulgatus, Bifidobacterium adolescentis, Bifidobacterium bifidum, Bifidobacterium breve, Bifidobacterium faecale, Bifidobacterium kashiwanohense, Bifidobacterium longum* subsp. *longum, Bifidobacterium pseudocatenulatum, Bifidobacterium stercoris, Blautia* (*Ruminococcus*) *coccoides, Blautia faecis, Blautia glucerasea, Blautia* (*Ruminococcus*) *hansenii, Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*), *Blautia* (*Ruminococcus*) *luti, Blautia* (*Ruminococcus*) *obeum, Blautia producta* (*Ruminococcus productus*), *Blautia* (*Ruminococcus*) *schinkii, Blautia stercoris, Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1), *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1), *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1), *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1), *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2), *Blautia wexlerae, Candidatus Arthromitus* sp. SFB-mouse-Yit, *Catenibacterium mitsuokai, Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13, *Clostridiales* bacterium 1_7_47FAA, *Clostridium asparagiforme, Clostridium bolteae, Clostridium clostridioforme, Clostridium glycyrrhizinilyticum, Clostridium* (*Hungatella*) *hathewayi, Clostridium histolyticum, Clostridium indolis, Clostridium leptum, Clostridium* (*Tyzzerella*) *nexile, Clostridium perfringens, Clostridium* (*Erysipelatoclostridium*) *ramosum, Clostridium scindens, Clostridium* sp. 14774, *Clostridium* sp. 7_3_54FAA, *Clostridium* sp. HGF2, *Clostridium symbiosum, Collinsella aerofaciens, Collinsella intestinalis, Coprobacillus* sp. D7, *Coprococcus catus, Coprococcus comes, Dorea formicigenerans, Dorea longicatena, Enterococcus faecalis, Enterococcus faecium, Erysipelotrichaceae* bacterium 3_1_53, *Escherichia coli, Escherichia coli* S88, *Eubacterium eligens, Eubacterium fissicatena, Eubacterium ramulus, Eubacterium rectale, Faecalibacterium prausnitzii, Flavonifractor plautii, Fusobacterium mortiferum, Fusobacterium nucleatum, Holdemania filiformis, Hydrogenoanaerobacterium saccharovorans, Klebsiella oxytoca, Lachnospiraceae* bacterium 3_1_57FAA_CT1, *Lachnospiraceae* bacterium 7_1_58FAA, *Lachnospiraceae* bacterium 5_1_57FAA, *Lactobacillus casei, Lactobacillus rhamnosus, Lactobacillus ruminis, Lactococcus casei, Odoribacter splanchnicus, Oscillibacter valericigenes, Parabacteroides gordonii, Parabacteroides johnsonii, Parabacteroides merdae, Pediococcus acidilactici, Peptostreptococcus asaccharolyticus, Propionibacterium granulosum, Roseburia intestinalis, Roseburia inulinivorans, Ruminococcus faecis, Ruminococcus gnavus, Ruminococcus* sp. ID8, *Ruminococcus torques, Slackia piriformis, Staphylococcus epidermidis, Staphylococcus saprophyticus, Streptococcus cristatus, Streptococcus dysgalactiae* subsp. *equisimilis, Streptococcus infantis, Streptococcus oralis, Streptococcus sanguinis, Streptococcus viridans, Streptococcus thermophiles, Veillonella dispar*, and combinations thereof.

140. The method of claim **11**, wherein the bacterial population comprises an isolated population of bacteria selected from the group consisting of *Acidaminococcus intestine, Acinetobacter baumannii, Acinetobacter lwoffii, Akkermansia muciniphila, Alistipes putredinis, Alistipes shahii, Anaerostipes hadrus, Anaerotruncus colihominis, Bacteroides caccae, Bacteroides cellulosilyticus, Bacteroides dorei, Bacteroides eggerthii, Bacteroides finegoldii, Bacteroides fragilis, Bacteroides massiliensis, Bacteroides ovatus, Bacteroides salanitronis, Bacteroides salyersiae, Bacteroides* sp. 1_1_6, *Bacteroides* sp. 3_1_23, *Bacteroides* sp. D20, *Bacteroides thetaiotaomicron, Bacteroides uniformis, Bacteroides vulgatus, Bifidobacterium adolescentis, Bifido-*

bacterium bifidum, Bifidobacterium breve, Bifidobacterium faecale, Bifidobacterium kashiwanohense, Bifidobacterium longum subsp. *longum, Bifidobacterium pseudocatenulatum, Bifidobacterium stercoris, Blautia* (*Ruminococcus*) *coccoides, Blautia faecis, Blautia glucerasea, Blautia* (*Ruminococcus*) *hansenii, Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*), *Blautia* (*Ruminococcus*) *luti, Blautia* (*Ruminococcus*) *obeum, Blautia producta* (*Ruminococcus productus*), *Blautia* (*Ruminococcus*) *schinkii, Blautia stercoris, Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1), *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1), *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1), *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1), *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2), *Blautia wexlerae, Candidatus Arthromitus* sp. SFB-mouse-Yit, *Catenibacterium mitsuokai, Clostridiaceae* bacterium (*Dielma fastidiosa*) JC13, *Clostridiales* bacterium 1_7_47FAA, *Clostridium asparagiforme, Clostridium bolteae, Clostridium clostridioforme, Clostridium glycyrrhizinilyticum, Clostridium* (*Hungatella*) *hathewayi, Clostridium histolyticum, Clostridium indolis, Clostridium leptum, Clostridium* (*Tyzzerella*) *nexile, Clostridium perfringens, Clostridium* (*Erysipelatoclostridium*) *ramosum, Clostridium scindens, Clostridium* sp. 14774, *Clostridium* sp. 7_3_54FAA, *Clostridium* sp. HGF2, *Clostridium symbiosum, Collinsella aerofaciens, Collinsella intestinalis, Coprobacillus* sp. D7, *Coprococcus catus, Coprococcus comes, Dorea formicigenerans, Dorea longicatena, Enterococcus faecalis, Enterococcus faecium, Erysipelotrichaceae* bacterium 3_1_53, *Escherichia coli, Escherichia coli* S88, *Eubacterium eligens, Eubacterium fissicatena, Eubacterium ramulus, Eubacterium rectale, Faecalibacterium prausnitzii, Flavonifractor plautii, Fusobacterium mortiferum, Fusobacterium nucleatum, Holdemania filiformis, Hydrogenoanaerobacterium saccharovorans, Klebsiella oxytoca, Lachnospiraceae* bacterium 3_1_57FAA_CT1, *Lachnospiraceae* bacterium 7_1_58FAA, *Lachnospiraceae* bacterium 5_1_57FAA, *Lactobacillus casei, Lactobacillus rhamnosus, Lactobacillus ruminis, Lactococcus casei, Odoribacter splanchnicus, Oscillibacter valericigenes, Parabacteroides gordonii, Parabacteroides johnsonii, Parabacteroides merdae, Pediococcus acidilactici, Peptostreptococcus asaccharolyticus, Propionibacterium granulosum, Roseburia intestinalis, Roseburia inulinivorans, Ruminococcus faecis, Ruminococcus gnavus, Ruminococcus* sp. ID8, *Ruminococcus torques, Slackia piriformis, Staphylococcus epidermidis, Staphylococcus saprophyticus, Streptococcus cristatus, Streptococcus dysgalactiae* subsp. *equisimilis, Streptococcus infantis, Streptococcus oralis, Streptococcus sanguinis, Streptococcus viridans, Streptococcus thermophiles, Veillonella dispar*, and combinations thereof.

141. The pharmaceutical composition of claim **12**, wherein the bacterial population comprises an isolated population of bacteria selected from the group consisting of *Acidaminococcus intestine, Acinetobacter baumannii, Acinetobacter lwoffii, Akkermansia muciniphila, Alistipes putredinis, Alistipes shahii, Anaerostipes hadrus, Anaerotruncus colihominis, Bacteroides caccae, Bacteroides cellulosilyticus, Bacteroides dorei, Bacteroides eggerthii, Bacteroides finegoldii, Bacteroides fragilis, Bacteroides massiliensis, Bacteroides ovatus, Bacteroides salanitronis, Bacteroides salyersiae, Bacteroides* sp. 1_1_6, *Bacteroides* sp. 3_1_23, *Bacteroides* sp. D20, *Bacteroides thetaiotaomicron, Bacteroides uniformis, Bacteroides vulgatus, Bifidobacterium adolescentis, Bifidobacterium bifidum, Bifidobacterium breve, Bifidobacterium faecale, Bifidobacterium kashiwanohense, Bifidobacterium longum* subsp. *longum, Bifidobacterium pseudocatenulatum, Bifidobacterium stercoris, Blautia* (*Ruminococcus*) *coccoides, Blautia faecis, Blautia glucerasea, Blautia* (*Ruminococcus*) *hansenii, Blautia hydrogenotrophica* (*Ruminococcus hydrogenotrophicus*), *Blautia* (*Ruminococcus*) *luti, Blautia* (*Ruminococcus*) *obeum, Blautia producta* (*Ruminococcus productus*), *Blautia* (*Ruminococcus*) *schinkii, Blautia stercoris, Blautia* uncultured bacterium clone BKLE_a03_2 (GenBank: EU469501.1), *Blautia* uncultured bacterium clone SJTU_B_14_30 (GenBank: EF402926.1), *Blautia* uncultured bacterium clone SJTU_C_14_16 (GenBank: EF404657.1), *Blautia* uncultured bacterium clone S1-5 (GenBank: GQ898099.1), *Blautia* uncultured PAC000178_s (www.ezbiocloud.net/eztaxon/hierarchy?m=browse&k=PAC000178&d=2), *Blautia wexlerae, Candidatus Arthromitus* sp. SFB-mouse-Yit, *Catenibacterium mitsuokai, Clostridiaceae bacterium* (*Dielma fastidiosa*) JC13, *Clostridiales* bacterium 1_7_47FAA, *Clostridium asparagiforme, Clostridium bolteae, Clostridium clostridioforme, Clostridium glycyrrhizinilyticum, Clostridium* (*Hungatella*) *hathewayi, Clostridium histolyticum, Clostridium indolis, Clostridium leptum, Clostridium* (*Tyzzerella*) *nexile, Clostridium perfringens, Clostridium* (*Erysipelatoclostridium*) *ramosum, Clostridium scindens, Clostridium* sp. 14774, *Clostridium* sp. 7_3_54FAA, *Clostridium* sp. HGF2, *Clostridium symbiosum, Collinsella aerofaciens, Collinsella intestinalis, Coprobacillus* sp. D7, *Coprococcus catus, Coprococcus comes, Dorea formicigenerans, Dorea longicatena, Enterococcus faecalis, Enterococcus faecium, Erysipelotrichaceae* bacterium 3_1_53, *Escherichia coli, Escherichia coli* S88, *Eubacterium eligens, Eubacterium fissicatena, Eubacterium ramulus, Eubacterium rectale, Faecalibacterium prausnitzii, Flavonifractor plautii, Fusobacterium mortiferum, Fusobacterium nucleatum, Holdemania filiformis, Hydrogenoanaerobacterium saccharovorans, Klebsiella oxytoca, Lachnospiraceae* bacterium 3_1_57FAA_CT1, *Lachnospiraceae* bacterium 7_1_58FAA, *Lachnospiraceae* bacterium 5_1_57FAA, *Lactobacillus casei, Lactobacillus rhamnosus, Lactobacillus ruminis, Lactococcus casei, Odoribacter splanchnicus, Oscillibacter valericigenes, Parabacteroides gordonii, Parabacteroides johnsonii, Parabacteroides merdae, Pediococcus acidilactici, Peptostreptococcus asaccharolyticus, Propionibacterium granulosum, Roseburia intestinalis, Roseburia inulinivorans, Ruminococcus faecis, Ruminococcus gnavus, Ruminococcus* sp. ID8, *Ruminococcus torques, Slackia piriformis, Staphylococcus epidermidis, Staphylococcus saprophyticus, Streptococcus cristatus, Streptococcus dysgalactiae* subsp. *equisimilis, Streptococcus infantis, Streptococcus oralis, Streptococcus sanguinis, Streptococcus viridans, Streptococcus thermophiles, Veillonella dispar*, and combinations thereof.

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