

MICROBIAL CONSORTIA

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims priority to U.S. Provisional Patent Application No. 63/285,010, filed on December 1, 2021, and to U.S. Provisional Patent Application No. 63/305,476, filed on February 8, 2022, the content of each of which is incorporated by reference in its entirety, and to each of which priority is claimed.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted electronically in XML format and is hereby incorporated by reference in its entirety. Said XML copy, created on November 30, 2022, is named 091592.0106.xml and is 393,216 bytes in size.

FIELD OF THE INVENTION

The present disclosure generally relates to microbial consortia for administration to an animal for degradation of a disease-associated metabolic substrate.

BACKGROUND

The gastrointestinal tract comprises various biological niches along its longitudinal length having different physical, chemical, and nutrient compositions. As a consequence of these diverse conditions, specific microbial communities are established within a particular biological niche. The microbial species comprising a specific microbial community are highly responsive to their local environment and produce an array of bioactive molecules that facilitate host engraftment, inter-microbial communication, nutrient metabolism, and inclusion or exclusion of competing microbial species. Adding further complexity, there is substantial diversity of microbial species and strains in the human gastrointestinal tract between individuals, which is attributed to a number of factors including genetics, diet, antibiotic and antifungal use, surgical intervention (*e.g.*, gastric bypass/bowel resection), presence of inflammatory bowel disease and/or irritable bowel syndrome, and other environmental influences. However, despite this interindividual diversity, the functional attributes of the varying human gut microbiota are relatively consistent among healthy adults and comprise core metabolic pathways involved in carbohydrate metabolism, amino acid metabolism, fermentation, and oxidative phosphorylation.

Modulation of microbial species in the gastrointestinal tract through the use of antibiotics, antifungals, and more recently, fecal microbial transplantation ("FMT"), have been approaches clinically investigated for the treatment and/or prevention of certain diseases and disorders. For

example, Dodd *et al.* (*Nature*, 2007, 551: 648-652) have proposed FMT as a therapeutic to modulate the levels of aromatic amino acid metabolites in the serum of gnotobiotic mice, which affect intestinal permeability and systemic immunity. In further examples, administration of bacterial compositions have also been proposed as a method for treating *Clostridium difficile* infection, ulcerative colitis, cholestatic disease, and hyperoxaluria.

As a modality for treating various diseases and/or conditions, there is a need for microbial compositions comprising a plurality of microbial species having improved therapeutic efficacy and an ability to efficiently engraft in a host, grow, and metabolize pathogenic substrates to non-pathogenic metabolic products within the various biological niches of the gastrointestinal tract and within the diverse gastrointestinal environments of different individuals. Furthermore, there is an unmet need for a treatment of diseases using a complex microbial community that can engraft and function symbiotically in the human gastrointestinal tract to degradation of a disease-associated metabolic substrate.

SUMMARY OF THE INVENTION

The present disclosure relates to compositions and methods for reducing oxalate in a subject. In certain non-limiting embodiments, the present disclosure provides a composition comprising at least 1 oxalate-metabolizing microbial strain. In certain embodiments, the at least one strain expresses an enzyme selected from a formyl-CoA transferase, an oxalate-formate antiporter, and an oxalyl-CoA decarboxylase. In certain embodiments, the at least 1 oxalate-metabolizing microbial strain is from the *Oxalobacter* genus.

In certain embodiments, the composition comprises at least 3 oxalate-metabolizing microbial strains. In certain embodiments, the at least 3 oxalate-metabolizing microbial strains are different strains of the same species. In certain embodiments, the at least 3 oxalate-metabolizing microbial strains are different strains of different species.

In certain embodiments, the species is *Oxalobacter formigenes* (*O. formigenes*), and optionally wherein the number of oxalate-metabolizing microbial strains is 3 or more.

In certain embodiments:

- a) at least one strain is a low pH tolerance strain;
- b) at least one strain is a high oxalate tolerance strain; and/or
- c) at least one strain is a high growth rate strain.

In certain non-limiting embodiments, the present disclosure provides a composition comprising at least 2 *Oxalobacter formigenes* (*O. formigenes*) strains, wherein each of the strains comprises one or more of the following functions: a) a low pH tolerance strain; b) a high oxalate tolerance strain; and/or c) a high growth rate strain.

The present disclosure further provides a composition comprising at least 3 *Oxalobacter formigenes* (*O. formigenes*) strains, wherein: a) at least one strain is a low pH tolerance strain; b) at least one strain is a high oxalate tolerance strain; and c) at least one strain is a high growth rate strain.

In certain embodiments, the low pH tolerance strain can metabolize oxalate at a pH between about 4 and about 6. In certain embodiments, the low pH tolerance strain can metabolize oxalate at a pH of about 5. In certain embodiments, the high oxalate tolerance strain can metabolize oxalate at a concentration between about 5 mM to about 30 mM. In certain embodiments, the high oxalate tolerance strain can metabolize oxalate at a concentration of about 15 mM.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146. In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146. In certain embodiments, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

In certain embodiments, the composition further comprises one or more microbes metabolizing formate. In certain embodiments, the composition further comprises one or more microbes catalyzing fermentation of polysaccharides. In certain embodiments, the composition further comprises one or more microbes catalyzing fermentation of amino acids. In certain embodiments, the composition further comprises microbes catalyzing the synthesis of at least one molecules selected from the group consisting of methane, acetate, sulfide, propionate, and succinate. In certain embodiments, the composition further comprises microbes catalyzing deconjugation of conjugated bile acids to produce primary bile acids. In certain embodiments, the composition further comprises microbes catalyzing conversion of cholic acid (CA) to 7-oxocholic acid. In certain embodiments, the composition further comprises microbes catalyzing conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA). In certain embodiments, the composition further comprises microbes catalyzing conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid. In certain embodiments, the composition further comprises microbes catalyzing conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

In certain embodiments, the composition comprises: a) Consortia I or a functional equivalent thereof; b) Consortia II or a functional equivalent thereof; c) Consortia III or a functional equivalent thereof; d) Consortia IV or a functional equivalent thereof; e) Consortia V or a functional equivalent thereof; f) Consortia VI or a functional equivalent thereof; g) Consortia VII or a functional equivalent thereof.

thereof; h) Consortia VIII or a functional equivalent thereof; i) Consortia IX or a functional equivalent thereof; j) Consortia X or a functional equivalent thereof; k) Consortia XI or a functional equivalent thereof; l) Consortia XII or a functional equivalent thereof; m) Consortia XIII or a functional equivalent thereof; n) Consortia XIV or a functional equivalent thereof; o) Consortia XV
 5 or a functional equivalent thereof; p) Consortia XVI or a functional equivalent thereof; q) Consortia XVII or a functional equivalent thereof; r) Consortia XVIII or a functional equivalent thereof; or s) Consortia XIX or a functional equivalent thereof.

In certain embodiments, the composition further comprises a second composition comprising
Clostridium citroniae, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*,
 10 *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae* sp. FBI00033, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorisoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae* sp. FBI00071, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*,
 15 *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catemulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Clostridiaceae* sp. FBI00191, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*,
 20 *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*, *Acidaminococcus intestini*, *Emergencia timonensis*, *Bifidobacterium pseudocatemulatum*, *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, *Lachnospiraceae* sp. FBI00290, or a functional equivalent microbial consortium.

In certain embodiments, the composition further comprises FBI00001, FBI00002, FBI00010,
 25 FBI00013, FBI00029, FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211,
 30 FBI00220, FBI00221, FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, FBI00290, or a functional equivalent thereof.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36,
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SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID

NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

In certain embodiments, the composition further comprises a third composition comprising *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae* sp. FBI00097, *Gordonibacter pamelaee*, *Bacteroides uniformis*, *Gordonibacter pamelaee*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae* sp. FBI00233, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinhominis*, *Alistipes onderdonkii*, *Methanobrevibacter smithii*, or a functional equivalent thereof.

In certain embodiments, the composition further comprises FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099,

FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, FBI00292, or a functional equivalent thereof.

5 In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148, (b) at least about 90% identical
10 to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ
35 ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ

ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

In certain embodiments, the composition further comprises a fourth composition comprising *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, *Bacteroides xylanisolvens*, or a functional equivalent thereof.

In certain embodiments, the composition further comprises FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, FBI00271, or a functional equivalent thereof.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28,

SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139. In certain embodiments, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

In certain embodiments, the composition further comprises a fifth composition comprising *Alistipes putredinis*, *Dialister succinatiphilus*, *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*, *Bilophila wadsworthia*, *Holdemanella biformis*,

Parasutterella excrementihominis, *Alistipes* sp. FBI00180, *Bacteroides coprocola*, *Alistipes* sp. FBI00238, *Alistipes putredinis*, *Eubacterium xylanophilum*, *Senegalimassilia anaerobia*, or a functional equivalent thereof.

In certain embodiments, the composition further comprises FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, FBI00281, or a functional equivalent thereof.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144.

Moreover, the present disclosure provides a microbial consortium comprising microbial strains set forth in Table 1, Table 2, Table 3, Table 4, Table 5, Table 6, Table 7, Table 8, Table 9, Table 10, Table 11, Table 12, Table 13, Table 14, Table 15, Table 16, Table 17, Table 18, Table 19, or a functional equivalent thereof.

The present disclosure also provides a microbial consortium comprising microbial strains set forth in Table 22 or a functional equivalent thereof.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148. In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% to the nucleotide sequence set forth in SEQ ID NOs: 1-148. In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

The present disclosure further provides a composition comprising a microbial consortium disclosed herein.

In certain embodiments, the composition disclosed herein is a pharmaceutical composition.

In certain embodiments, the composition comprises from about 5×10^{10} to about 5×10^{11} viable cells. In certain embodiments, the composition comprises from about 5×10^9 to about 5×10^{10} viable cells. In certain embodiments, the composition comprises from about 5×10^{11} to about 5×10^{12} viable cells. In certain embodiments, the composition comprises up to about 5×10^{12} viable cells.

In certain embodiments, the composition comprises from about 10% to about 50% of oxalate-metabolizing microbial strains. In certain embodiments, the composition comprises from about 10% to about 50% of *O. formigenes* strains on a viable cell count basis. In certain embodiments, the composition comprises about 20% of *O. formigenes* strains on a viable cell count basis. In certain embodiments, the composition comprises about 30% of *O. formigenes* strains on a viable cell count basis. In certain embodiments, the composition comprises about 40% of *O. formigenes* strains on a viable cell count basis.

The present disclosure further provides a method of manufacturing the compositions or the microbial consortia disclosed herein. In certain embodiments, the method comprises obtaining and blending:

a) a first composition comprising *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae sp. FBI00033*, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorisoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae sp. FBI00071*, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides fingoldii*,

Clostridiaceae sp. FBI00191, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*, *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*, *Acidaminococcus intestini*, *Emergencia timonensis*, *Bifidobacterium pseudocatenulatum*,
 5 *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, and *Lachnospiraceae* sp. FBI00290, or a functional equivalent thereof;

b) a second composition comprising *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*,
 10 *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae* sp. FBI00097, *Gordonibacter pamelaee*, *Bacteroides uniformis*, *Gordonibacter pamelaee*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium*
 15 *bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae* sp. FBI00233, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinihominis*, *Alistipes onderdonkii*, and *Methanobrevibacter smithii*, or a functional equivalent thereof;

c) a third composition comprising *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*,
 20 *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*,
 25 *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, and *Bacteroides xylanisolvens*, or a functional equivalent thereof;

d) a fourth composition comprising *Alistipes putredinis*, *Dialister succinatiphilus*,
 30 *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*, *Bilophila wadsworthia*, *Holdemanella biformis*, *Parasutterella excrementihominis*, *Alistipes* sp. FBI00180, *Bacteroides coprocola*, *Alistipes* sp. FBI00238, *Alistipes putredinis*, *Eubacterium xylanophilum*, and *Senegalimassilia anaerobia*, or a functional equivalent thereof;

e) a fifth composition comprising a first *O. formigenes* strain;

35 f) a sixth composition comprising a second *O. formigenes* strain; and/or

g) a seventh composition comprising a third *O. formigenes* strain.

In certain embodiments, the method comprises obtaining and blending:

a) a first composition comprising FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, and FBI00290, or a functional equivalent thereof;

b) a second composition comprising FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, and FBI00292, or a functional equivalent thereof;

c) a third composition comprising FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, and FBI00271, or a functional equivalent thereof;

d) a fourth composition comprising FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, and FBI00281, or a functional equivalent thereof;

e) a fifth composition comprising FBI00067 or a functional equivalent thereof;

f) a sixth composition comprising FBI00133 or a functional equivalent thereof; and/or

g) a seventh composition comprising FBI00289 or a functional equivalent thereof.

In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148. In certain embodiments, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148. In certain embodiments, each

strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 1-148.

In certain embodiments, the fourth composition is obtained by growing microbes in presence of threonine. In certain embodiments, each composition comprises a lyoprotectant. In certain
5 embodiments, each composition comprises maltodextrin, inulin, or a combination thereof. In certain
embodiments, the maltodextrin is at a concentration of about 8%. In certain embodiments, the inulin
is at a concentration of about 0.5%. In certain embodiments, each composition is separately
lyophilized.

In certain embodiments, the functional equivalent is based on the characteristics set forth in
10 Table 24. In certain embodiments, the functional equivalent is based on the characteristics set forth
in Table 34. In certain embodiments, the functional equivalent is based on the characteristics set
forth in Table 35. In certain embodiments, the functional equivalent is based on the characteristics
set forth in Table 36. In certain embodiments, the functional equivalent is based on the characteristics
set forth in Tables 34-36.

15 In certain embodiments, the method comprises obtaining and blending microbes comprising
a gene regulating oxalate degradation, oxalate resistance, formate metabolism, metabolism of
macronutrients, production of microbial metabolites, cross-feeding activity, and/or mucin
degradation. In certain embodiments, the method comprises obtaining and blending microbes that
are known to protect against diseases and/or that are prevalent in healthy human gut. In certain
20 embodiments, the method comprises obtaining and blending microbes that utilize carbon sources set
forth in Table 35. In certain embodiments, each strain can optionally utilize a subset of the carbon
sources set forth in Table 35.

In certain embodiments, each composition is prepared using inoculation density adjustment.
In certain embodiments, each composition is cultured or has been cultured in presence of gas overlay.
25 In certain embodiments, each composition is cultured or has been cultured in absence of gas sparging.

The present disclosure also provides a composition prepared by the methods of manufacturing
disclosed herein.

Moreover, the present disclosure provides methods of treating hyperoxaluria in a subject in
need thereof, reducing the risk of developing hyperoxaluria in a subject in need thereof, and/or
30 reducing urinary oxalate in a subject in need thereof. In certain embodiments, the methods comprise
administering an effective amount of the compositions or the microbial consortia disclosed herein.

In certain embodiments, the hyperoxaluria is a primary hyperoxaluria, a secondary
hyperoxaluria, or an enteric hyperoxaluria. In certain embodiments, the secondary hyperoxaluria is
associated with bowel resection surgery. In certain embodiments, the hyperoxaluria is enteric
35 hyperoxaluria.

In certain embodiments, the methods further comprise administering at least one antibacterial agent, antiviral agent, antifungal agent, anti-inflammatory agent, immunosuppressive agent, prebiotic, or a combination thereof. In certain embodiments, the methods further comprise administering NOV-001, SYN8802, OX-1, Lumasiran, Nedosiran, BBP-711, CNK-336, PBGENE-PH1, or a combination thereof. In certain embodiments, the methods further comprise administering a low oxalate diet, a high hydration diet, calcium supplements, or a combination thereof. In certain embodiments, the composition or the microbial consortium is administered orally.

In certain embodiments, the methods comprise administering a first dose of the compositions or the microbial consortia disclosed herein.

In certain embodiments, the methods further comprise administering an antibiotic treatment. In certain embodiments, the antibiotic treatment is administered for about 2 days, about 3 days, about 4 days, about 5 days, about 6 days, or about 7 days. In certain embodiments, the antibiotic is metronidazole, clarithromycin, or a combination thereof. In certain embodiments, the antibiotic treatment is completed 1 day before administering the first dose. In certain embodiments, the antibiotic treatment is completed 2 days before administering the first dose.

In certain embodiments, the methods further comprise administering a bowel preparation treatment. In certain embodiments, the bowel preparation treatment is administered to the subject after the antibiotic treatment. In certain embodiments, the bowel preparation treatment is administered before the first dose.

In certain embodiments, the first dose comprises an effective amount of the compositions or the microbial consortia. In certain embodiments, the first dose comprises about 10^{12} viable cells. In certain embodiments, the first dose is administered for about 1 day. In certain embodiments, the first dose is administered for about 2 days.

In certain embodiments, the methods further comprise administering a second dose of the compositions or the microbial consortia. In certain embodiments, the second dose comprises an effective amount of the composition or the microbial consortium. In certain embodiments, the second dose comprises about 10^{11} viable cells. In certain embodiments, the second dose is administered up to about 8 days. In certain embodiments, the second dose is administered up to about 10 days.

In certain embodiments, the first dose is administered orally. In certain embodiments, the second dose is administered orally.

The present disclosure also provides a kit comprising the compositions or the microbial consortia disclosed herein. In certain embodiments, the kit comprises a container comprising a desiccant. In certain embodiments, the container comprises anaerobic conditions. In certain embodiments, the container is a blister. In certain embodiments, the kit further comprises written instructions for administering the composition or microbial consortium.

The present disclosure also provides a method of culturing a microbial strain from the *Akkermansia* genus comprising contacting the strain with N-Acetylgalactosamine (GalNAc). In certain embodiments, the strain is *Akkermansia muciniphila*.

The present disclosure also provides a microbial consortium comprising the functional properties set forth in Table 23, Table 24, Table 34, Table 35, Table 36. Finally, the present disclosure provides microbial consortia comprising FB-001 or a functional equivalent thereof.

BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A, 1B, and 1C. Figure 1A shows the reduction in urinary oxalate in mice fed a refined, sugary diet and gavaged with a Consortia described herein. Figure 1B shows the reduction in urinary oxalate in mice fed a complex, grain-free diet and gavaged with a Consortia described herein. Figures 1A and 1B collectively show that the efficacy of reducing urinary oxalate using a Consortia described herein is independent of diet. Figure 1C shows that the gastrointestinal microbiota present in an animal before treatment with a Consortia described herein does not affect the ability of the Consortia to reduce urinary oxalate levels.

Figures 2A and 2B. Figure 2A shows an exemplary coculture experiment and Figure 2B shows an exemplary coculture experiment that was modified to yield 100% strain detection following coculture.

Figures 3A and 3B. Figure 3A shows the design of the DS buckets for a Consortia and Figure 3B shows the yield of strains after coculture depending on the inoculum seed.

Figures 4A and 4B. Figures 4A and 4B show examples of different lyophilization excipients.

Figures 5A and 5B. Figures 5A and 5B show examples of different lyophilization excipients and reducing agents.

Figures 6A and 6B. Figures 6A and 6B show examples of different lyophilization excipients. **Figures 7A and 7B.** Figure 7A is a venn diagram showing the overlapping microbes of five representative consortia designed and disclosed herein. Figure 7B shows the breakdown of the type of microbe in each of the 5 representative consortia.

Figures 8A and 8B. Figure 8A shows a graph plotting the induction of EH in germ-free mice on different diets (control and oxalate diets as described in **Example 4**). Figure 8B are graphs showing the relative abundance of *O. formigenes* and oxalate degradation.

Figure 9. Figure 9 shows oxalate and Ox:Cr ratios of Germ-free and “humanized” mice fed oxalate diets.

Figures 10A-10D. Figure 10A shows the relative abundance of *O. formigenes* after dosing of Community I (Prevalence Based Community), Community II (2 Donor Community), Community III (Metabolism A Community), Community 4 (Metabolism B Community), or Community 5

(Diversity Community). Figure 10B shows the species richness of mice fed an Ox36 diet followed by dosing of one of the five representative consortia. Figure 10C shows the species richness of mice fed a 5021+0.875% Ox diet followed by dosing of one of the five representative consortia. Figure 10D shows the species richness of humanized mice dosed with one of the five representative consortia.

Figures 11A and 11B. Figures 11A and 11B show the schematics of the experimental designs of the studies described in Example 5.

Figure 12. Figure 12 shows that YCFAC + GalNAc is not able to support the growth of Akkermansia.

Figure 13. Figure 13 shows that Threonine supports the growth of Akkermansia in the absence of GalNAc.

Figure 14. Figure 14 shows a diagram of the coculture method of manufacture.

Figure 15. Figure 15 shows an overview of the strain isolation and purification process, RCB banking, and RCB identity/purity testing.

Figure 16. Figure 16 shows a method for generation of master cell banks (MCB).

Figure 17. Figure 17 shows a phylogenetic tree indicating the taxonomic composition of the FB-001 Consortium.

Figures 18A-18C. Figures 18A-18C show a table summarizing the strains and species of the microbial consortia disclosed herein.

Figures 19A and 19B. Figure 19A shows the effect FB-001 has on reducing gut permeability and Figure 19B shows the ability of FB-001 to produce short chain fatty acids (SCFA) at a level that is comparable to a normal, healthy gut. Butyrate, a SCFA, is important because it supports gastrointestinal epithelial cell health, energy metabolism and cell signaling to improve barrier function.

Figures 20A-20D. Figures 20A-20D show that FB-001 reduces urinary oxalate (UrOx) by 35-68% *in vivo* across different diets (i.e., the ability of FB-001 and DS1-DS4 to reduce urinary oxalate independent of diet and existing microbiota). Figure 20A shows a depiction of the study design. Figure 20B shows the Oxalate:Creatinine ratio of mice fed a complex, grain-based diet. Figure 20C shows the Oxalate:Creatinine ratio of mice fed a refined, high-sugar diet. Figure 20D shows the Oxalate:Creatinine ratio of humanized mice.

Figure 21. Figure 21 shows a comparison done by mathematical modelling of the oxalate degradation rate (per cell) of FB-001 compared to Novome's WW554 and WW626 hyperoxaluria drug products and Synlogics 8802 drug product). The data shows that FB-001 is able to achieve oxalate consumption at a significantly higher rate than the other drug products and suggests it will be more effective at treating hyperoxaluria in subjects in need thereof.

Figure 22. Figure 22 shows the manufacturing process used for *O. formigenes* in the production of the Consortia described herein. Furthermore, DS5-DS7 (i.e., the three *O. formigenes* drug substances) of FB-001 used this manufacturing process for GMP and non-GMP manufacture.

5 **Figure 23.** Figure 23 shows the manufacturing process used for DS1 in the production of the Consortia described herein. Furthermore, DS1 of FB-001 used this manufacturing process for GMP and non-GMP manufacture.

Figure 24. Figure 24 shows the manufacturing process used for DS2 in the production of the Consortia described herein. Furthermore, DS2 of FB-001 used this manufacturing process for GMP and non-GMP manufacture.

10 **Figure 25.** Figure 25 shows the manufacturing process used for DS3 in the production of the Consortia described herein. Furthermore, DS3 of FB-001 used this manufacturing process for GMP and non-GMP manufacture.

Figure 26. Figure 26 shows the manufacturing process used for DS4 in the production of the Consortia described herein. Furthermore, DS4 of FB-001 used this manufacturing process for GMP
15 and non-GMP manufacture.

DETAILED DESCRIPTION

The present disclosure relates to compositions and methods for reducing reducing oxalate in a subject. For clarity of description, and not by way of limitation, this section is divided into the following subsections:

- 20 (a) Definitions;
(b) Biological Niches;
(c) Physical Compartments;
(d) Metabolic Compartments;
(e) Consortia;
25 (f) Active Microbes;
(g) Oxalate-Metabolizing Active Microbes;
(h) Supportive Community of Microbes;
(j) Consortia Design;
(k) Methods of Preparation;
30 (i) Pharmaceutical Compositions;
(l) Functionally Equivalent and Identical Drug Products;
(m) Therapeutic Applications;
(n) Methods of Treating Hyperoxaluria;
(o) Dosages;

- (p) Combination Therapy;
- (q) Kits; and
- (r) Exemplary Embodiments.

Definitions

Unless defined otherwise, all technical and scientific terms used herein have the meaning commonly understood by a person skilled in the art. The following references provide one of skill with a general definition of many of the terms used in the presently disclosed subject matter: Singleton et al., Dictionary of Microbiology and Molecular Biology (2nd ed. 1994); The Cambridge Dictionary of Science and Technology (Walker ed., 1988); The Glossary of Genetics, 5th Ed., R. Rieger et al. (eds.), Springer Verlag (1991); and Hale & Marham, The Harper Collins Dictionary of Biology (1991). As used herein, the following terms have the meanings ascribed to them below, unless specified otherwise.

It is understood that aspects and embodiments of the present disclosure described herein include “comprising,” “consisting,” and “consisting essentially of” aspects and embodiments.

The terms “comprises” and “comprising” are intended to have the broad meaning ascribed to them in U.S. Patent Law and can mean “includes,” “including” and the like.

To facilitate an understanding of the present disclosure, a number of terms and phrases are defined below.

The term “a” and “an” as used herein mean “one or more” and include the plural unless the context is appropriate

As used herein, the term “active microbes” refers to microbes that express sufficient amounts of one or more than one metabolic enzyme to metabolize a substrate that causes or contributes to disease in an animal.

As used herein, the term “biomass,” refers to the total mass of one or more than one microbe, or consortium in a given area or volume.

As used herein, the terms “microbial consortia” and “microbial consortium” are used interchangeably and refer to a mixture of two or more isolated microbial strains that are expanded in culture, wherein one microbial strain in the mixture has a beneficial or desired effect on another microbial strain in the mixture.

As used herein, the term “Consortia” is used as a capitalized term to refer to one or more of the microbial consortia described herein.

As used herein, the term “gastrointestinal engraftment” or “engraft” or “engraftment” refers to the establishment of one or more than one microbe, or microbial consortium, in one or more than one niche of the gastrointestinal tract that, prior to administration of the one or more than one

microbe, or microbial consortium, is absent in the one or more than one microbe, or microbial consortium. Gastrointestinal engraftment may be transient, or may be persistent.

As used herein, the term “effective amount” refers to an amount sufficient to achieve a beneficial or desired result. In certain embodiments, an effective amount can be improved
5 gastrointestinal engraftment of one or more than one of the plurality of active microbes, increased biomass of one or more than one of the plurality of active microbes, increased metabolism of the first metabolic substrate, or improved longitudinal stability).

As used herein, the term “fermenting microbe” refers to a microbe that expresses sufficient amounts of one or more than one enzyme to catalyze a fermentation reaction in a gastrointestinal
10 niche.

As used herein, the term “longitudinal stability” refers to the ability of one or more than one microbe, or microbial consortium to remain engrafted and metabolically active in one of more than one niche of the gastrointestinal tract despite transient or long-term environmental changes to the gastrointestinal niche.

As used herein, the term “metabolism,” “metabolize,” “metabolization,” or variants thereof
15 refers to the biochemical conversion of a metabolic substrate to a metabolic product. In certain embodiments, metabolization includes isomerization.

As used herein, the term “microbe” or “microbiota” refers to a microbial organism including, but not limited to, bacteria, archaea, protozoa, and unicellular fungi.

As used herein, the term “pharmaceutical composition” refers to the combination of an active
20 agent with a carrier, inert or active, making the composition especially suitable for therapeutic use *in vivo* or *ex vivo*.

As used herein, the term “pharmaceutically acceptable carrier” refers to any of the standard pharmaceutical carriers, such as phosphate buffered saline solution, water, emulsions (*e.g.*, such as
25 oil/water or water/oil emulsions), and various types of wetting agents. The compositions also can include stabilizers and preservatives. For examples of carriers, stabilizers, and adjuvants, *see e.g.*, Martin, Remington’s Pharmaceutical Sciences, 15th Ed. Mack Publ. Co., Easton, PA [1975].

As used herein, “significantly” or “significant” refers to a change or alteration in a measurable parameter to a statistically significant degree as determined in accordance with an appropriate
30 statistically relevant test. For example, in certain non-limiting embodiments, a change or alteration is significant if it is statistically significant in accordance with, *e.g.*, a Student’s t-test, chi-square, or Mann Whitney test.

As used herein, the term “standardized substrate metabolization assay” refers to an experimental assay known to persons of ordinary skill in the art used to quantify the amount of
35 substrate converted to a metabolic product.

As used herein, the term “subject” refers to an organism to be treated by the microbial consortium and compositions described herein. Such organisms preferably include, but are not limited to, mammals (*e.g.*, murines, simians, equines, bovines, porcines, canines, felines, and the like), and more preferably include humans.

5 As used herein, the term “supportive community” refers to one or more than one microbial strain that, when administered with an active microbe, enhances one or more than one characteristic of the active microbe selected from the group consisting of gastrointestinal engraftment, biomass, metabolic substrate metabolism, and longitudinal stability.

10 As used herein, the term “synthesizing microbe” refers to a microbe that expresses sufficient amounts of one or more than one enzyme to catalyze the combination of one or more than one metabolite produced by an active microbe, and one or more than one fermentation product produced by a fermenting microbe in a gastrointestinal niche.

The term percent “identity” or “sequence identity,” in the context of two or more nucleic acid or polypeptide sequences, refer to two or more sequences or subsequences that have a specified
15 percentage of nucleotides or amino acid residues that are the same, when compared and aligned for maximum correspondence, as measured using one of the sequence comparison algorithms described below (*e.g.*, BLASTP and BLASTN or other algorithms available to persons of skill) or by visual inspection. Depending on the application, the percent “identity” can exist over a region of the sequence being compared, *e.g.*, over a functional domain, or, alternatively, exist over the full length
20 of the two sequences to be compared.

For sequence comparison, typically one sequence acts as a reference sequence to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are input into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. The sequence comparison algorithm then calculates
25 the percent sequence identity for the test sequence(s) relative to the reference sequence, based on the designated program parameters.

Optimal alignment of sequences for comparison can be conducted, *e.g.*, by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat’l. Acad. Sci. USA* 85:2444 (1988), by
30 computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by visual inspection (see generally Ausubel et al., *infra*).

One example of an algorithm that is suitable for determining percent sequence identity and
35 sequence similarity is the BLAST algorithm, which is described in Altschul et al., *J. Mol. Biol.*

215:403-410 (1990). Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (www.ncbi.nlm.nih.gov/).

When used in reference to 16S rRNA sequences, a “sequence identity” of at least 97% indicates that two microbial strains are likely to belong to the same species, whereas 16S rRNA sequences having less than 97% sequence identity indicate that two microbial strains likely belong to different species, and 16S rRNA sequences having less than 95% sequence identity indicates that two microbial strains likely belong to distinct genera (Stackebrandt E., and Goebel, B.M., *Int J Syst Bact*, 44 (1994) 846-849.).

As used herein, the terms “functional equivalent” or “functionally equivalent” refers to microbes, microbial consortia, and compositions that share similar or identical role (e.g., metabolism of oxalate). For example, without any limitation, two different microbial consortia that can catalyze high concentration of oxalate are functional equivalent to each other. In certain non-limiting embodiments, a microbe, a microbial consortium, and a composition that is functional equivalent can be based on the characteristic outlined in Table 24 (*see* Example section).

Throughout the description, where compositions are described as having, including, or comprising specific components, or where processes and methods are described as having, including, or comprising specific steps, it is contemplated that, additionally, there are compositions of the present disclosure that consist essentially of, or consist of, the recited components, and that there are processes and methods according to the present disclosure that consist essentially of, or consist of, the recited processing steps.

As a general matter, compositions specifying a percentage are by weight unless otherwise specified. Further, if a variable is not accompanied by a definition, then the previous definition of the variable controls.

Biological Niches

Disclosed herein are microbial consortia for administration to an animal comprising a plurality of active microbes which metabolize a first metabolic substrate which causes or contributes to disease in the animal. The microbial consortia disclosed herein further comprise an effective amount of a supportive community of microbes that metabolize one or more than one metabolite produced by the plurality of active microbes, and wherein the one or more than one metabolite inhibits metabolism of the plurality of active microbes. These microbial consortia are advantageous in having enhanced characteristics when administered to an animal as compared to administration of the plurality of active microbes alone. Enhanced characteristics of the microbial consortia include one or more of improved gastrointestinal engraftment, increased biomass, increased metabolism of the first metabolic substrate, and improved longitudinal stability.

The present disclosure provides microbial consortia capable of engrafting into one or more than one niche of a gastrointestinal tract where it is capable of metabolizing a substrate that causes or contributes to disease in an animal. These niches comprise specific microbial communities whose composition varies according to a number of environmental factors including, but not limited to, the particular physical compartment of the gastrointestinal tract inhabited by a microbial community, the chemical and physicochemical properties of the environment inhabited, the metabolic substrate composition of the environment inhabited, and other co-inhabiting microbial species.

Physical Compartments

A gastrointestinal tract comprises a number of physical compartments. For example, the human gastrointestinal tract includes the oral cavity, pharynx, esophagus, stomach, small intestine (duodenum, jejunum, ileum), cecum, large intestine (ascending colon, transverse colon, descending colon), and rectum. The pancreas, liver, gallbladder, and associated ducts, additionally comprise compartments of the human gastrointestinal tract. Each of these compartments has, for example, variable anatomical shape and dimension, aeration, water content, levels of mucus secretion, luminal presence of antimicrobial peptides, and presence or absence of peristaltic motility. Furthermore, the different gastrointestinal compartments vary in their pH. In humans, the pH of the oral cavity, upper stomach, lower stomach, duodenum, jejunum, ileum, and colon range from 6.5-7.5, 4.0-6.5, 1.5-4.0, 7.0-8.5, 4.0-7.0, and 4.0-7.0, respectively. Compartments of the gastrointestinal tract also differ in their levels of oxygenation which are subject to large degrees of fluctuation. For example, the luminal partial pressure of oxygen in the stomach of mice has been measured to be approximately 58 mm Hg, while the luminal partial pressure of oxygen in the distal sigmoid colon has been measured to be approximately 3 mm Hg (He *et al.*, 1999). Oxygen levels of the gastrointestinal tract are highly determinative of the biochemical pathways utilized by commensal microbes. For example, commensal bacteria utilize aerobic respiration at oxygen concentrations above 5 mbar of O₂, anaerobic respiration between 1-5 mbar of O₂, and fermentation at O₂ concentrations below 1 mbar. The sensitivity of microbes to O₂ levels and their ability to carry out metabolic reactions under aerobic and/or anaerobic conditions influences which microbial species engraft in a particular gastrointestinal compartment.

Metabolic Compartments

In addition to the various physical and chemical environments contributing to a gastrointestinal niche, different niches comprise different metabolic substrates.

Metabolic substrates that may be present in a gastrointestinal niche may include, but are not limited to, oxalate, fructan, inulin, glucuronoxylan, arabinoxylan, glucomannan, β -mannan, dextran,

starch, arabinan, xyloglucan, galacturonan, β -glucan, galactomannan, rhamnogalacturonan I, rhamnogalacturonan II, arabinogalactan, mucin O-linked glycans, yeast α -mannan, yeast β -glucan, chitin, alginate, porphyrin, laminarin, carrageenan, agarose, alternan, levan, xanthan gum, galactooligosaccharides, hyaluronan, chondroitin sulfate, dermatan sulfate, heparin sulfate, keratan sulfate, phenylalanine, tyrosine, tryptophan, leucine, valine, isoleucine, glycine, proline, asparagine, glutamine, aspartate, glutamate, cysteine, lysine, arginine, serine, methionine, alanine, arginine, histidine, ornithine, citrulline, carnitine, hydroxyproline, cholic acid, chenodeoxycholic acid, taurochenodeoxycholic acid, glycochenodeoxycholic acid, cholesterol, cinnamic acid, coumaric acid, sinapinic acid, ferulic acid, caffeic acid, quinic acid, chlorogenic acid, catechin, epicatechin, gallic acid, pyrogallol, catechol, quercetin, myricetin, campherol, luteolin, apigenin, naringenin, and hesperidin.

Consortia

The present disclosure provides Consortia comprising a plurality of active microbes and an effective amount of a supportive community of microbes. In certain embodiments, the Consortia comprises the microbiota listed in any of Tables 1-19. Tables 1-19 are provided below:

Table 1. Consortia I

Acidaminococcus intestini	Bacteroides stercoris	Blautia hydrogenotrophica	Coprococcus eutactus	Holdemanella biformis
Akkermansia muciniphila	Bacteroides stercoris	Blautia luti	Coprococcus eutactus	Holdemanella biformis
Alistipes fingoldii	Bacteroides thetaiotaomicron	Blautia luti	Desulfovibrio desulfuricans	Hungatella hathewayi
Alistipes onderdonkii	Bacteroides thetaiotaomicron	Blautia luti	Desulfovibrio desulfuricans	Hungatella hathewayi
Alistipes onderdonkii	Bacteroides thetaiotaomicron	Blautia obeum	Dialister invisus	Neglecta timonensis
Alistipes onderdonkii	Bacteroides uniformis	Blautia obeum	Dorea formicigenerans	Oxalobacter formigenes
Alistipes putredinis	Bacteroides uniformis	Blautia obeum	Dorea formicigenerans	Oxalobacter formigenes
Alistipes putredinis	Bacteroides uniformis	Blautia obeum	Dorea formicigenerans	Oxalobacter formigenes
Alistipes senegalensis	Bacteroides uniformis	Blautia wexlerae	Dorea longicatena	Parabacteroides distasonis
Alistipes senegalensis	Bacteroides vulgatus	Blautia wexlerae	Dorea longicatena	Parabacteroides distasonis
Alistipes shahii	Bacteroides vulgatus	Blautia wexlerae	Dorea longicatena	Parabacteroides distasonis
Alistipes shahii	Bacteroides vulgatus	Clostridium aldenense	Eggerthella lenta	Parabacteroides merdae
Alistipes shahii	Bacteroides vulgatus	Clostridium aldenense	Eggerthella lenta	Parabacteroides merdae
Alistipes timonensis	Bacteroides xylanisolvens	Clostridium amygdalinum	Eggerthella lenta	Parabacteroides merdae

Anaerofustis stercorihominis	Bacteroides xylanisolvens	Clostridium bolteae	Eggerthella lenta	Paraprevotella clara
Anaerostipes hadrus	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium eligens	Parasutterella excrementihominis
Anaerostipes hadrus	Bifidobacterium adolescentis	Clostridium citroniae	Eubacterium eligens	Parasutterella excrementihominis
Anaerotruncus colihominis	Bifidobacterium adolescentis	Clostridium citroniae	Eubacterium eligens	Roseburia hominis
Bacteroides caccae	Bifidobacterium catenulatum	Clostridium scindens	Eubacterium eligens	Roseburia hominis
Bacteroides caccae	Bifidobacterium dentium	Clostridium symbiosum	Eubacterium hallii	Roseburia hominis
Bacteroides cellulosilyticus	Bifidobacterium longum	Clostridium symbiosum	Eubacterium rectale	Roseburia hominis
Bacteroides coprocola	Bifidobacterium longum	Clostridium symbiosum	Eubacterium rectale	Ruminococcus bromii
Bacteroides finegoldii	Bifidobacterium longum	Collinsella aerofaciens	Eubacterium rectale	Ruminococcus bromii
Bacteroides fragilis	Bifidobacterium longum	Collinsella aerofaciens	Eubacterium rectale	Ruminococcus bromii
Bacteroides massiliensis	Bifidobacterium pseudocatenulatum	Collinsella aerofaciens	Eubacterium siraeum	Ruminococcus bromii
Bacteroides massiliensis	Bifidobacterium pseudocatenulatum	Collinsella aerofaciens	Eubacterium ventriosum	Ruminococcus faecis
Bacteroides nordii	Bifidobacterium pseudocatenulatum	Coprococcus comes	Eubacterium xylanophilum	Ruminococcus faecis
Bacteroides oleiciplenus	Blautia faecis	Coprococcus comes	Faecalibacterium prausnitzii	Turicibacter sanguinis
Bacteroides ovatus	Blautia faecis	Coprococcus comes	Faecalibacterium prausnitzii	
Bacteroides salyersiae	Blautia faecis	Coprococcus comes	Gordonibacter pamelaee	
Bacteroides stercoris	Blautia faecis	Coprococcus eutactus	Gordonibacter pamelaee	

Table 2. Consortia II

Akkermansia muciniphila	Bacteroides vulgatus	Clostridium amygdalinum	Eggerthella lenta	Oxalobacter formigenes
Alistipes onderdonkii	Bifidobacterium dentium	Clostridium citroniae	Eubacterium eligens	Parabacteroides distasonis
Alistipes putredinis	Bifidobacterium faecale	Clostridium citroniae	Eubacterium eligens	Parabacteroides distasonis
Alistipes shahii	Bifidobacterium longum	Clostridium scindens	Eubacterium rectale	Parabacteroides merdae
Alistipes timonensis	Bifidobacterium longum	Clostridium symbiosum	Eubacterium rectale	Paraprevotella clara
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Collinsella aerofaciens	Faecalibacterium prausnitzii	Parasutterella excrementihominis

Bacteroides koreensis	Bifidobacterium pseudocatenulatum	Coprococcus comes	Fusicatenibacter saccharivorans	Phascolarctobacterium faecium
Bacteroides kribbi	Bifidobacterium pseudocatenulatum	Coprococcus eutactus	Fusicatenibacter saccharivorans	Phascolarctobacterium faecium
Bacteroides kribbi	Blautia faecis	Desulfovibrio desulfuricans	Gordonibacter pamelaeae	Phascolarctobacterium faecium
Bacteroides nordii	Blautia faecis	Dialister succinatiphilus	Lachnoclostridium pacaense	Roseburia hominis
Bacteroides ovatus	Blautia obeum	Dorea formicigenerans	Lachnospira pectinoschiza	Ruminococcus bromii
Bacteroides salyersiae	Blautia obeum	Dorea longicatena	Monoglobus pectinilyticus	Ruminococcus bromii
Bacteroides thetaiotaomicron	Blautia obeum	Eggerthella lenta	Neglecta timonensis	Ruminococcus faecis
Bacteroides thetaiotaomicron	Blautia wexlerae	Eggerthella lenta	Oxalobacter formigenes	Sutterella massiliensis
Bacteroides uniformis	Blautia wexlerae	Eggerthella lenta	Oxalobacter formigenes	Sutterella wadsworthensis

Table 3. Consortia III

Akkermansia muciniphila	Bacteroides vulgatus	Clostridium scindens	Eubacterium rectale	Parabacteroides merdae
Anaerotruncus colihominis	Bacteroides vulgatus	Clostridium symbiosum	Eubacterium rectale	Ruminococcus bromii
Bacteroides caccae	Bacteroides vulgatus	Clostridium symbiosum	Eubacterium rectale	Ruminococcus bromii
Bacteroides caccae	Bifidobacterium adolescentis	Clostridium symbiosum	Eubacterium rectale	Ruminococcus bromii
Bacteroides cellulosilyticus	Bifidobacterium adolescentis	Collinsella aerofaciens	Eubacterium siraeum	Ruminococcus bromii
Bacteroides fragilis	Bifidobacterium bifidum	Collinsella aerofaciens	Faecalibacterium prausnitzii	Sutterella wadsworthensis
Bacteroides massiliensis	Bifidobacterium bifidum	Collinsella aerofaciens	Gordonibacter pamelaeae	Sutterella wadsworthensis
Bacteroides massiliensis	Bifidobacterium catenulatum	Collinsella aerofaciens	Gordonibacter pamelaeae	Sutterella wadsworthensis
Bacteroides salyersiae	Bifidobacterium dentium	Coprococcus comes	Hydrogenoanaerobacterium saccharovorans	Bacteroides vulgatus
Bacteroides stercoris	Bifidobacterium longum	Coprococcus comes	Lachnospiraceae sp.	Clostridium citroniae
Bacteroides stercoris	Bifidobacterium longum	Coprococcus comes	Lactonifactor longoviformis	Eggerthella lenta
Bacteroides stercoris	Bifidobacterium longum	Desulfovibrio desulfuricans	Neglecta timonensis	Parabacteroides merdae
Bacteroides thetaiotaomicron	Bifidobacterium longum	Desulfovibrio desulfuricans	Oxalobacter formigenes	Parabacteroides merdae

Bacteroides thetaiotaomicron	Bifidobacterium pseudocatenulatu m	Dorea longicatena	Oxalobacter formigenes	Eggerthella lenta
Bacteroides thetaiotaomicron	Bifidobacterium pseudocatenulatu m	Dorea longicatena	Oxalobacter formigenes	Clostridium citroniae
Bacteroides uniformis	Bifidobacterium pseudocatenulatu m	Dorea longicatena	Parabacteroides distasonis	Bacteroides uniformis
Bacteroides uniformis	Citrobacter freundii	Eggerthella lenta	Parabacteroides distasonis	
Bacteroides uniformis	Clostridium amygdalinum	Eggerthella lenta	Parabacteroides distasonis	

Table 4. Consortia IV

Alistipes finegoldii	Bacteroides vulgatus	Clostridium bolteae	Dorea longicatena	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium bolteae	Eggerthella lenta	Parabacteroides merdae
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium citroniae	Eggerthella lenta	Parabacteroides merdae
Anaerotruncus colihominis	Bacteroides xylanisolvens	Clostridium citroniae	Eggerthella lenta	Parabacteroides merdae
Bacteroides cacciae	Bacteroides xylanisolvens	Clostridium scindens	Eggerthella lenta	Ruminococcus bromii
Bacteroides cellulosilyticus	Bifidobacterium bifidum	Clostridium symbiosum	Eubacterium eligens	Ruminococcus bromii
Bacteroides coprocola	Bifidobacterium bifidum	Clostridium symbiosum	Eubacterium eligens	Ruminococcus bromii
Bacteroides fragilis	Bifidobacterium catenulatum	Clostridium symbiosum	Eubacterium eligens	Ruminococcus bromii
Bacteroides ovatus	Bifidobacterium dentium	Collinsella aerofaciens	Eubacterium eligens	Sutterella wadsworthensis
Bacteroides salyersiae	Bifidobacterium longum	Collinsella aerofaciens	Eubacterium hallii	
Bacteroides stercoris	Bifidobacterium longum	Collinsella aerofaciens	Eubacterium rectale	
Bacteroides stercoris	Bifidobacterium longum	Collinsella aerofaciens	Eubacterium siraeum	
Bacteroides stercoris	Bifidobacterium longum	Coprococcus comes	Eubacterium ventriosum	
Bacteroides thetaiotaomicron	Bifidobacterium pseudocatenulatum	Coprococcus eutactus	Faecalibacterium prausnitzii	
Bacteroides thetaiotaomicron	Bifidobacterium pseudocatenulatum	Coprococcus eutactus	Faecalibacterium prausnitzii	
Bacteroides thetaiotaomicron	Bifidobacterium pseudocatenulatum	Coprococcus eutactus	Hungatella hathewayi	
Bacteroides uniformis	Blautia hydrogenotrophica	Desulfovibrio desulfuricans	Hungatella hathewayi	
Bacteroides uniformis	Blautia obeum	Desulfovibrio desulfuricans	Neglecta timonensis	
Bacteroides vulgatus	Blautia obeum	Dorea formicigenerans	Oxalobacter formigenes	

Bacteroides vulgatus	Clostridium amygdalinum	Dorea longicatena	Oxalobacter formigenes	
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Table 5. Consortia V

Acidaminococcus intestini	Bacteroides uniformis	Clostridium citroniae	Eubacterium ventriosum	Phascolarctobacter ium faecium
Akkermansia muciniphila	Bacteroides vulgatus	Clostridium clostridioforme	Eubacterium siraeum	Phascolarctobacter ium faecium
Alistipes finegoldii	Bacteroides vulgatus	Clostridium scindens	Eubacterium xylanophilum	Phocaea massiliensis
Alistipes onderdonkii	Bacteroides xylanisolvens	Clostridium swellfunianum	Faecalibacterium prausnitzii	Phocaea massiliensis
Alistipes onderdonkii	Bacteroides xylanisolvens	Clostridium symbiosum	Faecalibacterium prausnitzii	Porphyromonas asaccharolytica
Alistipes putredinis	Barnesiella intestinihominis	Clostridium symbiosum	Faecalicatena contorta	Porphyromonas asaccharolytica
Alistipes putredinis	Bifidobacterium adolescentis	Collinsella aerofaciens	Fusicatenibacter saccharivorans	Roseburia hominis
Alistipes senegalensis	Bifidobacterium adolescentis	Collinsella aerofaciens	Fusicatenibacter saccharivorans	Roseburia hominis
Alistipes senegalensis	Bifidobacterium bifidum	Coprococcus comes	Gordonibacter pamelaeae	Ruminococcus bromii
Alistipes shahii	Bifidobacterium bifidum	Coprococcus comes	Gordonibacter pamelaeae	Ruminococcus bromii
Alistipes timonensis	Bifidobacterium catenulatum	Coprococcus eutactus	Holdemanella biformis	Ruminococcus faecis
Anaerofustis stercorihominis	Bifidobacterium dentium	Coprococcus eutactus	Holdemanella biformis	Ruminococcus faecis
Anaerostipes hadrus	Bifidobacterium faecale	Desulfovibrio desulfuricans	Hungatella effluvii	Ruthenibacterium lactatiformans
Anaerostipes hadrus	Bifidobacterium longum	Desulfovibrio desulfuricans	Hungatella hathewayi	Senegalimassilia anaerobia
Anaerotruncus colihominis	Bifidobacterium longum	Dialister invisus	Hungatella hathewayi	Sutterella massiliensis
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dialister succinatophilus	Hydrogenoanaerob acterium saccharovorans	Sutterella wadsworthensis
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lachnoclostridium pacaense	Sutterella wadsworthensis
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dorea formicigenerans	Lachnoclostridium pacaense	Turicibacter sanguinis
Bacteroides faecis	Blautia faecis	Dorea formicigenerans	Lachnospira pectinoschiza	
Bacteroides finegoldii	Blautia faecis	Dorea longicatena	Lachnospira pectinoschiza	
Bacteroides fragilis	Blautia hydrogenotrophica	Dorea longicatena	Lactonifactor longoviformis	
Bacteroides koreensis	Blautia luti	Eggerthella lenta	Longicatena caecimuris	
Bacteroides koreensis	Blautia obeum	Eggerthella lenta	Megasphaera massiliensis	
Bacteroides kribbi	Blautia obeum	Eggerthella lenta	Monoglobus pectinilyticus	

Bacteroides kribbi	Blautia wexlerae	Eggerthella lenta	Monoglobus pectinilyticus	
Bacteroides massiliensis	Blautia wexlerae	Eisenbergiella tayi	Neglecta timonensis	
Bacteroides nordii	Butyricimonas faecihominis	Eisenbergiella tayi	Oxalobacter formigenes	
Bacteroides oleiciplenus	Catabacter hongkongensis	Emergencia timonensis	Oxalobacter formigenes	
Bacteroides ovatus	Citrobacter freundii	Eubacterium eligens	Oxalobacter formigenes	
Bacteroides salyersiae	Clostridium aldenense	Eubacterium eligens	Parabacteroides distasonis	
Bacteroides stercoris	Clostridium aldenense	Eubacterium hallii	Parabacteroides merdae	
Bacteroides stercoris	Clostridium amygdalinum	Eubacterium oxidoreducens	Parabacteroides merdae	
Bacteroides thetaiotaomicron	Clostridium bolteae	Eubacterium rectale	Paraprevotella clara	
Bacteroides thetaiotaomicron	Clostridium bolteae	Eubacterium rectale	Parasutterella excrementihominis	
Bacteroides uniformis	Clostridium citroniae	Eubacterium ruminantium	Parasutterella excrementihominis	

Table 6. Consortia VI

Acidaminococcus intestini	Bacteroides stercorisoris	Butyricimonas sp. FBI00158	Enterococcus casseliflavus	Longicatena caecimuris
Acidaminococcus intestini	Bacteroides stercoris	Catabacter hongkongensis	Enterococcus casseliflavus	Megasphaera massiliensis
Acutalibacter timonensis	Bacteroides stercoris	Citrobacter portucalensis	Enterococcus durans	Methanobrevibacter smithii
Akkermansia muciniphila	Bacteroides thetaiotaomicron	Clostridiaceae sp. FBI00191	Enterococcus durans	Monoglobus pectinilyticus
Alistipes onderdonkii	Bacteroides thetaiotaomicron	Clostridium aldenense	Enterococcus durans	Monoglobus pectinilyticus
Alistipes onderdonkii	Bacteroides uniformis	Clostridium aldenense	Enterococcus faecalis	Oxalobacter formigenes
Alistipes putredinis	Bacteroides uniformis	Clostridium bolteae	Enterococcus faecium	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium bolteae	Escherichia flexneri	Oxalobacter formigenes
Alistipes senegalensis	Bacteroides vulgatus	Clostridium citroniae	Eubacterium eligens	Parabacteroides distasonis
Alistipes shahii	Bacteroides xylanisolvens	Clostridium citroniae	Eubacterium eligens	Parabacteroides distasonis
Alistipes shahii	Bacteroides xylanisolvens	Clostridium clostridioforme	Eubacterium hallii	Parabacteroides merdae
Alistipes sp. FBI00180	Bacteroides xylanisolvens	Clostridium fessum	Eubacterium rectale	Parabacteroides merdae
Alistipes sp. FBI00238	Barnesiella intestinihominis	Clostridium fessum	Eubacterium rectale	Paraprevotella clara
Alistipes timonensis	Bifidobacterium adolescentis	Clostridium scindens	Eubacterium siraeum	Parasutterella excrementihominis
Anaerofustis stercorihominis	Bifidobacterium adolescentis	Collinsella aerofaciens	Eubacterium ventriosum	Parasutterella excrementihominis

Anaerostipes hadrus	Bifidobacterium adolescentis	Collinsella aerofaciens	Eubacterium xylanophilum	Phascolarctobacterium faecium
Anaerostipes hadrus	Bifidobacterium adolescentis	Coprococcus comes	Faecalibacterium prausnitzii	Phascolarctobacterium faecium
Anaerotruncus massiliensis	Bifidobacterium bifidum	Coprococcus comes	Faecalibacterium prausnitzii	Porphyromonas asaccharolytica
Bacteroides caccae	Bifidobacterium bifidum	Coprococcus eutactus	Faecalicatena contorta	Porphyromonas asaccharolytica
Bacteroides caccae	Bifidobacterium catenulatum	Dialister invisus	Fusicatenibacter saccharivorans	Roseburia hominis
Bacteroides cellulosilyticus	Bifidobacterium dentium	Coprococcus eutactus	Fusicatenibacter saccharivorans	Roseburia hominis
Bacteroides cellulosilyticus	Bifidobacterium longum	Dialister succinatiphilus	Gordonibacter pamelaiae	Ruminococcaceae sp. FBI00097
Bacteroides coprocola	Bifidobacterium longum	Dialister succinatiphilus	Gordonibacter pamelaiae	Ruminococcaceae sp. FBI00097
Bacteroides dorei	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Holdemanella bififormis	Ruminococcaceae sp. FBI00233
Bacteroides dorei	Bifidobacterium pseudocatenulatum	Dorea formicigenerans	Holdemanella bififormis	Ruminococcus bromii
Bacteroides faecis	Bilophila wadsworthia	Dorea formicigenerans	Hungatella effluvii	Ruminococcus bromii
Bacteroides finegoldii	Bilophila wadsworthia	Dorea longicatena	Hungatella effluvii	Ruminococcus faecis
Bacteroides fragilis	Blautia faecis	Dorea longicatena	Hungatella effluvii	Ruminococcus faecis
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia faecis	Eggerthella lenta	Lachnospiraceae sp. FBI00033	Ruthenibacterium lactatiformans
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia hydrogenotrophica	Eggerthella lenta	Lachnospiraceae sp. FBI00033	Senegalimassilia anaerobia
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia luti	Eisenbergiella tayi	Lachnospiraceae sp. FBI00033	Sutterella massiliensis
Bacteroides massiliensis	Blautia massiliensis	Emergencia timonensis	Lachnospiraceae sp. FBI00071	Sutterella wadsworthensis
Bacteroides massiliensis	Blautia obeum	Eisenbergiella tayi	Lachnospiraceae sp. FBI00150	Sutterella wadsworthensis
Bacteroides nordii	Blautia obeum	Enterobacter himalayensis	Lachnospiraceae sp. FBI00290	Turicibacter sanguinis
Bacteroides ovatus	Blautia wexlerae	Enterobacter hormaechei	Lactobacillus rogosae	
Bacteroides salyersiae	Blautia wexlerae	Enterococcus casseliflavus	Lactobacillus rogosae	
Bacteroides salyersiae	Butyrivibrio faecihominis	Enterococcus casseliflavus	Lactonifactor longoviformis	

Table 7. Consortia VII

Acidaminococcus intestini	Bacteroides thetaiotaomicron	Citrobacter portucalensis	Eubacterium eligens	Oxalobacter formigenes
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Acutalibacter timonensis	Bacteroides uniformis	Clostridiaceae sp. FBI00191	Eubacterium hallii	Parabacteroides distasonis
Akkermansia muciniphila	Bacteroides uniformis	Clostridium aldenense	Eubacterium rectale	Parabacteroides merdae
Alistipes onderdonkii	Bacteroides vulgatus	Clostridium aldenense	Eubacterium rectale	Parabacteroides merdae
Alistipes onderdonkii	Bacteroides vulgatus	Clostridium bolteae	Eubacterium siraeum	Paraprevotella clara
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium ventriosum	Parasutterella excrementihominis
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium citroniae	Faecalibacterium prausnitzii	Parasutterella excrementihominis
Alistipes senegalensis	Bacteroides xylanisolvens	Clostridium citroniae	Eubacterium xylanophilum	Phascolarctobacterium faecium
Alistipes shahii	Barnesiella intestinihominis	Clostridium clostridioforme	Faecalibacterium prausnitzii	Phascolarctobacterium faecium
Alistipes sp. FBI00180	Bifidobacterium adolescentis	Clostridium fessum	Faecalicatena contorta	Porphyromonas asaccharolytica
Alistipes sp. FBI00238	Bifidobacterium adolescentis	Clostridium fessum	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica
Alistipes timonensis	Bifidobacterium adolescentis	Clostridium scindens	Fusicatenibacter saccharivorans	Roseburia hominis
Anaerofustis stercorihominis	Bifidobacterium bifidum	Collinsella aerofaciens	Gordonibacter pamelaeae	Roseburia hominis
Anaerostipes hadrus	Bifidobacterium bifidum	Collinsella aerofaciens	Gordonibacter pamelaeae	Ruminococcaceae sp. FBI00097
Anaerostipes hadrus	Bifidobacterium catenulatum	Coprococcus comes	Holdemanella bififormis	Ruminococcaceae sp. FBI00097
Anaerotruncus massiliensis	Bifidobacterium dentium	Coprococcus comes	Holdemanella bififormis	Ruminococcaceae sp. FBI00233
Bacteroides caccae	Bifidobacterium longum	Coprococcus eutactus	Hungatella effluvii	Ruminococcus bromii
Bacteroides caccae	Bifidobacterium longum	Coprococcus eutactus	Hungatella effluvii	Ruminococcus bromii
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dialister invisus	Hungatella effluvii	Ruminococcus faecis
Bacteroides faecis	Bifidobacterium pseudocatenulatum	Dialister succinatiphilus	Lachnoclostridium pacaense	Ruminococcus faecis
Bacteroides finegoldii	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lachnoclostridium pacaense	Ruthenibacterium lactatiformans
Bacteroides fragilis	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00033	Senegalimassilia anaerobia
Bacteroides kribbi / Bacteroides koreensis species cluster	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00071	Sutterella massiliensis
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia faecis	Dorea longicatena	Lachnospiraceae sp. FBI00290	Sutterella wadsworthensis
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia faecis	Dorea longicatena	Lactobacillus rogosae	Sutterella wadsworthensis

Bacteroides massiliensis	Blautia hydrogenotrophica	Eggerthella lenta	Lactobacillus rogosae	Turicibacter sanguinis
Bacteroides nordii	Blautia massiliensis	Eggerthella lenta	Lactonifactor longoviformis	
Bacteroides ovatus	Blautia obeum	Eggerthella lenta	Longicatena caecimuris	
Bacteroides salyersiae	Blautia obeum	Eggerthella lenta	Megasphaera massiliensis	
Bacteroides stercorisoris	Blautia wexlerae	Eisenbergiella tayi	Monoglobus pectinilyticus	
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Monoglobus pectinilyticus	
Bacteroides stercoris	Butyricimonas faecihominis	Emergencia timonensis	Oxalobacter formigenes	
Bacteroides thetaiotaomicron	Catabacter hongkongensis	Eubacterium eligens	Oxalobacter formigenes	

Table 8. Consortia VIII

Acidaminococcus intestini	Bacteroides thetaiotaomicron	Butyricimonas faecihominis	Eisenbergiella tayi	Monoglobus pectinilyticus
Acutalibacter timonensis	Bacteroides thetaiotaomicron	Catabacter hongkongensis	Emergencia timonensis	Monoglobus pectinilyticus
Akkermansia muciniphila	Bacteroides uniformis	Citrobacter portucalensis	Eubacterium eligens	Oxalobacter formigenes
Alistipes onderdonkii	Bacteroides uniformis	Clostridiaceae sp. FBI00191	Eubacterium eligens	Oxalobacter formigenes
Alistipes onderdonkii	Bacteroides vulgatus	Clostridium aldenense	Eubacterium hallii	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium rectale	Parabacteroides distasonis
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium rectale	Parabacteroides merdae
Alistipes senegalensis	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium siraeum	Parabacteroides merdae
Alistipes shahii	Bacteroides xylanisolvens	Clostridium citroniae	Eubacterium ventriosum	Paraprevotella clara
Alistipes sp. FBI00180	Barnesiella intestinihominis	Clostridium citroniae	Faecalibacterium prausnitzii	Parasutterella excrementihominis
Alistipes sp. FBI00238	Bifidobacterium adolescentis	Clostridium clostridioforme	Eubacterium xylanophilum	Parasutterella excrementihominis
Alistipes timonensis	Bifidobacterium adolescentis	Clostridium fessum	Faecalibacterium prausnitzii	Phascolarctobacterium faecium
Anaerofustis stercorihominis	Bifidobacterium adolescentis	Clostridium fessum	Faecalicatena contorta	Phascolarctobacterium faecium
Anaerostipes hadrus	Bifidobacterium bifidum	Clostridium scindens	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica
Anaerostipes hadrus	Bifidobacterium bifidum	Collinsella aerofaciens	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica
Anaerotruncus massiliensis	Bifidobacterium catenulatum	Collinsella aerofaciens	Gordonibacter pamelaecae	Roseburia hominis
Bacteroides caccae	Bifidobacterium dentium	Coprococcus comes	Gordonibacter pamelaecae	Roseburia hominis
Bacteroides caccae	Bifidobacterium longum	Coprococcus comes	Holdemanella bififormis	Ruminococcaceae sp. FBI00097

Bacteroides coprocola	Bifidobacterium longum	Coprococcus eutactus	Holdemanella biformis	Ruminococcaceae sp. FBI00097
Bacteroides faecis	Bifidobacterium pseudocatenulatum	Coprococcus eutactus	Hungatella effluvii	Ruminococcaceae sp. FBI00233
Bacteroides finegoldii	Bifidobacterium pseudocatenulatum	Dialister invisus	Hungatella effluvii	Ruminococcus bromii
Bacteroides fragilis	Bifidobacterium pseudocatenulatum	Dialister succinatiphilus	Hungatella effluvii	Ruminococcus bromii
Bacteroides kribbi / Bacteroides korensis species cluster	Bilophila wadsworthia	Dielma fastidiosa	Lachnoclostridium pacaense	Ruminococcus faecis
Bacteroides kribbi / Bacteroides korensis species cluster	Bilophila wadsworthia	Dorea formicigenerans	Lachnoclostridium pacaense	Ruminococcus faecis
Bacteroides kribbi / Bacteroides korensis species cluster	Blautia faecis	Dorea formicigenerans	Lachnospiraceae sp. FBI00033	Ruthenibacterium lactatiformans
Bacteroides massiliensis	Blautia faecis	Dorea longicatena	Lachnospiraceae sp. FBI00071	Senegalimassilia anaerobia
Bacteroides nordii	Blautia hydrogenotrophica	Dorea longicatena	Lachnospiraceae sp. FBI00290	Sutterella massiliensis
Bacteroides ovatus	Blautia massiliensis	Eggerthella lenta	Lactobacillus rogosae	Sutterella wadsworthensis
Bacteroides salyersiae	Blautia obeum	Eggerthella lenta	Lactobacillus rogosae	Sutterella wadsworthensis
Bacteroides stercorisoris	Blautia obeum	Eggerthella lenta	Lactonifactor longoviformis	Turicibacter sanguinis
Bacteroides stercoris	Blautia wexlerae	Eggerthella lenta	Longicatena caecimuris	
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Megasphaera massiliensis	

Table 9. Consortia IX

Acidaminococcus intestini	Bacteroides thetaiotaomicron	Butyricimonas faecihominis	Eubacterium eligens	Neglecta timonensis
Akkermansia muciniphila	Bacteroides thetaiotaomicron	Catabacter hongkongensis	Eubacterium eligens	Oxalobacter formigenes
Alistipes onderdonkii	Bacteroides uniformis	Clostridiaceae sp. FBI00191	Eubacterium hallii	Oxalobacter formigenes
Alistipes onderdonkii	Bacteroides uniformis	Clostridiales sp. FBI00377	Eubacterium rectale	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium rectale	Parabacteroides distasonis
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium siraeum	Parabacteroides distasonis
Alistipes senegalensis	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium ventriosum	Parabacteroides merdae
Alistipes shahii	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium xylanophilum	Parabacteroides merdae
Alistipes shahii	Bacteroides xylanisolvens	Clostridium citroniae	Faecalibacterium prausnitzii	Paraprevotella clara

Alistipes sp. FBI00180	Barnesiella intestinihominis	Clostridium citroniae	Fusicatenibacter saccharivorans	Parasutterella excrementihominis
Alistipes sp. FBI00238	Bifidobacterium adolescentis	Clostridium clostridioforme	Fusicatenibacter saccharivorans	Parasutterella excrementihominis
Alistipes timonensis	Bifidobacterium adolescentis	Clostridium fessum	Gordonibacter pamelaeae	Phascolarctobacterium faecium
Anaerofustis stercorihominis	Bifidobacterium adolescentis	Clostridium scindens	Gordonibacter pamelaeae	Porphyromonas asaccharolytica
Anaerostipes hadrus	Bifidobacterium bifidum	Collinsella aerofaciens	Holdemanella bififormis	Porphyromonas asaccharolytica
Anaerostipes hadrus	Bifidobacterium catenulatum	Collinsella aerofaciens	Hungatella effluvii	Roseburia hominis
Anaerotruncus massiliensis	Bifidobacterium dentium	Coprococcus comes	Hungatella effluvii	Roseburia hominis
Bacteroides caccae	Bifidobacterium longum	Coprococcus comes	Hungatella effluvii	Ruminococcaceae sp. FBI00082 FBI00097
Bacteroides caccae	Bifidobacterium longum	Coprococcus eutactus	Lachnoclostridium pacaense	Ruminococcaceae sp. FBI00233
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dialister invisus	Lachnoclostridium pacaense	Ruminococcus bromii
Bacteroides faecis	Bifidobacterium pseudocatenulatum	Dialister succinatiphilus	Lachnospiraceae sp. FBI00033	Ruminococcus bromii
Bacteroides finegoldii	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lachnospiraceae sp. FBI00071	Ruminococcus faecis
Bacteroides fragilis	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00290	Ruminococcus faecis
Bacteroides kribbi / Bacteroides koreensis species cluster	Bilophila wadsworthia	Dorea formicigenerans	Lactobacillus rogosae	Ruthenibacterium lactatiformans
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia faecis	Dorea longicatena	Lactobacillus rogosae	Senegalimassilia anaerobia
Bacteroides massiliensis	Blautia faecis	Dorea longicatena	Longicatena caecimuris	Sutterella massiliensis
Bacteroides nordii	Blautia hydrogenotrophica	Eggerthella lenta	Megasphaera massiliensis	Sutterella wadsworthensis
Bacteroides ovatus	Blautia massiliensis	Eggerthella lenta	Methanobrevibacter smithii	Sutterella wadsworthensis
Bacteroides salyersiae	Blautia obeum	Eggerthella lenta	Methanobrevibacter smithii	Turicibacter sanguinis
Bacteroides stercorisoris	Blautia obeum	Eggerthella lenta	Monoglobus pectinilyticus	
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Monoglobus pectinilyticus	
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Neglecta timonensis	

Table 10. Consortia X

Acidaminococcus intestini	Bacteroides thetaiotaomicron	Butyricimonas faecihominis	Eubacterium eligens	Monoglobus pectinilyticus
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Akkermansia muciniphila	Bacteroides thetaiotaomicron	Catabacter hongkongensis	Eubacterium eligens	Neglecta timonensis
Alistipes onderdonkii	Bacteroides uniformis	Clostridiaceae sp. FBI00191	Eubacterium hallii	Neglecta timonensis
Alistipes onderdonkii	Bacteroides uniformis	Clostridiales sp. FBI00377	Eubacterium rectale	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium rectale	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium siraeum	Oxalobacter formigenes
Alistipes senegalensis	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium ventriosum	Parabacteroides distasonis
Alistipes shahii	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium xylanophilum	Parabacteroides distasonis
Alistipes shahii	Bacteroides xylanisolvens	Clostridium citroniae	Faecalibacterium prausnitzii	Parabacteroides merdae
Alistipes sp. FBI00180	Barnesiella intestinihominis	Clostridium citroniae	Faecalibacterium prausnitzii	Parabacteroides merdae
Alistipes sp. FBI00238	Bifidobacterium adolescentis	Clostridium clostridioforme	Fusicatenibacter saccharivorans	Paraprevotella clara
Alistipes timonensis	Bifidobacterium adolescentis	Clostridium fessum	Fusicatenibacter saccharivorans	Parasutterella excrementihominis
Anaerofustis stercorihominis	Bifidobacterium adolescentis	Clostridium scindens	Gordonibacter pamelaeae	Parasutterella excrementihominis
Anaerostipes hadrus	Bifidobacterium bifidum	Collinsella aerofaciens	Gordonibacter pamelaeae	Phascolarctobacterium faecium
Anaerostipes hadrus	Bifidobacterium catenulatum	Collinsella aerofaciens	Holdemanella bififormis	Porphyromonas asaccharolytica
Anaerotruncus massiliensis	Bifidobacterium dentium	Coprococcus comes	Holdemanella bififormis	Porphyromonas asaccharolytica
Bacteroides caccae	Bifidobacterium longum	Coprococcus comes	Hungatella effluvii	Roseburia hominis
Bacteroides caccae	Bifidobacterium longum	Coprococcus eutactus	Hungatella effluvii	Roseburia hominis
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dialister invisus	Hungatella effluvii	Ruminococcaceae sp. FBI00082 FBI00097
Bacteroides faecis	Bifidobacterium pseudocatenulatum	Dialister succinatiphilus	Lachnoclostridium pacaense	Ruminococcaceae sp. FBI00233
Bacteroides finegoldii	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lachnoclostridium pacaense	Ruminococcus bromii
Bacteroides fragilis	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00033	Ruminococcus bromii
Bacteroides kribbi / Bacteroides koreensis species cluster	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00071	Ruminococcus faecis
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia faecis	Dorea longicatena	Lachnospiraceae sp. FBI00290	Ruminococcus faecis
Bacteroides massiliensis	Blautia faecis	Dorea longicatena	Lactobacillus rogosae	Ruthenibacterium lactatiformans

Bacteroides nordii	Blautia hydrogenotrophica	Eggerthella lenta	Lactobacillus rogosae	Senegalimassilia anaerobia
Bacteroides ovatus	Blautia massiliensis	Eggerthella lenta	Longicatena caecimuris	Sutterella massiliensis
Bacteroides salyersiae	Blautia obeum	Eggerthella lenta	Megasphaera massiliensis	Sutterella wadsworthensis
Bacteroides stercorisoris	Blautia obeum	Eggerthella lenta	Methanobrevibacter smithii	Sutterella wadsworthensis
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Methanobrevibacter smithii	Turicibacter sanguinis
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Monoglobus pectinilyticus	

Table 11. Consortia XI

Acidaminococcus intestini	Bifidobacterium longum	Fusicatenibacter saccharivorans	Bacteroides xylanisolvens	Clostridium bolteae
Akkermansia muciniphila	Bilophila wadsworthia	Gordonibacter pamelaee	Turicibacter sanguinis	Collinsella aerofaciens
Alistipes onderdonkii	Blautia hydrogenotrophica	Hungatella effluvii	Bifidobacterium adolescentis	Coprococcus comes
Alistipes putredinis	Blautia massiliensis	Lachnoclostridium pacaense	Bifidobacterium pseudocatenulatum	Dorea formicigenerans
Alistipes senegalensis	Blautia obeum	Lachnospiraceae sp. FBI00033	Blautia faecis	Dorea longicatena
Alistipes shahii	Blautia wexlerae	Lachnospiraceae sp. FBI00071	Clostridium citroniae	Eggerthella lenta
Alistipes sp. FBI00180	Butyrivibrio faecihominis	Lachnospiraceae sp. FBI00290	Faecalibacterium prausnitzii	Eggerthella lenta
Alistipes sp. FBI00238	Catabacter hongkongensis	Lactobacillus rogosae	Holdemanella bififormis	Eggerthella lenta
Alistipes timonensis	Clostridiaceae sp. FBI00191	Longicatena caecimuris	Bacteroides xylanisolvens	Eisenbergiella tayi
Anaerofustis stercorihominis	Clostridiales sp. FBI00377	Megasphaera massiliensis	Bifidobacterium adolescentis	Eubacterium eligens
Anaerostipes hadrus	Clostridium aldenense	Methanobrevibacter smithii	Bifidobacterium pseudocatenulatum	Eubacterium rectale
Anaerotruncus massiliensis	Clostridium bolteae	Monoglobus pectinilyticus	Blautia faecis	Fusicatenibacter saccharivorans
Bacteroides caccae	Clostridium clostridioforme	Neglecta timonensis	Alistipes onderdonkii	Gordonibacter pamelaee
Bacteroides coprocola	Clostridium fessum	Oxalobacter formigenes	Clostridium citroniae	Hungatella effluvii
Bacteroides faecis	Clostridium scindens	Oxalobacter formigenes	Alistipes putredinis	Hungatella effluvii
Bacteroides finegoldii	Collinsella aerofaciens	Oxalobacter formigenes	Alistipes shahii	Lachnoclostridium pacaense
Bacteroides fragilis	Coprococcus comes	Parabacteroides distasonis	Anaerostipes hadrus	Lactobacillus rogosae
Bacteroides kribbi /	Coprococcus eutactus	Parabacteroides merdae	Bacteroides caccae	Methanobrevibacter smithii

Bacteroides koreensis species cluster				
Bacteroides massiliensis	Dialister invisus	Paraprevotella clara	Bacteroides kribbi / Bacteroides koreensis species cluster	Monoglobus pectinilyticus
Bacteroides nordii	Dialister succinatiphilus	Parasutterella excrementihominis	Bacteroides stercoris	Neglecta timonensis
Bacteroides ovatus	Dielma fastidiosa	Phascolarctobacterium faecium	Bacteroides thetaiotaomicron	Parabacteroides distasonis
Bacteroides salyersiae	Dorea formicigenerans	Porphyromonas asaccharolytica	Bacteroides uniformis	Parabacteroides merdae
Bacteroides stercorisoris	Dorea longicatena	Roseburia hominis	Bacteroides vulgatus	Parasutterella excrementihominis
Bacteroides stercoris	Eggerthella lenta	Ruminococcaceae sp. FBI00082 FBI00097	Bacteroides xylanisolvens	Porphyromonas asaccharolytica
Bacteroides thetaiotaomicron	Eisenbergiella tayi	Ruminococcaceae sp. FBI00233	Bifidobacterium adolescentis	Roseburia hominis
Bacteroides uniformis	Eubacterium eligens	Ruminococcus bromii	Bifidobacterium longum	Ruminococcus bromii
Bacteroides vulgatus	Eubacterium hallii	Ruminococcus faecis	Bifidobacterium pseudocatenulatum	Ruminococcus faecis
Barnesiella intestinihominis	Eubacterium rectale	Ruthenibacterium lactatiformans	Bilophila wadsworthia	Sutterella wadsworthensis
Bifidobacterium bifidum	Eubacterium siraeum	Senegalimassilia anaerobia	Blautia obeum	
Bifidobacterium catenulatum	Eubacterium ventriosum	Sutterella massiliensis	Blautia wexlerae	
Bifidobacterium dentium	Eubacterium xylanophilum	Sutterella wadsworthensis	Clostridium aldenense	

Table 12. Consortia XII

Acidaminococcus intestini	Bacteroides uniformis	Clostridium bolteae	Faecalibacterium prausnitzii	Parasutterella excrementihominis
Akkermansia muciniphila	Bacteroides vulgatus	Clostridium bolteae	Faecalibacterium prausnitzii	Phascolarctobacterium faecium
Alistipes onderdonkii	Bacteroides vulgatus	Clostridium citroniae	Fusicatenibacter saccharivorans	Phascolarctobacterium faecium
Alistipes onderdonkii	Bacteroides xylanisolvens	Clostridium citroniae	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium clostridioforme	Gordonibacter pamelaeae	Porphyromonas asaccharolytica
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium fessum	Gordonibacter pamelaeae	Roseburia hominis

Alistipes senegalensis	Barnesiella intestinihominis	Clostridium fessum	Holdemanella biformis	Roseburia hominis
Alistipes shahii	Bifidobacterium adolescentis	Clostridium scindens	Holdemanella biformis	Ruminococcaceae sp. FBI00082 FBI00097
Alistipes shahii	Bifidobacterium adolescentis	Collinsella aerofaciens	Hungatella effluvii	Ruminococcaceae sp. FBI00082 FBI00097
Alistipes sp. FBI00180	Bifidobacterium adolescentis	Collinsella aerofaciens	Hungatella effluvii	Ruminococcaceae sp. FBI00233
Alistipes sp. FBI00238	Bifidobacterium bifidum	Coprococcus comes	Hungatella effluvii	Ruminococcus bromii
Alistipes timonensis	Bifidobacterium bifidum	Coprococcus comes	Lachnoclostridium pacaense	Ruminococcus bromii
Anaerofustis stercorihominis	Bifidobacterium catenulatum	Coprococcus eutactus	Lachnoclostridium pacaense	Ruminococcus faecis
Anaerostipes hadrus	Bifidobacterium dentium	Coprococcus eutactus	Lachnospiraceae sp. FBI00033	Ruminococcus faecis
Anaerostipes hadrus	Bifidobacterium longum	Dialister invisus	Lachnospiraceae sp. FBI00071	Ruthenibacterium lactatiformans
Anaerotruncus massiliensis	Bifidobacterium longum	Dialister succinatiphilus	Lachnospiraceae sp. FBI00290	Senegalimassilia anaerobia
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lactobacillus rogosae	Sutterella massiliensis
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dorea formicigenerans	Lactobacillus rogosae	Sutterella wadsworthensis
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dorea formicigenerans	Longicatena caecimuris	Sutterella wadsworthensis
Bacteroides faecis	Bilophila wadsworthia	Dorea longicatena	Megasphaera massiliensis	Turicibacter sanguinis
Bacteroides finegoldii	Bilophila wadsworthia	Dorea longicatena	Methanobrevibacter smithii	Bacteroides thetaiotaomicron
Bacteroides fragilis	Blautia faecis	Eggerthella lenta	Methanobrevibacter smithii	Bacteroides uniformis
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia faecis	Eggerthella lenta	Monoglobus pectinilyticus	Clostridium aldenense
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia hydrogenotrophica	Eggerthella lenta	Monoglobus pectinilyticus	Clostridium aldenense
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia massiliensis	Eggerthella lenta	Neglecta timonensis	Eubacterium ventriosum
Bacteroides massiliensis	Blautia obeum	Eisenbergiella taylori	Neglecta timonensis	Eubacterium xylanophilum
Bacteroides nordii	Blautia obeum	Eisenbergiella taylori	Oxalobacter formigenes	Paraprevotella clara

Bacteroides ovatus	Blautia wexlerae	Eubacterium eligens	Oxalobacter formigenes	Parasutterella excrementihominis
Bacteroides salyersiae	Blautia wexlerae	Eubacterium eligens	Oxalobacter formigenes	Bacteroides thetaiotaomicron
Bacteroides stercorisoris	Butyricimonas faecihominis	Eubacterium hallii	Parabacteroides distasonis	Clostridiales sp. FBI00377
Bacteroides stercoris	Catabacter hongkongensis	Eubacterium rectale	Parabacteroides distasonis	Eubacterium siraeum
Bacteroides stercoris	Clostridiaceae sp. FBI00191	Eubacterium rectale	Parabacteroides merdae	Parabacteroides merdae

Table 13. Consortia XIII

Acidaminococcus intestini	Bacteroides thetaiotaomicron	Butyricimonas faecihominis	Eubacterium eligens	Monoglobus pectinilyticus
Akkermansia muciniphila	Bacteroides thetaiotaomicron	Catabacter hongkongensis	Eubacterium eligens	Neglecta timonensis
Alistipes onderdonkii	Bacteroides uniformis	Clostridiaceae sp. FBI00191	Eubacterium hallii	Neglecta timonensis
Alistipes onderdonkii	Bacteroides uniformis	Clostridiales sp. FBI00377	Eubacterium rectale	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium rectale	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium siraeum	Oxalobacter formigenes
Alistipes senegalensis	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium ventriosum	Parabacteroides distasonis
Alistipes shahii	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium xylanophilum	Parabacteroides distasonis
Alistipes shahii	Bacteroides xylanisolvens	Clostridium citroniae	Faecalibacterium prausnitzii	Parabacteroides merdae
Alistipes sp. FBI00180	Barnesiella intestinihominis	Clostridium citroniae	Faecalibacterium prausnitzii	Parabacteroides merdae
Alistipes sp. FBI00238	Bifidobacterium adolescentis	Clostridium clostridioforme	Fusicatenibacter saccharivorans	Paraprevotella clara
Alistipes timonensis	Bifidobacterium adolescentis	Clostridium fessum	Fusicatenibacter saccharivorans	Parasutterella excrementihominis
Anaerofustis stercorihominis	Bifidobacterium adolescentis	Clostridium scindens	Gordonibacter pamelaeae	Parasutterella excrementihominis
Anaerostipes hadrus	Bifidobacterium bifidum	Collinsella aerofaciens	Gordonibacter pamelaeae	Phascolarctobacterium faecium
Anaerostipes hadrus	Bifidobacterium catenulatum	Collinsella aerofaciens	Holdemanella bififormis	Porphyromonas asaccharolytica
Anaerotruncus massiliensis	Bifidobacterium dentium	Coprococcus comes	Holdemanella bififormis	Porphyromonas asaccharolytica
Bacteroides caccae	Bifidobacterium longum	Coprococcus comes	Hungatella effluvii	Roseburia hominis
Bacteroides caccae	Bifidobacterium longum	Coprococcus eutactus	Hungatella effluvii	Roseburia hominis
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dialister invisus	Hungatella effluvii	Ruminococcaceae sp. FBI00082 FBI00097

Bacteroides faecis	Bifidobacterium pseudocatenulatum	Dialister succinatiphilus	Lachnoclostridium pacaense	Ruminococcaceae sp. FBI00233
Bacteroides finegoldii	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lachnoclostridium pacaense	Ruminococcus bromii
Bacteroides fragilis	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00033	Ruminococcus bromii
Bacteroides kribbi / Bacteroides koreensis species cluster	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00071	Ruminococcus faecis
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia faecis	Dorea longicatena	Lachnospiraceae sp. FBI00290	Ruminococcus faecis
Bacteroides massiliensis	Blautia faecis	Dorea longicatena	Lactobacillus rogosae	Ruthenibacterium lactatiformans
Bacteroides nordii	Blautia hydrogenotrophica	Eggerthella lenta	Lactobacillus rogosae	Senegalimassilia anaerobia
Bacteroides ovatus	Blautia massiliensis	Eggerthella lenta	Longicatena caecimuris	Sutterella massiliensis
Bacteroides salyersiae	Blautia obeum	Eggerthella lenta	Megasphaera massiliensis	Sutterella wadsworthensis
Bacteroides stercorisoris	Blautia obeum	Eggerthella lenta	Methanobrevibacter smithii	Sutterella wadsworthensis
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Methanobrevibacter smithii	Turicibacter sanguinis
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Monoglobus pectinilyticus	

Table 14. Consortia XIV

Acidaminococcus intestini	Bacteroides uniformis	Clostridium citroniae	Eubacterium siracum	Parasutterella excrementihominis
Akkermansia muciniphila	Bacteroides uniformis	Clostridium citroniae	Eubacterium ruminantium	Parasutterella excrementihominis
Alistipes finegoldii	Bacteroides vulgatus	Clostridium clostridioforme	Eubacterium ventriosum	Phascolarctobacterium faecium
Alistipes onderdonkii	Bacteroides vulgatus	Clostridium scindens	Eubacterium xylanophilum	Phascolarctobacterium faecium
Alistipes onderdonkii	Bacteroides xylanisolvens	Clostridium swellfunianum	Faecalibacterium prausnitzii	Phoceae massiliensis
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium symbiosum	Faecalibacterium prausnitzii	Phoceae massiliensis
Alistipes putredinis	Barnesiella intestinihominis	Clostridium symbiosum	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica
Alistipes senegalensis	Bifidobacterium adolescentis	Collinsella aerofaciens	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica

Alistipes senegalensis	Bifidobacterium adolescentis	Collinsella aerofaciens	Gordonibacter pamelaeae	Roseburia hominis
Alistipes shahii	Bifidobacterium bifidum	Coprococcus comes	Gordonibacter pamelaeae	Roseburia hominis
Alistipes shahii	Bifidobacterium bifidum	Coprococcus comes	Holdemanella bififormis	Ruminococcus bromii
Alistipes timonensis	Bifidobacterium catenulatum	Coprococcus eutactus	Holdemanella bififormis	Ruminococcus bromii
Anaerofustis stercorihominis	Bifidobacterium dentium	Coprococcus eutactus	Hungatella effluvii	Ruminococcus faecis
Anaerostipes hadrus	Bifidobacterium faecale	Desulfovibrio desulfuricans	Hungatella hathewayi	Ruminococcus faecis
Anaerostipes hadrus	Bifidobacterium longum	Desulfovibrio desulfuricans	Hungatella hathewayi	Ruthenibacterium lactatiformans
Anaerotruncus colihominis	Bifidobacterium longum	Dialister invisus	Hydrogenoanaerobacterium saccharovorans	Senegalimassilia anaerobia
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dialister succinatiphilus	Lachnoclostridium pacaense	Sutterella massiliensis
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lachnoclostridium pacaense	Sutterella wadsworthensis
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dorea formicigenans	Lachnospira pectinoschiza	Sutterella wadsworthensis
Bacteroides faecis	Blautia faecis	Dorea formicigenans	Lachnospira pectinoschiza	Turicibacter sanguinis
Bacteroides finegoldii	Blautia faecis	Dorea longicatena	Longicatena caecimuris	Bacteroides stercoris
Bacteroides fragilis	Blautia hydrogenotrophica	Dorea longicatena	Megasphaera massiliensis	Bacteroides stercoris
Bacteroides koreensis	Blautia luti	Eggerthella lenta	Methanobrevibacter smithii	Bacteroides thetaiotaomicron
Bacteroides koreensis	Blautia obeum	Eggerthella lenta	Methanobrevibacter smithii	Bacteroides thetaiotaomicron
Bacteroides kribbi	Blautia obeum	Eggerthella lenta	Monoglobus pectinilyticus	Clostridium aldenense
Bacteroides kribbi	Blautia wexlerae	Eggerthella lenta	Monoglobus pectinilyticus	Clostridium aldenense
Bacteroides massiliensis	Blautia wexlerae	Eisenbergiella tayi	Neglecta timonensis	Clostridium bolteae
Bacteroides nordii	Butyricimonas faecihominis	Eisenbergiella tayi	Oxalobacter formigenes	Clostridium bolteae
Bacteroides oleiciplenus	Catabacter hongkongensis	Emergencia timonensis	Oxalobacter formigenes	Parabacteroides merdae
Bacteroides ovatus	Citrobacter freundii	Eubacterium eligens	Oxalobacter formigenes	Parabacteroides merdae
Bacteroides salyersiae	Clostridiaceae sp.	Eubacterium eligens	Parabacteroides distasonis	Paraprevotella clara
Eubacterium rectale	Eubacterium rectale	Eubacterium hallii	Parabacteroides distasonis	Eubacterium oxidoreducens

Table 15. Consortia XV

Acidaminococcus s. intestini	Bacteroides thetaiotaomicron	Butyricimonas faecihominis	Eubacterium eligens	Monoglobus pectinilyticus
Akkermansia muciniphila	Bacteroides thetaiotaomicron	Catabacter hongkongensis	Eubacterium eligens	Neglecta timonensis
Alistipes onderdonkii	Bacteroides uniformis	Clostridiaceae sp. FBI00191	Eubacterium hallii	Neglecta timonensis
Alistipes onderdonkii	Bacteroides uniformis	Clostridiales sp. FBI00377	Eubacterium rectale	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium rectale	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium siraeum	Oxalobacter formigenes
Alistipes senegalensis	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium ventriosum	Parabacteroides distasonis
Alistipes shahii	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium xylanophilum	Parabacteroides distasonis
Alistipes shahii	Bacteroides xylanisolvens	Clostridium citroniae	Faecalibacterium prausnitzii	Parabacteroides merdae
Alistipes sp. FBI00180	Barnesiella intestinihominis	Clostridium citroniae	Faecalibacterium prausnitzii	Parabacteroides merdae
Alistipes sp. FBI00238	Bifidobacterium adolescentis	Clostridium clostridioforme	Fusicatenibacter saccharivorans	Paraprevotella clara
Alistipes timonensis	Bifidobacterium adolescentis	Clostridium fessum	Fusicatenibacter saccharivorans	Parasutterella excrementihominis
Anaerofustis stercorihominis	Bifidobacterium adolescentis	Clostridium scindens	Gordonibacter pamelaeae	Parasutterella excrementihominis
Anaerostipes hadrus	Bifidobacterium bifidum	Collinsella aerofaciens	Gordonibacter pamelaeae	Phascolarctobacteriu m faecium
Anaerostipes hadrus	Bifidobacterium catenulatum	Collinsella aerofaciens	Holdemanella biformis	Porphyromonas asaccharolytica
Anaerotruncus massiliensis	Bifidobacterium dentium	Coprococcus comes	Holdemanella biformis	Porphyromonas asaccharolytica
Bacteroides caccae	Bifidobacterium longum	Coprococcus comes	Hungatella effluvii	Roseburia hominis
Bacteroides caccae	Bifidobacterium longum	Coprococcus eutactus	Hungatella effluvii	Roseburia hominis
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dialister invisus	Hungatella effluvii	Ruminococcaceae sp. FBI00082 FBI00097
Bacteroides faecis	Bifidobacterium pseudocatenulatu m	Dialister succinatophilus	Lachnoclostridium pacaense	Ruminococcaceae sp. FBI00233
Bacteroides finegoldii	Bifidobacterium pseudocatenulatu m	Dielma fastidiosa	Lachnoclostridium pacaense	Ruminococcus bromii
Bacteroides fragilis	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00033	Ruminococcus bromii
Bacteroides kribbi / Bacteroides koreensis species cluster	Bilophila wadsworthia	Dorea formicigeneran s	Lachnospiraceae sp. FBI00071	Ruminococcus faecis

Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia faecis	Dorea longicatena	Lachnospiraceae sp. FBI00290	Ruminococcus faecis
Bacteroides massiliensis	Blautia faecis	Dorea longicatena	Lactobacillus rogosae	Ruthenibacterium lactatiformans
Bacteroides nordii	Blautia hydrogenotrophica	Eggerthella lenta	Lactobacillus rogosae	Senegalimassilia anaerobia
Bacteroides ovatus	Blautia massiliensis	Eggerthella lenta	Longicatena caecimuris	Sutterella massiliensis
Bacteroides salyersiae	Blautia obeum	Eggerthella lenta	Megasphaera massiliensis	Sutterella wadsworthensis
Bacteroides stercorisoris	Blautia obeum	Eggerthella lenta	Methanobrevibacter smithii	Sutterella wadsworthensis
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Methanobrevibacter smithii	Turicibacter sanguinis
Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Monoglobus pectinilyticus	

Table 16. Consortia XVI

Acidaminococcus intestini	Bacteroides uniformis	Clostridium citroniae	Eubacterium ventriosum	Parasutterella excrementihominis
Akkermansia muciniphila	Bacteroides uniformis	Clostridium clostridioforme	Eubacterium siraeum	Phascolarctobacterium faecium
Alistipes finegoldii	Bacteroides vulgatus	Clostridium scindens	Eubacterium xylanophilum	Phascolarctobacterium faecium
Alistipes onderdonkii	Bacteroides vulgatus	Clostridium swellexianum	Faecalibacterium prausnitzii	Phoceamassiliensis
Alistipes onderdonkii	Bacteroides xylanisolvens	Clostridium symbiosum	Faecalibacterium prausnitzii	Phoceamassiliensis
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium symbiosum	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica
Alistipes putredinis	Barnesiella intestinihominis	Collinsella aerofaciens	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica
Alistipes senegalensis	Bifidobacterium adolescentis	Collinsella aerofaciens	Gordonibacter pamelaeae	Roseburia hominis
Alistipes senegalensis	Bifidobacterium adolescentis	Coprococcus comes	Gordonibacter pamelaeae	Roseburia hominis
Alistipes shahii	Bifidobacterium bifidum	Coprococcus comes	Holdemanella bififormis	Ruminococcus bromii
Alistipes shahii	Bifidobacterium bifidum	Coprococcus eutactus	Holdemanella bififormis	Ruminococcus bromii
Alistipes timonensis	Bifidobacterium catenulatum	Coprococcus eutactus	Hungatella effluvii	Ruminococcus faecis
Anaerofustis stercorihominis	Bifidobacterium dentium	Desulfovibrio desulfuricans	Hungatella hathewayi	Ruminococcus faecis
Anaerostipes hadrus	Bifidobacterium faecale	Desulfovibrio desulfuricans	Hungatella hathewayi	Ruthenibacterium lactatiformans

Anaerostipes hadrus	Bifidobacterium longum	Dialister invisus	Hydrogenoanaerobacterium saccharovorans	Senegalimassilia anaerobia
Anaerotruncus colihominis	Bifidobacterium longum	Dialister succinatiphilus	Lachnoclostridium pacaense	Sutterella massiliensis
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lachnoclostridium pacaense	Sutterella wadsworthensis
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dorea formicigenerans	Lachnospira pectinoschiza	Sutterella wadsworthensis
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dorea formicigenerans	Lachnospira pectinoschiza	Turicibacter sanguinis
Bacteroides faecis	Blautia faecis	Dorea longicatena	Longicatena caecimuris	Bacteroides stercoris
Bacteroides finegoldii	Blautia faecis	Dorea longicatena	Megasphaera massiliensis	Bacteroides stercoris
Bacteroides fragilis	Blautia hydrogenotrophica	Eggerthella lenta	Methanobrevibacter smithii	Bacteroides thetaiotaomicron
Bacteroides koreensis	Blautia luti	Eggerthella lenta	Methanobrevibacter smithii	Bacteroides thetaiotaomicron
Bacteroides koreensis	Blautia obeum	Eggerthella lenta	Monoglobus pectinilyticus	Clostridium aldenense
Bacteroides kribbi	Blautia obeum	Eggerthella lenta	Monoglobus pectinilyticus	Clostridium bolteae
Bacteroides kribbi	Blautia wexlerae	Eisenbergiella tayi	Neglecta timonensis	Clostridium bolteae
Bacteroides massiliensis	Blautia wexlerae	Eisenbergiella tayi	Oxalobacter formigenes	Clostridium citroniae
Bacteroides nordii	Butyrivibrio faecihominis	Emergencia timonensis	Oxalobacter formigenes	Eubacterium oxidoreducens
Bacteroides oleiciplenus	Catabacter hongkongensis	Eubacterium eligens	Oxalobacter formigenes	Eubacterium rectale
Bacteroides ovatus	Clostridiaceae sp.	Eubacterium eligens	Parabacteroides distasonis	Eubacterium rectale
Bacteroides salyersiae	Clostridium aldenense	Eubacterium hallii	Parabacteroides distasonis	Eubacterium ruminantium
Parasutterella excrementihominis	Paraprevotella clara	Parabacteroides merdae	Parabacteroides merdae	

Table 17. Consortia XVII

Acidaminococcus intestini	Bacteroides uniformis	Clostridium bolteae	Faecalicatena contorta	Roseburia hominis
Acutalibacter timonensis	Bacteroides vulgatus	Clostridium citroniae	Fusicatenibacter saccharivorans	Roseburia hominis
Akkermansia muciniphila	Bacteroides vulgatus	Clostridium citroniae	Fusicatenibacter saccharivorans	Ruminococcaceae sp. FBI00097
Alistipes onderdonkii	Bacteroides xylanisolvens	Clostridium clostridioforme	Gordonibacter pamelaeae	Ruminococcaceae sp. FBI00097

Alistipes onderdonkii	Bacteroides xylanisolvens	Clostridium fessum	Gordonibacter pamelaee	Ruminococcaceae sp. FBI00233
Alistipes putredinis	Bacteroides xylanisolvens	Clostridium fessum	Holdemanella biformis	Ruminococcus bromii
Alistipes putredinis	Barnesiella intestinihominis	Clostridium scindens	Holdemanella biformis	Ruminococcus bromii
Alistipes senegalensis	Bifidobacterium adolescentis	Collinsella aerofaciens	Hungatella effluvii	Ruminococcus faecis
Alistipes shahii	Bifidobacterium adolescentis	Collinsella aerofaciens	Hungatella effluvii	Ruminococcus faecis
Alistipes sp. FBI00180	Bifidobacterium adolescentis	Coprococcus comes	Hungatella effluvii	Ruthenibacterium lactatiformans
Alistipes sp. FBI00238	Bifidobacterium bifidum	Coprococcus comes	Lachnoclostridium pacaense	Senegalimassilia anaerobia
Alistipes timonensis	Bifidobacterium bifidum	Coprococcus eutactus	Lachnoclostridium pacaense	Sutterella massiliensis
Anaerofustis stercorihominis	Bifidobacterium catenulatum	Coprococcus eutactus	Lachnospiraceae sp. FBI00033	Sutterella wadsworthensis
Anaerostipes hadrus	Bifidobacterium dentium	Dialister invisus	Lachnospiraceae sp. FBI00071	Sutterella wadsworthensis
Anaerostipes hadrus	Bifidobacterium longum	Dialister succinatiphilus	Lachnospiraceae sp. FBI00290	Turicibacter sanguinis
Anaerotruncus massiliensis	Bifidobacterium longum	Dielma fastidiosa	Lactobacillus rogosae	Bacteroides stercoris
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dorea formicigenerans	Lactobacillus rogosae	Bacteroides stercoris
Bacteroides caccae	Bifidobacterium pseudocatenulatum	Dorea formicigenerans	Lactonifactor longoviformis	Bacteroides thetaiotaomicron
Bacteroides coprocola	Bilophila wadsworthia	Dorea longicatena	Longicatena caecimuris	Bacteroides thetaiotaomicron
Bacteroides faecis	Bilophila wadsworthia	Dorea longicatena	Megasphaera massiliensis	Bacteroides uniformis
Bacteroides finegoldii	Blautia faecis	Eggerthella lenta	Monoglobus pectinilyticus	Citrobacter portucalensis
Bacteroides fragilis	Blautia faecis	Eggerthella lenta	Monoglobus pectinilyticus	Clostridiaceae sp. FBI00191
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia hydrogenotrophica	Eisenbergiella tayi	Oxalobacter formigenes	Clostridium aldenense
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia massiliensis	Eisenbergiella tayi	Oxalobacter formigenes	Clostridium aldenense
Bacteroides kribbi / Bacteroides koreensis species cluster	Blautia obeum	Emergencia timonensis	Oxalobacter formigenes	Clostridium bolteae
Bacteroides massiliensis	Blautia obeum	Eubacterium eligens	Parabacteroides distasonis	Eubacterium siraeum

Bacteroides nordii	Blautia wexlerae	Eubacterium eligens	Parabacteroides merdae	Eubacterium ventriosum
Bacteroides ovatus	Blautia wexlerae	Eubacterium hallii	Parabacteroides merdae	Eubacterium xylanophilum
Bacteroides salyersiae	Butyricimonas faecihominis	Eubacterium rectale	Paraprevotella clara	Faecalibacterium prausnitzii
Bacteroides stercorisoris	Catabacter hongkongensis	Eubacterium rectale	Parasutterella excrementihominis	Faecalibacterium prausnitzii
Phascolarctobacterium faecium	Phascolarctobacterium faecium	Porphyromonas asaccharolytica	Parasutterella excrementihominis	Porphyromonas asaccharolytica

Table 18. Consortia XVIII

Bacteroides caccae	Bifidobacterium longum	Clostridium scindens	Eggerthella lenta	Parabacteroides merdae
Bacteroides salyersiae	Bifidobacterium pseudocatenulatum	Clostridium symbiosum	Eggerthella lenta	Ruminococcus bromii
Bacteroides thetaiotaomicron	Bifidobacterium pseudocatenulatum	Collinsella aerofaciens	Faecalibacterium prausnitzii	Ruminococcus bromii
Bacteroides thetaiotaomicron	Bifidobacterium pseudocatenulatum	Desulfovibrio desulfuricans	Neglecta timonensis	
Bacteroides vulgatus	Clostridium amygdalinum	Dorea longicatena	Oxalobacter formigenes	
Bifidobacterium dentium	Clostridium citroniae	Eggerthella lenta	Oxalobacter formigenes	
Bifidobacterium longum	Clostridium citroniae	Eggerthella lenta	Oxalobacter formigenes	

Table 19. Consortia XIX

Acidaminococcus intestini	Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Monoglobus pectinilyticus
Acutalibacter timonensis	Bacteroides stercoris	Blautia wexlerae	Eisenbergiella tayi	Monoglobus pectinilyticus
Akkermansia muciniphila	Bacteroides thetaiotaomicron	Butyricimonas faecihominis	Emergencia timonensis	Parabacteroides distasonis
Alistipes onderdonkii	Bacteroides thetaiotaomicron	Catabacter hongkongensis	Eubacterium eligens	Oxalobacter formigenes
Alistipes onderdonkii	Bacteroides uniformis	Clostridiaceae sp. FBI00191	Eubacterium eligens	Oxalobacter formigenes
Alistipes putredinis	Bacteroides uniformis	Clostridium aldenense	Eubacterium hallii	Oxalobacter formigenes
Alistipes putredinis	Bacteroides vulgatus	Clostridium aldenense	Eubacterium rectale	Parabacteroides distasonis
Alistipes senegalensis	Bacteroides vulgatus	Clostridium bolteae	Eubacterium rectale	Parabacteroides merdae
Alistipes shahii	Bacteroides xylanisolvens	Clostridium bolteae	Eubacterium siraeum	Parabacteroides merdae
Alistipes shahii	Bacteroides xylanisolvens	Clostridium citroniae	Eubacterium ventriosum	Paraprevotella clara
Alistipes sp. FBI00180	Bacteroides xylanisolvens	Clostridium citroniae	Eubacterium xylanophilum	Parasutterella excrementihominis

Alistipes sp. FBI00238	Barnesiella intestinihominis	Clostridium clostridioforme	Faecalibacterium prausnitzii	Parasutterella excrementihominis
Alistipes timonensis	Bifidobacterium adolescentis	Clostridium fessum	Fusicatenibacter saccharivorans	Phascolarctobacterium faecium
Anaerofustis stercorihominis	Bifidobacterium adolescentis	Clostridium scindens	Fusicatenibacter saccharivorans	Porphyromonas asaccharolytica
Anaerostipes hadrus	Bifidobacterium bifidum	Collinsella aerofaciens	Gordonibacter pamelaecae	Roseburia hominis
Anaerostipes hadrus	Bifidobacterium catenulatum	Collinsella aerofaciens	Gordonibacter pamelaecae	Roseburia hominis
Anaerotruncus massiliensis	Bifidobacterium dentium	Coprococcus comes	Holdemanella biformis	Ruminococcaceae sp. FBI00097
Bacteroides caccae	Bifidobacterium longum	Coprococcus comes	Hungatella effluvii	Ruminococcaceae sp. FBI00233
Bacteroides caccae	Bifidobacterium longum	Coprococcus eutactus	Hungatella effluvii	Ruminococcus bromii
Bacteroides coprocola	Bifidobacterium pseudocatenulatum	Dialister invisus	Hungatella hathewayi	Ruminococcus bromii
Bacteroides faecis	Bifidobacterium pseudocatenulatum	Dialister succinatiphilus	Lachnoclostridium pacaense	Ruminococcus faecis
Bacteroides finegoldii	Bifidobacterium pseudocatenulatum	Dielma fastidiosa	Lachnoclostridium pacaense	Ruminococcus faecis
Bacteroides fragilis	Bifidobacterium adolescentis	Dorea formicigenerans	Lachnospiraceae sp. FBI00033	Ruthenibacterium lactatiformans
Bacteroides kribbi	Bilophila wadsworthia	Dorea formicigenerans	Lachnospiraceae sp. FBI00071	Senegalimassilia anaerobia
Bacteroides kribbi	Bilophila wadsworthia	Dorea longicatena	Lachnospiraceae sp. FBI00290	Sutterella massiliensis
Bacteroides massiliensis	Blautia faecis	Dorea longicatena	Lactobacillus rogosae	Sutterella wadsworthensis
Bacteroides nordii	Blautia hydrogenotrophica	Eggerthella lenta	Lactobacillus rogosae	Sutterella wadsworthensis
Bacteroides ovatus	Blautia massiliensis	Eggerthella lenta	Longicatena caecimuris	Turicibacter sanguinis
Bacteroides salyersiae	Blautia obeum	Eggerthella lenta	Megasphaera massiliensis	
Bacteroides stercorisoris	Blautia obeum	Eggerthella lenta	Methanobrevibacter smithii	

In certain embodiments, the Consortia comprises the microbiota listed in Table 1. In certain embodiments, the Consortia comprises the microbiota listed in Table 2. In certain embodiments, the Consortia comprises the microbiota listed in Table 3. In certain embodiments, the Consortia comprises the microbiota listed in Table 4. In certain embodiments, the Consortia comprises the microbiota listed in Table 5. In certain embodiments, the Consortia comprises the microbiota listed in Table 6. In certain embodiments, the Consortia comprises the microbiota listed in Table 7. In certain embodiments, the Consortia comprises the microbiota listed in Table 8. In certain embodiments, the Consortia comprises the microbiota listed in Table 9. In certain embodiments, the

Consortia comprises the microbiota listed in Table 10. In certain embodiments, the Consortia comprises the microbiota listed in Table 11. In certain embodiments, the Consortia comprises the microbiota listed in Table 12. In certain embodiments, the Consortia comprises the microbiota listed in Table 13. In certain embodiments, the Consortia comprises the microbiota listed in Table 14. In certain embodiments, the Consortia comprises the microbiota listed in Table 15. In certain embodiments, the Consortia comprises the microbiota listed in Table 16. In certain embodiments, the Consortia comprises the microbiota listed in Table 17. In certain embodiments, the Consortia comprises the microbiota listed in Table 18. In certain embodiments, the Consortia comprises the microbiota listed in Table 19.

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at least 90% or at least 95% identical to those listed in Table 18. In certain embodiments, the Consortia comprises the microbiota that are at least 90% or at least 95% identical to those listed in Table 19.

In certain embodiments, a microbial consortium described herein comprises a microbial strain having a relative abundance of approximately 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 10%, 5%, 1%, 0.1%, 0.01%, 0.001%, 0.0001%, 0.00001%, or 0.000001% of the total microbial consortium. In certain embodiments, the relative abundance of a microbial strain is determined by metagenomic sequencing and calculated as the percentage of reads that are classified as an identified microbial strain, divided by the genome size. In certain embodiments, the relative abundance of a microbial strain of the present disclosure is determined by metagenomic shotgun sequencing.

In certain embodiments, the Consortia comprises the microbiota that are at least 90% or at least 95% identical to those listed in Table 22. Table 22 is provided below:

Table 22. FB-001 Drug Substances

Drug Substance (DS) (aka CoCulture, CoC)	Strain ID	Strain Species
DS1	FBI00001	<i>Clostridium citroniae</i>
	FBI00002	<i>Bacteroides salyersiae</i>
	FBI00010	<i>Blautia obeum</i>
	FBI00013	<i>Parabacteroides merdae</i>
	FBI00029	<i>Parabacteroides distasonis</i>
	FBI00032	<i>Anaerostipes hadrus</i>
	FBI00033	<i>Lachnospiraceae</i> sp. FBI00033
	FBI00034	<i>Eubacterium eligens</i>
	FBI00043	<i>Bifidobacterium dentium</i>
	FBI00044	<i>Blautia wexlerae</i>
	FBI00048	<i>Fusicatenibacter saccharivorans</i>
	FBI00050	<i>Bacteroides nordii</i>
	FBI00051	<i>Dorea formicigenerans</i>
	FBI00057	<i>Dorea longicatena</i>
	FBI00059	<i>Bacteroides stercorisoris</i>
	FBI00060	<i>Bifidobacterium longum</i>
	FBI00070	<i>Bacteroides kribbi</i>
	FBI00071	<i>Lachnospiraceae</i> sp. FBI00071
	FBI00076	<i>Bacteroides thetaiotaomicron</i>
	FBI00079	<i>Clostridium clostridioforme</i>
	FBI00087	<i>Clostridium scindens</i>
	FBI00093	<i>Roseburia hominis</i>
	FBI00102	<i>Clostridium fessum</i>
	FBI00109	<i>Coprococcus comes</i>
	FBI00117	<i>Blautia faecis</i>
	FBI00120	<i>Hungatella hathewayi</i>
	FBI00125	<i>Bacteroides stercoris</i>
	FBI00127	<i>Collinsella aerofaciens</i>
	FBI00128	<i>Hungatella effluvii</i>
	FBI00145	<i>Bifidobacterium adolescentis</i>
	FBI00162	<i>Bifidobacterium catenulatum</i>
	FBI00174	<i>Lactobacillus rogosae</i>
	FBI00184	<i>Bacteroides faecis</i>

	FBI00190	Bacteroides finegoldii
	FBI00191	Clostridiaceae sp. FBI00191
	FBI00194	Ruminococcus faecis
	FBI00198	Lachnoclostridium pacaense
	FBI00199	Clostridium boltea
	FBI00200	Longicatena caecimuris
	FBI00201	Eggerthella lenta
	FBI00205	Blautia massiliensis
	FBI00206	Bacteroides xylanisolvens
	FBI00211	Bacteroides vulgatus
	FBI00220	Megasphaera massiliensis
	FBI00221	Butyricimonas faecihominis
	FBI00236	Eisenbergiella tayi
	FBI00245	Acidaminococcus intestini
	FBI00248	Emergencia timonensis
	FBI00251	Bifidobacterium pseudocatenulatum
	FBI00254	Eubacterium hallii
	FBI00267	Anaerofustis stercorihominis
	FBI00278	Eubacterium ventriosum
	FBI00288	Blautia hydrogenotrophica
	FBI00290	Lachnospiraceae sp. FBI00290
DS2	FBI00004	Acutalibacter timonensis
	FBI00012	Alistipes onderdonkii
	FBI00015	Bacteroides uniformis
	FBI00018	Eubacterium rectale
	FBI00019	Alistipes timonensis
	FBI00021	Bacteroides kribbi
	FBI00038	Coprococcus eutactus
	FBI00040	Bilophila wadsworthia
	FBI00046	Bacteroides caccae
	FBI00061	Alistipes shahii
	FBI00066	Parasutterella excrementihominis
	FBI00075	Paraprevotella clara
	FBI00077	Sutterella wadsworthensis
	FBI00080	Sutterella massiliensis
	FBI00081	Porphyromonas asaccharolytica
	FBI00085	Ruminococcus bromii
	FBI00092	Monoglobus pectinilyticus
	FBI00097	Ruminococcaceae sp. FBI00097
	FBI00099	Gordonibacter pamelaeae
	FBI00112	Bacteroides uniformis
	FBI00132	Gordonibacter pamelaeae
	FBI00137	Bacteroides fragilis
	FBI00140	Phascolarctobacterium faecium
	FBI00149	Monoglobus pectinilyticus
	FBI00151	Clostridium aldenense
	FBI00176	Ruthenibacterium lactatiformans
	FBI00189	Bacteroides ovatus
	FBI00197	Bifidobacterium bifidum
	FBI00208	Anaerotruncus massiliensis
	FBI00212	Clostridium aldenense
	FBI00224	Sutterella wadsworthensis
	FBI00226	Catabacter hongkongensis
	FBI00229	Alistipes senegalensis
	FBI00233	Ruminococcaceae sp. FBI00233
	FBI00235	Alistipes shahii
	FBI00237	Dielma fastidiosa
	FBI00243	Eubacterium siraeum

	FBI00244	Faecalibacterium prausnitzii
	FBI00258	Turicibacter sanguinis
	FBI00260	Eubacterium rectale
	FBI00263	Bacteroides caccae
	FBI00270	Methanobrevibacter smithii
	FBI00273	Barnesiella intestinihominis
	FBI00277	Alistipes onderdonkii
	FBI00292	Methanobrevibacter smithii
DS3	FBI00009	Bifidobacterium adolescentis
	FBI00011	Bifidobacterium longum
	FBI00016	Bifidobacterium pseudocatenulatum
	FBI00020	Bacteroides thetaiotaomicron
	FBI00025	Coprococcus comes
	FBI00027	Fusicatenibacter saccharivorans
	FBI00030	Eggerthella lenta
	FBI00047	Eubacterium eligens
	FBI00052	Bacteroides xylanisolvens
	FBI00053	Lactobacillus rogosae
	FBI00056	Clostridium citroniae
	FBI00062	Collinsella aerofaciens
	FBI00078	Blautia obeum
	FBI00096	Eggerthella lenta
	FBI00104	Blautia wexlerae
	FBI00110	Lachnoclostridium pacaense
	FBI00111	Bacteroides vulgatus
	FBI00113	Parabacteroides merdae
	FBI00115	Dorea formicigenerans
	FBI00116	Ruminococcus faecis
	FBI00123	Roseburia hominis
	FBI00124	Anaerostipes hadrus
	FBI00126	Bifidobacterium adolescentis
	FBI00135	Bifidobacterium pseudocatenulatum
	FBI00147	Clostridium bolteae
	FBI00159	Eisenbergiella tavi
	FBI00167	Dorea longicatena
	FBI00170	Eggerthella lenta
	FBI00232	Bacteroides stercoris
	FBI00255	Hungatella hathewayi
	FBI00271	Bacteroides xylanisolvens
DS4	FBI00022	Alistipes putredinis
	FBI00049	Dialister succinatiphilus
	FBI00068	Akkermansia muciniphila
	FBI00069	Ruminococcus bromii
	FBI00152	Dialister invisus
	FBI00165	Bacteroides massiliensis
	FBI00171	Bilophila wadsworthia
	FBI00175	Holdemanella bififormis
	FBI00177	Parasutterella excrementihominis
	FBI00180	Alistipes sp. FBI00180
	FBI00182	Bacteroides coprocola
	FBI00238	Alistipes sp. FBI00238
	FBI00269	Alistipes putredinis
	FBI00274	Eubacterium xylanophilum
	FBI00281	Senegalimassilia anaerobia
DS5 (DS-OF1)	FBI00067	Oxalobacter formigenes
DS6 (DS-OF2)	FBI00133	Oxalobacter formigenes
DS7 (DS-OF3)	FBI00289	Oxalobacter formigenes

In certain embodiments, the Consortia comprises the microbiota that are at least 90% or at least 95% identical to those listed in any of Tables 1-19.

In certain embodiments, a Consortia comprises a microbial strain having a relative abundance of approximately 90%, 80%, 70%, 60%, 50%, 40%, 30%, 20%, 10%, 5%, 1%, 0.1%, 0.01%, 0.001%, 0.0001%, 0.00001%, or 0.000001% of the total microbial consortium. In certain embodiments, the relative abundance of a microbial strain is determined by metagenomic sequencing and calculated as the percentage of reads that are classified as an identified microbial strain, divided by the genome size. In certain embodiments, the relative abundance of a microbial strain of the present disclosure is determined by metagenomic shotgun sequencing.

10 *Active Microbes*

The Consortia described herein comprise a plurality of active microbes capable of metabolizing a first metabolic substrate that causes or contributes to disease in an animal. In certain embodiments, the current disclosure provides a microbial consortium capable of metabolizing the first metabolic substrate at a pH within a range of 4 to 8. For example, in certain non-limiting
15 embodiments, one or more than one of the plurality of active microbes is capable of metabolizing a first metabolic substrate at a pH within a range of about 4 to about 8, about 4.2 to about 8, about 4.4 to about 8, about 4.6 to about 8, about 4.8 to about 8, about 5 to about 8, about 5.2 to about 8, about 5.4 to about 8, about 5.6 to about 8, about 5.8 to about 8, about 6 to about 8, about 6.2 to about 8, about 6.4 to about 8, about 6.6 to about 8, about 6.8 to about 8, about 7 to about 8, about 7.2 to about
20 8, about 7.4 to about 8, about 7.6 to about 8, about 7.8 to about 8, about 4 to about 7, about 4.2 to about 7, about 4.4 to about 7, about 4.6 to about 7, about 4.8 to about 7, about 5 to about 7, about 5.2 to about 7, about 5.4 to about 7, about 5.6 to about 7, about 5.8 to about 7, about 6 to about 7, about 6.2 to about 7, about 6.4 to about 7, about 6.6 to about 7, about 6.8 to about 7, about 4 to about 6, about 4.2 to about 6, about 4.4 to about 6, about 4.6 to about 6, about 4.8 to about 6, about 5 to about
25 6, about 5.2 to about 6, about 5.4 to about 6, about 5.6 to about 6, about 5.8 to about 6, about 4 to about 6, about 4.2 to about 6, about 4.4 to about 6, about 4.6 to about 6, about 4.8 to about 6, about 5 to about 6, about 5.2 to about 6, about 5.4 to about 6, about 5.6 to about 6, or about 5.8 to about 6.

In certain embodiments, the plurality of active microbes comprises one microbial strain having a significantly different first metabolic substrate-metabolizing activity in a standard substrate-metabolizing assay conducted at two pH values differing by 1 pH unit and within a pH range of
30 about 4 to about 8. In certain embodiments, the difference between the two pH values is about 1.0, about 1.1, about 1.2, about 1.3, about 1.4, about 1.5, about 1.6, about 1.7, about 1.8, about 1.9, about 2.0, about 2.1, about 2.2, about 2.3, about 2.4, about 2.5, about 2.6, about 2.7, about 2.8, about 2.9,

about 3.0, about 3.2, about 3.3, about 3.4, about 3.5, about 3.6, about 3.7, about 3.8, about 3.9, or about 4.0 pH units. For example, in certain non-limiting embodiments, one microbial strain has significantly different first metabolic substrate-metabolizing activities in a standard substrate metabolizing assay at pH 4 and pH 8, pH 5 and pH 8, pH 6 and pH 8, pH 7 and pH 8, pH 4 and pH 7, pH 5 and pH 7, pH 6 and pH 7, pH 4 and pH 6, pH 5 and pH 6, or pH 4 and pH 5.

As used herein, “lower pH” or a “low pH” refers to a pH in a standardized substrate metabolization assay that is lower in value as compared to another pH value. For example, a standardized substrate metabolization assay performed at pH 4.5 has a lower pH as compared to a standardized substrate metabolization assay performed at a pH of 7.5. “Higher pH,” as used herein, refers to a pH in a standardized substrate metabolization assay that is higher in value as compared to another pH value. For example a standardized substrate metabolization assay performed at pH 7.5 has a higher pH as compared to a standardized substrate metabolization assay performed at a pH of 4.5.

As used herein, “higher first metabolic substrate-metabolizing activity” means either a first metabolic substrate-metabolizing activity of a microbial strain that is higher as compared to a first metabolic substrate-metabolizing activity of the same microbial strain under different conditions, and/or a first metabolic substrate-metabolizing activity of a microbial strain that is higher as compared to a first metabolic substrate-metabolizing activity of a different microbial strain under the same conditions.

In certain embodiments, the plurality of active microbes comprises two microbial strains having significantly different first metabolic substrate-metabolizing activities. For example, in certain non-limiting embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a lower pH as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at the same lower pH. In certain embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5, respectively. In certain embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a higher pH as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at the same higher pH. In certain embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0 as compared to the first metabolic substrate-metabolizing activity

of another microbial strain in the plurality of active microbes at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0, respectively.

In certain embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a lower pH as compared to its first metabolic substrate-metabolizing activity at a higher pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 than it does at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0. In certain embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a higher pH as compared to its first metabolic substrate-metabolizing activity at a lower pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0 than it does at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5.

In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at a lower pH and another microbe having a higher first metabolic substrate-metabolizing activity at a higher pH. For example, in certain non-limiting embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.5. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.6. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.7. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.8. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.9. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.0 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 8.0. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 4.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.5. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first

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metabolizing activity at pH 7.8. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at pH 6.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 7.9. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first
5 metabolic substrate-metabolizing activity at pH 6.5 and another microbe having a higher first metabolic substrate-metabolizing activity at pH 8.0.

In certain embodiments, the plurality of active microbes comprises one microbial strain having a significantly different first metabolic substrate-metabolizing activity in a standard substrate-metabolizing assay conducted at a first metabolic substrate concentration as compared to its first
10 metabolic substrate-metabolizing activity in a standard substrate-metabolizing assay conducted at a different first metabolic substrate concentration, wherein the difference between the two first metabolic substrate concentrations is within a 100 fold range. In certain embodiments, the difference between the two first metabolic concentrations is about 1.2 fold. For example, in certain non-limiting
15 embodiments, the difference between the two first metabolic substrate concentrations is at least about 1.2 fold, about 1.4 fold, about 1.6 fold, about 1.8 fold, about 2.0 fold, about 4 fold, about 6 fold, about 8 fold, about 10 fold, about 20 fold, about 30 fold, about 40 fold, about 50 fold, about 60 fold, about 70 fold, about 80 fold, about 90 fold, or about 100 fold or greater.

As used herein, “lower concentration of first metabolic substrate” refers to a substrate concentration in a standardized substrate metabolization assay that is lower in value as compared to
20 another substrate concentration. “Higher concentration of first metabolic substrate,” as used herein, refers to a substrate concentration in a standardized substrate metabolization assay that is higher in value as compared to another substrate concentration.

In certain embodiments, the plurality of active microbes comprises two microbial strains having significantly different first metabolic substrate-metabolizing activities. For example, in
25 certain non-limiting embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a lower concentration of first metabolic substrate as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at the same lower concentration of first metabolic substrate. In certain
30 embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a higher concentration of first metabolic substrate as compared to the first metabolic substrate-metabolizing activity of another microbial strain in the plurality of active microbes at the same higher concentration of first metabolic substrate.

In certain embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a lower concentration of first metabolic substrate as

compared to its first metabolic substrate-metabolizing activity at a higher concentration of first metabolic substrate. In certain embodiments, one of the plurality of active microbes has a significantly higher first metabolic substrate-metabolizing activity at a higher concentration of first metabolic substrate as compared to its first metabolic substrate-metabolizing activity at a lower concentration of first metabolic substrate.

In certain embodiments, the plurality of active microbes comprises an active microbe having a higher first metabolic substrate-metabolizing activity at a lower concentration of first metabolic substrate and another microbe having a higher first metabolic substrate-metabolizing activity at a higher concentration of first metabolic substrate. For example, in certain non-limiting embodiments, the difference between the lower concentration of first metabolic substrate and the higher concentration of first metabolic substrate is at least about 1.2 fold, about 1.4 fold, about 1.6 fold, about 1.8 fold, about 2.0 fold, about 4 fold, about 6 fold, about 8 fold, about 10 fold, about 20 fold, about 30 fold, about 40 fold, about 50 fold, about 60 fold, about 70 fold, about 80 fold, about 90 fold, or about 100 fold or greater.

In certain embodiments, the plurality of active microbes comprises two microbial strains having significantly different growth rates. For example, in certain non-limiting embodiments, one of the plurality of active microbes has a significantly higher growth rate at a lower pH as compared to the growth rate of another microbial strain in the plurality of active microbes at the same lower pH. In certain embodiments, one of the plurality of active microbes has a significantly higher growth rate at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 as compared to the growth rate of another microbial strain in the plurality of active microbes at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5, respectively. In certain embodiments, one of the plurality of active microbes has a significantly higher growth rate at a higher pH as compared to the growth rate of another microbial strain in the plurality of active microbes at the same higher pH. In certain embodiments, one of the plurality of active microbes has a significantly higher growth rate at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0 as compared to the growth rate of another microbial strain in the plurality of active microbes at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0, respectively.

In certain embodiments, one of the plurality of active microbes has a significantly higher growth rate at a lower pH as compared to its growth rate at a higher pH. For example, in some embodiments one of the plurality of active microbes has a significantly higher growth rate at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 than it does at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0. In certain embodiments, one of the plurality of active microbes has a significantly higher growth rate at a higher pH as compared to its growth rate at a lower pH. For example, in some embodiments one of the plurality of active

microbes has a significantly higher growth rate at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0 than it does at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5.

In certain embodiments, the plurality of active microbes comprises one microbial strain having a significantly higher growth rate when cultured in media containing a certain concentration of first metabolic substrate concentration as compared to the growth rate of another microbial strain in the plurality of active microbes cultured in the same media containing the same concentration of the first metabolic substrate. In certain embodiments, the difference between the two growth rates is at least about 0.2 fold, at least about 0.4 fold, at least about 0.6 fold, at least about 0.8 fold, at least about 1.0 fold, at least about 1.2 fold, at least about 1.4 fold, at least about 1.6 fold, at least about 1.8 fold, or at least about 2.0 fold.

In certain embodiments, the first metabolic substrate may be selected from, but not limited to, oxalate and a bile acid (*e.g.*, lithocholic acid (LCA), deoxycholic acid (DCA)).

In certain embodiments, the current disclosure provides a microbial consortium comprising a plurality of active microbes capable of metabolizing a first metabolic substrate to one or more than one metabolite. For example, in certain non-limiting embodiments, the one or more than one metabolite may be selected from, but not limited to, formate, CO₂, and a secondary bile acid (*e.g.*, 3-oxo-deoxycholic acid (3 oxoDCA), 3-oxo-lithocholic acid (3oxoLCA), iso-lithocholic acid (iso-LCA), or iso-deoxycholic acid (iso-DCA)). In certain embodiments, the plurality of active microbes can comprise 2 to 200 microbial strains. For example, in certain non-limiting embodiments, a microbial consortium comprises 2 to 10, 2 to 15, 2 to 20, 2 to 25, 2 to 30, 2 to 35, 2 to 40, 2 to 45, 2 to 50, 2 to 75, 2 to 100, 2 to 125, 2 to 150, 2 to 175, or 2 to 200 active microbial strains. In certain embodiments, the plurality of active microbes can comprise 2 to 20 microbial strains.

Oxalate-Metabolizing Active Microbes

The Consortia described herein comprise a plurality of active microbes that metabolize oxalate. In certain embodiments, each of the plurality of active microbes that metabolize oxalate express sufficient amounts of one or more than one enzyme involved in oxalate metabolism. For example, in certain non-limiting embodiments, one or more than one active microbe expresses formyl-CoA transferase (*Frc*), an oxalate-formate antiporter (*e.g.*, *OxIT*), and oxalyl-CoA decarboxylase (*e.g.*, *OxC*), and/or oxalate decarboxylase (*e.g.*, *OxD*).

In certain embodiments, the plurality of active microbes that metabolize oxalate comprise 2 to 20 oxalate-metabolizing microbial strains. In certain embodiments, the plurality of active microbes that metabolize oxalate comprise 2 to 5 oxalate-metabolizing microbial strains. In certain embodiments, the plurality of active microbes that metabolize oxalate comprise 2 to 7 oxalate-

metabolizing microbial strains. In certain embodiments, the plurality of active microbes that metabolize oxalate comprise 2 to 7 oxalate-metabolizing microbial strains. In certain embodiments, the plurality of active microbes that metabolize oxalate comprise more than 20 oxalate-metabolizing microbial strains. In certain embodiments, the plurality of active microbes comprises 3 strains of oxalate-metabolizing microbes. In certain embodiments, 2 or more of the active microbes are different strains of the same species.

In certain embodiments, the plurality of active microbes that metabolize oxalate may comprise one or more microbial species selected from, but not limited to *Oxalobacter formigenes*, *Bifidobacterium* sp., *Bifidobacterium dentium*, *Dialister invisus*, *Lactobacillus acidophilus*, *Lactobacillus gasseri*, *Lactobacillus helveticus*, *Lactobacillus reuteri*, *Eggerthella lenta*, *Lactobacillus rhamnosus*, *Enterococcus faecalis*, *Enterococcus gallinarum*, *Enterococcus faecium*, *Providencia rettgeri*, *Streptococcus thermophilus*, *Lactobacillus plantarum*, *Lactobacillus casei*, *Lactobacillus salivarius*, *Lactobacillus johnsii*, *Bifidobacterium infantis*, *Bifidobacterium animalis*, *Clostridium sporogenes*, *Leuconostoc lactis*, or *Leuconostoc mesenteroides*.

In certain embodiments, the Consortia described herein comprise 3 strains of *Oxalobacter formigenes*. In certain embodiments, the Consortia described herein comprise 3 strains of *Oxalobacter formigenes*, each with different phenotypic properties. In certain embodiments, the Consortia described herein comprise 3 strains of *Oxalobacter formigenes* wherein 1 strain is low pH tolerant, 1 strain is high oxalate tolerant, and 1 strain has a high growth rate. In certain embodiments, the low pH tolerance is approximately pH 5. In certain embodiments, the high oxalate tolerance is approximately 150mM. In certain embodiments, the high oxalate tolerance is approximately 15 mM.

In certain embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146. In certain embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146. In certain embodiments, the plurality of active microbes comprises three *Oxalobacter formigenes* strains, wherein the first, second, and third have a respective 16S sequence that is identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146. In certain embodiments, the plurality of active microbes comprises three *Oxalobacter formigenes* strains, wherein the first, second, and third have a respective 16S sequence that is at least about 90%, at least about 91%, at

least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146. In certain embodiments, the plurality of active microbes comprises three *Oxalobacter formigenes* strains, wherein the first, second, and third have a respective 16S sequence that is at least about 97% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

In some embodiments the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 42 and an *Oxalobacter formigenes* strain having a 16S sequence at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 79. In certain embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%, identical to the nucleotide sequence set forth in SEQ ID NO: 42 and an *Oxalobacter formigenes* strain having a 16S sequence at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to the nucleotide sequence set forth in SEQ ID NO: 79.

In some embodiments the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 42 and an *Oxalobacter formigenes* strain having a 16S sequence at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 146. In certain embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to the nucleotide sequence set forth in SEQ ID NO: 42 and an *Oxalobacter formigenes* strain having a 16S sequence at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to the nucleotide sequence set forth in SEQ ID NO: 146.

In some embodiments the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least 80% identical to the nucleotide sequence set forth in SEQ ID NO: 79 and an *Oxalobacter formigenes* strain having a 16S sequence at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 146. In certain embodiments, the plurality of active microbes comprises an *Oxalobacter formigenes* strain having a 16S sequence at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at

least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to the nucleotide sequence set forth in SEQ ID NO: 79 and an *Oxalobacter formigenes* strain having a 16S sequence at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99% identical to the nucleotide sequence set forth in SEQ ID NO: 146.

As used herein, “substantially metabolizing oxalate,” “substantial metabolization of oxalate,” and variants thereof, refer to a statistically significant reduction in the amount of oxalate in an *in vitro* assay. In certain embodiments, one or more than one of the plurality of active microbes is capable of substantially metabolizing oxalate at a pH within a range of 4 to 8. In certain embodiments, one or more than one of the plurality of active microbes is capable of metabolizing oxalate at a pH within a range of about 4 to about 8, about 4.2 to about 8, about 4.4 to about 8, about 4.6 to about 8, about 4.8 to about 8, about 5 to about 8, about 5.2 to about 8, about 5.4 to about 8, about 5.6 to about 8, about 5.8 to about 8, about 6 to about 8, about 6.2 to about 8, about 6.4 to about 8, about 6.6 to about 8, about 6.8 to about 8, about 7 to about 8, about 7.2 to about 8, about 7.4 to about 8, about 7.6 to about 8, about 7.8 to about 8, about 4 to about 7, about 4.2 to about 7, about 4.4 to about 7, about 4.6 to about 7, about 4.8 to about 7, about 5 to about 7, about 5.2 to about 7, about 5.4 to about 7, about 5.6 to about 7, about 5.8 to about 7, about 6 to about 7, about 6.2 to about 7, about 6.4 to about 7, about 6.6 to about 7, about 6.8 to about 7, about 4 to about 6, about 4.2 to about 6, about 4.4 to about 6, about 4.6 to about 6, about 4.8 to about 6, about 5 to about 6, about 5.2 to about 6, about 5.4 to about 6, about 5.6 to about 6, about 5.8 to about 6, about 4 to about 6, about 4.2 to about 6, about 4.4 to about 6, about 4.6 to about 6, about 4.8 to about 6, about 5 to about 6, about 5.2 to about 6, about 5.4 to about 6, about 5.6 to about 6, or about 5.8 to about 6.

In certain embodiments, the plurality of active microbes comprises one microbial strain having a significantly different oxalate-metabolizing activity in a standard oxalate metabolizing assay conducted at two pH values differing by at least 1 pH unit and within a pH range of 4 to 8. In certain embodiments, one microbial strain has significantly different oxalate-metabolizing activities in a standard oxalate metabolizing assay at pH 4 and pH 8, pH 5 and pH 8, pH 6 and pH 8, pH 7 and pH 8, pH 4 and pH 7, pH 5 and pH 7, pH 6 and pH 7, pH 4 and pH 6, pH 5 and pH 6, or pH 4 and pH 5.

In certain embodiments, oxalate-metabolizing activity is detected using a standard oxalate metabolization assay. In certain embodiments, oxalate-metabolizing activity is detected using a colorimetric enzyme assay that measures the activity of oxalate oxidase. In certain embodiments, relative changes in oxalate abundance in culture media inoculated with microbial strains are measured using a commercial oxalate assay kit (*e.g.*, Sigma-Aldrich, Catalog# MAK315). In certain embodiments, oxalate-metabolizing activity is detected using liquid chromatography–mass

spectrometry (LC-MS/MS). In certain embodiments, relative changes in oxalate abundance is compared between the abundance of oxalate at the beginning of incubation (*i.e.* $t=0$), and after about 2 hours, about 4 hours, about 6 hours, about 8, hours, about 10 hours, about 12 hours, about 14 hours, about 16 hours, about 18 hours, about 24 hours, about 30 hours, about 36 hours, about 48 hours, about 60 hours, about 72 hours, about 84 hours, about 96 hours, about 120 hours, or about 144 hours incubation.

As used herein, “higher oxalate metabolizing activity” means either an oxalate metabolizing activity of a microbial strain that is higher as compared to an oxalate metabolizing activity of the same microbial strain under different conditions, and/or an oxalate metabolizing activity of a microbial strain that is higher as compared to an oxalate metabolizing activity of a different microbial strain under the same conditions.

In certain embodiments, the plurality of active microbes comprises two microbial strains having significantly different oxalate metabolizing activities. In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a lower pH as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at the same lower pH. In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5, respectively. In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a higher pH as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at the same higher pH. In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0 as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0, respectively.

In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a lower pH as compared to its oxalate metabolizing activity at a higher pH. In certain embodiments one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5 than it does at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0. In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a higher pH as compared to its oxalate metabolizing activity at a lower pH. In certain embodiments one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at pH 7.5, 7.6, 7.7, 7.8, 7.9, or 8.0 than it does at pH 4.0, 4.5, 5.0, 5.5, 6.0, or 6.5.

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[illegible]

plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.0 and another microbe having a higher oxalate metabolizing activity at pH 8.0. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.5. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.6. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.7. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.8. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 7.9. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at pH 6.5 and another microbe having a higher oxalate metabolizing activity at pH 8.0.

In certain embodiments, one or more than one of the plurality of active microbes is capable of substantially metabolizing oxalate at an oxalate concentration of about 0.75 mM to about 40 mM of oxalate. In certain embodiments, one or more than one of the plurality of active microbes is capable of substantially metabolizing oxalate at an oxalate concentration within a range of about 0.75 mM to about 40 mM, of about 1 mM to about 40 mM, of about 2.5 mM to about 40 mM, of about 5 mM to about 40 mM, of about 7.5 mM to about 40 mM, of about 10 mM to about 40 mM, of about 15 mM to about 40 mM, of about 20 mM to about 40 mM, of about 25 mM to about 40 mM, of about 30 mM to about 40 mM, of about 0.75 mM to about 30 mM, of about 1 mM to about 30 mM, of about 2.5 mM to about 30 mM, of about 5 mM to about 30 mM, of about 7.5 mM to about 30 mM, of about 10 mM to about 30 mM, of about 15 mM to about 30 mM, of about 20 mM to about 30 mM, of about 25 mM to about 30 mM, of about 0.75 mM to about 25 mM, of about 1 mM to about 25 mM, of about 2.5 mM to about 25 mM, of about 5 mM to about 25 mM, of about 7.5 mM to about 25 mM, of about 10 mM to about 25 mM, of about 15 mM to about 25 mM, of about 20 mM to about 25 mM, of about 0.75 mM to about 20 mM, of about 1 mM to about 20 mM, of about 2.5 mM to about 20 mM, of about 5 mM to about 20 mM, of about 7.5 mM to about 20 mM, of about 10 mM to about 20 mM, of about 15 mM to about 20 mM, of about 0.75 mM to about 15 mM, of about 1 mM to about 15 mM, of about 2.5 mM to about 15 mM, of about 5 mM to about 15 mM, of about 7.5 mM to about 15 mM, of about 10 mM to about 15 mM, of about 0.75 mM to about 10 mM, of

about 1 mM to about 10 mM, of about 2.5 mM to about 10 mM, of about 5 mM to about 10 mM, of about 7.5 mM to about 10 mM, of about 0.75 mM to about 5 mM, of about 1 mM to about 5 mM, of about 2.5 mM to about 5 mM, or of about 0.75 mM to about 1 mM.

In certain embodiments, the plurality of active microbes comprises one microbial strain
5 having a significantly different oxalate-metabolizing activity in a standard *in vitro* oxalate
metabolizing assay at an oxalate concentration as compared to its oxalate-metabolizing activity in a
standard *in vitro* oxalate metabolizing assay conducted at a different oxalate concentration, wherein
the difference between the two oxalate concentrations is within 100 fold. In certain embodiments,
one microbial strain has significantly different oxalate-metabolizing activities in a standard oxalate
10 metabolizing assay conducted at about 0.75 mM oxalate and about 40 mM oxalate, about 1 mM and
about 40 mM, about 2.5 mM and about 40 mM, about 5 mM and about 40 mM, about 7.5 mM and
about 40 mM, about 10 mM and about 40 mM, about 15 mM and about 40 mM, about 20 mM and
about 40 mM, about 25 mM and about 40 mM, about 30 mM and about 40 mM, about 0.75 mM and
about 30 mM, about 1 mM and about 30 mM, about 2.5 mM and about 30 mM, about 5 mM and
15 about 30 mM, about 7.5 mM and about 30 mM, about 10 mM and about 30 mM, about 15 mM and
about 30 mM, about 20 mM and about 30 mM, about 25 mM and about 30 mM, about 0.75 mM and
about 25 mM, about 1 mM and about 25 mM, about 2.5 mM and about 25 mM, about 5 mM and
about 25 mM, about 7.5 mM and about 25 mM, about 10 mM and about 25 mM, about 15 mM and
about 25 mM, about 20 mM and about 25 mM, about 0.75 mM and about 20 mM, about 1 mM and
20 about 20 mM, about 2.5 mM and about 20 mM, about 5 mM and about 20 mM, about 7.5 mM and
about 20 mM, about 10 mM and about 20 mM, about 15 mM and about 20 mM, about 0.75 mM and
about 15 mM, about 1 mM and about 15 mM, about 2.5 mM and about 15 mM, about 5 mM and
about 15 mM, about 7.5 mM and about 15 mM, about 10 mM and about 15 mM, about 0.75 mM and
about 10 mM, about 1 mM and about 10 mM, about 2.5 mM and about 10 mM, about 5 mM and
25 about 10 mM, about 7.5 mM and about 10 mM, about 0.75 mM and about 5 mM, about 1 mM and
about 5 mM, about 2.5 mM and about 5 mM, or about 0.75 mM and about 1 mM.

In certain embodiments, the plurality of active microbes comprises two microbial strains
having significantly different oxalate metabolizing activities. In certain embodiments, one of the
plurality of active microbes has a significantly higher oxalate metabolizing activity at a lower
30 concentration of oxalate as compared to the oxalate metabolizing activity of another microbial strain
in the plurality of active microbes at the same lower concentration of oxalate. In certain
embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing
activity at an oxalate concentration of about 0.75 mM, about 1 mM, about 2.5 mM, about 5 mM, or
about 7.5 mM, as compared to the oxalate metabolizing activity of another microbial strain in the

plurality of active microbes at an oxalate concentration of about 0.75 mM, about 1 mM, about 2.5 mM, about 5 mM, or about 7.5 mM, respectively. In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a higher concentration of oxalate as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at the same higher concentration of oxalate. In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at an oxalate concentration of about 15 mM, about 20 mM, about 25 mM, about 30 mM, or about 40 mM as compared to the oxalate metabolizing activity of another microbial strain in the plurality of active microbes at an oxalate concentration of about 15 mM, about 20 mM, about 25 mM, about 30 mM, or about 40 mM, respectively.

In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a lower oxalate concentration as compared to its oxalate metabolizing activity at a higher oxalate concentration. In certain embodiments one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at about 0.75 mM, about 1 mM, about 2.5 mM, about 5 mM, or about 7.5 mM of oxalate than it does at about 15 mM, about 20 mM, about 25 mM, about 30 mM, or about 40 mM of oxalate. In certain embodiments, one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at a higher oxalate concentration as compared to its oxalate metabolizing activity at a lower oxalate concentration. In certain embodiments one of the plurality of active microbes has a significantly higher oxalate metabolizing activity at about 15 mM, about 20 mM, about 25 mM, about 30 mM, or about 40 mM of oxalate than it does at about 0.75 mM, about 1 mM, about 2.5 mM, about 5 mM, or about 7.5 mM of oxalate.

In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at a lower concentration of oxalate and another microbe having a higher oxalate metabolizing activity at a higher concentration of oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 0.75 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 40 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 1 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 40 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 2.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 40 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 5 mM

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having a higher oxalate metabolizing activity at about 20 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 2.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 20 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 20 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 7.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 20 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 0.75 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 1 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 2.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate. In certain embodiments, the plurality of active microbes comprises an active microbe having a higher oxalate metabolizing activity at about 7.5 mM oxalate and another active microbe having a higher oxalate metabolizing activity at about 15 mM oxalate.

In certain embodiments, when tested in an *in vitro* oxalate metabolization assay a plurality of active microbes of the present disclosure significantly reduces the concentration of oxalate present in a sample by at least about 20%, by at least about 30%, by at least about 40%, by at least about 50%, by at least about 60%, by at least about 70%, or by at least about 80%.

In certain embodiments, a plurality of active microbes of the present disclosure significantly reduces the concentration of oxalate present in a sample of blood, serum, bile, stool, or urine when administered to a subject by at least about 20%, by at least about 30%, by at least about 40%, by at least about 50%, by at least about 60%, by at least about 70%, or by at least about 80% as compared to an untreated control subject or pre-administration levels. Concentrations of oxalate in a blood, serum, bile, stool or urine sample can be measured using a liquid chromatography–mass spectrometry (LC-MS).

Supportive Community of Microbes

The microbial consortia of the present disclosure further comprise a supportive community of microbes that enhances one or more than one characteristic of the plurality of active microbes. For example, in certain non-limiting embodiments, the supportive community of microbes enhances gastrointestinal engraftment of the plurality of active microbes. In other embodiments, the supportive community of microbes enhances biomass of the plurality of active microbes. In other embodiments, the supportive community of microbes enhances metabolism of the first metabolic substrate by the plurality of active microbes. In other embodiments, the supportive community of microbes enhances longitudinal stability of the plurality of active microbes.

The supportive community of microbes disclosed herein metabolize one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one metabolite inhibits metabolism of the plurality of active microbes. For example, in certain non-limiting embodiments, the supportive community of microbes metabolizes formate produced by the plurality of active microbes, wherein the presence of formate inhibits the metabolism of oxalate by the plurality of active microbes. In certain embodiments, the supportive community of microbes of the current disclosure catalyzes the fermentation of polysaccharides to one or more than one of the group consisting of acetate, acetoin, 2-oxoglutarate, propionate, 1,3-propanediol, succinate, ethanol, lactate, butyrate, 2,3-butanediol, acetone, butanol, formate, H₂, and CO₂. In certain embodiments, the supportive community of microbes catalyzes the fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate, 2-methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3-(1H-indol-3-yl)propanoate, 5-aminopentanoate, H₂, H₂S, and CO₂. In certain embodiments, the supportive community catalyzes the synthesis of one or more than one of the group consisting of methane from H₂ and CO₂, methane from formate and H₂, acetate from H₂ and CO₂, acetate from formate and H₂, acetate and sulfide from H₂, CO₂, and sulfate, propionate and CO₂ from succinate, succinate from H₂ and fumarate; synthesis of succinate from formate and fumarate, and butyrate, acetate, H₂, and CO₂ from lactate. In certain embodiments, the supportive community of microbes of the current disclosure catalyzes the deconjugation of conjugated bile acids to produce primary bile acids, the conversion of cholic acid (CA) to 7-oxocholic acid, the conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), the conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and/or the conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

Consortia Design

In certain embodiments, microbial consortia disclosed herein are designed to meet one or more than one of the following criteria:

- (i) an ability to eliminate or reduce levels of a first metabolic substrate causing or contributing to a disease in an animal;
- (ii) an ability to metabolize or convert one or more than one metabolite produced by the metabolism of the first metabolic substrate;
- (iii) an ability to metabolize one or more than one nutrient typically found in the human diet;
- (iv) an ability to fulfill unique and potentially beneficial biological functions in the gastrointestinal (GI) tract (e.g., bile salt hydrolase activity or butyrate production);
- (v) an ability to engraft in various biological niches and physical and metabolic compartments of the GI tract of an animal;
- (vi) an ability to increase biomass upon engraftment in the GI tract;
- (vii) an ability to have longitudinal stability in the GI tract of an animal;
- (viii) an ability to increase the flux of a precursor of the first metabolic substrate into a biochemical pathway that converts said precursor into a metabolite that is not the first metabolic substrate;
- (ix) diversity of component microbial species across one or more than one taxonomic phyla; and
- (x) natural prevalence of component microbial species in the GI tract of healthy adults.

In certain embodiments, the microbial consortia of the present disclosure are designed to comprise a plurality of active microbes capable of metabolizing a first metabolic substrate that causes or contributes to disease in an animal. In certain embodiments, the first metabolic substrate may be selected from, but not limited to, oxalate and a bile acid (e.g., lithocholic acid (LCA), deoxycholic acid (DCA)). In certain embodiments, the microbial consortium is designed to be capable of metabolizing the first metabolic substrate across a variety of pH ranges found within the GI tract (e.g., pH 4 to 8). In certain embodiments, the microbial consortium is designed to be capable of metabolizing the first metabolic substrate in the presence of various concentrations of first metabolic substrate as they exist in different regions of the GI tract.

In certain embodiments, the Consortia is FB-001 (Table 22) or a functional equivalent thereof. In certain embodiments, FB-001 is defined by its function. In certain embodiments, FB-001 is defined by its function as set forth in Tables 23 and/or 24. In certain embodiments, FB-001 is defined by its function as set forth in Tables 23 and 24. In certain embodiments, FB-001 is defined by its function as set forth in Table 23 or 24. In certain embodiments, FB-001 is defined by its function as

set forth in Tables 34, 35, and 36. In certain embodiments, FB-001 is defined by its function as set forth in one or more of Tables 34, 35, and 36. In certain embodiments, FB-001 is defined by its function as set forth in Tables 23, 24, 34, 35, and 36. In certain embodiments, FB-001 is defined by its function as set forth in one or more of Tables 23, 24, 34, 35, and 36. In certain embodiments, methods for determining function of FB-001 are provided in Examples 6 and 7.

Methods of Preparation

The present disclosure also provides methods for preparing and/or manufacturing the microbial consortia described herein. Figures 14-16 illustrate certain methods for the preparation and manufacturing of the microbial consortia described herein.

In certain embodiments, the methods comprise obtaining a donor stool and preparing a stool dilution. In certain embodiments, the stool dilution is plated onto an agar plate. In certain embodiments, the agar plate includes an anaerobic media. In certain embodiments, the agar plate includes colonies. Characterization and quality analysis of these colonies can be performed. For example, but without any limitation, 16s RNA and/or MALDI mass spectrometry could be performed. In certain embodiments, the characterized colonies can be further expanded in a broth culture. After growth and expansion, the microbes can be stored in vials for further use.

In certain embodiments, the microbes can be further expanded in a bioreactor including a cell culture medium. In certain embodiments, the cell culture medium can include:

a) soytone, D-cellobiose, yeast extract, dextrose (glucose), maltose monohydrate, magnesium sulfate heptahydrate, calcium chloride dihydrate, potassium phosphate monobasic, potassium phosphate dibasic, sodium chloride, sodium bicarbonate, volatile fatty acid solution, L-cysteine HCl monohydrate, hemin solution, vitamin solution, or a combination thereof; or

b) soytone, D-cellobiose, yeast extract, dextrose (glucose), maltose monohydrate, magnesium sulfate heptahydrate, calcium chloride dihydrate, potassium phosphate monobasic, potassium phosphate dibasic, sodium chloride, ammonium sulfate, sodium bicarbonate, volatile fatty acid solution, L-cysteine HCl monohydrate, hemin solution, vitamin solution, or a combination thereof.

In certain embodiments, the cell culture medium is YCFAC. In certain embodiments, the cell culture medium further comprises threonine.

In certain embodiments, the microbes can be expanded in a bioreactor in anaerobic conditions. In certain embodiments, the microbes can be expanded in a bioreactor in the presence of gas overlay. In certain embodiments, the microbes can be expanded in a bioreactor in absence of gas sparing.

In certain embodiments, the methods include expanding microbes in mixed cultures.

In certain embodiments, the methods comprise expanding microbes in a first mixed culture or composition comprising:

- a) *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*,
 5 *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae* sp. FBI00033, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorisoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae* sp. FBI00071, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*,
 10 *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catemulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Clostridiaceae* sp. FBI00191, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*,
 15 *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*, *Acidaminococcus intestini*, *Emergencia timonensis*, *Bifidobacterium pseudocatemulatum*, *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, and *Lachnospiraceae* sp. FBI00290, or a functional equivalent thereof; or

- b) FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034,
 20 FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248,
 25 FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, and FBI00290, or a functional equivalent thereof.

In certain embodiments, the methods comprise expanding microbes in a second mixed culture or composition comprising:

- a) *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae* sp. FBI00097, *Gordonibacter pamelaee*, *Bacteroides uniformis*, *Gordonibacter pamelaee*, *Bacteroides fragilis*, *Phascolarctobacterium*

faecium, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae* sp. FBI00233, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*,
 5 *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinihominis*, *Alistipes onderdonkii*, and *Methanobrevibacter smithii*, or a functional equivalent thereof; or

b) FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085,
 10 FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, and FBI00292, or a functional equivalent thereof.

In certain embodiments, the methods comprise expanding microbes in a third mixed culture
 15 or composition comprising:

a) *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatemulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia*
 20 *wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatemulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, and *Bacteroides xylanisolvens*, or a functional equivalent thereof; or

b) FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, and FBI00271, or a functional
 25 equivalent thereof.

In certain embodiments, the methods comprise expanding microbes in a fourth mixed culture
 30 or composition comprising:

a) *Alistipes putredinis*, *Dialister succinatiphilus*, *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*, *Bilophila wadsworthia*, *Holdemanella bififormis*, *Parasutterella excrementihominis*, *Alistipes* sp. FBI00180, *Bacteroides coprocola*, *Alistipes* sp.

FBI00238, *Alistipes putredinis*, *Eubacterium xylanophilum*, and *Senegalimassilia anaerobia*, or a functional equivalent thereof; or

b) FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, and FBI00281, or a functional equivalent thereof.

In certain embodiments, the methods include expanding microbes in single cultures.

In certain embodiments, the methods comprise expanding microbes in a first single culture (or fifth composition) comprising a) a first *O. formigenes* strain; or b) FBI00067 or a functional equivalent thereof.

In certain embodiments, the methods comprise expanding microbes in a second single culture (or sixth composition) comprising a) a second *O. formigenes* strain; or b) FBI00133 or a functional equivalent thereof.

In certain embodiments, the methods comprise expanding microbes in a third single culture (or seventh composition) comprising a) a third *O. formigenes* strain; or b) FBI00289 or a functional equivalent thereof.

In certain embodiments, the methods comprise lyophilizing cultures and compositions described herein. In certain embodiments, the cultures and compositions comprises a lyoprotectant. In certain embodiments, the lyoprotectant comprises maltodextrin. In certain embodiments, the lyoprotectant comprises inulin. In certain embodiments, the lyoprotectant comprises maltodextrin and inulin. In certain embodiments, the maltodextrin is present at a concentration of about 8%. In certain embodiments, the inulin is present at a concentration of about 0.5%.

In certain embodiments, the methods comprise blending and/or mixing lyophilized cultures and compositions outlined above. Additional information on the strains for each composition can be found in Table 22.

In certain embodiments, DS1 as described in Table 22 is prepared using the method described in Figure 23. In certain embodiments, DS2 as described in Table 22 is prepared using the method described in Figure 24. In certain embodiments, DS3 as described in Table 22 is prepared using the method described in Figure 25. In certain embodiments, DS4 as described in Table 22 is prepared using the method described in Figure 26. In certain embodiments, DS5-DS7 (i.e., the manufacture of *O. formigenes*) as described in Table 22 are prepared using the method described in Figure 22. In certain embodiments, the manufacture of FB-001 comprises the separate manufacture of each of DS1-DS7 as described in Figures 22-26, followed by blending to achieve a uniform distribution of each of the DSs. In certain embodiments, the blending of DS1-DS7 is followed by encapsulation for oral administration.

Pharmaceutical Compositions

The present disclosure also provides pharmaceutical compositions that contain an effective amount of a microbial consortium described herein. The composition can be formulated for use in a variety of delivery systems. One or more physiologically acceptable buffer(s) or carrier(s) can also be included in the composition for proper formulation. Suitable formulations for use in the present disclosure are found in Remington's Pharmaceutical Sciences, Mack Publishing Company, Philadelphia, Pa., 17th ed., 1985. For a brief review of methods for drug delivery, *see, e.g.*, Langer (Science 249:1527-1533, 1990).

In certain embodiments, microbial cells of the present disclosure are harvested by microfiltration and centrifugation. In certain embodiments, microfiltration is done with a membrane comprising a nonreactive polymer. For example, in certain non-limiting embodiments, said membrane comprises Polyvinylidene fluoride, Polysulfones, or nitrocellulose. In certain embodiments, a membrane for microfiltration has a pore size of approximately 0.2 to 0.45 μm . In certain embodiments, the cells are centrifuged at approximately 1000 to 30000, 5000 to 30000, 10000 to 30000, 15000 to 30000, 20000 to 30000, 25000 to 30000, 1000 to 25000, 5000 to 25000, 10000 to 25000, 15000 to 25000, 20000 to 25000, 1000 to 20000, 5000 to 20000, 10000 to 20000, 15000 to 20000, 1000 to 15000, 5000 to 15000, 10000 to 15000, 1000 to 10000, 5000 to 10000, 1000 to 5000 g force. In certain embodiments, the cells are concentrated to approximately 1×10^6 CFUs per milliliter to 1×10^{12} CFUs per milliliter, 1×10^7 CFUs per milliliter to 1×10^{12} CFUs per milliliter, 1×10^8 CFUs per milliliter to 1×10^{12} CFUs per milliliter, 1×10^9 CFUs per milliliter to 1×10^{12} CFUs per milliliter, 1×10^{10} CFUs per milliliter to 1×10^{12} CFUs per milliliter, 1×10^{11} CFUs per milliliter to 1×10^{12} CFUs per milliliter, 1×10^6 CFUs per milliliter to 1×10^{11} CFUs per milliliter, 1×10^7 CFUs per milliliter to 1×10^{11} CFUs per milliliter, 1×10^8 CFUs per milliliter to 1×10^{11} CFUs per milliliter, 1×10^9 CFUs per milliliter to 1×10^{11} CFUs per milliliter, 1×10^{10} CFUs per milliliter to 1×10^{11} CFUs per milliliter, 1×10^6 CFUs per milliliter to 1×10^{10} CFUs per milliliter, 1×10^7 CFUs per milliliter to 1×10^{10} CFUs per milliliter, 1×10^8 CFUs per milliliter to 1×10^{10} CFUs per milliliter, 1×10^9 CFUs per milliliter to 1×10^{10} CFUs per milliliter, 1×10^6 CFUs per milliliter to 1×10^9 CFUs per milliliter, 1×10^7 CFUs per milliliter to 1×10^9 CFUs per milliliter, 1×10^8 CFUs per milliliter to 1×10^9 CFUs per milliliter, 1×10^6 CFUs per milliliter to 1×10^8 CFUs per milliliter, 1×10^7 CFUs per milliliter to 1×10^8 CFUs per milliliter, or 1×10^6 CFUs per milliliter to 1×10^7 CFUs per milliliter.

In certain embodiments, microbial cells of the present disclosure are frozen. In certain embodiments, the microbial cells of the present disclosure are mixed with one or more cryoprotective agents (CPAs) before freezing. In certain embodiments, the ratio of cells to CPA is approximately 25:1, 10:1, 5:1, 4:1, 3:1, 2:1, 1:1, 1:2, 1:3, 1:4, 1:5, 1:10, or 1:25. In certain embodiments, a CPA

comprises one or more of glycerol, maltodextrin, sucrose, inulin, trehalose, and alginate. In certain embodiments, a CPA further comprises one or more antioxidants. In certain embodiments, an antioxidant is selected from the list of cysteine, ascorbic acid, and riboflavin.

5 In certain embodiments, the microbial cells of the present disclosure are lyophilized. In certain embodiments, the lyophilized cells are used to make an orally-administered dose of the disclosure. In certain embodiments, primary drying is conducted below approximately -20 °C. In certain embodiments, primary drying is followed by a secondary drying at a higher temperature, *e.g.* greater than 0 °C, greater than 5 °C, or greater than 10 °C.

Functionally Equivalent and Identical Drug Products to FB-001

10 The strains included in FB-001 are described herein by 16S RNA sequences and functional characteristics. Based on this, equivalent Consortia to FB-001 can be generated by screening multiple of the same strain to find equivalent strains with equivalent function to those that comprise FB-001. Accordingly, identical strains may theoretically have different functions, strains can be screened using 16S RNA and Biolog as described herein to identify functionally identical and equivalent
15 strains from any fecal collection using the methods of collection described herein.

It is important to note that FB-001 was articulately designed to have multiple of the same strain in the Consortia. The reason for this to have redundancy to ensure function; however, such redundancy is not required for equivalent function so long as one of the otherwise redundant strains is included in the final drug product at a sufficient viable cell count amount to achieve *in vivo* function
20 in a subject. Accordingly, a Consortia that is equivalent or identical to FB-001 may contain all redundancies (*see* Table 22) or alternatively may contain no or fewer redundancies per strain so long as the included strains achieve *in vivo* function in a subject.

In an alternative approach to creating a functionally equivalent Consortia to FB-001, one of skill in the art could recreate a consortia of supportive microbes from healthy fecal donors and
25 supplement the supportive microbes with one or more *O. formigenes* strains. In certain embodiments, the supportive microbes will be supplemented with two or more *O. formigenes* strains or specifically three *O. formigenes* strains. The supportive microbes may comprise anywhere between 10 and 200 microbes so long as such supportive community supports and encourages the growth, health, and engraftment of the *O. formigenes* strain(s) in a subject. FB-001 was designed to have 148 microbes
30 to mimic a complete, healthy microbiome. Accordingly, equivalent Consortia may comprise approximately 148 microbes, including *O. formigenes* strain(s). However, it is interesting to note that older subjects often have smaller microbiomes; accordingly, a functionally equivalent Consortia

to FB-001 may also have far fewer microbes (e.g., 30-40, 40-50, 50-60, 60-70, 70-80, 8-90, 90-100, 100-110, 110-120, 120-130, 130-140, or 140-150 microbes, including *O. formigenes* strain(s)).

Therapeutic Applications

The present disclosure provides Consortia capable of engrafting into one or more than one niche of a gastrointestinal tract where it is capable of metabolizing a first metabolic substrate that causes or contributes to disease in an animal. In certain embodiments, the animal is a human.

In certain embodiments of the disclosure, when administered to an animal, the animal is pre-treated with one or more antibiotics prior to administration of the Consortium. In certain embodiments, the one or more antibiotics is selected from ampicillin, enrofloxacin, clarithromycin, and metronidazole. In certain embodiments, the animal is pre-treated with a polyethylene glycol bowel-preparation procedure.

In certain embodiments, when administered to an animal, the Consortia significantly reduces the concentration of a first metabolic substrate present in the blood, serum, bile, stool or urine as compared to samples collected pretreatment from the same animal or from corresponding control animal that have not been administered with the microbial consortium.

In certain embodiments, a Consortia is used to treat a subject having or at risk of developing a metabolic disease or condition. In certain embodiments, the metabolic disease is primary hyperoxaluria. In certain embodiments, the metabolic disease is secondary hyperoxaluria. In certain embodiments, the metabolic disease is enteric hyperoxaluria. In certain embodiments, the metabolic disease is secondary hyperoxaluria associated with bowel resection surgery or IBD. In certain embodiments, a Consortium significantly reduces the concentration of oxalate present in a sample of blood, serum, bile, stool, or urine when administered to a subject by at least about 20%, by at least about 30%, by at least about 40%, by at least about 50%, by at least about 60%, by at least about 70%, or by at least about 80% as compared to untreated subjects or pre-administration concentrations.

In certain embodiments, a Consortia significantly alters the profile and/or concentration of bile acids present in an animal. For example, in certain non-limiting embodiments, a Consortia significantly alters the profile and/or concentration of T β -MCA, T α -MCA, TUDCA, THDCA, TCA, 7 β -CA, 7-oxo-CA, TCDCA, T ω -MCA, TDCA, α -MCA, β -MCA, ω -MCA, Muro-CA, d4-CA, CA, TLCA, UDCA, HDCA, CDCA, DCA, and LCA in an animal.

In certain embodiments, a high-complexity defined gut microbial community of the present disclosure can be used to treat an animal having a cholestatic disease, such as, for example, primary sclerosing cholangitis, primary biliary cholangitis, progressive familial intrahepatic cholestasis, or

nonalcoholic steatohepatitis. For example, in certain non-limiting embodiments, the animal may be a mammal, and more particularly a human.

In certain embodiments, a Consortia can be administered via an enteric route. For example, in certain non-limiting embodiments, a microbial consortium is administered orally, rectally (e.g., by enema, suppository, or colonoscope), or by oral or nasal tube.

In certain embodiments, a Consortia is administered orally. In certain embodiments the oral administration is by a powder. In certain embodiments the oral administration is by a slurry. In certain embodiments the oral administration is by pills or capsules.

In certain embodiments, a Consortia can be administered to a specific location along the gastrointestinal tract. For example, in certain non-limiting embodiments, a microbial consortium can be administered into one or more than one gastrointestinal location including the mouth, esophagus, stomach, small intestine (duodenum, jejunum, ileum), large intestine (cecum, ascending colon, transverse colon, descending colon), or rectum. In certain embodiments, a microbial consortium can be administered in all regions of the gastrointestinal tract.

15 ***Methods of Treating Hyperoxaluria***

In certain embodiments, a Consortia is used to treat hyperoxaluria. Hyperoxaluria is a metabolic disorder characterized by a significant increase in urinary oxalate (UOx) excretion (>40 mg/24 h) that can lead to the formation of kidney stones and ultimately kidney damage. It is either due to a genetic defect that results in overproduction of oxalate by the liver (primary) or from absorption of too much oxalate from the diet (secondary). Secondary hyperoxaluria is further characterized as either dietary, due to excessive intake of oxalate or its precursors, or enteric hyperoxaluria (EH). Enteric hyperoxaluria is a complex medical condition characterized by excess absorption of dietary oxalate, usually caused by malabsorption of fat, for example after gastric bypass surgery, or an increased permeability of the gut for oxalate due to underlying gastrointestinal diseases.

25 Twenty-four-hour UOx excretion is an established biomarker of disease that is routinely measured in clinical practice to diagnose and manage patients at risk for EH and calcium oxalate kidney stones. While an increase in UOx increases the risk for kidney stone events, it is believed that a decrease of 20% or more will reduce the incidence of kidney stones by 25% or more. The increase in UOx excretion (>40 mg/24 h) that characterizes EH occurs because non-absorbed fatty acids bind to calcium in the small intestine, thereby making it unavailable to precipitate oxalate. Soluble oxalate consequently builds up to a relatively high concentration in the lumen and can diffuse passively out of the colon into the blood for excretion in the urine. Calcium oxalate crystals can precipitate within kidney tubules, bind to epithelial cells, and cause obstruction. Attached crystals can be phagocytosed

and transcytosed into the kidney interstitium, thereby releasing inflammatory mediators that can contribute to oxalate nephropathy and potentially progressive loss of kidney function.

In certain embodiments, while the presentation of hyperoxaluria can be variable, the first clinical manifestation is often the occurrence of a kidney stone (nephrolithiasis), which can be extremely painful and debilitating and sometimes requires surgical removal. As oxalate can complex with calcium to form insoluble crystals, chronically elevated UOx levels are a major risk factor for the development of kidney stones and ultimately kidney damage. Regardless of the frequency of kidney stones, oxalate nephropathy in patients with severe hyperoxaluria can lead to progressive kidney deterioration, chronic kidney disease (CKD) and eventually end stage renal disease (ESRD) which can be fatal.

The prevalence of EH has increased in recent years affecting over 250,000 Americans. Of the 250,000 patients with EH in the US in 2019, approximately 60% were a result of RYGB surgery for the treatment of obesity. As the global prevalence of obesity has increased in recent years, bariatric surgery procedures, RYGB in particular, have emerged as a widely used procedure to treat obesity. While the RYGB procedure can be advantageous for patients, including increasing life expectancy and reducing the risk of obesity related cancers, it can also lead to EH within 6 to 24 months of surgery, which can then progress to kidney stones and, in severe cases, kidney damage. A 36.4% increase in UOx was identified as a key lithogenic risk factor after RYGB in an analysis of seven studies including 277 patients before and after RYGB. Additionally, plasma oxalate and urine calcium oxalate supersaturation were found to be significantly increased compared with presurgical levels at 6 and 12 months following RYGB. Collectively, biomarkers such as urinary and plasma oxalate as well as calcium oxalate supersaturation are excellent prognostic indicators of EH, kidney stone formation and kidney damage and reduction of these markers may lead to improved outcomes.

There are currently no approved therapies for the reduction of UOx excretion in patients with EH. The management or standard of care options for patients with EH are limited to high fluid intake to increase urine output, correcting the underlying GI disease to reduce fat malabsorption, intensive dietary modifications to reduce intake of oxalate, and the use of calcium salts to bind oxalate in the GI tract. Compliance with these strategies tends to be low and many patients continue to experience hyperoxaluria with recurrent kidney stones and are at continued risk for long-term significant, irreversible, and progressive kidney damage.

In certain embodiments, the Consortia described herein comprise one or more *O. formigenes* strain(s) and can be administered to subjects for the treatment of enteric hyperoxaluria. In certain embodiments, the Consortia described herein comprise one or more *O. formigenes* strain(s) and can be administered to subjects for the treatment of hyperoxaluria. In certain embodiments, the Consortia

described herein comprise one or more *O. formigenes* strain(s) and can be administered to subjects for the treatment of primary hyperoxaluria. In certain embodiments, the Consortia described herein comprise one or more *O. formigenes* strain(s) and can be administered to subjects for the treatment of secondary hyperoxaluria. In certain embodiments, the FB-001 can be administered to subjects for the treatment of enteric hyperoxaluria. In certain embodiments, the FB-001 can be administered to subjects for the treatment of hyperoxaluria. In certain embodiments, the FB-001 can be administered to subjects for the treatment of primary hyperoxaluria. In certain embodiments, the FB-001 can be administered to subjects for the treatment of secondary hyperoxaluria. In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises the reduction of gut permeability (**Figure 19**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises the increased production or production equivalent to a normal, healthy gut of SCFAs (**Figure 20**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises the reduction of urinary oxalate independent of diet (**Figures 20A-20D**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation (**Figure 21**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation at a rate of at least 10^3 fg/cell/hr oxalate consumption (**Figure 21**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation at a rate of at least 10^2 fg/cell/hr oxalate consumption (**Figure 21**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation at a rate of at least 10^4 fg/cell/hr oxalate consumption (**Figure 21**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation at a rate of at least 10^3 mg/dose/hr oxalate consumption (**Figure 21**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation at a rate of at least 10^1 mg/dose/hr oxalate consumption (**Figure 21**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation at a rate of at least 10^2 mg/dose/hr oxalate consumption (**Figure 21**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation at a rate of greater than 10^3 mg/dose/hr oxalate consumption (**Figure 21**). In certain embodiments, the treatment of hyperoxaluria by FB-001 or a functionally equivalent Consortia thereof comprises oxalate degradation at a rate of at least 10^{-1} mg/dose/hr oxalate consumption (**Figure 21**).

Dosages

In certain embodiments, a Consortia is administered as a single dose or as multiple doses. In certain embodiments, a Consortia is administered once a day for 2 days, 3 days, 4 days, 5 days, 6 days, 1 week, 2 weeks 3 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, or 1 year. In certain embodiments, a Consortia is administered multiple times daily. In certain
5 embodiments, a Consortia is administered twice daily, three times daily, 4 times daily, or 5 times daily. In certain embodiments, a Consortia is administered intermittently. In certain embodiments, a Consortia is administered once weekly, once monthly, or when a subject is in need thereof.

In certain embodiments, a Consortia is administered at an effective dose to allow for
10 engraftment and substrate metabolism. In certain embodiments, a Consortia is administered at an effective dose to allow for engraftment and oxalate metabolism. In certain embodiments, a Consortia is administered at an effective dose to allow for engraftment and urinary oxalate reduction.

In certain embodiments, a Consortia is administered at a first loading dose and then followed by maintenance doses. In certain embodiments, the first loading dose is administered for 1 day, 2
15 days, 3 days, 4 days, 5 days, 6 days, 7 days, 8 days, 9 days, or 10 days. In certain embodiments, the loading dose is administered for 1-3 days. In certain embodiments, the loading dose is administered for 2-4 days. In certain embodiments, the loading dose is administered for 2-3 days. In certain embodiments, the loading dose is administered for 3-5 days. In certain embodiments, the loading dose is administered for 4-6 days. In certain embodiments, the loading dose is administered for 5-7
20 days. In certain embodiments, the loading dose is administered for 1 day. In certain embodiments, the loading dose is administered for 3 days. In certain embodiments, the loading dose is administered for 2 days. In certain embodiments, the maintenance doses are administered for 5-10 days following the last loading dose. In certain embodiments, the maintenance doses are administered for 7-12 days following the last loading dose. In certain embodiments, the maintenance doses are administered for
25 10-14 days following the last loading dose. In certain embodiments, the maintenance doses are administered for 14-21 days following the last loading dose. In certain embodiments, the maintenance doses are administered for 21-28 days following the last loading dose. In certain embodiments, the maintenance doses are administered for 14 days following the last loading dose. In certain embodiments, the maintenance doses are administered for 21 days following the last loading dose.
30 In certain embodiments, the maintenance doses are administered for 28 days following the last loading dose. In certain embodiments, the maintenance doses are administered for about 8 days following the last loading dose. In certain embodiments, the maintenance doses are administered for about 7 days following the last loading dose. In certain embodiments, the maintenance doses are administered for about 6 days following the last loading dose. In certain embodiments, the

5 maintenance doses are administered for about 9 days following the last loading dose. In certain embodiments, the maintenance doses are administered for about 10 days following the last loading dose. In certain embodiments, the loading dose is administered for 2 days and the maintenance dose is administered for 6 days (for a total of a 8day course of treatment). In certain embodiments, the loading dose is administered for 2 days and the maintenance dose is administered for 7 days (for a total of a 9 day course of treatment). In certain embodiments, the loading dose is administered for 2 days and the maintenance dose is administered for 8 days (for a total of a 10 day course of treatment). In certain embodiments, the loading dose is administered for 9 days and the maintenance dose is administered for 9 days (for a total of a 11 day course of treatment). In certain embodiments, the loading dose is administered for 2 days and the maintenance dose is administered for 10 days (for a total of a 12 day course of treatment). In certain embodiments, the Consortia is FB-001. In certain embodiments, the loading dose follows the pretreatment with antibiotics as described in the Combination Therapy section below. In certain embodiments, the loading dose follows the pretreatment with a bowel preparation as described in the Combination Therapy section below. In certain embodiments, the loading dose follows the pretreatment with antibiotics and a bowel preparation as described in the Combination Therapy section below.

20 In certain embodiments, FB-001 (i.e., FB-001), is formulated by blending the seven lyophilized DSs containing the 148 microbial species and filling them into coated enteric capsules. In certain embodiments, the capsules are provided in blister packaging or alternative packaging to allow for no or low oxygen exposure (e.g., packaging to sustain the viability of anaerobic microbes). In certain embodiments, each capsule contains a range of 5×10^{10} to 5×10^{11} viable cells/capsule. In certain embodiments, each capsule contains a range of 5×10^9 to 5×10^{10} viable cells/capsule. In certain embodiments, each capsule contains a range of 5×10^{11} to 5×10^{12} viable cells/capsule. In certain embodiments, FB-001 is orally dosed at up to 10^{12} viable cells on Days 1 and 2, and up to 10^{11} viable cells on Days 3 to 10. In certain embodiments, maltodextrin is included as an excipient in the capsules.

30 In certain embodiments, the FB-001 is comprised of approximately 10-15% *O. formigenes*. In certain embodiments, the FB-001 is comprised of approximately 15-20% *O. formigenes*. In certain embodiments, the FB-001 is comprised of approximately 20-25% *O. formigenes*. In certain embodiments, the FB-001 is comprised of approximately 25-30% *O. formigenes*. In certain embodiments, the FB-001 is comprised of approximately 30-35% *O. formigenes*. In certain embodiments, the FB-001 is comprised of approximately 35-40% *O. formigenes*. In certain embodiments, the FB-001 is comprised of approximately 45-50% *O. formigenes*. In certain embodiments, the three strains of *O. formigenes* with 16S RNA sequences of SEQ ID NOS: 42, 79,

and 146 are provided in approximately equal amounts. In certain embodiments, the three strains of *O. formigenes* with 16S RNA sequences of SEQ ID NOs: 42, 79, and 146 are provided in unequal amounts. In certain embodiments, the three strains of *O. formigenes* with 16S RNA sequences of SEQ ID NOs: 42, 79, and 146 are provided in similar amounts. In certain embodiments, the three strains of *O. formigenes* with 16S RNA sequences of SEQ ID NOs: 42, 79, and 146 are provided in equal amounts.

In certain embodiments, the total *O. formigenes* content of each capsule is approximately 25-35% on a relative abundance basis. In certain embodiments, the total *O. formigenes* content of each capsule is approximately 20%, 21%, 22%, 23%, 24% or 25% on a relative abundance basis. In certain embodiments, the total *O. formigenes* content of each capsule is approximately 15%, 16%, 17%, 18% or 19% on a relative abundance basis. In certain embodiments, the total *O. formigenes* content of each capsule is approximately 20%, 21%, 22%, 23%, 24% or 25% on a relative abundance basis. In certain embodiments, the total *O. formigenes* content of each capsule is approximately 30%, 31%, 32%, 33%, 34% or 35% on a relative abundance basis.

In certain embodiments, the total *O. formigenes* content of each capsule is approximately 32% on a relative abundance basis. In certain embodiments, this translates to a total *O. formigenes* content of 40% on a viable cell count basis. In certain embodiments, for the remaining strains, relative abundance values ranged from 18% to 0.015%, or three orders of magnitude. In certain embodiments, the distribution is typical of the human microbiome, which follows a power law distribution in which most species are at a low relative abundance. In certain embodiments, the absence of detection of a strain should not be interpreted as its absence from the drug substance. In certain embodiments, the 60 detected strains account for 95.932% of the biomarkers detected in FB-001 DP. In certain embodiments, the remaining 88 strains therefore account for 4.068% of the biomarkers. In certain embodiments, the relative abundance profile is expected to vary between batches and data will continue to be collected during development to understand the magnitude of the variability.

In certain embodiments, each capsule of FB-001 contains a range of 5×10^{10} to 5×10^{11} viable cells/capsule with approximately 40% *O. formigenes* and a viable cell count basis and with relative abundance values of the remaining 145 strains ranging from 18% to 0.015%.

In certain embodiments, the dosage comprises treatment for 10 days consisting of a loading dose of 10 capsules (1×10^{12} viable cells) on Day 1 and Day 2 and a dose of 1 capsule (1×10^{11} viable cells) on Day 3 to Day 10. In certain embodiments, this dosing scheme follows pretreatment with antibiotics as described herein. In certain embodiments, the pretreatment with antibiotics comprises pretreatment with 500mg metronidazole and 500mg clarithromycin as described herein.

In certain embodiments, this dosing scheme follows pretreatment with a bowel preparation as described herein. In certain embodiments, the bowel preparation comprises pretreatment with MiraLax. In certain embodiments, this dosing scheme follows pretreatment with antibiotics as and pretreatment with a bowel preparation as described herein.

5 *Combination Therapy*

In certain embodiments, a Consortia can be administered in combination with other agents. In certain embodiments, a Consortia can be administered with an antimicrobial agent, an antifungal agent, an antiviral agent, an antiparasitic agent or a prebiotic. In certain embodiments, a Consortia can be administered subsequent to administration of an antimicrobial agent, an antifungal agent, an antiviral agent, an antiparasitic agent or a prebiotic. In certain embodiments, administration may be sequential over a period of hours or days, or simultaneously.

For example, in certain non-limiting embodiments, a microbial consortium can be administered with, or pre-administered with, one or more than one antibacterial agent selected from fluoroquinolone antibiotics (ciprofloxacin, Levaquin, floxin, tequin, avelox, and norflox); cephalosporin antibiotics (cephalexin, cefuroxime, cefadroxil, cefazolin, cephalothin, cefaclor, cefamandole, cefoxitin, cefprozil, and ceftobiprole); penicillin antibiotics (amoxicillin, ampicillin, penicillin V, dicloxacillin, carbenicillin, vancomycin, and methicillin); tetracycline antibiotics (tetracycline, minocycline, oxytetracycline, and doxycycline); and carbapenem antibiotics (ertapenem, doripenem, imipenem/cilastatin, and meropenem).

For example, in certain non-limiting embodiments, a microbial consortium can be administered with one or more than one antiviral agent selected from 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.

In certain embodiments, a microbial consortium can be administered with one or more than one antifungal agent selected from 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; polygodial; benzoic acid; ciclopirox; tolnaftate; undecylenic acid; flucytosine or 5-fluorocytosine; griseofulvin; and haloprogin.

In certain embodiments, a microbial consortium can be administered with one or more than one anti-inflammatory and/or immunosuppressive agent selected from cyclophosphamide, mycophenolate mofetil, corticosteroids, mesalazine, mesalamine, sulfasalazine, sulfasalazine derivatives, cyclosporin A, mercaptopurine, azathiopurine, prednisone, methotrexate, antihistamines, glucocorticoids, epinephrine, theophylline, cromolyn sodium, anti-leukotrienes, anticholinergics, monoclonal anti-IgE, immunomodulatory peptides, immunomodulatory small molecules, immunomodulatory cytokines, immunomodulatory antibodies, and vaccines.

In certain embodiments, a Consortia can be administered with one or more than one probiotic selected from, but not limited to, amino acids, biotin, fructooligosaccharides, galactooligosaccharides, inulin, lactulose, mannan oligosaccharides, oligofructose-enriched inulin, oligofructose, oligodextrose, tagatose, trans-galactooligosaccharide, and xylooligosaccharides.

In certain embodiments, a Consortia described herein is administered in combination with NOV-001 (Novome). In certain embodiments, the Consortia is administered prior to the administration of NOV-001 (Novome). In certain embodiments, the Consortia is administered after to the administration of NOV-001 (Novome). In certain embodiments, the Consortia is administered concurrently with the administration of NOV-001 (Novome). In certain embodiments, the consortia administered in combination with NOV-001 (Novome) is FB-001.

In certain embodiments, a Consortia is administered in combination with SYN8802 (Synlogic). In certain embodiments, the Consortia is administered prior to the administration of SYN8802 (Synlogic). In certain embodiments, the Consortia is administered after to the administration of SYN8802 (Synlogic). In certain embodiments, the Consortia is administered concurrently with the administration of SYN8802 (Synlogic). In certain embodiments, the consortia administered in combination with SYN8802 (Synlogic) is FB-001.

In certain embodiments, a Consortia is administered in combination with OX-1 (Oxidien). In certain embodiments, the Consortia is administered prior to the administration of OX-1 (Oxidien). In certain embodiments, the Consortia is administered after to the administration of OX-1 (Oxidien). In certain embodiments, the Consortia is administered concurrently with the administration of OX-1 (Oxidien). In certain embodiments, the consortia administered in combination with OX-1 (Oxidien) is FB-001.

In certain embodiments, a Consortia is administered in combination with Lumasiran (Alnylam). In certain embodiments, the Consortia is administered prior to the administration of Lumasiran (Alnylam). In certain embodiments, the Consortia is administered after to the

administration of Lumasiran (Alnylam). In certain embodiments, the Consortia is administered concurrently with the administration of Lumasiran (Alnylam). In certain embodiments, the consortia administered in combination with Lumasiran (Alnylam) is FB-001.

5 In certain embodiments, a Consortia is administered in combination with Nedosiran (Dicerna). In certain embodiments, the Consortia is administered prior to the administration of Nedosiran (Dicerna). In certain embodiments, the Consortia is administered after to the administration of Nedosiran (Dicerna). In certain embodiments, the Consortia is administered concurrently with the administration of Nedosiran (Dicerna). In certain embodiments, the consortia administered in combination with Nedosiran (Dicerna) is FB-001.

10 In certain embodiments, a Consortia is administered in combination with BBP-711 (Cantero/Bridge Bio). In certain embodiments, the Consortia is administered prior to the administration of BBP-711 (Cantero/Bridge Bio). In certain embodiments, the Consortia is administered after to the administration of BBP-711 (Cantero/Bridge Bio). In certain embodiments, the Consortia is administered concurrently with the administration of BBP-711 (Cantero/Bridge Bio).
15 In certain embodiments, the consortia administered in combination with BBP-711 (Cantero/Bridge Bio) is FB-001.

In certain embodiments, a Consortia is administered in combination with CNK-336 (Chinook). In certain embodiments, the Consortia is administered prior to the administration of CNK-336 (Chinook). In certain embodiments, the Consortia is administered after to the
20 administration of CNK-336 (Chinook). In certain embodiments, the Consortia is administered concurrently with the administration of CNK-336 (Chinook). In certain embodiments, the consortia administered in combination with CNK-336 (Chinook) is FB-001.

In certain embodiments, a Consortia is administered in combination with PBGENE-PH1 (Precision Bio). In certain embodiments, the Consortia is administered prior to the administration of
25 PBGENE-PH1 (Precision Bio). In certain embodiments, the Consortia is administered after to the administration of PBGENE-PH1 (Precision Bio). In certain embodiments, the Consortia is administered concurrently with the administration of PBGENE-PH1 (Precision Bio). In certain embodiments, the consortia administered in combination with PBGENE-PH1 (Precision Bio) is FB-001.

30 In certain embodiments, a Consortia is administered in combination with a low oxalate diet. In certain embodiments, a Consortia is administered in combination with a high hydration diet. In certain embodiments, a Consortia is administered in combination with calcium supplements. In certain embodiments, a Consortia is administered in combination with a low oxalate diet and with calcium supplements. In certain embodiments, the Consortia is FB-001 and FB-001 is administered

in combination with a low oxalate diet, with calcium supplements, or with a low oxalate diet and calcium supplements. In certain embodiments, calcium supplements comprise a diet with sufficient calcium without additional supplementation.

In certain embodiments, a Consortia is administered in combination with 1) one of NOV-001, 2) OX-1, (Oxidien), Lumasiran (Alnylam), Nedosiran (Dicerna), BBP-711 (Cantero/Bridge Bio), CNK-336 (Chinook), and PBGENE-PH1 (Precision Bio), and 2) a low oxalate diet. In certain embodiments, a Consortia is administered in combination with 1) one of NOV-001, 2) OX-1, (Oxidien), Lumasiran (Alnylam), Nedosiran (Dicerna), BBP-711 (Cantero/Bridge Bio), CNK-336 (Chinook), and PBGENE-PH1 (Precision Bio), and 2) a high calcium diet (including but not limited to calcium supplements). In certain embodiments, a Consortia is administered in combination with 1) one of NOV-001, 2) OX-1, (Oxidien), Lumasiran (Alnylam), Nedosiran (Dicerna), BBP-711 (Cantero/Bridge Bio), CNK-336 (Chinook), and PBGENE-PH1 (Precision Bio), 2) a low oxalate diet, and 3) a high calcium diet (including but not limited to calcium supplements). In certain embodiments, FB-001 is administered in combination with 1) one of NOV-001, 2) OX-1, (Oxidien), Lumasiran (Alnylam), Nedosiran (Dicerna), BBP-711 (Cantero/Bridge Bio), CNK-336 (Chinook), and PBGENE-PH1 (Precision Bio), and 2) a low oxalate diet. In certain embodiments, FB-001 is administered in combination with 1) one of NOV-001, 2) OX-1, (Oxidien), Lumasiran (Alnylam), Nedosiran (Dicerna), BBP-711 (Cantero/Bridge Bio), CNK-336 (Chinook), and PBGENE-PH1 (Precision Bio), and 2) a high calcium diet (including but not limited to calcium supplements). In certain embodiments, FB-001 is administered in combination with 1) one of NOV-001, 2) OX-1, (Oxidien), Lumasiran (Alnylam), Nedosiran (Dicerna), BBP-711 (Cantero/Bridge Bio), CNK-336 (Chinook), and PBGENE-PH1 (Precision Bio), 2) a low oxalate diet, and 3) a high calcium diet (including but not limited to calcium supplements). In certain embodiments within this paragraph, “in combination” refers to concurrent, prior to, or after the administration of a Consortia. In certain embodiments within this paragraph, “in combination” refers to concurrent, prior to, or after the administration of FB-001.

In certain embodiments, the combination treatment of a Consortia comprises the pretreatment with antibiotics. In certain embodiments, the pretreatment of antibiotics comprises a 2, 3, 4, 5, 6, or 7 day pretreatment. In certain embodiments, the pretreatment is 4, 5, or 6 days. In certain embodiments, the pretreatment is 5 days. In certain embodiments, the pretreatment of antibiotics comprises 500mg metronidazole. In certain embodiments, the pretreatment of antibiotics comprises 500mg clarithromycin. In certain embodiments, the pretreatment of antibiotics comprises 500mg metronidazole and 500mg clarithromycin. In certain embodiments, the pretreatment of antibiotics consists of 500mg metronidazole and 500mg clarithromycin. In certain embodiments, the dose of

antibiotics may be adjusted based on the body mass of a subject. In certain embodiments, the 500mg metronidazole and 500mg clarithromycin are administered every 12hrs (Q12h). In certain embodiments, there is a 1 day gap between the last dose of antibiotics and the administration of a Consortia. In certain embodiments, there is a 2 day gap between the last dose of antibiotics and the administration of a Consortia. In certain embodiments, metronidazole and/or clarithromycin may be substituted for one or more different antibiotics with a similar or substantially similar mode of action (e.g., type of anti-bacterial). In certain embodiments, metronidazole and/or clarithromycin may be substituted for one or more different antibiotics with a similar or substantially similar mode of action (e.g., type of anti-bacterial) if a subject has a sensitivity or allergy to metronidazole and/or clarithromycin, respectively. In certain embodiments, the Consortia is FB-001. In certain embodiments, the Consortia is FB-001 and the pretreatment is 500mg metronidazole and 500mg clarithromycin administered as a 5 day Q12h pretreatment. In certain embodiments, the Consortia is FB-001 and the pretreatment is 500mg metronidazole and 500mg clarithromycin administered as a 5 day Q12h pretreatment with a 1 day gap between the administration of the last dose of the antibiotics and the first dose of FB-001. In certain embodiments, the Consortia is FB-001 and the pretreatment is 500mg metronidazole and 500mg clarithromycin administered as a 5 day Q12h pretreatment with no gap between the administration of the last dose of the antibiotics and the first dose of FB-001.

In certain embodiments, a bowel preparation (e.g., MiraLax) is administered in the late afternoon or early evening following the final dose of antibiotics, wherein the final dose of antibiotics is administered the morning of the same day. In certain embodiments, a bowel preparation (e.g., MiraLax) is administered in the late afternoon or early evening following the final dose of 500mg metronidazole and 500mg clarithromycin, wherein the final dose of 500mg metronidazole and 500mg clarithromycin is administered the morning of the same day. In certain embodiments, the MiraLax is administered at least 8 hrs after the last dose of 500mg metronidazole and 500mg clarithromycin. In certain embodiments, metronidazole and/or clarithromycin may be substituted for one or more different antibiotics with a similar or substantially similar mode of action (e.g., type of anti-bacterial). In certain embodiments, the bowel prep is MiraLax. In certain embodiments, 238g of MiraLax is administered. In certain embodiments, the MiraLax is mixed with a flavored hydration beverage such as Gatorade, a sugar-free Gatorade, or a similar brand of alike. In certain embodiments, the MiraLax is mixed with approximately 2L of a flavored hydration beverage. In certain embodiments, the MiraLax is mixed with approximately 1.5-2L of a flavored hydration beverage. In certain embodiments, the MiraLax is mixed with approximately 1.9L of a flavored hydration beverage. In certain embodiments, the diluted MiraLax is consumed by the subject at approximately 8oz every 10-20min. In certain embodiments, the diluted MiraLax is consumed by the subject at approximately

8oz every 10-15min. In certain embodiments, the diluted MiraLax is fully consumed by the subject within 90-150min. In certain embodiments, the diluted MiraLax is fully consumed by the subject within 100-140min. In certain embodiments, the diluted MiraLax is fully consumed by the subject within 100-130min. In certain embodiments, the diluted MiraLax is fully consumed by the subject within 100-120min. In certain embodiments, the diluted MiraLax is fully consumed by the subject within 120min. In certain embodiments, the Consortia is FB-001. In certain embodiments, the MiraLax pretreatment comprises 238g of MiraLax mixed (i.e., diluted) in approximately 1.9L of a flavored hydration beverage (e.g., zero sugar Gatorade) that is fully consumed by the subject within approximately 120min (e.g., 8oz every 10-20min) at least 8hrs following the last dose of 500mg metronidazole and 500mg clarithromycin; wherein a Consortia is administered the day following the MiraLax administration. In certain embodiments, the Consortia is FB-001 and the MiraLax pretreatment comprises 238g of MiraLax mixed (i.e., diluted) in approximately 1.9L of a flavored hydration beverage (e.g., zero sugar Gatorade) that is fully consumed by the subject within approximately 120min (e.g., 8oz every 10-20min) at least 8hrs following the last dose of 500mg metronidazole and 500mg clarithromycin; wherein FB-001 is administered the day following the MiraLax administration.

Kits

The presently disclosed subject matter provides kits for treating hyperoxaluria, enteric hyperoxaluria, primary hyperoxaluria, and secondary hyperoxaluria in a subject. In certain embodiments, the kit comprises an effective amount of presently disclosed Consortia or a pharmaceutical composition comprising thereof. In certain embodiments, the kit comprises an effective amount of FB-001 or a pharmaceutical composition comprising thereof. In certain embodiments, the kit comprises an effective amount of a functionally equivalent Consortia to FB-001 or a pharmaceutical composition comprising thereof. In certain embodiments, the kit comprises an effective amount of a functionally identical Consortia to FB-001 or a pharmaceutical composition comprising thereof. In certain embodiments, the kit comprises an effective amount of a substantially similar Consortia to FB-001 or a pharmaceutical composition comprising thereof. In certain embodiments, the kit comprises an effective amount of a similar Consortia to FB-001 or a pharmaceutical composition comprising thereof. In certain embodiments, the kit comprises a sterile container; such containers can be boxes, ampules, bottles, vials, tubes, bags, pouches, blister-packs, or other suitable container forms known in the art. Such containers can be made of plastic, glass, laminated paper, metal foil, or other materials suitable for holding medicaments. In certain non-limiting embodiments, the kit includes anaerobic containers to hold the Consortia(s) described herein.

In certain non-limiting embodiments, the kit includes blister packs to hold the Consortia(s) described herein in the presence of no or limited amounts of oxygen. In certain non-limiting embodiments, the kit includes blister packs with desiccant to hold the Consortia(s) described herein in the presence of no or limited amounts of oxygen. In certain non-limiting embodiments, the kit includes bottles with desiccant to hold the Consortia(s) described herein in the presence of no or limited amounts of oxygen.

In certain embodiments, the kits include instructions for administering the Consortia as described herein. In certain embodiments, the instructions include directions for administering the loading and the maintenance dose.

In certain embodiments, the kits include storage instructions. In certain embodiments, the storage instructions are for storage at approximately -20°C. In certain embodiments, the storage instructions are for storage at less than -5°C. In certain embodiments, the storage instructions are for storage at less than approximately -15 to -20°C, -10 to -20°C, -10 to -15°C, -5 to -10°C, 0 to -5°C, below 0°C, or 0 to -20°C. In certain embodiments, the storage instructions are for storage at less than approximately 4°C. In certain embodiments, the storage instructions are for storage at room temperature.

In certain embodiments, the kits include instructions for maintaining the Consortia in no or low oxygen conditions.

In certain embodiments, the kits include instructions for a low oxalate and/or high calcium diet. In certain embodiments, the kits include instructions for remaining hydrated.

In certain embodiments, the kits include instructions for the subject to remain off all antibiotics during treatment with the Consortia.

In certain embodiments, the kit includes FB-001 and instructions for administering FB-001.

Exemplary Embodiments

In certain non-limiting embodiments, the present disclosure is directed to a composition comprising a microbial consortia comprising at least 1 oxalate-metabolizing microbial strain, wherein the at least one strain expresses an enzyme selected from a formyl-CoA transferase, an oxalate-formate antiporter, and an oxalyl-CoA decarboxylase.

In certain embodiments of the compositions disclosed herein, the at least 1 oxalate-metabolizing microbial strain is from the *Oxalobacter* genus.

In certain embodiments of the compositions disclosed herein, the composition comprises at least 3 oxalate-metabolizing microbial strains, wherein the at least 3 oxalate-metabolizing microbial strains are different strains of the same species.

In certain embodiments of the compositions disclosed herein, the composition comprises at least 3 oxalate-metabolizing microbial strains, wherein the at least 3 oxalate-metabolizing microbial strains are different strains of different species.

In certain embodiments of the compositions disclosed herein, the species is *Oxalobacter formigenes* (*O. formigenes*), and optionally wherein the number of oxalate-metabolizing microbial strains is 3 or more.

In certain embodiments of the compositions disclosed herein:

- a) at least one strain is a low pH tolerance strain;
- b) at least one strain is a high oxalate tolerance strain; and/or
- c) at least one strain is a high growth rate strain.

In certain non-limiting embodiments, the present disclosure is directed to a composition comprising at least 2 *Oxalobacter formigenes* (*O. formigenes*) strains, wherein each of the strains comprises one or more of the following functions:

- a) a low pH tolerance strain;
- b) a high oxalate tolerance strain; and/or
- c) a high growth rate strain.

In certain non-limiting embodiments, the present disclosure is directed to a composition comprising at least 3 *Oxalobacter formigenes* (*O. formigenes*) strains, wherein: a) at least one strain is a low pH tolerance strain; b) at least one strain is a high oxalate tolerance strain; and c) at least one strain is a high growth rate strain.

In certain embodiments of the compositions disclosed herein, the low pH tolerance strain can metabolize oxalate at a pH between about 4 and about 6.

In certain embodiments of the compositions disclosed herein, the low pH tolerance strain can metabolize oxalate at a pH of about 5.

In certain embodiments of the compositions disclosed herein, the high oxalate tolerance strain can metabolize oxalate at a concentration between about 5 mM to about 30 mM.

In certain embodiments of the compositions disclosed herein, the high oxalate tolerance strain can metabolize oxalate at a concentration of about 15 mM.

In certain embodiments of the compositions disclosed herein, each strain comprises a RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

5 In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

In certain embodiments of the compositions disclosed herein, the composition further comprises one or more microbes metabolizing formate.

10 In certain embodiments of the compositions disclosed herein, the composition further comprises one or more microbes catalyzing fermentation of polysaccharides.

In certain embodiments of the compositions disclosed herein, the composition further comprises one or more microbes catalyzing fermentation of amino acids.

15 In certain embodiments of the compositions disclosed herein, the composition further comprises microbes catalyzing the synthesis of at least one molecules selected from the group consisting of methane, acetate, sulfide, propionate, and succinate.

In certain embodiments of the compositions disclosed herein, the composition further comprises microbes catalyzing: a) deconjugation of conjugated bile acids to produce primary bile acids; b) conversion of cholic acid (CA) to 7-oxocholic acid; c) conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA); d) conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid; and/or e) conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

25 In certain embodiments of the compositions disclosed herein, the composition comprises: a) Consortia I or a functional equivalent thereof; b) Consortia II or a functional equivalent thereof; c) Consortia III or a functional equivalent thereof; d) Consortia IV or a functional equivalent thereof; e) Consortia V or a functional equivalent thereof; f) Consortia VI or a functional equivalent thereof; g) Consortia VII or a functional equivalent thereof; h) Consortia VIII or a functional equivalent thereof; i) Consortia IX or a functional equivalent thereof; j) Consortia X or a functional equivalent thereof; k) Consortia XI or a functional equivalent thereof; l) Consortia XII or a functional equivalent thereof; m) Consortia XIII or a functional equivalent thereof; n) Consortia XIV or a functional equivalent thereof; o) Consortia XV or a functional equivalent thereof; p) Consortia XVI or a functional equivalent thereof; q) Consortia XVII or a functional equivalent thereof; r) Consortia XVIII or a functional equivalent thereof; or s) Consortia XIX or a functional equivalent thereof.

30 In certain embodiments of the compositions disclosed herein, the composition further comprises a second composition comprising *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia*

obeum, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*,
Lachnospiraceae sp. FBI00033, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*,
Fusicatenibacter saccharivorans, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*,
Bacteroides stercorisoris, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae* sp.
5 *FBI00071*, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*,
Roseburia hominis, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*,
Bacteroides stercoris, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*,
Bifidobacterium catemulatum, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides finegoldii*,
Clostridiaceae sp. FBI00191, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium*
10 *bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*,
Bacteroides vulgatus, *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*,
Acidaminococcus intestini, *Emergencia timonensis*, *Bifidobacterium pseudocatemulatum*,
Eubacterium hallii, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia*
hydrogenotrophica, *Lachnospiraceae* sp. FBI00290, or a functional equivalent microbial
15 consortium.

In certain embodiments of the compositions disclosed herein, the composition further
 comprises FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034,
 FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060,
 FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109,
 20 FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174,
 FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201,
 FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248,
 FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, FBI00290, or a functional equivalent
 thereof.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s
 RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth
 in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20,
 SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO:
 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID
 30 NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ
 ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77,
 SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID
 NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO:
 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116,

SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115,

SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

In certain embodiments of the compositions disclosed herein, the composition further comprises a third composition comprising *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae sp. FBI00097*, *Gordonibacter pamelaee*, *Bacteroides uniformis*, *Gordonibacter pamelaee*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae sp. FBI00233*, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinhominis*, *Alistipes onderdonkii*, *Methanobrevibacter smithii*, or a functional equivalent thereof.

In certain embodiments of the compositions disclosed herein, the composition further comprises FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226,

FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, FBI00292, or a functional equivalent thereof.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID

NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, 5 SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16S RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148. 15

In certain embodiments of the compositions disclosed herein, the composition further comprises a fourth composition comprising *Bifidobacterium adolescentis*, *Bifidobacterium longum*, 20 *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, 25 *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, *Bacteroides xylanisolvens*, or a functional equivalent thereof.

In certain embodiments of the compositions disclosed herein, the composition further comprises FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, 30 FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, FBI00271, or a functional equivalent thereof.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80,

SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

In certain embodiments of the compositions disclosed herein, the composition further comprises a fifth composition comprising *Alistipes putredinis*, *Dialister succinatiphilus*,
5 *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*,
Bilophila wadsworthia, *Holdemanella biformis*, *Parasutterella excrementihominis*, *Alistipes sp. FBI00180*, *Bacteroides coprocola*, *Alistipes sp. FBI00238*, *Alistipes putredinis*, *Eubacterium xylanophilum*, *Senegalimassilia anaerobia*, or a functional equivalent thereof.

In certain embodiments of the compositions disclosed herein, the composition further
10 comprises FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175,
FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, FBI00281, or a functional
equivalent thereof.

In certain embodiments of the compositions disclosed herein, each strain comprises a 16s
RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth
15 in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID
NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ
ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144, (b) at least about 90% identical
to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID
NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ
20 ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO:
144, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ
ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93,
SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO:
137, SEQ ID NO: 141, or SEQ ID NO: 144.

25 In certain embodiments of the compositions disclosed herein, each strain comprises a 16s
RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide
sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID
NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ
ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144.

30 In certain embodiments of the compositions disclosed herein, each strain comprises a 16s
RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: SEQ ID NO:
15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID
NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ
ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144

In certain non-limiting embodiments, the present disclosure is directed to a microbial consortium comprising microbial strains set forth in Table 1, Table 2, Table 3, Table 4, Table 5, Table 6, Table 7, Table 8, Table 9, Table 10, Table 11, Table 12, Table 13, Table 14, Table 15, Table 16, Table 17, Table 18, Table 19, or a functional equivalent thereof.

5 In certain non-limiting embodiments, the present disclosure is directed to a microbial consortium comprising microbial strains set forth in Table 22 or a functional equivalent thereof.

In certain embodiments of the microbial consortia disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, (b) at least about 90% identical to the nucleotide sequence set forth in
10 SEQ ID NOs: 1-148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

In certain embodiments of the microbial consortia disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

15 In certain embodiments of the microbial consortia disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

In certain non-limiting embodiments, the present disclosure is directed to a composition comprising a microbial consortium disclosed herein.

20 In certain embodiments of the compositions disclosed herein, the composition is a pharmaceutical composition.

In certain embodiments of the compositions disclosed herein, the composition comprises from about 5×10^{10} to about 5×10^{11} viable cells.

In certain embodiments of the compositions disclosed herein, the composition comprises
25 from about 5×10^9 to about 5×10^{10} viable cells.

In certain embodiments of the compositions disclosed herein, the composition comprises from about 5×10^{11} to about 5×10^{12} viable cells.

In certain embodiments of the compositions disclosed herein, the composition comprises up to about 5×10^{12} viable cells.

30 In certain embodiments of the compositions disclosed herein, the composition comprises from about 10% to about 50% of oxalate-metabolizing microbial strains.

In certain embodiments of the compositions disclosed herein, the composition comprises from about 10% to about 50% of *O. formigenes* strains on a viable cell count basis.

In certain embodiments of the compositions disclosed herein, the composition comprises about 20% of *O. formigenes* strains on a viable cell count basis.

In certain embodiments of the compositions disclosed herein, the composition comprises about 30% of *O. formigenes* strains on a viable cell count basis.

5 In certain embodiments of the compositions disclosed herein, the composition comprises about 40% of *O. formigenes* strains on a viable cell count basis.

In certain non-limiting embodiments, the present disclosure is directed to a method of manufacturing the compositions or the microbial consortia disclosed herein. In certain embodiments of the methods of manufacturing disclosed herein, the method comprises obtaining and blending:

- 10 a) a first composition comprising *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae* sp. FBI00033, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorisoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae* sp. FBI00071, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Clostridiaceae* sp. FBI00191, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*, *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*, *Acidaminococcus intestini*, *Emergencia timonensis*, *Bifidobacterium pseudocatenulatum*, *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, and *Lachnospiraceae* sp. FBI00290, or a functional equivalent thereof;
- 25 b) a second composition comprising *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae* sp. FBI00097, *Gordonibacter pamelaee*, *Bacteroides uniformis*, *Gordonibacter pamelaee*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae* sp. FBI00233, *Alistipes shahii*, *Dielma*
- 30

fastidiosa, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinihominis*, *Alistipes onderdonkii*, and *Methanobrevibacter smithii*, or a functional equivalent thereof;

c) a third composition comprising *Bifidobacterium adolescentis*, *Bifidobacterium longum*,
 5 *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*,
Fusicatenibacter saccharivorans, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*,
Eggerthella lenta, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*,
Parabacteroides merdae, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*,
 10 *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*,
Clostridium bolteae, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, and *Bacteroides xylanisolvens*, or a functional equivalent thereof;

d) a fourth composition comprising *Alistipes putredinis*, *Dialister succinatiphilus*,
Akkermansia muciniphila, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*,
 15 *Bilophila wadsworthia*, *Holdemanella biformis*, *Parasutterella excrementihominis*, *Alistipes* sp.
FBI00180, *Bacteroides coprocola*, *Alistipes* sp. *FBI00238*, *Alistipes putredinis*, *Eubacterium xylanophilum*, and *Senegalimassilia anaerobia*, or a functional equivalent thereof;

e) a fifth composition comprising a first *O. formigenes* strain;

f) a sixth composition comprising a second *O. formigenes* strain; and/or

20 g) a seventh composition comprising a third *O. formigenes* strain.

In certain embodiments of the methods of manufacturing disclosed herein, the method comprises obtaining and blending:

a) a first composition comprising FBI00001, FBI00002, FBI00010, FBI00013, FBI00029,
 FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051,
 25 FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087,
 FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128,
 FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198,
 FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221,
 FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, and
 30 FBI00290, or a functional equivalent thereof;

b) a second composition comprising FBI00004, FBI00012, FBI00015, FBI00018, FBI00019,
 FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077,
 FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132,
 FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208,

FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, and FBI00292, or a functional equivalent thereof;

5 c) a third composition comprising FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, and FBI00271, or a functional equivalent thereof;

10 d) a fourth composition comprising FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, and FBI00281, or a functional equivalent thereof;

e) a fifth composition comprising FBI00067 or a functional equivalent thereof;

f) a sixth composition comprising FBI00133 or a functional equivalent thereof; and/or

g) a seventh composition comprising FBI00289 or a functional equivalent thereof.

15 In certain embodiments of the methods of manufacturing disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

20 In certain embodiments of the methods of manufacturing disclosed herein, each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

In certain embodiments of the methods of manufacturing disclosed herein, each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID
25 NO: 1-148.

In certain embodiments of the methods of manufacturing disclosed herein, the fourth composition is obtained by growing microbes in presence of threonine.

In certain embodiments of the methods of manufacturing disclosed herein, each composition comprises a lyoprotectant.

30 In certain embodiments of the methods of manufacturing disclosed herein, each composition comprises maltodextrin, inulin, or a combination thereof.

In certain embodiments of the methods of manufacturing disclosed herein, the maltodextrin is at a concentration of about 8%.

In certain embodiments of the methods of manufacturing disclosed herein, the inulin is at a concentration of about 0.5%.

In certain embodiments of the methods of manufacturing disclosed herein, each composition is separately lyophilized.

5 In certain embodiments of the methods of manufacturing disclosed herein, the functional equivalent is based on the characteristics set forth in Table 24.

In certain embodiments of the methods of manufacturing disclosed herein, the functional equivalent is based on the characteristics set forth in Table 34.

10 In certain embodiments of the methods of manufacturing disclosed herein, the functional equivalent is based on the characteristics set forth in Table 35.

In certain embodiments of the methods of manufacturing disclosed herein, the functional equivalent is based on the characteristics set forth in Table 36.

In certain embodiments of the methods of manufacturing disclosed herein, the functional equivalent is based on the characteristics set forth in Tables 34-36.

15 In certain embodiments of the methods of manufacturing disclosed herein, the method comprises obtaining and blending microbes comprising a gene regulating oxalate degradation, oxalate resistance, formate metabolism, metabolism of macronutrients, production of microbial metabolites, cross-feeding activity, and/or mucin degradation.

20 In certain embodiments of the methods of manufacturing disclosed herein, the method comprises obtaining and blending microbes that are known to protect against diseases and/or that are prevalent in healthy human gut.

In certain embodiments of the methods of manufacturing disclosed herein, the method comprises obtaining and blending microbes that utilize carbon sources set forth in Table 35.

25 In certain embodiments of the methods of manufacturing disclosed herein, each strain can optionally utilize a subset of the carbon sources set forth in Table 35.

In certain embodiments of the methods of manufacturing disclosed herein, each composition is prepared using inoculation density adjustment.

In certain embodiments of the methods of manufacturing disclosed herein, each composition is cultured or has been cultured in presence of gas overlay.

30 In certain embodiments of the methods of manufacturing disclosed herein, each composition is cultured or has been cultured in absence of gas sparging.

In certain non-limiting embodiments, the present disclosure is directed to a composition prepared by the methods of manufacturing disclosed herein.

In certain non-limiting embodiments, the present disclosure is directed to a method of treating hyperoxaluria in a subject in need thereof comprising administering an effective amount of the compositions or the microbial consortia disclosed herein.

5 In certain non-limiting embodiments, the present disclosure is directed to a method of reducing the risk of developing hyperoxaluria in a subject in need thereof comprising administering an effective amount of the compositions or the microbial consortia disclosed herein.

In certain non-limiting embodiments, the present disclosure is directed to a method of reducing urinary oxalate in a subject in need thereof comprising administering an effective amount of the compositions or the microbial consortia disclosed herein.

10 In certain embodiments of the methods disclosed herein, the hyperoxaluria is a primary hyperoxaluria, a secondary hyperoxaluria, or an enteric hyperoxaluria.

In certain embodiments of the methods disclosed herein, the secondary hyperoxaluria is associated with bowel resection surgery.

15 In certain embodiments of the methods disclosed herein, the hyperoxaluria is enteric hyperoxaluria.

In certain embodiments of the methods disclosed herein, the method further comprises administering at least one antibacterial agent, antiviral agent, antifungal agent, anti-inflammatory agent, immunosuppressive agent, prebiotic, or a combination thereof.

20 In certain embodiments of the methods disclosed herein, the method further comprises administering NOV-001, SYN8802, OX-1, Lumasiran, Nedosiran, BBP-711, CNK-336, PBGENE-PH1, or a combination thereof.

In certain embodiments of the methods disclosed herein, the method further comprises administering a low oxalate diet, a high hydration diet, calcium supplements, or a combination thereof.

25 In certain embodiments of the methods disclosed herein, the composition or the microbial consortium is administered orally.

In certain non-limiting embodiments, the present disclosure is directed to a method of treating hyperoxaluria in a subject in need thereof comprising administering a first dose of the compositions or microbial consortia disclosed herein.

30 In certain non-limiting embodiments, the present disclosure is directed to a method of reducing the risk of developing hyperoxaluria in a subject in need thereof comprising administering a first dose of the compositions or microbial consortia disclosed herein.

In certain non-limiting embodiments, the present disclosure is directed to a method of reducing urinary oxalate in a subject in need thereof comprising administering a first dose of the compositions or microbial consortia disclosed herein.

5 In certain embodiments of the methods disclosed herein, the hyperoxaluria is a primary hyperoxaluria, a secondary hyperoxaluria, or an enteric hyperoxaluria.

In certain embodiments of the methods disclosed herein, the secondary hyperoxaluria is associated with bowel resection surgery.

In certain embodiments of the methods disclosed herein, the hyperoxaluria is enteric hyperoxaluria.

10 In certain embodiments of the methods disclosed herein, the method further comprises administering an antibiotic treatment.

In certain embodiments of the methods disclosed herein, the antibiotic treatment is administered for about 2 days, about 3 days, about 4 days, about 5 days, about 6 days, or about 7 days.

15 In certain embodiments of the methods disclosed herein, the antibiotic is metronidazole, clarithromycin, or a combination thereof.

In certain embodiments of the methods disclosed herein, the antibiotic treatment is completed 1 day before administering the first dose.

20 In certain embodiments of the methods disclosed herein, the antibiotic treatment is completed 2 days before administering the first dose.

In certain embodiments of the methods disclosed herein, the method further comprises administering a bowel preparation treatment.

In certain embodiments of the methods disclosed herein, the bowel preparation treatment is administered to the subject after the antibiotic treatment.

25 In certain embodiments of the methods disclosed herein, the bowel preparation treatment is administered before the first dose.

In certain embodiments of the methods disclosed herein, the first dose comprises an effective amount of the composition or the microbial consortium.

30 In certain embodiments of the methods disclosed herein, the first dose comprises about 10^{12} viable cells.

In certain embodiments of the methods disclosed herein, the first dose is administered for about 1 day.

In certain embodiments of the methods disclosed herein, the first dose is administered for about 2 days.

In certain embodiments of the methods disclosed herein, the method further comprises administering a second dose of the compositions or microbial consortia disclosed herein.

In certain embodiments of the methods disclosed herein, the second dose comprises an effective amount of the composition or the microbial consortium.

5 In certain embodiments of the methods disclosed herein, the second dose comprises about 10^{11} viable cells.

In certain embodiments of the methods disclosed herein, the second dose is administered up to about 8 days.

10 In certain embodiments of the methods disclosed herein, the second dose is administered up to about 10 days.

In certain embodiments of the methods disclosed herein, the first dose is administered orally.

In certain embodiments of the methods disclosed herein, the second dose is administered orally.

15 In certain non-limiting embodiments, the present disclosure is directed to a kit comprising the compositions or the microbial consortia disclosed herein.

In certain embodiments of the kits disclosed herein, the kit comprises a container comprising a desiccant.

In certain embodiments of the kits disclosed herein, the container comprises anaerobic conditions.

20 In certain embodiments of the kits disclosed herein, the container is a blister.

In certain embodiments of the kits disclosed herein, the kit further comprises written instructions for administering the composition or microbial consortium.

25 In certain non-limiting embodiments, the present disclosure is directed to a method of culturing a microbial strain from the *Akkermansia* genus comprising contacting the strain with N-Acetylgalactosamine (GalNAc).

In certain embodiments of the methods of culturing disclosed herein, the strain is *Akkermansia muciniphila*.

In certain non-limiting embodiments, the present disclosure is directed to a microbial consortium comprising the functional properties set forth in Table 23.

30 In certain non-limiting embodiments, the present disclosure is directed to a microbial consortium comprising the functional properties set forth in Table 24.

In certain non-limiting embodiments, the present disclosure is directed to a microbial consortium comprising the functional properties set forth in Table 34.

In certain non-limiting embodiments, the present disclosure is directed to a microbial consortium comprising the functional properties set forth in Table 35.

In certain non-limiting embodiments, the present disclosure is directed to a microbial consortium comprising the functional properties set forth in Table 36.

5 In certain non-limiting embodiments, the present disclosure is directed to a microbial consortia comprising FB-001 or a functional equivalent thereof.

In certain non-limiting embodiments, the present disclosure is directed to any method or composition described herein.

EXAMPLES

10 *Example 1: Design of Consortia*

While microbial consortia of two or more microbial strains have been made before, limitations existed that prevent manufacturing and clinical efficacy. Specifically, manufacturing limitations have prevented the design and generation of large consortia that are able to engraft in the gastrointestinal tract and build a functional microbiota system.

15 *Isolation of donor-derived microbial strains.* Microbial strains were isolated and identified using the methods described in PCT/US2021/021790.

Generation of Consortia. Using the microbial strains identified using the isolation and identification methods described in PCT/US2021/021790, over 30 large consortia were made and examined for their functional ability to metabolize oxalate, absence of phages, acceptable endotoxin
20 levels, and their ability to be manufactured in multi-strain drug substances. The reason for the large number of experimental large consortia was because it was unknown what combination of microbial strains would be optimal given the considerations above. More so, the optimal combination of microbial strains could not be predicted with algorithms and required wet laboratory work to determine efficacy and manufacturability.

25 Nineteen exemplary consortia are provided in Tables 1-19.

Drug products comprising each of the consortia above were tested for the ability to metabolize oxalate using in vitro and/or in vivo assays.

In exemplary experiments, in vitro studies were performed on germ-free mice. determine whether diet and existing gastrointestinal microbiota had an effect on the efficacy of Consortia in
30 reducing oxalate *in vivo*. Germ-free mice were divided into three groups: 1) diet was a refined, sugary diet, 2) diet was a complex, grain-based diet, and 3) diet was a complex, grain-based diet and the mice were colonized with human FMT. The mice from groups 1-3 were then given one of Consortia I-VIII. The refined, sugary diet (also referred to as the Ox36 diet) consisted of 316.22 g/kg sucrose,

280 g/kg corn starch, 200 g/kg casein, 50 g/kg corn oil, 35 g/kg inulin, 35 g/kg pectin, 25 g/kg cellulose, 16.23 g/kg sodium chloride, 13.37 g/kg mineral mix (Ca-P deficient), 11.4 g/kg potassium phosphate monobasic, 10 g/kg vitamin mix (Teklad), 3.72 g/kg sodium oxalate, 3 g/kg DL-methionine, 1.05 g/kg calcium chloride, and 0.01 g/kg ethoxyquin (antioxidant). As formulated, the Ox36 diet contained 0.372% sodium oxalate, 1.88% NaCl, 2.5% cellulose, 3.5% inulin and 3.5% pectin and the nutritional breakdown of the diet was 58.3% carbohydrates, 17.7% protein, and 5.2% fat (by weight). The complex, grain-based diet consisted of 22.7% protein by weight, 40.3% carbohydrate by weight, 5% fat by weight and was made using the PMI Laboratory Autoclavable Rodent Diet (Envigo Cat No 5010) with the addition of sodium oxalate and sodium chloride (final product consisting of 970.82 g/Kg PMI Laboratory Autoclavable Rodent Diet, 21.5g/Kg sodium oxalate, and 7.68 g/Kg sodium chloride).

In these experiments, the germ-free C57Bl/6 mice are fed either the refined, sugary diet or the complex, grain-based diet to induce hyperoxaluria. After one week, one of Consortias I-VIII were introduced via oral gavage to the mice. Mice were sampled thereafter to determine microbiome composition and urinary oxalate levels. Specifically, on day -7, the mice began the diets, on day 0 the mice were gavaged, on day 7 fecal samples were taken and food consumption was measured, and on day 14 the mice were taken down to collect urine and feces and serum samples, cecal images, and kidney/liver inspection and/or images were taken when possible. The negative control for these experiments were a gavage with PBS instead of a Consortia.

Oxalate and creatinine were measured by LC-MS/MS from urine samples acquired on day 14.

Representative data from mice fed the complex, grain-based diet that were gavaged with Consortias is provided in Tables 20 and 21.

Table 20. Oxalate urine Concentrations, μ M

Treatment	R1	R2	R3	R4	R5	Ave	SD	CV, %
PBS Control	9,157	3,962	6,452	6,999	6,778	6,669	1,850	27.73
Consortia I	1,313	1,858	3,874	3,517		2,640	1,247	47.23
Consortia II	2,118	3,270	4,237	3,422		3,261	873	26.76
Consortia III	1,468	1,783	2,153	2,353		1,939	393	20.27
Consortia IV	972	1,596	1,249	713		1,132	379	33.46
Consortia V	1,173	750	846	801		893	191	21.42

Table 21. Creatinine Urine Concentrations, μ M

Treatment	R1	R2	R3	R4	R5	Ave	SD	CV, %
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PBS Control	2,563	3,346	3,977	4,129	2,906	3,384	673	19.88
Consortia I	1,417	1,413	1,820	1,975		1,656	286	17.25
Consortia II	1,702	1,822	2,218	1,476		1,805	311	17.22
Consortia III	1,449	1,363	1,661	1,723		1,549	171	11.03
Consortia IV	1,219	1,304	1,190	1,245		1,239	49	3.92
Consortia V	923	897	1,264	1,250		1,084	201	18.51

Furthermore, it was surprising to see that the ability of the Consortia to reduce urinary oxalate was independent of diet. Representative data from mice fed either the complex grain based diet or the refined sugary diet that were gavaged with Consortia VI (**Figure 1A**) or VIII (**Figure 1B**) show the ability of the Consortia to reduce urinary oxalate is independent of diet.

An additional question that was unknown was whether existing microbiota in the gastrointestinal tract would affect the efficacy of the Consortias. Accordingly, the experiments described above were repeated in germ-free mice that were colonized with human FMT prior to the initiation of the oxalate diets (either the refined, sugary diet or the complex, grain-based diet). As shown in **Figure 1C**, the pre-existing microbiota did not affect the efficacy of the Consortia (Consortia VII, in this example). The ability of the Consortia to have an active effect on the reduction of urinary oxalate levels regardless of the existing microbiota was unexpected because literature suggested that it was necessary to eliminate existing microbiota using antibiotics in order for microbiome products to engraft and function in a gastrointestinal tract.

While Table 20 shows that Consortia V was most effective at oxalate metabolism and degradation (i.e., Consortia V had the lowest concentration of urinary oxalate), additional investigation and modification of the Consortia was needed to design a product for the treatment of disease, specifically a disease that causes or is caused by decrease ability or inability to effectively metabolize and degrade oxalate in the gastrointestinal tract. Accordingly, modifications of Consortia V were made to determine which microbiota provided functional benefits, including but not limited consortia growth, oxalate metabolism and degradation, consortia engraftment, and consortia survival, and which microbiota were either not needed or provided a detriment to the patient receiving the consortia as treatment of the disease or a detriment to the function of the consortia as a whole (including but not limited consortia growth, oxalate metabolism and degradation, consortia engraftment, and consortia survival). Examples of such designed and investigated consortia are Consortia IX-XVI.

Of Consortia IX-XVI that were designed and tested, Consortia IX was selected as the lead for clinical development. Key changes made as variations of the consortia were made to modify for the treatment of disease, specifically a disease that causes or is caused by decrease ability or inability to

effectively metabolize and degrade oxalate in the gastrointestinal tract, include removing the *Citrobacter freundii* strain because through experimentation it was determined to be facultative anaerobes (see e.g., strain removal between Consortia XIII and XV and between Consortia XXIV and XIII and XII), replacement of one *Bacteroides kribbi* species with a different *Bacteroides kribbi* species cluster (see e.g., strain replacements between Consortia XV and XVI), replacement of one *Blautia faecis* species with a different *Blautia faecis* species (see e.g., strain replacements between Consortia XV and XVI), strains that were determined to be duplicative strains based on Whole Genome Sequencing cluster (see e.g., strain removals between Consortia XVII and XVI), replacement of one *Bifidobacterium adolescentis* with an alternate *Bifidobacterium adolescentis* to improve growth in culture (see e.g., strain replacement between Consortia X and XII), replacement of one *Bifidobacterium pseudocatenulatum* with an alternate *Bifidobacterium pseudoactenulatum* to improve growth in culture (see e.g., strain replacement between Consortia X and XII), replacement of one *Bacteroides xylanisolvens* with an alternate *Bacteroides xylanisolvens* to improve growth in culture (see e.g., strain replacement between Consortia X and XII), replacement of one *Clostridium citroniae* with an alternate *Clostridium citroniae* to improve growth in culture (see e.g., strain replacement between Consortia X and XII), replacement of one *Blautia faecis* with an alternate *Blautia faecis* in order to identify a *Blautia* strain that was able to grow sufficiently to produce a master cell bank (see e.g., strain replacement between Consortia X and XII), removal of *Holdemanella biformis* to eliminate phage risk because while a phage was not detected in co-culture it was detected using bioinformatic methods (see e.g., strain replacement between Consortia X and XII), and removal of *Faecalibacterium prasnitzii* to eliminate phage risk because while a phage was not detected in co-culture it was detected using bioinformatic methods (see e.g., strain replacement between Consortia X and XII).

Example 2: Oxalobacter formigenes Microbiota

Oxalobacter formigenes (*O. formigenes*) is a key active microbiota for the degradation and metabolism of oxalate and it is included in the Consortia I-XIX. However, as shown in Tables 1-19 above, certain Consortia have *O. formigenes* listed three times in each of the Consortia. The reason for this is because there are multiple strains of *O. formigenes* and it was determined through experimentation that the different strains identified had different physiologies that directly affected engraftment and function in the gastrointestinal tract. The three *O. formigenes* strains that were selected for Consortia I-XIX comprise 1) one strain with a low pH tolerance, 2) one strain with a high oxalate tolerance, and 3) one strain that has a high growth rate.

While any set of *O. formigenes* strains that meet the criteria of 1-3 above can be used in a consortium designed to increase oxalate metabolism and degradation, the strains used in Consortia I-XIX comprise the 16S RNA sequences of SEQ ID NO:42, SEQ ID NO: 79, and SEQ ID NO: 146.

Example 3: Drug Product Design and Manufacture

As shown in Example 1, the Consortia described herein were designed to be a complex community of anaerobic microbiota that can engraft and function in a gastrointestinal tract. However, prior methods known to one of skill in the art were not capable of manufacturing such large consortia. Accordingly, new methods of manufacture were needed in order to grow the microbiota in discrete groups (i.e., drug substances) to then form a final drug product.

Conventionally, Live Biotherapeutic Products (LBPs) are manufactured one strain at a time (i.e., single strain manufacturing). Single strain manufacture necessitates fermentation scale-up of each single strain followed by lyophilization to make individual drug substances (each a “DS”). Thereafter the multiple DSs of individual lyophilized stains are then blended into a mixture and filled into capsules or other suitable packaging/filling to make a final drug product (a “DP”). While this works for small consortia, it is not feasible to grow 100+ strains separately, make 100+ DSs, and then blend 100+ DSs into a stable DP. In addition to stability limitations, current technology would require 1 or more year(s) to manufacture a single DP. Accordingly, conventional manufacturing using current technology was not an option for a DP comprising 100+ strains, and preferably 145+ strains as provided in Consortia IX.

As the Consortia were designed and modified as described in Examples 1 and 2, manufacturing methods were developed that were capable of manufacturing the 145+ strain consortia that comprise over 90 species, and 4 or more or the 6 taxonomic phyla found in the human gastrointestinal tract microbiome. More so, methods were developed to modify for Consortia IX that comprises approximately 99 species across the taxonomic phyla of Bacteroidetes, Firmicutes, Actinobacteria, Proteobacteria, and Archaea. The methods developed and described herein are mixed co-culture methods that are capable of stably growing greater than 50 strains in one co-culture to generate DSs with greater than 50 strains.

Strains were selected for co-culture by based on growth rates and the manufacturing was initially designed to add strains to the co-culture at different times throughout the manufacturing process in order to achieve optimal growth of each strain. This approach was termed “time of addition” manufacturing. The rationale behind this initial approach was to ensure the strains reanimate in the gastrointestinal tract to increase efficacy of engraftment (i.e., allow for engraftment before the strains are excreted. Optimal reanimation and engraftment of the lyophilized strains

require preserving the strains in an “active state” (i.e., active growth state). However, this “time of addition” manufacturing approach was not successful because growth rates of the strains in the Consortia described herein are highly variable which makes it difficult to achieve exponential growth simultaneously for diverse strains in coculture. Accordingly, it was determined that additional experimentation was needed in order to understand each strain’s unique growth kinetics to enable binning of strains based on growth rate and further modification of time of addition to the bioreactor. Growth kinetic assays were performed using HTP anaerobic growth kinetic assays on each individual strain in each of Consortia IX-XVI at 8 different inoculation densities.

While experimentation to understand each strain’s unique growth kinetics proved helpful with the time of addition manufacturing, ultimately the highly variable nature of growing strains from a lyophilized powder to an active consortia in a bioreactor proved undesirable for the time of addition methods.

Accordingly, a second approach for coculture was developed. Instead of applying different time of additions, the second approach used inoculation density adjustment for each strain to synchronize growth and control of strain distribution at the time of harvest from the co-culture (“inoculation density” manufacturing). Using the unique growth kinetics determined for each strain in the Consortia, specifically Consortia IX-XVI, optimal growth zones were determined for each strain. In doing so, it was determined that coculture was effective and possible if each strain was added to culture at an initial time point based on inoculum density (i.e., number of cells per strain added to the co-culture) such that higher inoculum densities of certain strains resulted in shorter growth lag time for such strains. Based on this, higher inoculum density of slow growing strains and lower inoculum density of fast growing strains resulted in a synchronized harvest time. As shown by means of example in **Figures 2A** and **2B**, modifying inoculation densities of individual strains allowed control over the strain distribution and improved strain recovery in cocultures (i.e., even distribution of strains as well as higher number of strain recovery are achieved by adjusting inoculum densities). **Figure 2A** shows an example of a co-culture of 21 fast growing strains where only 4 of the 21 strains were undetectable by metagenomics in the final product. However, it is important to note that even if a strain is not detected in the final product, the strain may still provide a community advantage to allow for more efficient and robust growth of other strains that are detectable in the final product. **Figure 2B** shows a further modified experiment of that show in **Figure 2A** where the time of harvest and strain detection was modified. As shown the different timing of growth and culture led to a better distribution of strains and detection of all 21 strains.

Further modification of the coculture process was needed to improve fermentation. For example, additional modification was performed to control for pH and to achieve conditions of growth based on the bioreactor container (i.e., the type of container and the size of the container).

Using the methods developed and described herein, Consortia IX-XVI were each
 5 manufactured using only 7 DSs. One exemplary 7 DS Drug Product comprises: 3 *O. formigenes* monocultures (see the 3 phenotypes of the 3 *O. formigenes* cultures described in Example 2), the strains of DS1 (e.g., listed in Table 22), the strains of DS2 (e.g., listed in Table 22), the strains of DS3 (e.g., listed in Table 22), the strains of DS4 (e.g., listed in Table 22).

In order to identify each DS without sequencing the entire genome of all strains and in order
 10 to ensure proper growth throughout the coculture process, identifier strains were developed. For DS1, the identifier strains were *Bacteroides thetaiotaomicron*, *Bifidobacterium pseudocatenulatum*, and *Megasphaera massiliensis*. For DS2, the identifier strains were *Bacteroides ovatus*, *Faecalibacterium prausnitzii*, and *Phascolarctobacterium faecium*. For DS3, the identifier strains were *Blautia wexlerae*, *Anaerostipes hadrus*, and *Clostridium bolteae*. For DS4, the identifier strains
 15 were *Holdemanella biformis*, *Parasutterella excrementihominis*, and *Dialister invisus*.

As described herein, the number of strains detected at the conclusion of the co-culture may be less than the number of strains added at the beginning of the culture. This may be a result of limited detection methods. Furthermore, while not all strains may be detected at the conclusion of the coculture process, the inclusion of the undetected strains may still be vital for the survival and
 20 propagation of other strains that are detected.

In one experiment, DS1 consisted of 54 initial strains and 50 strains were detected at the end of the coculture process; DS2 consisted of 47 initial strains and 39 strains were detected at the end of the coculture process; DS3 consisted of 33 initial strains and 30 strains were detected at the end of the coculture process; and DS4 consisted of 14 initial strains and 11 strains were detected at the end
 25 of the coculture process. Accordingly, in this experiment 148 strains were detectable at the beginning of the coculture and 130 strains were detected at the completion of the culture.

This achievement of 130/148 strains was achieved through development of a fermentation process that allowed for optimal growth of diverse strains in coculture. Variables that were investigated include growth kinetics of each strain, nutritional requirements for each strain,
 30 competition for nutritional sources in each DS, selection of the optimal starting inoculum concentration to achieve strain growth and distribution in each DS. For example growth curves were performed and used to define DS buckets as well as starting inoculum composition. This is shown in **Figures 3A** and **3B**. **Figure 3A** shows the design of strain segregation into 4 DS buckets based on slow and fast growing strains. **Figure 3B** shows the starting inoculum seed design for fast and

very fast growing strains. Using 5 iterations of the strain segregation and inoculum seed design methods, the DS1, for example, was able to increase its yield rate from approximately 35/54 strains detected at the conclusion of the coculture process to 50/54 strains detected at the conclusion of the coculture process.

5 Additional experimentation was required to successfully manufacture the DSs at large scale. For example, experimentation was performed on sterilization procedures and raw materials used in the media, gas solubility in the bioreactor (i.e., fermenter), shear stress caused by the impeller and gas sparging in the bioreactor, and mass transfer and mixing times. Each of these factors are necessary in order develop a process that could successfully produce a complex consortia such as
10 any of the Consortia described herein. For example, through experimentation, it was determined that nitrogen sparging lead to higher sheering and impacted gas solubility. Accordingly, experiments were performed to adjust the speed of the sparger, location of the sparger, and replacement of sparging to gas overlay. The data showed that gas overlay was the only approach that provided successful coculture of DSs. For example, data from different sparging conditions only allowed for
15 the detection of up to 36 out of 54 strains from DS1 while gas overlay allowed for detection of an additional 11 species at the conclusion of the coculture (i.e., 47/54 strains).

The next step in the manufacturing process that had to be developed was a method of storing the final product in a way that preserved the stability and activity of the strains. Freezing and lyophilization methods were investigated to determine what would preserve the activity and viability
20 of the strains for each DS.

In order to determine if lyophilization would be better than freezing to preserve the activity and viability of the strains in each DS, lyophilization processes had to be developed because none were known in the art for the complexity of the DSs and Consortia provided herein. Key variables that were investigated in order to develop lyophilization process for each DS included but were not
25 limited to: formulation of the broth or alternative microbiota suspension media, methods to prevent oxygen contamination during the lyophilization process, excipient:broth ratio, parameters for freezing the microbiota suspension prior to the lyophilization, cycle parameters for the lyophilization, sterilization requirements, methods for reviving the microbiota following lyophilized storage, buffers for reviving the microbiota, and storage of the lyophilized DS.

30 By means of example, high throughput, foil covered plates were used as one of the test options for storage of the lyophilized DS. This was presumed to work because the foil cover should prevent oxygen exposure. However, it was determined that foil covered plates in fact did not prevent oxygen contamination because there was no way to partially stopper the plate. Another storage method that was investigated was glass and plastic tray vials with multiplexed stoppers. The theoretical

advantage of this approach was hypothesized to be the ability to do high throughput screening without the need to individually stopper each vial because the multiplexed stoppers can be pushed into the vials in a single step. However, this method proved ineffective because oxygen contamination occurred with the removal of the multiplexed stoppers. After exploring additional options for
5 methods of preserving the lyophilized product, it was determined that individual glass vials with individual stoppers allowed for long term storage without oxygen contamination.

By means of a second example, it was necessary to determine the correct formulation for the lyophilization buffer/media. The following lyoprotectants were investigated to determine the correct formulation for each DS: sorbitol, maltodextrin, OPS diagnostics buffer, sucrose, inulin, alginate,
10 mannitol, trehalose, and skim milk. For example, **Figure 4A** shows examples of different viabilities of DS2 based on different lyoprotectants and **Figure 4B** shows examples of different viabilities of DS1 based on different lyoprotectants. The addition of reducing agents including but not limited to cysteine HCL and riboflavin were also investigated as shown in **Figure 5A** (DS2) and **Figure 5B** (DS1). Additional lyophilization formulations that were tested include 8% Maltodextrin+ 0.5%
15 Inulin + RA, 5% Sucrose + 10% Glycerol + 0.3% Inulin + RA, 7% Trehalose+8% Maltodextrin+RA, 3% Sucrose+5% Maltodextrin + 0.5% Inulin + RA, 5% Maltodextrin+OPS Diag+ 0.5% Inulin + RA, and 5% maltodextrin+10% Glycerol+0.3% Inulin+RA.

Based on freeze thaw and lyophilization experiments, data suggested that 10-12% solids was the selected dose. However, additional experiments were performed to determine if a lower dose
20 would be possible. One exemplary experiment on DS2 is shown in **Figure 6A** and a second exemplary experiment is shown in **Figure 6B**.

Assays were then performed to determine the success rates of cell revival. Cell revival was done using the Anaerobe systems YCFAC media and dilution schemes were conducted using 100 fold dilution to the lyophilized powder (e.g., 50 mg (0.05 g) of powder was diluted in 5.0 mL of
25 YCFAC media). Revival was then detected using flow cytometry and the Coulter Counter.

The experiments performed herein and the data generated determined that lyophilized material produced comparable colonization of strains in mice.

Example 4: EH Mouse Models and Efficacy of Consortia

As described herein, enteric hyperoxaluria (EH) is caused by excess absorption of dietary
30 oxalate leading to elevated urinary oxalate (UOx) levels. Once absorbed, oxalate can complex with calcium to form insoluble crystals, and as a result chronically elevated UOx levels are a major risk factor for the development of kidney stones and progression to kidney damage. There are currently no approved therapies for EH; the standard of care options is limited to supportive measures and

dietary restrictions that have relatively low compliance. Most oxalate degradation in the human GI is carried out by *Oxalobacter formigenes*, a fastidious human commensal that metabolizes dietary oxalate as its primary energy source. However, it is hypothesized that increased antibiotic usage and western diets have decreased the prevalence of *O. formigenes*. Preliminary human studies have explored the therapeutic use of orally dosed *O. formigenes* and demonstrated limited engraftment of *O. formigenes*, leading to reduced durability of UOx reduction. Therefore, we reasoned that the metabolic support of a diverse consortia of GI commensals will enable engraftment of *O. formigenes* and maximum degradation of oxalate. To this end, microbial consortia were designed as described herein that mimic the taxonomic, phylogenetic, and functional structure of a healthy human microbiome. These consortia are not only enriched in *O. formigenes* to maximize oxalate metabolism but also contain numerous bacterial species to support the metabolism of formate, a byproduct of oxalate metabolism. A candidate was selected for clinical development in part by evaluating these consortia for their ability to engraft and reduce UOx in mouse models of diet-induced hyperoxaluria (HO).

Methods. Metagenomics and liquid chromatography-mass spectrophotometry (LC-MS) were used to evaluate bacterial species and urinary metabolites, respectively. Metagenomic sequencing was performed on select fecal samples from each study to evaluate *O. formigenes* engraftment, species richness, and community-specific strain level engraftment. LC-MS was used to evaluate levels of oxalate and creatinine from terminal spot urine samples collected.

Isolation and Processing. Isolation of bacterial strains to create synthetic consortia: bacterial strains to create consortia were isolated from healthy human stool samples collected under anaerobic conditions, homogenized, and then bacterial species from each sample were identified using whole-genome sequencing (WGS). From there, the bacterial strains and abundance thereof were identified.

Stool samples were then processed and bacterial strains isolated for culture on appropriate culture media (e.g. BHI, blood agar). Isolation of oxalate degraders and strains specific to metabolize EH-related pathways were prioritized along with fastidious and unique strains and strains associated with a healthy gut microbiome. Following culture, strains were purified and sequenced using metagenomics. From the cultured, isolated strains, communities to treat enteric hyperoxaluria were created based on the notion of our bacteria to fill critical functional niches in the gut, support normal GI physiology, support engraftment of specialty strains such as *O. formigenes*, and degrade oxalate.

Diversity of synthetic consortia: consortia were created to support engraftment of *O. formigenes* in the GI and each consortium contains unique species and strains to cover various metabolic phenotypes (e.g. bile acid metabolism, short chain fatty acid synthesis, oxalate degradation). A core set of 31 bacterial strains were similar between synthetic consortia and each

community had its unique signature as indicated in the Venn diagram. The number of species present in each consortium created ranged from 40 to 103 species and the number of strains ranged from 75 to 195 as shown **Figures 7A and 7B**. The species and strains comprised varying proportions of the phylum-level diversity where the Bacteroidetes to firmicutes ratio ranges from 51% to 96% indicating that the general composition varied.

EH Model Development. Diet induced EH mouse models were created. Dietary components for induction of EH: three diets (Ox36, 5021 + 0.875% oxalate in drinking water (DW), and 5010 1.51) were created to induce EH for three weeks in germ-free mice with different caloric intake and sodium oxalate. Diet 1 (Ox36): Fat (% kcal): 13.5, Carbohydrate (% kcal): 66.0, Protein (% kcal): 20.5, Fiber (%): 6.0, and Sodium Oxalate (g/kg): 3.7. Diet 2 (5021): Fat (% kcal): 23.7, Carbohydrate (% kcal): 53.2, Protein (% kcal): 23.1, Fiber (%): 3.7, and Sodium Oxalate (g/kg): in drinking water. Diet 3 (5010 1.51): Fat (% kcal): 15.0, Carbohydrate (% kcal): 54.3, Protein (% kcal): 30.6, Fiber (%): 4.2, and Sodium Oxalate (g/kg): 21.5.

Induction of EH in germ-free and humanized mice: terminal urine samples were collected to measure UOx (urinary oxalate). BioIVT10 was identified as a possible FMT sample to develop and humanized, germ-free model of EH as the fecal sample was unable to control oxalate excretion and did not have *O. formigenes* present. This fecal sample showed that it could not degrade oxalate when colonized in a germ-free mouse and when supplemented with *O. formigenes* it was able to degrade oxalate. Additionally, this material showed no presence of *O. formigenes*. See **Figures 8A and 8B**.

Synthetic consortia reduce UOx and UOx:UCr ratio in EH-induced murine models: the three diets described above were tested in the development of microbial consortia to treat EH. All mice were dosed, via gavage, with 200 μ L of each consortium on day 1. Two sets of mice were used: 1) Taconic germ-free C57BL/6NTac F (7-9 weeks old) that were Germ-Free, and 2) Taconic germ-free C57BL/6NTac F (7-9 weeks old) that were Humanized. For the Germ-Free mice, dietary EH induction began on D-7, consortia dosing began on D1, and the endpoint for feces and urine collection was on D15. For the Humanized mice, FMT was administered on D-21, dietary EH induction began on D-14, antibiotic treatment occurred on D-7, consortia dosing began on D1, and the endpoint for feces and urine collection was on D15. It was demonstrated that in using germ-free mice, a significant, 3-5 fold increase in urinary oxalate levels are observed across all diets. Furthermore, the 5010 1.51 diet was used in a humanization model where mice were colonized with an FMT. Three different FMT materials with and without *O. formigenes* were used and it was shown that an FMT that does not have *O. formigenes* present was unable to reduce oxalate degradation compared to control.

Synthetic consortia reduce UOx and UOx:UCr ratio in EH-induced murine models. After establishing that hyperoxaluria could be induced in germ-free mice, the question of whether or not oxalate excretion could be controlled with the administration of a consortia described herein. To do that, the germ free mice were induced for hyperoxaluria for 7 days by providing one of the three diets described above, given a single dose of one of the consortia, and then euthanized for terminal urine collection 14 days later. The diets were sown to effectively induce hyperoxaluria. On average, the consortia described herein reduced levels of oxalate in terminal urine samples collected. Because spot urine samples were collected, the oxalate to creatinine ratio was calculated as a more robust measure of EH and the Prevalence-based and Diversity Communities consistently reduced the UOx:UCr ratio across all diets. The average % reduction in UOx:UCr across consortia was between 40 to 55%. See **Figure 9**.

As described above, humanized mice were also created by providing an FMT to a germ-free mouse using a stool sample that cannot degrade oxalate. These mice were provided a complex high oxalate diet and then were pre-treated with antibiotic to reduce the host microbiome. After a 1-week course of antibiotics, mice were dosed with one of the consortia described herein. The consortia described herein had varying degrees of oxalate reduction.

Consortia engraftment in various EH-induced models: the engraftment of *O. formigenes* and other consortia members were evaluated using metagenomic sequencing. *O. formigenes* engrafted to robust levels across all diets tested with Prevalence-based and Diversity Communities engrafting at the greatest relative abundance. Additionally, a greater proportion of strains and species in Prevalence-based and Diversity Communities engrafted to detectable levels as shown in species richness plots. Lastly, the Diversity Community had greater species richness compared to Five rationally-designed, synthetic consortia were created from donor fecal samples with varying degrees of diversity, fortified with *O. formigenes*, to control oxalate metabolism in the GI tract baseline in the “humanized” model, indicating that in a complex model, the Diversity Community stably engrafts and displaces a previously established human community in germ-free mice. See, **Figures 10A, 10B, 10C, and 10D**.

Based on these experiments, it was determined that the five rationally-designed, synthetic consortia used in this experiment had varying degrees of diversity and were able to control oxalate metabolism in the GI tract to varying degrees. It was further shown that the diverse consortia described herein are able to engraft following dosing. Specifically, the experiments described herein show that *O. formigenes* was one of the microbes that were able to engraft. Furthermore, it was shown that the consortia described herein were able to reduce oxalate excretion (UOx and UOx:UCr ratio) in dietary induced EH models to varying degrees and that the Community V, the consortium

with the greatest diversity described in this Example 5, had the ability to stably engraft *O. formigenes*, therapeutically reduce UOx, and lead to a healthy human microbiome.

Example 5: The Manufacture of Threonine Auxotrophic Microorganisms

Certain microorganisms are auxotrophs. This means that the microorganism is not able to synthesize a particular organic compound required for its growth. One such organic compound that certain microorganisms are incapable of synthesizing themselves is threonine. Furthermore, while some microorganisms are not per se auxotrophs of threonine, they are inefficient producers of threonine which prevent effective growth in commonly used growth medias.

N-Acetylgalactosamine (GalNAc) is an amino sugar derivative of galactose that is typically the first monosaccharide that connects serine or threonine in particular forms of protein O-glycosylation. While it is possible to supplement certain small batch growth medias with GalNAc to grow threonine auxotrophs without the addition of threonine, such supplementation is not preferred for large batch manufacture because GalNAc is costly and large amounts are needed for effective growth of microorganisms that require such galactose derivative. Furthermore, certain medias such as YCFAC media is incapable of effectively growing certain threonine auxotrophs even in the presence of GalNAc.

Accordingly, a method of improving the expansion and growth of inefficient producers of threonine is needed to effectively grow such microorganisms.

One such microorganism included in the consortia described herein is *Akkermansia muciniphilia*. *Akkermansia* is not capable of synthesizing threonine itself and thus is not able to effectively expand and grow in culture that is lacking a GalNAc source (or a primary source that can be metabolized into GalNAc). Furthermore, GalNAc is the preferred carbon source for *Akkermansia* and thus known methods of effectively growing and manufacturing *Akkermansia* comprise the addition of GalNAc to the growth media.

Accordingly, experiments were designed to identify novel methods of growing *Akkermansia* in large batches without large amounts of GalNAc. Specifically, three different growth medias were tested: YCFAC + GalNAc, YCFAC + GalNAc + Threonine, and YCFAC + Threonine. Since BHI is an animal-based media that contains threonine, BHI media was used as a positive control (specifically BHI media + GalNAc + Hemin + VitaminK). Because GalNAc is the preferred carbon source for *Akkermansia*, it was expected to be needed in all medias in order to allow expansion and growth of the microorganism; however, the expected question was how much GalNAc is needed, not whether GalNAc was needed at all, if threonine is also added. Surprisingly, it was determined that 1) YCFAC + 0.5g/L GalNAc did not support *Akkermansia* growth, 2) YCFAC + 0.5g/L GalNAc +

10mM threonine did support growth, and that 3) YCFAC + 10mM threonine alone supports the growth of Akkermansia. In these experiments, a seed culture containing 0.5g/L GalNAc in YCFAC was used to initiate cell growth before being transferred to large fermenter for growth and expansion with the 3 medias described above.

5 However, certain of the consortia described herein comprise more than 100 different microorganisms, Akkermansia being only one of the more than 100 different microorganisms. Furthermore, the manufacturing methods described herein allow for the growth and manufacturing of multiple microorganisms in a single large batch culture (e.g., in a fermenter). The question then became how to grow Akkermansia in a large co-culture when it is the only microorganism that is a
10 threonine auxotroph that has a preferred carbon source of GalNAc. Accordingly, an experiment was designed to determine if it was possible to start a seed culture with Akkermansia alone and then combine it with a second seed culture of multiple microorganisms for the large batch expansion.

 This experiment comprised : 1) a seed culture was first grown to allow the Akkermansia to begin growing in a small culture (i.e., a seed culture) of 10mL before expansion into a large batch
15 fermenter, 2) concurrently with the Akkermansia seed culture, a second 100mL seed culture of all other microorganism in the drug substance was separately grown, 3) the 100mL seed co-culture and the 10mL Akkermansia seed culture were combined into a large batch fermenter (e.g., 1L or more), and 4) the strains of the drug substance were detected and the ability of Akkermansia to grow and expand in the co-culture was assessed. A diagram of this experiment is shown in **Figure 11A**.

20 As shown in **Figure 12**, it was surprising to see that Akkermansia was unable to grow in YCFAC media that was supplemented with GalNAc, Hemin, and VitaminK (0.0000% Akkermansia detected) compared to BHI media that was supplemented with GalNAc, Hemin, and VitaminK. Accordingly, it was determined that YCFAC + GalNAc cannot support the growth of Akkermansia. The question then became whether the addition of threonine could recover the growth of the
25 Akkermansia.

 The next question was whether GalNAc was needed for if threonine was added. Specifically, the question was how would Akkermansia grow in YCFAC + 10mM threonine (72hr growth) compared to a media comprising YCFAC + 10mM threonine + 0.5 g/L GalNAc (48hr growth). It was surprising to find that the results showed comparable growth with and without the GalNAc (an
30 OD of 0.25 for w/o GalNAc and an OD of 0.35 for w/ GalNAc).

 A co-culture experiment similar to that described above and shown in **Figure 11A** was designed to evaluate the need for GalNAc and threonine. In this experiment, two seed cultures were used: 1) Akkermansia seed grown in YCFAC + 10mM threonine + 0.5 g/L GalNAc, and 2) the other microorganisms in the drug substance (14 microorganisms) grown in YCFAC alone. The seed

cultures were then combined into a large batch fermenter comprising YCFAC + 10mM threonine (i.e., no GalNAc). See **Figure 11B**. This study showed that no GalNAc was needed in the presence of 10mM threonine in a large batch fermenter in order for Akkermansia to grow in a co-culture with other microorganisms that are not threonine auxotrophs. Furthermore, in the 10mM threonine YCFAC media, Akkermansia was detected at all growth time points (**Figure 13**).

Additional experiments further showed that GalNAc was not even needed in the seed culture in order to achieve Akkermansia growth.

The ability to grow Akkermansia without GalNAc was very surprising given that GalNAc is Akkermansia's preferred carbon source. Furthermore, the ability to grow Akkermansia in a media without GalNAc provides a means of making microbial drug products comprising GalNAc wherein the Akkermansia is grown in a co-culture of multiple microbes.

Example 6: Clinical Candidate Selection

As described above, Consortia IX was selected as the clinical candidate for clinical trials and was termed FB-001. FB-001 comprises 148 different anaerobic microbial strains that was designed to emulate the metabolic and phylogenetic diversity of the human microbiome (**Figure 17**) and was split into 7 different drug substances for manufacturing purposes. Table 22 shows the 7 different drug substances. Species were identified by 16S rRNA gene sequencing and whole genome sequencing of RCBs. The species in the consortium span six of the major phyla found in the GI tracts of healthy adults (King, Desai et al. 2019) with the deliberate exception of Fusobacteria, a phylum generally associated with human infections and enriched for opportunistic pathogens. The 148 strains encompass 10 distinct classes, 18 orders, 26 families, and 59 genera.

Prior to lyophilization, the cell pellet containing the FB-001 microbial strains was resuspended in YCFAC media with lyoprotectants and then lyophilized. The YCFAC media and lyoprotectants were chosen to stabilize the DS during the lyophilization step. The lyoprotectant combination of 8% maltodextrin + 0.5% inulin was chosen for the final DS formulation as it demonstrated high viability of the FB-001 microbial strains in formulation development studies.

Maltodextrin was also added as a filler during DP manufacturing.

The capsules to encapsulate the DP were enteric coated and were chosen to release the DP in the small intestine and resist the gastric acids as they pass through the gastrointestinal tract. The dissolution of these capsules was tested per USP <701> at a pH of 1.2 and showed no disintegration for 2 hours. At a pH of 6.8, the capsules fully disintegrated within 30 minutes, which is the target release pH in the GI tract for FB-001 DP (Hydroxypropyl methylcellulose [HPMC] Capsule COA).

Function Properties of FB-001. FB-001 was manufactured using 7 individual drug substances (DS) that contain a total of 148 anaerobic microbial strains and is enriched for species performing beneficial or normalizing functions in the human GI tract.

The first of these beneficial or normalizing functions is oxalate degradation, which is the primary EH disease modifying mechanism of FB-001. *Oxalobacter formigenes* is the principal driver of oxalate degradation in the human GI tract. *O. formigenes* uses oxalate as its exclusive energy source, metabolizing significant concentrations of oxalate for energy generation and biomass production. The metabolism of oxalate is mediated by a series of enzymatic and transport reactions that ultimately consume oxalate and release CO₂ and formate.

Formate, as a by-product of oxalate metabolism, can ultimately inhibit further oxalate metabolism *in vitro* if it is not removed. Therefore, FB-001 also contains strains capable of formate degradation. These formate-utilizing bacteria help to clear the potentially inhibitory metabolic byproducts of oxalate metabolism.

FB-001 also contains strains that are oxalate resistant, able to grow in the presence of oxalate concentrations that are over a magnitude or higher than the physiologically normal concentrations of oxalate. This enrichment of oxalate-tolerant strains in the FB-001 consortium may support stable engraftment despite potentially elevated levels of free oxalate in the GI lumen of patients with EH, as the abundance of the key oxalotrophs will naturally increase with spikes in oxalate concentration.

The FB-001 consortium was specifically designed to contain phylogenetically diverse microbial species that function mutualistically to maximize the metabolic flux of oxalate (primary mechanism) and improve the dysbiosis associated with malabsorption (secondary mechanism). To ensure execution of both mechanisms, the FB-001 consortium is enriched for oxalate degrading strains to reduce free oxalate concentrations in the GI tract, as well as numerous species intended to support the community by restoring essential metabolic functions that reduce the malabsorption of any oxalate that is not degraded. The strains that make up the FB-001 consortium were selected based on their predicted ability to perform a variety of supportive metabolic functions that would contribute to engraftment regardless of differences in patient physiology or diet. Metabolism of macronutrients and dietary molecules that are not digested or utilized by host cells may result in the release of metabolic products that feed other members of the microbiome community.

Other strains in FB-001 were evaluated for unique and potentially beneficial biological functions in the GI tract, including production of short-chain fatty acids (SCFAs), cross-feeding activity, and mucin degradation. SCFAs are absorbed by the host and have been recognized to confer a range of health-promoting functions by acting as key energy substrates for colonocytes, enterocytes, and hepatocytes, while also acting as signaling molecules recognized by specific G-protein couple

receptors targeting primarily enteroendocrine and immune cells in the lamina propria of the intestinal mucosa. Strains in FB-001 were evaluated for their cross-feeding activity, a process in which bacteria make by-products that feed other bacteria. Cross-feeding stabilizes the gut microbiome and creates novel niches. Strains in FB-001 were also evaluated for putative protective and/or anti-inflammatory properties.

Table 23 summarizes the number of strains in FB-001 that contribute to each of these functional properties, and characteristics that are associated with each FB-001 species are summarized in Table 24.

Table 23. Function Properties of FB-001 DP

Properties	Classification	Number of FB-001 DP Strains
Oxalate and formate metabolism	Oxalate degradation	7
	Oxalate resistance	38
	Formate metabolism	45
Supportive metabolic functions	Metabolism of macronutrients	98
	Production of microbial metabolites	70
	Production of short-chain fatty acids	131
	Cross-feeding activity	12
	Mucin degradation	4
Putative protection against disease		22
Prevalence in healthy human gut		97

Table 24. Species Included in FB-001 Drug Product and Characteristics

Species (by phylum)	# strains	Oxalate Degradation	Oxalate Resistance	Formate Metabolism	Metabolism of Macronutrients	Production of Microbial Metabolites	Production of Short-Chain Fatty Acids	Cross-Feeding Activity	Mucin Degradation	Putative Protection Against Disease	Known Prevalence in Healthy Human Gut
Actinobacteria											
Bifidobacterium adolescentis	3				•	•	•				•

<i>Bifidobacterium bifidum</i>	1				•			•	•		•
<i>Bifidobacterium catenulatum</i>	1				•	•	•				•
<i>Bifidobacterium dentium</i>	1	•			•	•	•				•
<i>Bifidobacterium longum</i>	2				•	•	•			•	•
<i>Bifidobacterium pseudocatenulatum</i>	3	•			•	•	•				•
<i>Collinsella aerofaciens</i>	2			•	•	•	•				•
<i>Eggerthella lenta</i>	4		•	•	•		•				•
<i>Gordonibacter pamelaeae</i>	2			•	•		•				•
<i>Senegalimassilia anaerobia</i>	1			•							
Bacteroidetes											
<i>Alistipes onderdonkii</i>	2				•	•	•			•	•
<i>Alistipes putredinis</i>	2					•	•				•
<i>Alistipes senegalensis</i>	1				•						•
<i>Alistipes shahii</i>	2				•		•			•	•
<i>Alistipes timonensis</i>	1			•	•		•				•
<i>Alistipes</i> sp. FBI00180	1						•		•		
<i>Alistipes</i> sp. FBI00238	1						•				
<i>Bacteroides caccae</i>	2				•		•			•	•
<i>Bacteroides coprocola</i>	1										•
<i>Bacteroides faecis</i>	1			•		•	•				•
<i>Bacteroides finegoldii</i>	1			•							•
<i>Bacteroides fragilis</i>	1				•		•				•
<i>Bacteroides kribbi</i>	2			•	•		•				
<i>Bacteroides massiliensis</i>	1				•		•				•
<i>Bacteroides nordii</i>	1						•				•
<i>Bacteroides ovatus</i>	1			•	•					•	•
<i>Bacteroides salyersiae</i>	1			•			•				•
<i>Bacteroides stercorisoris</i>	1			•			•				
<i>Bacteroides stercoris</i>	2				•	•	•				•
<i>Bacteroides thetaiotaomicron</i>	2		•	•	•	•	•	•			•
<i>Bacteroides uniformis</i>	2				•		•	•			•
<i>Bacteroides vulgatus</i>	2			•	•	•	•				•
<i>Bacteroides xylanisolvens</i>	3		•	•	•	•	•				•
<i>Barnesiella intestinihominis</i>	1									•	•
<i>Butyricimonas faecihominis</i>	1				•	•	•				
<i>Parabacteroides distasonis</i>	1		•		•	•	•				•

Parabacteroides merdae	2				•		•				•
Paraprevotella clara	1			•	•	•	•				•
Porphyromonas asaccharolytica	1						•				•
Euryarchaeota											
Methanobrevibacter smithii	2			•	•	•	•				•
Acidaminococcus intestini	1					•	•				•
Acutalibacter timonensis	1		•				•				
Anaerofustis stercorihominis	1		•		•	•	•				•
Anaerostipes hadrus	2				•	•	•	•			•
Anaerotruncus massiliensis	1			•	•						•
Blautia faecis	1		•			•	•				•
Blautia hydrogenotrophica	1			•		•	•				•
Blautia massiliensis	1			•		•	•				
Blautia obeum	2		•		•	•	•			•	•
Blautia wexlerae	2			•	•	•	•			•	
Catabacter hongkongensis	1		•		•						•
Clostridiaceae sp. FBI00191	1						•				
Clostridium aldenense	2		•		•		•				•
Clostridium bolteae	2		•	•	•		•				•
Clostridium citroniae	2		•		•		•				•
Clostridium clostridioforme	1						•				•
Clostridium fessum	1						•				
Clostridium scindens	1				•		•				
Coprococcus comes	2				•	•	•				•
Coprococcus eutactus	1						•				•
Dialister invisus	1						•				•
Dialister succinatiphilus	1		•		•	•	•				
Dielma fastidiosa	1				•						
Dorea formicigenerans	2			•	•		•				•
Dorea longicatena	2				•		•				•
Eisenbergiella tayi	2					•	•				
Emergencia timonensis	1				•	•					
Eubacterium eligens	2				•		•			•	
Eubacterium hallii	1				•	•	•				•
Eubacterium rectale	2				•		•	•			•
Eubacterium siraeum	1				•						

Eubacterium ventriosum	1				•					•	•
Eubacterium xylanophilum	1				•	•	•				•
Faecalibacterium prausnitzii	1			•	•	•	•		•	•	•
Fusicatenibacter saccharivorans	2					•	•				
Holdemanella bififormis	1					•				•	•
Hungatella effluvii	1						•				
Hungatella hathewayi	2			•	•	•					
Lachnoclostridium pacaense	2						•				
Lachnospiraceae sp. FBI00033	1						•				
Lachnospiraceae sp. FBI00071	1						•				
Lachnospiraceae sp. FBI00290	1						•				
Lactobacillus rogosae	2						•				
Longicatena caecimuris	1						•				
Megasphaera massiliensis	1			•		•	•				
Monoglobus pectinilyticus	2		•		•	•	•				
Phascolarctobacterium faecium	1		•			•	•				
Roseburia hominis	2		•		•	•	•			•	•
Ruminococcaceae sp. FBI00097	1					•	•				
Ruminococcaceae sp. FBI00233	1					•	•				
Ruminococcus bromii	2		•		•		•	•			•
Ruminococcus faecis	2		•		•	•	•				
Ruthenibacterium lactatiformans	1				•	•	•				
Turicibacter sanguinis	1						•			•	
Proteobacteria											
Bilophila wadsworthia	2			•	•		•				
Oxalobacter formigenes	3	•	•								
Parasutterella excrementihominis	2			•		•	•				•
Sutterella massiliensis	1		•	•		•	•				
Sutterella wadsworthensis	2		•	•			•				•
Verrucomicrobia											
Akkermansia muciniphila	1				•		•	•	•		•

Formate Metabolism. The FB-001 DP consortium also contains formate-utilizing bacteria to maintain maximal carbon flux through the pathway. Formate, as a by-product of oxalate metabolism, can ultimately inhibit further oxalate metabolism *in vitro* if it is not removed. Symbiotic bacterial species such as methanogens found in the human GI tract can efficiently remove formate via

reduction to methane in the presence of hydrogen gas produced by microbial fermenters. Therefore, the FB-001 Consortia includes *Methanobrevibacter smithii* (DS-CoC2), the most prevalent and abundant archaeal methanogen in the gut, and one that efficiently metabolizes formate, as well as the acetogenic gut commensal *Blautia hydrogenotrophica* (DS-CoC1), which utilizes formate to generate acetate for short-chain fatty acid (SCFA) synthesis, and a panel of anaerobes (eg, *Sutterella* and *Parasutterella*, found in DS-CoC2 and DS-CoC4) that express cytochrome- dependent formate dehydrogenases that oxidize formate to CO₂. These formate-utilizing bacteria therefore help to clear the potentially inhibitory metabolic byproducts of oxalate metabolism.

Supportive Metabolic Functions. FB-001 also contains a diverse panel of broadly functional commensals that fulfill unique and potentially beneficial biological functions in the GI tract, including metabolism of macro-nutrients, production of short-chain fatty acids, cross- feeding activity, and mucin degradation.

Composition of FB-001 DP. FB-001 DP is a highly complex, mixed fermentation of 148 microbial strains, chosen for their potential role in supporting a healthy GI tract. To support clinical studies, FB-001 DP was characterized for relative abundance of individual species in the final DP using metagenomic sequencing, as well as for total *O. formigenes* content. In metagenomic sequencing and analysis, strains were first confirmed to be present in the sample by positive identification of pre-specified biomarkers (short sequences of DNA) that are unique to the strain of interest. Then, the results of metagenomic sequencing were reported as the relative abundance of each strain, which approximates the percentage of genome copies that belong to each strain and can range from 0 to 100%. The relative abundance was then calculated by comparing the number and frequency of detected biomarkers to the total number of strain-specific biomarkers and the number of sequencing reads. The percent contribution of each strain in the FB-001 DP comprises a predominant portion of the three *O. formigenes* strains identified by 16S RNA and carbon source analysis described below as follows: approximately 32% *O. formigenes* on a relative abundance basis (i.e., approximately 40% on a viable cell count basis) with the other 145 strains having relative abundance values ranging from 18% to 0.015% (distribution of a typical human microbiome).

FB-001 DP was manufactured as a single batch. A single capsule of DP from was collected and stored at -20°C ± 5 until DNA extraction. FB-001 DP was sequenced via shotgun metagenomics and the metagenomic sequences of DP were analyzed to determine the composition of FB-001 DP. Results were reported as the relative abundance of each strain. Relative abundance approximates the percentage of FB-001 DP genome copies that belong to each strain and can range from 0 to 100%. A total of 60 of 148 strains were detected at or above their qualified limit of detection, including 21 strains from DS-CoC1, 13 strains from DS-CoC2, 16 strains from DS-CoC3,

7 strains from DS-CoC4, and each of DS- OF1, DS-OF2, and DS-OF3. The absence of detection of a strain should not be interpreted as its absence from the drug substance. The 60 detected strains account for 95.932% of the biomarkers detected in FB-001 DP. The remaining 88 strains therefore account for 4.068% of the biomarkers. The relative abundance profile is expected to vary between
 5 batches and data will continue to be collected during development to understand the magnitude of the variability. Furthermore, the exact percentages should not be interpreted as limiting or exclusive; rather each batch of DP may vary in its microbial distribution based on natural growth of bacterial in co-cultures. An example of the relative abundance profile of the microbes in one lot of FB-001 is provided in Table 25.

10 **Table 25. Relative Abundance Profile of a FB-001 DP Lot**

Strain	Relative Abundance (%)	Strain	Relative Abundance (%)	Strain	Relative Abundance (%)
FBI00180	18	FBI00245	0.076	FBI00097	< LoD
FBI00289	11	FBI00043	0.063	FBI00099	< LoD
FBI00067	11	FBI00237	0.059	FBI00109	< LoD
FBI00133	10	FBI00206	0.052	FBI00113	< LoD
FBI00038	4.3	FBI00032	0.04	FBI00115	< LoD
FBI00175	4.1	FBI00243	0.038	FBI00117	< LoD
FBI00255	3.9	FBI00116	0.035	FBI00123	< LoD
FBI00120	3.3	FBI00002	0.032	FBI00126	< LoD
FBI00177	2.5	FBI00167	0.031	FBI00127	< LoD
FBI00212	2.4	FBI00068	0.015	FBI00132	< LoD
FBI00025	2.2	FBI00010	< LoD	FBI00137	< LoD
FBI00060	1.8	FBI00011	< LoD	FBI00145	< LoD
FBI00048	1.6	FBI00012	< LoD	FBI00149	< LoD
FBI00104	1.5	FBI00013	< LoD	FBI00159	< LoD
FBI00151	1.5	FBI00015	< LoD	FBI00162	< LoD
FBI00220	1.1	FBI00018	< LoD	FBI00165	< LoD
FBI00004	1	FBI00019	< LoD	FBI00170	< LoD
FBI00020	0.93	FBI00021	< LoD	FBI00174	< LoD
FBI00251	0.91	FBI00022	< LoD	FBI00182	< LoD
FBI00016	0.73	FBI00030	< LoD	FBI00184	< LoD
FBI00079	0.72	FBI00033	< LoD	FBI00189	< LoD
FBI00102	0.71	FBI00034	< LoD	FBI00190	< LoD
FBI00233	0.65	FBI00040	< LoD	FBI00191	< LoD
FBI00171	0.64	FBI00044	< LoD	FBI00194	< LoD
FBI00029	0.63	FBI00046	< LoD	FBI00200	< LoD
FBI00076	0.56	FBI00047	< LoD	FBI00201	< LoD
FBI00147	0.53	FBI00049	< LoD	FBI00208	< LoD

FBI00128	0.5	FBI00050	< LoD	FBI00221	< LoD
FBI00197	0.49	FBI00051	< LoD	FBI00224	< LoD
FBI00110	0.47	FBI00052	< LoD	FBI00229	< LoD
FBI00112	0.47	FBI00053	< LoD	FBI00235	< LoD
FBI00135	0.47	FBI00056	< LoD	FBI00236	< LoD
FBI00226	0.44	FBI00057	< LoD	FBI00238	< LoD
FBI00199	0.43	FBI00059	< LoD	FBI00244	< LoD
FBI00152	0.43	FBI00061	< LoD	FBI00248	< LoD
FBI00027	0.42	FBI00066	< LoD	FBI00254	< LoD
FBI00211	0.4	FBI00069	< LoD	FBI00258	< LoD
FBI00232	0.37	FBI00070	< LoD	FBI00260	< LoD
FBI00111	0.31	FBI00071	< LoD	FBI00267	< LoD
FBI00140	0.3	FBI00075	< LoD	FBI00269	< LoD
FBI00263	0.25	FBI00077	< LoD	FBI00270	< LoD
FBI00124	0.24	FBI00078	< LoD	FBI00271	< LoD
FBI00001	0.23	FBI00080	< LoD	FBI00273	< LoD
FBI00198	0.21	FBI00081	< LoD	FBI00274	< LoD
FBI00176	0.2	FBI00085	< LoD	FBI00277	< LoD
FBI00125	0.2	FBI00087	< LoD	FBI00278	< LoD
FBI00205	0.17	FBI00092	< LoD	FBI00288	< LoD
FBI00062	0.096	FBI00093	< LoD	FBI00290	< LoD
FBI00281	0.095	FBI00096	< LoD	FBI00292	< LoD
FBI00009	0.09				

Process Development. The blending process during DP manufacture was developed to create a homogenous mixture of the DSs. During the development phase, the blend-sieve-blend technique for mixing the DSs was tested. Using this technique, several of the DSs were blended in a Turbula mixer for 15 minutes at 43 rpm followed by sieving of the material through #50 sieve. The material was again blended for 15 minutes at 43 rpm. An aliquot of blended material from the top, middle and bottom of the container were taken and evaluated for TCC, VCC and strain distribution by relative abundance. The blending study results showed that the DS material was homogeneously mixed with blend-sieve-blend mixing technique. The VCC/g, TCC/g and relative abundance of the three *O. formigenes* strains in the top, middle and bottom of the mixing container are very similar, which indicates a homogenous blend of DSs in the blending container.

A diagram of the coculture method of manufacture is provided in **Figure 14**.

Manufacture of DS1. Yeast casitone fatty acids with carbohydrates (YCFAC) medium, pH 7, was prepared at 1X concentration in batches of 4 L each for Seed 1 fermentation and Seed 2 fermentation. The medium was prepared by adding the components indicated in Table 26 to 3.46

kg of water for injection, boiling for 5 to 10 minutes, then allowing the medium to cool down. Upon reaching a temperature of 50°C or lower, the medium was sparged with N₂ while the rest of the components were added in the following order: sodium bicarbonate, 50X volatile fatty acid solution, L-cysteine HCl monohydrate, 0.5% hemin solution, and 25X vitamin solution. The pH was adjusted to 7 with 10 N NaOH or sulfuric acid, and the medium was autoclaved at 122.5°C for 45 minutes. The medium was incubated at 37°C for a minimum of 24 hours prior to inoculation for a contamination check.

Table 26. YCFAC Media

Reagent Description	Quantity/4.0L of Medium	Unit	Final Conc. (1X)	Addition
Soytone	40.00	g	1% w/w	Boiled for 5 to 10 minutes in 3.46 kg Water for Injection (WFI)
D-cellobiose	8.00	g	0.2% w/w	
Yeast extract	10.00	g	0.25% w/w	
Dextrose (glucose)	20.00	g	0.5% w/w	
Maltose monohydrate	8.00	g	0.2% w/w	
Magnesium sulfate heptahydrate	0.36	g	0.009% w/w	
Calcium chloride dihydrate	0.36	g	0.009% w/w	
Potassium phosphate monobasic	1.80	g	0.045% w/w	
Potassium phosphate dibasic	1.80	g	0.045% w/w	
Sodium chloride	3.60	g	0.09% w/w	
Sodium bicarbonate (7.5%)	213.0	mL	5.325% w/w	Added after the media cools down to 50°C or lower
Volatile fatty acid solution (50X)	11.56	mL	1X volatile fatty acid solution ^b	
L-cysteine HCl monohydrate	4.0	g	0.1% w/w	
Hemin solution (0.5% w/w)	8.00	mL	0.2% w/w	
Vitamin solution (25X)	160.00	mL	1X vitamin solution	

A 5X concentration media was also made for use in the main fermentation. The 5X stock was made using the same proportions as described in Table 26, scaled up to 5X. The 5X media was diluted to a 1X concentration before the main fermentation process.

Resuspension medium was also made and comprised YCFAC medium with reducing agents L-cysteine HCl and riboflavin, pH 7. To prepare resuspension medium, 0.6 g of riboflavin and 2.0 g of cysteine-HCl are added per kg of YCFAC medium. The medium is stirred until completely dissolved, then titrated with 10 N NaOH or sulfuric acid to obtain a final pH of 7. The medium is

filtered with a 0.22 µm polyethersulfone (PES) filter. The final concentration of Riboflavin was 0.06% and the final concentration of L-cysteine HCL was 0.2%, in YCFAC media.

The volatile fatty acid solution (50X) for the YCFAC media was made and comprised Glacial acetic acid (65.7%w/w for the 50X concentration; 1.31%w/w for the 1X concentration), Propionic acid (24.2%w/w for the 50X concentration; 0.48%w/w for the 1X concentration), Iso-butyric acid (3.1%w/w for the 50X concentration; 0.06%w/w for the 1X concentration), n-Valeric acid (3.5%w/w for the 50X concentration; 0.07%w/w for the 1X concentration), and Iso-valeric acid (3.5%w/w for the 50X concentration; 0.07%w/w for the 1X concentration).

The vitamin solution (25X) for the YCFAC media comprised Biotin powder (1.31 Quantity/6kg WFI (g)), Folic acid (1.31 Quantity/6kg WFI (g)), Pyridoxine hydrochloride (6.56 Quantity/6kg WFI (g)), Thiamine-HCl-2H₂O (3.28 Quantity/6kg WFI (g)), Riboflavin (0.13 Quantity/6kg WFI (g)), Nicotinic acid (3.28 Quantity/6kg WFI (g)), D-calcium pantothenate (3.28 Quantity/6kg WFI (g)), Vitamin B12 (0.07 Quantity/6kg WFI (g)), 4-aminobenzoic acid (3.28 Quantity/6kg WFI (g)), and DL-alfa-lipoic acid (3.28 Quantity/6kg WFI (g)).

Microbial strains intended for FB-001 DS-CoC1 were isolated from stool samples obtained after extensive donor screening. An overview of the strain isolation and purification process, RCB banking, and RCB identity/purity testing is provided in **Figure 15**. The entire stool sample homogenization and aliquoting was carried out under anaerobic conditions, starting with transfer of the stool sample to the anaerobic chamber within 15 to 30 minutes of the collection, followed by homogenization and addition of a 1:1 solution of PBS and 50% glycerol prior to aliquoting into 6 to 9 separate cryovials and transferring to ≤ -65°C for storage until further processing.

To isolate individual strains, fecal samples were serially diluted and then plated onto a variety of agar plates containing anaerobic microbial cultivation media (counted as passage 1). The plates were incubated at 37°C under anaerobic conditions. Single colonies from these initial growth plates were picked for further isolation on appropriate microbial cultivation agar media plates (counted as passage 2). After incubation at 37°C, if the single-colony plating resulted in isolated colonies with uniform morphology, the culture was further characterized for strain identification. Preliminary strain identification was performed either by 16S rRNA gene sequencing or by creating and analyzing proteomic fingerprinting using high-throughput matrix-assisted laser desorption/ionization-time of flight spectrometry. If the single-colony plating resulted in multiple colony morphologies, each unique colony type was picked from this plating for further isolation on an appropriate cultivation agar plate until uniform colony morphology was achieved (counted as passage 3 or more). The passage history of each strain in FB-001 DS-CoC1 and the agar and broth medias are listed in Table 27.

Table 27. Isolation of Research Cell Banks Used in FB-001 DS-CoC1

FBI Strain ID	RCB Agar Passaging		RCB Broth Passaging	
	Agar Type	Passage #	Broth Type	Passage #
FBI00001	Bifidobacterium selective agar + 40 mM oxalate	1	YCFAC, pH 6.0 + 40 mM oxalate	1
	Bifidobacterium selective agar	2		
FBI00002	Bifidobacterium selective agar + 40 mM oxalate	1	YCFAC, pH 6.0 + 40 mM oxalate	1
	Bifidobacterium selective agar	2		
FBI00010	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00013	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00029	Brain heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
FBI00032	Bifidobacterium selective agar	3	YCFAC, pH 6.0	1
	YCFAC agar	1		
FBI00033	YCFAC-B agar + 20 mM oxalate	1	YCFAC, pH 6.0 + 20 mM oxalate	1
	YCFAC-BO 40 mM agar	2		
	YCFAC agar	1		
FBI00034	Brain heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
FBI00043	Reinforced clostridial agar	2	YCFAC, pH 6.0	1
FBI00044	Chocolate agar	2	YCFAC, pH 6.0	1
FBI00048	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00050	Bifidobacterium selective agar + 40 mM oxalate	1	YCFAC, pH 6.0 + 40 mM oxalate	1
	YCFAC-BO 40 mM agar	2		
FBI00051	YCFAC-B agar	2	YCFAC, pH 6.0	1
	YCFAC agar	1		
FBI00057	Reinforced clostridial agar	2	YCFAC, pH 6.0	1
	YCFAC agar	1		
FBI00059	Columbia agar with 5% sheep blood	3	YCFAC, pH 6.0	1
FBI00060	YCFAC-B agar	3	YCFAC, pH 6.0	1
	YCFAC-BO 40 mM agar	2		
FBI00070	YCFAC agar	1	YCFAC, pH 6.0 + 40 mM oxalate	1
	YCFAC-B agar	3		
FBI00071	YCFAC-BO 80 mM agar	2	YCFAC, pH 6.0	1
	YCFAC agar	1		
FBI00076	YCFAC agar	1	YCFAC, pH 6.0	1
	Chocolate agar	2		
FBI00079	Brain heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
	YCFAC agar	1		
FBI00087	YCFAC agar	1	YCFAC, pH 6.0	1
FBI00093	YCFAC-BO 40 mM agar	2	YCFAC, pH 6.0	1
FBI00102	YCFAC-BO 40 mM agar	2	YCFAC, pH 6.0	1
FBI00109	YCFAC-B agar	4	YCFAC, pH 6.0	1
	YCFAC-BO 80 mM agar	2		
FBI00117	YCFAC agar	1	YCFAC, pH 6.0	2
	YCFAC-BO 80 mM agar	2		
FBI00120	YCFAC-BO 80 mM agar	2	YCFAC, pH 6.0	1
FBI00125	YCFAC-BO 80 mM agar	2	YCFAC, pH 6.0	1
FBI00127	YCFAC-B agar	3	YCFAC, pH 6.0	1
	YCFAC-BO 80 mM agar	2		
FBI00128	YCFAC-BO 40 mM agar	1	YCFAC, pH 6.0	1
	YCFAC-BO 80 mM agar	2		
FBI00145	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00162	Reinforced clostridial agar	2	YCFAC, pH 6.0	1
FBI00174	YCFAC-B agar	2	YCFAC, pH 6.0	1
FBI00184	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00190	Brain heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1

FBI00191	OxyPras plus brucella blood agar	2	YCFAC, pH 6.0 + BBL™ Vitamin K1-Hemin Solution	1
FBI00194	Brain heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
FBI00198	YCFAC-BO 40 mM agar	3	YCFAC, pH 6.0	1
FBI00199	YCFAC-BO 40 mM agar	3	YCFAC, pH 6.0	1
FBI00200	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00201	Columbia agar with 5% sheep blood	3	YCFAC, pH 6.0	1
FBI00205	YCFAC-BO 40 mM agar	3	YCFAC, pH 6.0	1
FBI00206	YCFAC-BO 40 mM agar	3	YCFAC, pH 6.0	1
FBI00211	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00220	Brain heart infusion agar with hemin and vitamin K	4	YCFAC, pH 6.0	1
FBI00221	Brain heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
FBI00236	YCFAC-BO 40 mM agar	2	YCFAC pH 6.0	1
FBI00245	Columbia agar with 5% sheep blood	4	YCFAC, pH 6.0 + BBL™ Vitamin K1-Hemin Solution	1
FBI00248	Brain heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00251	Reinforced clostridial agar	2	YCFAC, pH 6.0	1
FBI00254	Brain heart infusion with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00267	YCFAC-BO 80 mM agar	3	YCFAC, pH 6.0	1
FBI00278	Brain heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00288	Brain heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	2
	YCFAC agar	3		
	YCFAC-B agar	1		
FBI00290	Brain heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	2

Abbreviations: FBI = Federation Bio isolate; RCA = reinforced clostridial agar; RCB = research cell bank; YCFAC = yeast casitone fatty acids with carbohydrates

To bank the RCBs used in FB-001 DS-CoC1, monocultures were inoculated into culture tubes containing appropriate broth media and incubated under anaerobic conditions at 37°C until sufficient growth was observed. Sterile glycerol solution was added to achieve a final glycerol concentration of 25% prior to aliquoting approximately 0.2 mL into 2D-barcode cryo-vials. After removing the cryovials from the anaerobic gas chambers, the 2D bar codes at the bottom of the vials were scanned promptly and the vials were transferred to $\leq -65^{\circ}\text{C}$ as the final step in the banking of the RCBs.

After at least 10 hours of freezing, one vial of each purified frozen RCB was retrieved from the freezer and thawed under anaerobic conditions followed by plating on agar plates containing appropriate growth media. The plates were incubated under anaerobic conditions at 37°C. Growth on the plate was observed to confirm revival and uniform colony morphology for each purified isolate.

Following confirmation of uniform colony morphology for each RCB, individual colonies were analyzed by 16S rRNA gene sequencing (see Sequence Listing). RCBs were further characterized using whole-genome sequencing followed by genome assembly. Strain-level identification was performed using both 16S rRNA gene sequences and whole-genome assemblies.

An explicit criterion for inclusion of each strain in FB-001 DS-CoC1 was demonstrated susceptibility to at least 2 FDA-approved antibiotics. The anaerobic microbes in the FB-001 DS-CoC1 were tested against multiple FDA-approved, clinically relevant antimicrobials, most of which show especially potent activity against anaerobes. All strains in FB-001 DS-CoC1 were found to demonstrate sensitivity *in vitro* to 2 or more clinically relevant antibiotics, implying a straightforward means for biological control. Importantly, no strain in the FB-001 DS-CoC1 were resistant to both clindamycin and amoxicillin-clavulanate, suggesting that a combination of the 2 agents could cover all FB-001 DS-CoC1 strains.

Fgu described in **Figure 16**. The first step of MCB generation for DS-CoC1 strains involved reviving each RCB by plating on YCFAC agar plates followed by incubation under anaerobic conditions at 37°C. Isolated colonies were used for inoculating MCB precultures in 30 to 45 mL of YCFAC broth and were incubated anaerobically at 37°C. Each MCB was passaged 2 to 3 times in YCFAC broth prior to banking. Growth of precultures was monitored using total cell counts and viable cell counts to determine suitable time, inoculation, and culture volumes for MCB cultures. Sterility monitoring was performed by incubating a sterile agar plate or broth during the entire culturing process. A minimum total cell count of 2×10^8 cells per mL was targeted for the harvest of the MCB culture. When required, cells were harvested by centrifugation to allow concentration of the biomass. Sterile glycerol was added as cryoprotectant to a final concentration of 25% v/v prior to aliquoting cells from MCB culture into 2D barcoded cryovials. The barcodes of cryovials were scanned and entered into an electronic inventory system, then the vials are transferred to long-term storage at $\leq -65^\circ\text{C}$. All MCBs are stored in at least 2 physically distinct locations.

Manufacture of DS2. The same YCFAC media used for DS1 was used for DS2. Similarly, the same general strain isolation methods were used as described above for DS1. The specific agar types, passages, and broth types used for DS2 strains is provided in Table 28.

Table 28. Isolation of Research Cell Banks Used in FB-001 DS-CoC2

FBI Strain ID	RCB Agar Passaging		RCB Broth Passaging	
	Agar Type	Passage #	Broth Type	Passage #
FB100004	YCFAC-B agar + 80 mM oxalate	1	YCFAC, pH 6.0 + 80 mM oxalate	1
	YCFAC-BO 80 mM agar	2		
	Bacteroides bile esculin agar	2		

FBI00012	YCFAC-B agar	1	YCFAC, pH 6.0	1
	YCFAC-B agar	2		
FBI00015	YCFAC agar	1	YCFAC, pH 6.0	1
FBI00018	Bifidobacterium selective agar	3	YCFAC, pH 6.0	1
	Bacteroides bile esculin agar	2		
FBI00019	YCFAC-B agar	1	YCFAC, pH 6.0	1
	YCFAC-B agar + 80 mM oxalate	1		
FBI00021	YCFAC-BO 80 mM agar	2	YCFAC, pH 6.0 + 80 mM oxalate	1
FBI00038	Chocolate agar	2	YCFAC, pH 6.0	1
	Bacteroides bile esculin agar	2		
FBI00040	YCFAC-B agar	1	YCFAC, pH 6.0	1
FBI00046	YCFAC-B agar	3	YCFAC, pH 6.0	1
	Bacteroides bile esculin	2		
FBI00061	Brain heart infusion agar with hemin and vitamin K	1	YCFAC, pH 6.0	1
	Bacteroides bile esculin	2		
FBI00066	YCFAC-B agar	1	YCFAC, pH 6.0	1
FBI00075	YCFAC-B agar	3	YCFAC, pH 6.0	1
	Lactobacillus MRS agar + 20 mM oxalate	2		
FBI00077	YCFAC	1	YCFAC, pH 6.0	1
	Lactobacillus MRS agar + 40 mM oxalate	2		
FBI00080	YCFAC agar	1	YCFAC, pH 6.0	1
FBI00081	Columbia agar with 5% sheep blood	3	YCFAC, pH 6.0	1
FBI00085	Reinforced clostridial agar	2	YCFAC, pH 6.0	1
FBI00092	YCFAC-BO 40 mM agar	2	YCFAC, pH 6.0	1
	Brain heart infusion agar with hemin and vitamin K	2		
FBI00097			YCFAC, pH 6.0	2
	YCFAC agar	2		
FBI00099	Chocolate agar	2	YCFAC, pH 6.0	1
	Brain heart infusion agar with hemin and vitamin K	2		
FBI00112	YCFAC agar	1	YCFAC, pH 6.0	1
	YCFAC-BO 80 mM agar	2		
FBI00132	YCFAC-BO 80 mM agar	1	YCFAC, pH 6.0	1
FBI00137	YCFAC-BO 40 mM agar	2	YCFAC, pH 6.0	1
	YCFAC-BO 160 mM agar	1		
FBI00140	YCFAC-BO 80 mM agar	2	YCFAC, pH 6.0 + 80 mM oxalate	1
	YCFAC-BO 80 mM agar	1		
FBI00149	YCFAC-BO 80 mM agar	1	YCFAC, pH 6.0	1
	YCFAC-BO 40 mM agar	1		
	YCFAC-BO 80 mM agar	1		
FBI00151	YCFAC-BO 80 mM agar	1	YCFAC, pH 6.0	1
	YCFAC-BO 40 mM agar	2		
FBI00176	Brain heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
	YCFAC-BO 40 mM agar	3		
FBI00189	YCFAC-BO 40 mM agar	1	YCFAC, pH 6.0	1
FBI00197	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00208	YCFAC-BO 40 mM agar	3	YCFAC, pH 6.0	1
FBI00212	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00224	YCFAC-BO 40 mM agar	3	YCFAC, pH 6.0	1
			YCFAC, pH 6.0 with BBL™ Vitamin K1-Hemin Solution	
FBI00226	YCFAC-BO 40 mM agar	3		1
FBI00229	Brain heart infusion agar with hemin and vitamin K	4	Thioglycollate broth with hemin and vitamin K	1
	Brain heart infusion agar with hemin and vitamin K			
FBI00233		4	YCFAC, pH 6.0 with BBL™ Vitamin K1-Hemin Solution	1

FBI00235	Brain heart infusion agar with hemin and vitamin K	4	YCFAC, pH 6.0	1
FBI00237	Brain heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00243	Brain heart infusion agar with hemin and vitamin K	4	YCFAC, pH 6.0	1
	YCFAC agar	1		
FBI00244	YCFAC-BO 40 mM agar	3	YCFAC, pH 6.0	1
	YCFAC-B agar + 40 mM oxalate	3		
	YCFAC agar	1		
FBI00258	Modified Eggerth-Gagnon medium agar	3	Thioglycollate broth with hemin and vitamin K	1
FBI00260	Brain heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00263	Modified Eggerth-Gagnon medium agar	3	YCFAC, pH 6.0	1
FBI00270	Columbia agar with 5% sheep blood + antibiotics ^b	2	SAB mediac	1
	Columbia agar with 5% sheep blood	3		
FBI00273	Brain heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00277	Brain heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00292	Columbia agar with 5% sheep blood	3	SAB mediac	1

Abbreviations: FBI = Federation Bio isolate; RCB = research cell bank; YCFAC = yeast casitone fatty acids with carbohydrates, YCFAC-B = yeast casitone fatty acids with carbohydrates and sheep blood; YCFAC-BO = yeast casitone fatty acids with carbohydrates, sheep blood, and oxalate

5 ^a Modified Eggerth-Gagnon medium agar is prepared in house and consists of peptone (1% w/v), Na₂HPO₄ (0.32% w/v), mucin (0.2% w/v), BactoAgar (1.5% w/v), and sheep blood (5% v/v), pH 7.45.

^b Antibiotics used for isolation of FBI00270 included vancomycin (100 µg/mL), penicillin 100 units/mL, streptomycin (100 µg/mL), and amphotericin B (0.25 µg/mL).

10 ^c SAB media was prepared as described in (Khelaifia, Raoult et al. 2013).

Characterization and banking of the DS2 strains were performed as described above for DS1. It is important to note that while not all DS2 strains were sensitive to both clindamycin and amoxicillin-clavulanate as were the DS1 strains, all strains were still sensitive to at least 2 FDA
15 approved antibiotics.

Manufacture of DS3. The same YCFAC media used for DS1 was used for DS2. Similarly, the same general strain isolation methods were used as described above for DS1. The specific agar types, passages, and broth types used for DS2 strains is provided in Table 29.

Table 29. Isolation of Research Cell Banks Used in FB-001 DS-CoC3

FBI Strain ID	RCB Agar Passaging		RCB Broth Passaging	
	Agar Type	Passage #	Broth Type	Passage #
FBI00009	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00011	Bifidobacterium selective agar	3	YCFAC, pH 6.0	1
FBI00016	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00020	Bifidobacterium selective agar + 40 mM oxalate	1	YCFAC, pH 6.0 with 40 mM Oxalate	1
	YCFAC-BO 40 mM agar	1		
	YCFAC-BO 40 mM agar	1		
FBI00025	Chocolate agar	2	YCFAC, pH 6.0	1
FBI00027	Brain-heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
FBI00030	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00047	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00052	YCFAC-BO 40 mM agar	2	YCFAC, pH 6.0 with 40 mM Oxalate	1
	YCFAC agar	1		
FBI00053	YCFAC-BO 40 mM agar	2	YCFAC, pH 6.0 with 40 mM Oxalate	1
	YCFAC agar	1		
FBI00056	YCFAC-BO 80 mM agar	2	YCFAC, pH 6.0 with 80 mM Oxalate	1
	YCFAC agar	1		
FBI00062	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00078	YCFAC-B agar	2	YCFAC, pH 6.0	1
FBI00096	Brain-heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
	YCFAC agar	1		
FBI00104	Brain-heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
	YCFAC agar	1		
FBI00110	YCFAC-BO 80 mM agar	2	YCFAC, pH 6.0	1
	YCFAC agar	1		
	YCFAC-B agar	1		
FBI00111	YCFAC-BO 80 mM agar	2	YCFAC, pH 6.0	1
	YCFAC agar	1		
	YCFAC-B agar	1		
FBI00113	Brain-heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	1
	YCFAC-B agar	1		
FBI00115	Brain-heart infusion agar with hemin and vitamin K	2	YCFAC, pH 6.0	2
	YCFAC agar	3		
FBI00116	Bifidobacterium selective agar + 40 mM oxalate	1	YCFAC, pH 6.0 with 40 mM Oxalate	1
	Bifidobacterium selective agar	2		
	YCFAC-BO 160 mM agar	1		
FBI00123	YCFAC-B agar	2	YCFAC, pH 6.0	1
FBI00124	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00126	YCFAC-BO 40 mM agar	1	YCFAC, pH 6.0	1
	YCFAC-BO 40 mM agar	1		
FBI00135	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00147	YCFAC-BO 80 mM agar	1	YCFAC, pH 6.0	1
	YCFAC-BO 80 mM agar	1		
	YCFAC-BO 40 mM agar	1		
FBI00159	YCFAC-BO 160 mM agar	1	YCFAC, pH 6.0	1
	YCFAC-BO 80 mM agar	2		
FBI00167	YCFAC-B agar	2	YCFAC, pH 6.0	1

FBI00170	YCFAC-BO 80 mM agar	1	YCFAC, pH 6.0	2
	YCFAC-BO 80 mM agar	1		
	YCFAC-BO 40 mM agar	1		
FBI00232	Columbia agar with 5% sheep blood	4	YCFAC, pH 6.0	1
FBI00255	YCFAC-BO 80 mM agar	3	YCFAC, pH 6.0	1
FBI00271	Brain-heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1

Abbreviations: FBI = Federation Bio isolate; RCB = research cell bank; YCFAC = yeast casitone fatty acids with carbohydrates, YCFAC-B = yeast casitone fatty acids with carbohydrates and sheep blood; YCFAC-BO = yeast casitone fatty acids with carbohydrates, sheep blood and oxalate

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Characterization and banking of the DS3 strains were performed as described above for DS1. It is important to note that while not all DS2 strains were sensitive to both clindamycin and amoxicillin-clavulanate as were the DS1 strains, all strains were still sensitive to at least 2 FDA approved antibiotics.

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Manufacture of DS4. YCFAC media with ammonium sulfate, pH 7 for Seed 1 Fermentation was prepared at 1X concentration in batches of 4 L. The medium is prepared by adding the components indicated in Table 30 to 3.46 kg of water for injection and boiling for 5 to 10 minutes. Then the media was sparged for at least 30 minutes with N₂ and allowed to cool down. Upon reaching a temperature of 50°C or lower, the rest of the components were added in the following order while

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sparging continues: sodium bicarbonate, 50X volatile fatty acid solution, L- cysteine HCl monohydrate, and 0.5% hemin solution. The medium was adjusted to a pH of 7 with 10 N NaOH or sulfuric acid and was autoclaved at 122.5°C for 45 minutes. Vitamin solution (25X) was filtered using a 0.22 µm filter and added post-sterilization. The medium was incubated at 37°C for a minimum of 24 hours prior to inoculation for a contamination check.

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Table 30. Yeast Casitone Fatty Acids With Carbohydrates Medium Composition (1X) For Seed 1 Fermentation

Reagent Description	Quantity/4.0 L of Medium	Unit	Final Conc. (1X)	Addition
Soytone	40.00	g	1% (w/w)	Boiled for 5 to 10 minutes in 3.46 kg WFI; sparging initiated
D-cellobiose	8.00	g	0.2% (w/w)	
Yeast extract	10.00	g	0.25% (w/w)	
Dextrose (glucose)	20.00	g	0.5% (w/w)	
Maltose monohydrate	8.00	g	0.2% (w/w)	
Magnesium sulfate heptahydrate	0.36	g	0.009% (w/w)	
Calcium chloride dihydrate	0.36	g	0.009% (w/w)	

Potassium phosphate monobasic	1.80	g	0.045% (w/w)	
Potassium phosphate dibasic	1.80	g	0.045% (w/w)	
Sodium chloride	3.60	g	0.09% (w/w)	
Ammonium sulfate	3.60	g	0.09% (w/w)	
Sodium bicarbonate (7.5% w/w)	213	mL	5.325% (w/w)	Added after the media cools down to 50°C or lower (sparging continues)
Volatile fatty acid solution (50X)	11.6	mL	1X volatile fatty acid solution	
L-cysteine HCl monohydrate	4.0	g	0.1%	
Hemin solution (0.5% w/w)	8.00	mL	0.2% w/w hemin	
Vitamin solution (25X)	160.00	mL	1X vitamin solution	Added post- sterilization

YCFAC medium with ammonium sulfate, threonine, and N-acetylgalactosamine, pH 7.4 for Seed 2 Fermentation (Stage 1 and Stage 2) is prepared at 1X concentration in batches of 4 L. The medium is prepared by adding the components indicated in Table 31 to 3.46 kg of water for injection and boiling for 5 to 10 minutes. Then the media is sparged for at least 30 minutes with N₂ and allowed to cool down. Upon reaching a temperature of 50°C or lower, the rest of the components are added in the following order while sparging continues: sodium bicarbonate, 50X volatile fatty acid solution, L-cysteine HCl monohydrate, and 0.5% hemin solution. The medium is adjusted to a pH of 7 with 10 N NaOH or sulfuric acid and is autoclaved at 122.5°C for 45 minutes. Sterile 25X vitamin solution (25X), threonine solution, and N-acetylgalactosamine solution are added post-sterilization. The medium is incubated at 37°C for a minimum of 24 hours prior to inoculation for a contamination check.

Table 31. Yeast Casitone Fatty Acids With Carbohydrates Medium Composition (1X) For Seed 2 Fermentation

Reagent Description	Quantity/4.0 L of Medium	Unit	Final Conc. (1X)	Addition
Soytone	40.00	g	1% (w/w)	Boiled for 5 to 10 minutes in 3.46 kg WFI; sparging initiated
D-cellobiose	8.00	g	0.2% (w/w)	
Yeast extract	10.00	g	0.25% (w/w)	
Dextrose (glucose)	20.00	g	0.5% (w/w)	
Maltose monohydrate	8.00	g	0.2% (w/w)	
Magnesium sulfate heptahydrate	0.36	g	0.009% (w/w)	
Calcium chloride dihydrate	0.36	g	0.009% (w/w)	

Potassium phosphate monobasic	1.80	g	0.045% (w/w)	Added after the media cools down to 50°C or lower (sparging continues)
Potassium phosphate dibasic	1.80	g	0.045% (w/w)	
Sodium chloride	3.60	g	0.09% (w/w)	
Ammonium sulfate	3.60	g	0.09% (w/w)	
Sodium bicarbonate (7.5% w/w)	213	mL	5.325% (w/w)	
Volatile fatty acid solution (50X)	11.6	mL	1X volatile fatty acid solution	
L-cysteine HCl monohydrate	4.0	g	0.1%	
Hemin solution (0.5% w/w)	8.00	mL	0.2% w/w hemin	Added post- sterilization
Vitamin solution (25X)	160.00	mL	1X vitamin solution	
N-acetylgalactosamine solution (1% w/w)	20	mL	0.5% (w/w)	
Threonine	59.6	g	1.5% (w/w)	

YCFAC medium with ammonium sulfate and threonine, pH 7, used for the main fermentation, is prepared at 5X. The 5X medium is prepared by adding the components indicated in Table 32 to 40.0 kg of water for injection, mixing, then autoclaving. The medium is incubated at 37°C for a minimum of 24 hours prior to inoculation for a contamination check. After pumping the 5X solution into the fermenter, 50X volatile fatty acid solution, threonine solution, 25X vitamin solution, L-cysteine HCl solution, and WFI are added for a final 1X concentration.

Table 32. Yeast Casitone Fatty Acids with Carbohydrates Medium Composition (5X)

Reagent Description	Quantity/60.0 kg YCFAC (5X) Medium	Unit	Final Conc. (1X)
Soytone	3.00	kg	1% (w/w)
D-(+) cellobiose	600	g	0.2% (w/w)
Yeast extract	750	g	0.25% (w/w)
Dextrose (glucose)	1.50	kg	0.5% (w/w)
Maltose monohydrate	600.0	g	0.2% (w/w)
Magnesium sulfate heptahydrate	27.0	g	0.009% (w/w)
Calcium chloride dihydrate	27.0	g	0.009% (w/w)
Potassium phosphate monobasic	135	g	0.045% (w/w)
Potassium phosphate dibasic	135	g	0.045% (w/w)
Sodium chloride	270	g	0.09% (w/w)
Ammonium sulfate	270	g	0.09% (w/w)
Sodium bicarbonate (7.5% w/w)	16.0	kg	5.33% (w/w)
Hemin solution (0.5% w/w)	600	mL	0.2% (w/w)
Volatile fatty acid solution (50X)			1X
L-cysteine HCl monohydrate solution (3% w/w)			3.32% (w/w)
Vitamin solution (25X)			1X
Threonine solution (7.2% w/w)			4.0% (w/w)

The specific agar types, passages, and broth types used for DS2 strains is provided in Table 33.

Table 33. Isolation of Research Cell Banks Used in FB-001 DS-CoC4

FBI Strain ID	RCB Agar Passaging		RCB Broth Passaging	
	Agar Type	Passage #	Broth Type	Passage #
FBI00022	Bacteroides bile esculin agar	2	YCFAC, pH 6.0	1
	YCFAC-B agar	1		
FBI00049	YCFAC-B agar	3	YCFAC, pH 6.0	1
FBI00068	Bicarbonate-buffered basal medium agar ^a	2	YCFAC, pH 6.0	2
	YCFAC-B agar	1		
FBI00069	Bifidobacterium selective agar + 40 mM oxalate	1	YCFAC, pH 6.0	1
	Bifidobacterium selective agar	2		
FBI00152	YCFAC-B agar	2	YCFAC, pH 6.0 with BBL™ Vitamin K1-Hemin Solution	1
FBI00165	Brain-heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00171	YCFAC-BO 80 mM agar	1	YCFAC, pH 6.0	2
	YCFAC-BO 80 mM agar	1		
	YCFAC-BO 40 mM agar	1		
FBI00175	YCFAC-B agar	2	YCFAC, pH 6.0 with BBL Vitamin K1-Hemin Solution	1
FBI00177	Bacteroides bile esculin agar	2	YCFAC, pH 6.0	1
FBI00180	Bacteroides bile esculin agar	2	YCFAC, pH 6.0	1
FBI00182	YCFAC-B agar	2	YCFAC, pH 6.0	1
FBI00238	Columbia agar with 5% sheep blood	3	YCFAC, pH 6.0	1
FBI00269	Brain-heart infusion agar with hemin and vitamin K	3	YCFAC, pH 6.0	1
FBI00274	YCFAC-BO 80 mM agar	3	YCFAC, pH 6.0	1
FBI00281	Reinforced clostridial agar	3	YCFAC, pH 6.0	1

Abbreviations: FBI = Federation Bio isolate; RCA = reinforced clostridial agar; RCB = research cell bank; YCFAC = yeast casitone fatty acids with carbohydrates, YCFAC-B = yeast casitone fatty acids with carbohydrates and sheep blood; YCFAC-BO = yeast casitone fatty acids with carbohydrates, sheep blood, and oxalate; Bicarbonate-buffered basal medium was prepared as described in Derrien 2004 (Derrien, Vaughan et al. 2004).

Characterization and banking of the DS4 strains was performed as described above for DS1. It is important to note that while not all DS2 strains were sensitive to both clindamycin and amoxicillin-clavulanate as were the DS1 strains, all strains were still sensitive to at least 2 FDA approved antibiotics.

Example 7: Functional Characterization of DS1-7

FB-001 was characterized through 16S sequence identity, macronutrient utilization, metabolite production and Biolog analysis of individual strains. At the species level, FB-001 was

characterized by the DNA sequences of 16S rRNA genes which represent 100 species. 16S sequence length varied by strain, from a minimum of 1177 bp (FBI00109, *Coprococcus comes*) to a maximum of 1532 bp (FBI00087, *Clostridium scindens*). The 148 16S DNA sequences uniquely identified the majority of the 148 strains within FB-001, with exceptions for closely related strains such as two of the *Oxalobacter formigenes* strains (FBI00133 and FBI00289) which share identical 16S sequences. To provide phenotypic characterization, Biolog assays were used to characterize the strains in FB-001, as described below.

Biolog phenotype assays were used to determine unique macronutrient signatures for FB-001 strains. These data provide empirical characterization of growth features of each strain. The 148 strains of FB-001 fit into several broad categories of growth characteristics based on our Biolog analyses: 98 strains showed positive growth signatures; 41 strains did not have positive growth signatures; 9 were not tested using Biolog due to insufficient growth. Table 34 shows the 98 strains with positive growth signatures, with the specific macronutrients that supported growth listed along with the Genus species identification of each strain. Of the 98 strains with positive growth signatures, 60 were tested against the 190 individual carbon and energy sources present in the 96 well plate format of PM1 and 2 plates and the remaining 38 were tested using 2 plates alone. Each 96 well plate contains one negative control well that lacks any additional carbon or energy source. The total number of substrates utilized by any single strain in this assay showed great diversity, ranging from 1 to 59 substrates that yield growth. Furthermore, each of the 98 strains with growth on at least one substrate presented with an entirely unique growth fingerprint, or combination of permissive growth substrates, relative to every other strain in the set.

Table 34. Characterization of strain-level macronutrient utilization by Biolog assay in 98 strains with positive growth signatures. For each strain, the Biolog PM plates tested are given along with the Genus species identity and the macronutrients that supported growth. Positive growth is defined as an increase of 0.1 or more in optical density at 600 nm above the negative control that contained no supplied carbon and energy source.

Strain	PM	Macronutrient growth
FBI00001	1,2	2-Deoxy-D-Ribose; D-Fructose; D-Fructose-6-Phosphate; D-Galactose; D-Galacturonic Acid; D-Gluconic Acid; D-Glucosamine; D-Glucuronic Acid; D-Mannose; D-Ribose; D-Saccharic Acid; D-Trehalose; D-Xylose; Inosine; L-Arabinose; L-Galactonic Acid-g-Lactone; Maltose; Mucic Acid; N-Acetyl-D-Glucosamine; N-Acetyl-Neuraminic Acid; Sucrose; Thymidine; Uridine; a-D-Glucose; b-D-Allose
FBI00002	1,2	D-Galactose; a-D-Glucose; a-D-Lactose
FBI00004	1,2	D-Glucose-6-Phosphate; Maltose; Maltotriose

FBI00010	1,2	D-Arabinose; D-Cellobiose; D-Fructose; D-Fucose; D-Galactose; D-Mannose; D-Raffinose; D-Ribose; D-Sorbitol; D-Xylose; L-Arabinose; L-Fucose; L-Rhamnose; Maltose; Maltotriose; Stachyose; a-D-Glucose; a-D-Lactose
FBI00013	1,2	Caproic Acid; D-Melibiose; L-Pyroglutamic Acid; Melibionic Acid; N-Acetyl-D-Glucosamine; N-Acetyl-L-Glutamic Acid; Oxalic Acid; a-D-Glucose; a-D-Lactose
FBI00015	1,2	3-Hydroxy 2-Butanone; 3-Methyl Glucose; Amygdalin; Arbutin; D-Cellobiose; D-Glucosamine; D-Glucuronic Acid; D-Melibiose; D-Raffinose; Inulin; L-Galactonic Acid-g-Lactone; Lactulose; N-Acetyl-D-Galactosamine; N-Acetyl-b-D-Mannosamine; Palatinose; Salicin; a-D-Lactose; a-Methyl-D-Galactoside; b-Cyclodextrin; b-Methyl-D-Galactoside
FBI00025	1,2	D-Fructose; D-Fucose; D-Galactose; D-Melibiose; D-Raffinose; D-Xylose; Glycogen; L-Arabinose; Lactulose; Maltose; Maltotriose; Stachyose; Sucrose; a-D-Glucose; a-D-Lactose
FBI00027	1,2	D-Cellobiose; D-Galactose; D-Glucosamine; D-Raffinose; L-Tartaric Acid; Lactulose; Maltitol; Maltose; Maltotriose; Palatinose; Pectin; Stachyose; Sucrose; a-D-Glucose; a-D-Lactose; a-Methyl-D-Galactoside; a-Methyl-D-Glucoside; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside; b-Methyl-D-Xyloside
FBI00030	1,2	D-Mannitol; D-Trehalose; D-Xylose; Glycogen; Palatinose; a-D-Lactose
FBI00033	1,2	Lactulose; a-D-Lactose
FBI00044	1,2	Amygdalin; Arbutin; D-Arabinose; D-Cellobiose; D-Fructose; D-Galactose; D-Glucosamine; D-Mannitol; D-Melezitose; D-Melibiose; D-Raffinose; D-Sorbitol; D-Trehalose; D-Xylose; Gentiobiose; L-Arabinose; L-Fucose; Lactitol; Lactulose; Maltitol; Maltose; Maltotriose; N-Acetyl-Neuraminic Acid; Palatinose; Pectin; Salicin; Stachyose; Sucrose; Turanose; a-D-Glucose; a-D-Lactose; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside
FBI00046	1,2	D-Arabinose; D-Cellobiose; D-Fructose; D-Galactose; D-Galacturonic Acid; D-Glucosamine; D-Glucuronic Acid; D-Mannose; D-Melezitose; D-Melibiose; D-Raffinose; D-Ribose; D-Trehalose; D-Xylose; Gentiobiose; L-Arabinose; L-Fucose; L-Galactonic Acid-g-Lactone; Lactitol; Lactulose; Maltitol; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; Palatinose; Pectin; Salicin; Stachyose; Sucrose; Turanose; Uridine; a-D-Glucose; a-D-Lactose; a-Methyl-D-Glucoside; b-Methyl-D-Galactoside
FBI00047	1,2	D-Gluconic Acid
FBI00048	1,2	Arbutin; D-Cellobiose; D-Fructose; D-Galactose; D-Glucosamine; D-Glucosaminic Acid; D-Melibiose; D-Raffinose; Gentiobiose; L-Arabinose; Lactitol; Lactulose; Maltitol; Maltose; Maltotriose; Melibionic Acid; Palatinose; Pectin; Salicin; Stachyose; Sucrose; Turanose; a-D-Glucose; a-D-Lactose; a-Methyl-D-Glucoside; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside
FBI00050	1,2	3-Methyl Glucose; Amygdalin; Chondroitin Sulfate C; D-Cellobiose; D-Fructose; D-Galactose; D-Galacturonic Acid; D-Glucosamine; D-Glucuronic Acid; D-Mannose; D-Melibiose; D-Raffinose; D-Xylose; Dextrin; Gentiobiose; Glycogen; Inulin; L-Fucose; L-Galactonic Acid-g-Lactone; L-Lyxose; L-Rhamnose; Lactulose; Laminarin; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-b-D-Mannosamine; Palatinose; Pectin; Stachyose; Sucrose; Thymidine; Uridine; a-Cyclodextrin; a-D-Glucose; a-D-Lactose; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin

FBI00051	1,2	D-Fructose; D-Galactose; D-Galacturonic Acid; D-Sorbitol; Inulin; L-Arabinose; L-Galactonic Acid-g-Lactone; L-Tartaric Acid; Maltose; Maltotriose; N-Acetyl-Neuraminic Acid; a-D-Glucose
FBI00053	1,2	D-Galacturonic Acid; D-Gluconic Acid; D-Glucuronic Acid; L-Galactonic Acid-g-Lactone
FBI00057	1,2	Arbutin; D-Cellobiose; D-Fructose; D-Glucosamine; D-Raffinose; D-Sorbitol; L-Arabinose; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-Neuraminic Acid; Stachyose; Turanose; a-D-Glucose; a-D-Lactose; m-Inositol
FBI00059	1,2	Amygdalin; Arbutin; D-Arabinose; D-Galacturonic Acid; D-Glucosamine; D-Glucuronic Acid; D-Ribose; L-Fucose; Lactulose; Laminarin; N-Acetyl-D-Glucosamine; Pectin; a-D-Lactose; b-Methyl-D-Galactoside
FBI00070	1,2	3-0-b-D-Galacto-pyranosyl-D-Arabinose; Amygdalin; Arbutin; Chondroitin Sulfate C; D-Arabinose; D-Cellobiose; D-Fructose; D-Fructose-6-Phosphate; D-Galactose; D-Galacturonic Acid; D-Glucosamine; D-Glucose-1-Phosphate; D-Glucose-6-Phosphate; D-Glucuronic Acid; D-Mannose; D-Melezitose; D-Melibiose; D-Raffinose; D-Ribose; D-Trehalose; D-Xylose; Dextrin; Gentiobiose; Glycogen; L-Arabinose; L-Fucose; L-Galactonic Acid-g-Lactone; L-Rhamnose; Lactitol; Lactulose; Maltitol; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-b-D-Mannosamine; Palatinose; Pectin; Salicin; Stachyose; Sucrose; Thymidine; Turanose; Uridine; a-Cyclodextrin; a-D-Glucose; a-D-Lactose; a-Methyl-D-Galactoside; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside; g-Cyclodextrin
FBI00078	1,2	D-Arabinose; D-Cellobiose; D-Fructose; D-Galactose; D-Mannose; D-Melibiose; D-Raffinose; D-Ribose; D-Sorbitol; D-Xylose; L-Arabinose; L-Fucose; L-Lyxose; L-Rhamnose; L-Sorbose; Lactitol; Lactulose; Maltose; Maltotriose; Pectin; Sedoheptulosan; Stachyose; Sucrose; Xylitol; a-D-Glucose; a-D-Lactose; b-Methyl-D-Galactoside
FBI00079	1,2	5-Keto-D-Gluconic Acid; Amygdalin; Arbutin; D-Cellobiose; D-Fructose; D-Galactonic Acid-g-Lactone; D-Galactose; D-Gluconic Acid; D-Glucosamine; D-Glucose-1-Phosphate; D-Glucuronic Acid; D-Mannose; D-Ribono-1,4-Lactone; D-Ribose; D-Saccharic Acid; D-Xylose; Gentiobiose; L-Arabinose; L-Fucose; L-Galactonic Acid-g-Lactone; Lactulose; Maltose; Maltotriose; Mucic Acid; N-Acetyl-D-Glucosamine; N-Acetyl-Neuraminic Acid; N-Acetyl-b-D-Mannosamine; Pectin; Salicin; Sucrose; Thymidine; Uridine; a-D-Glucose; a-D-Lactose; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside
FBI00087	1,2	D-Arabitol; D-Fructose; D-Galactose; D-Gluconic Acid; D-Ribose; D-Sorbitol; D-Xylose; L-Arabinose; Sucrose; a-D-Glucose
FBI00102	1,2	Amygdalin; Chondroitin Sulfate C; D-Arabinose; D-Cellobiose; D-Fructose; D-Galactose; D-Galacturonic Acid; D-Glucosamine; D-Glucuronic Acid; D-Mannose; D-Melibiose; D-Raffinose; D-Ribose; D-Trehalose; D-Xylose; Dextrin; Gentiobiose; Glycogen; Inulin; L-Arabinose; L-Fucose; L-Galactonic Acid-g-Lactone; L-Rhamnose; Lactulose; Laminarin; Maltitol; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-b-D-Mannosamine; Palatinose; Pectin; Salicin; Sucrose; Turanose; Uridine; a-Cyclodextrin; a-D-Glucose; a-D-Lactose; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00104	1,2	Amygdalin; D-Arabinose; D-Cellobiose; D-Fructose; D-Galactose; D-Glucosamine; D-Melibiose; D-Raffinose; D-Sorbitol; D-Xylose; L-Arabinose;

		L-Fucose; L-Rhamnose; Maltose; N-Acetyl-Neuraminic Acid; Stachyose; Uridine; a-D-Glucose; a-D-Lactose
FBI00109	1,2	Arbutin; D-Fructose; D-Galactose; D-Melibiose; D-Raffinose; D-Sorbitol; Maltose; Maltotriose; Salicin; Stachyose; a-D-Glucose; a-D-Lactose; b-Methyl-D-Glucoside
FBI00110	1,2	5-Keto-D-Gluconic Acid; Arbutin; D-Cellobiose; D-Fructose; D-Fructose-6-Phosphate; D-Galactose; D-Gluconic Acid; D-Glucosamine; D-Mannose; D-Melezitose; D-Raffinose; D-Ribose; D-Trehalose; D-Xylose; Gentiobiose; Inosine; L-Arabinose; L-Fucose; Lactulose; Maltose; Maltotriose; N-Acetyl-D-Glucosamine; Palatinose; Salicin; Stachyose; Sucrose; Thymidine; Turanose; a-D-Glucose; b-D-Allose; b-Methyl-D-Glucoside
FBI00113	1,2	Arbutin; N-Acetyl-D-Galactosamine; a-Methyl-D-Galactoside
FBI00115	1,2	D-Fructose; D-Galactose; D-Xylose; L-Arabinose; Maltose; Maltotriose; N-Acetyl-Neuraminic Acid; Turanose; a-D-Glucose
FBI00117	1,2	Arbutin; Maltotriose
FBI00125	1,2	Chondroitin Sulfate C; D-Fructose; D-Galactose; D-Glucosamine; D-Mannose; Gentiobiose; Lactulose; Laminarin; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; Pectin; Sucrose; a-Cyclodextrin; a-D-Glucose; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00128	1,2	1,2-Propanediol; D-Fructose-6-Phosphate; a-D-Glucose
FBI00137	1,2	D-Fructose; D-Galactose; D-Glucosamine; D-Glucuronic Acid; D-Mannose; D-Melibiose; D-Raffinose; D-Xylose; Dextrin; Glycogen; Inulin; L-Fucose; Lactitol; Lactulose; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-Neuraminic Acid; Sucrose; a-Cyclodextrin; a-D-Glucose; a-D-Lactose; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00147	1,2	2-Deoxy-D-Ribose; D-Fructose; D-Galactose; D-Gluconic Acid; D-Glucosamine; D-Glucuronic Acid; D-Mannose; D-Melibiose; D-Psicose; D-Raffinose; D-Ribose; D-Sorbitol; D-Trehalose; D-Xylose; L-Arabinose; Lactulose; Maltose; Maltotriose; N-Acetyl-D-Glucosamine; N-Acetyl-Neuraminic Acid; Palatinose; Stachyose; Sucrose; Thymidine; Uridine; a-D-Glucose
FBI00165	1,2	N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-Neuraminic Acid
FBI00167	1,2	Amygdalin; Arbutin; D-Cellobiose; D-Fructose; D-Galactose; D-Glucosamine; D-Raffinose; D-Sorbitol; Gentiobiose; L-Arabinose; Lactulose; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-Neuraminic Acid; Salicin; Stachyose; Sucrose; Thymidine; Uridine; a-D-Glucose; a-D-Lactose; b-Methyl-D-Glucoside; m-Inositol
FBI00174	1,2	Adenosine; D-Fructose-6-Phosphate; D-Galacturonic Acid; D-Gluconic Acid; D-Glucose-1-Phosphate; D-Glucuronic Acid; D-Melezitose; D-Trehalose; Inosine; L-Fucose; L-Galactonic Acid-g-Lactone; Laminarin; N-Acetyl-D-Glucosamine; Pectin
FBI00180	1,2	Inulin; b-D-Allose
FBI00182	1,2	Amygdalin; Arbutin; D-Cellobiose; D-Fructose; D-Galactose; D-Galacturonic Acid; D-Mannose; D-Melibiose; D-Raffinose; Dextrin; Dihydroxy Acetone; Gentiobiose; L-Galactonic Acid-g-Lactone; L-Rhamnose; Lactulose; Maltose; Maltotriose; N-Acetyl-D-Glucosamine; Pectin; Salicin; Stachyose; Sucrose; a-D-Glucose; a-D-Lactose; a-Methyl-D-Galactoside; b-Methyl-D-Galactoside; g-Cyclodextrin

FBI00184	1,2	Amygdalin; D-Galactose; D-Glucosamine; D-Mannose; D-Melibiose; D-Raffinose; D-Trehalose; Gentiobiose; Lactulose; Maltitol; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-b-D-Mannosamine; Palatinose; Salicin; Stachyose; Sucrose; Turanose; Uridine; a-Cyclodextrin; a-D-Glucose; a-D-Lactose; a-Methyl-D-Glucoside; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00189	1,2	Amygdalin; Arbutin; D-Arabinose; D-Cellobiose; D-Galactose; D-Glucosamine; D-Mannitol; D-Mannose; D-Melibiose; D-Raffinose; D-Sorbitol; D-Trehalose; Gentiobiose; Glycogen; L-Arabinose; L-Fucose; Lactitol; Lactulose; Maltitol; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; Palatinose; Salicin; Stachyose; Sucrose; Turanose; a-Cyclodextrin; a-D-Glucose; a-D-Lactose; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside; g-Cyclodextrin
FBI00190	1,2	Amygdalin; Arbutin; Chondroitin Sulfate C; D-Arabinose; D-Cellobiose; D-Fructose; D-Fructose-6-Phosphate; D-Galactose; D-Galacturonic Acid; D-Glucosamine; D-Glucose-1-Phosphate; D-Glucose-6-Phosphate; D-Glucuronic Acid; D-Mannose; D-Melezitose; D-Melibiose; D-Raffinose; D-Trehalose; D-Xylose; Dextrin; Gentiobiose; Glycogen; Glycyl-L-Aspartic Acid; L-Arabinose; L-Fucose; L-Galactonic Acid-g-Lactone; L-Rhamnose; Lactitol; Lactulose; Laminarin; Maltitol; Maltose; Maltotriose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-b-D-Mannosamine; Palatinose; Pectin; Salicin; Stachyose; Sucrose; Thymidine; Turanose; Uridine; a-D-Glucose; a-D-Lactose; a-Methyl-D-Galactoside; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside
FBI00191	1,2	D-Trehalose; L-Arabinose; Maltotriose; N-Acetyl-D-Glucosamine; a-Cyclodextrin; b-Cyclodextrin
FBI00194	1,2	Arbutin; D-Arabinose; D-Fructose; D-Galactose; D-Glucosamine; D-Melibiose; D-Raffinose; D-Sorbitol; D-Trehalose; Gentiobiose; L-Fucose; Lactulose; Maltose; Maltotriose; N-Acetyl-D-Glucosamine; Salicin; Stachyose; Sucrose; Turanose; a-D-Glucose; a-D-Lactose
FBI00198	1,2	2-Deoxy Adenosine; Arbutin; D-Cellobiose; D-Fructose; D-Galactose; D-Galacturonic Acid; D-Gluconic Acid; D-Glucosamine; D-Glucuronic Acid; D-Mannose; D-Melezitose; D-Melibiose; D-Raffinose; D-Ribose; D-Trehalose; D-Xylose; Inosine; L-Arabinose; L-Fucose; Lactulose; Maltose; Maltotriose; N-Acetyl-D-Glucosamine; N-Acetyl-Neuraminic Acid; Palatinose; Stachyose; Thymidine; Turanose; a-D-Glucose; a-D-Lactose; b-D-Allose
FBI00199	1,2	D-Fructose; D-Galactonic Acid-g-Lactone; D-Galactose; D-Gluconic Acid; D-Glucosamine; D-Glucose-1-Phosphate; D-Glucose-6-Phosphate; D-Mannose; D-Melibiose; D-Psicose; D-Raffinose; D-Ribose; D-Sorbitol; D-Trehalose; D-Xylose; L-Arabinose; L-Serine; L-Tartaric Acid; Lactulose; Maltose; Maltotriose; N-Acetyl-D-Glucosamine; N-Acetyl-Neuraminic Acid; Palatinose; Stachyose; Sucrose; Uridine; a-D-Glucose
FBI00200	1,2	D-Galacturonic Acid; D-Gluconic Acid; D-Glucuronic Acid; L-Galactonic Acid-g-Lactone; Pectin
FBI00201	1,2	Dextrin; Glycogen; Inulin; Laminarin; g-Cyclodextrin
FBI00205	1,2	3-0-b-D-Galacto-pyranosyl-D-Arabinose; Arbutin; D-Arabinose; D-Fructose; D-Galactose; D-Gluconic Acid; D-Mannitol; D-Melibiose; D-Raffinose; D-Sorbitol; D-Xylose; L-Fucose; L-Rhamnose; L-Tartaric Acid; Lactitol;

		Lactulose; Maltitol; Maltose; Maltotriose; Melibiononic Acid; N-Acetyl-D-Glucosamine; Palatinose; Pectin; Salicin; Stachyose; Sucrose; Turanose; a-D-Glucose; a-D-Lactose; a-Methyl-D-Galactoside; b-Methyl-D-Galactoside; m-Inositol
FBI00220	1,2	D-Arabitol; D-Fructose; D-Galacturonic Acid; D-Gluconic Acid; D-Mannitol; D-Xylose; L-Serine; Maltose; Maltotriose; Pyruvic Acid; Sucrose; a-D-Glucose
FBI00232	1,2	Chondroitin Sulfate C; D-Galactose; Glycogen; Inulin; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; Pectin; Sucrose; a-Cyclodextrin; b-Cyclodextrin; g-Cyclodextrin
FBI00235	1,2	1,2-Propanediol; 2-Hydroxy Benzoic Acid; 5-Keto-D-Gluconic Acid; Acetic Acid; Amygdalin; D-Arabinose; D-Fucose; D-Ribose; D-Tagatose; D-Threonine; L-Arabitol; L-Arginine; L-Pyroglutamic Acid; L-Rhamnose; Maltitol; N-Acetyl-L-Glutamic Acid; Oxalic Acid; Quinic Acid; Sebacic Acid; Stachyose; Succinamic Acid; Turanose; a-D-Lactose; a-Hydroxy Glutaric Acid-g-Lactone; a-Keto-Butyric Acid; a-Keto-Valeric Acid; a-Methyl-D-Galactoside; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Methyl-D-Xyloside; d-Amino Valeric Acid; g-Amino Butyric Acid; g-Hydroxy Butyric Acid
FBI00236	1,2	D-Galactose; D-Mannose; D-Melibiose; D-Raffinose; D-Trehalose; L-Fucose; Maltose; Maltotriose; N-Acetyl-D-Glucosamine; Stachyose; Turanose; a-Methyl-D-Galactoside; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside; b-Methyl-D-Xyloside
FBI00245	1,2	Amygdalin; Chondroitin Sulfate C; D-Arabinose; D-Cellobiose; D-Fructose; D-Galactose; D-Galacturonic Acid; D-Gluconic Acid; D-Glucosamine; D-Glucuronic Acid; D-Mannose; D-Melezitose; D-Melibiose; D-Raffinose; D-Ribose; D-Saccharic Acid; D-Trehalose; D-Xylose; Dextrin; Gentiobiose; Glycogen; Inulin; L-Arabinose; L-Fucose; L-Galactonic Acid-g-Lactone; L-Glutamine; L-Histidine; L-Pyroglutamic Acid; L-Rhamnose; Lactitol; Lactulose; Maltitol; Maltose; Maltotriose; Mannan; Mucic Acid; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-b-D-Mannosamine; Palatinose; Pectin; Pyruvic Acid; Salicin; Stachyose; Sucrose; Turanose; Uridine; a-Cyclodextrin; a-D-Glucose; a-D-Lactose; a-Keto-Butyric Acid; a-Keto-Glutaric Acid; a-Methyl-D-Galactoside; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside; b-Methyl-D-Glucoside; g-Cyclodextrin
FBI00263	1,2	D-Galactose; D-Glucosamine; D-Mannose; D-Melibiose; D-Raffinose; D-Trehalose; L-Arabinose; L-Fucose; Lactulose; Maltitol; Maltose; N-Acetyl-D-Galactosamine; N-Acetyl-D-Glucosamine; N-Acetyl-Neuraminic Acid; Stachyose; Sucrose; Turanose; a-D-Glucose; a-D-Lactose; a-Methyl-D-Glucoside; b-Methyl-D-Galactoside
FBI00269	1,2	D,L-a-Glycerol-Phosphate; D-Gluconic Acid; D-Glucuronic Acid; Dextrin; Gelatin; Glycogen; Inulin; Laminarin; g-Cyclodextrin
FBI00278	1,2	Glycogen; Thymidine
FBI00281	1,2	D-Ribose; N-Acetyl-Neuraminic Acid
FBI00290	1,2	Glycogen
FBI00009	2	Acetamide; D-Raffinose; g-Cyclodextrin
FBI00011	2	4-Hydroxy Benzoic Acid; Capric Acid; D,L-Carnitine; D,L-Octopamine; D-Glucosamine; D-Ribono-1,4-Lactone; Dihydroxy Acetone; Glycine; Inulin; L-

		Alaninamide; L-Arginine; L-Histidine; L-Homoserine; N-Acetyl-L-Glutamic Acid; Putrescine; Quinic Acid; Turanose
FBI00016	2	D-Arabinose; D-Glucosamine; D-Raffinose; Dextrin; Glycogen; Lactitol; N-Acetyl-D-Galactosamine; N-Acetyl-Neuraminic Acid; Palatinose; Stachyose; a-Cyclodextrin; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00020	2	Amygdalin; D-Arabinose; D-Glucosamine; D-Melezitose; D-Raffinose; Gentiobiose; Maltitol; N-Acetyl-D-Galactosamine; Palatinose; Salicin; Stachyose; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00021	2	Amygdalin; Arbutin; D-Arabinose; D-Arabitol; D-Glucosamine; D-Melezitose; D-Raffinose; Gentiobiose; Glycogen; Lactitol; Maltitol; N-Acetyl-D-Galactosamine; Palatinose; Pectin; Salicin; Stachyose; Turanose; a-Cyclodextrin; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00029	2	Amygdalin; Arbutin; D-Glucosamine; D-Melezitose; D-Raffinose; Dextrin; Gentiobiose; Inulin; Lactitol; Laminarin; Maltitol; N-Acetyl-D-Galactosamine; N-Acetyl-Neuraminic Acid; Palatinose; Salicin; Stachyose; Turanose; a-Cyclodextrin; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00032	2	5-Keto-D-Gluconic Acid; Arbutin; D-Glucosamine; Inulin; L-Sorbose; L-Tartaric Acid; Lactitol; Maltitol; N-Acetyl-D-Glucosaminitol; Palatinose; Pectin; Salicin; Turanose; a-Methyl-D-Mannoside
FBI00043	2	2-Hydroxy Benzoic Acid; Amygdalin; D-Arabinose; D-Ribono-1,4-Lactone; Dextrin; Dihydroxy Acetone; Glycine; L-Leucine; Maltitol; N-Acetyl-Neuraminic Acid; Oxalomalic Acid; Palatinose; Quinic Acid; Sebacic Acid; Stachyose; a-Methyl-D-Glucoside; b-Methyl-D-Galactoside
FBI00049	2	b-Cyclodextrin; g-Cyclodextrin
FBI00052	2	Amygdalin; Arbutin; D-Arabinose; D-Glucosamine; D-Melezitose; D-Raffinose; Gentiobiose; Maltitol; N-Acetyl-D-Galactosamine; Palatinose; Salicin; Turanose; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Methyl-D-Galactoside
FBI00056	2	Amygdalin; D-Raffinose; Dextrin; Gentiobiose; Maltitol; N-Acetyl-Neuraminic Acid; Palatinose; Stachyose; Turanose; b-Methyl-D-Galactoside
FBI00060	2	Amygdalin; Arbutin; D-Arabinose; D-Glucosamine; D-Melezitose; D-Raffinose; Dextrin; Gentiobiose; Glycogen; Lactitol; Maltitol; N-Acetyl-D-Galactosamine; Palatinose; Salicin; Turanose; a-Cyclodextrin; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00062	2	Dextrin; Lactitol; Maltitol; Palatinose; Salicin; Stachyose; Turanose; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00075	2	b-Methyl-D-Galactoside
FBI00076	2	Amygdalin; D-Arabinose; D-Glucosamine; D-Melezitose; D-Raffinose; Gentiobiose; Glycogen; Inulin; Laminarin; Maltitol; N-Acetyl-D-Galactosamine; Palatinose; Pectin; Salicin; Turanose; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00080	2	Amygdalin; Arbutin; D-Melezitose; D-Raffinose; Dextrin; L-Arginine; Laminarin; Maltitol; N-Acetyl-Neuraminic Acid; Pectin; Stachyose; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside
FBI00111	2	D-Arabinose; D-Glucosamine; D-Raffinose; Stachyose; b-D-Allose

FBI00112	2	Amygdalin; Arbutin; D-Arabinose; D-Glucosamine; Inulin; N-Acetyl-D-Galactosamine; Salicin; a-Cyclodextrin; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00116	2	Amygdalin; D-Arabinose; D-Glucosamine; D-Raffinose; Gentiobiose; Palatinose; Pectin; Stachyose; Turanose
FBI00124	2	D-Glucosamine; D-Raffinose; Lactitol; Pectin; Stachyose; a-Methyl-D-Mannoside
FBI00126	2	Arbutin; D-Glucosamine; D-Tagatose; N-Acetyl-D-Galactosamine; Pectin
FBI00127	2	Amygdalin; Arbutin; Lactitol; Pectin; Salicin; Turanose; b-Methyl-D-Galactoside
FBI00135	2	Amygdalin; D-Glucosamine; N-Acetyl-D-Galactosamine; N-Acetyl-Neuraminic Acid
FBI00140	2	Dextrin; Gentiobiose; Glycogen; Laminarin; Stachyose; a-Cyclodextrin; b-Cyclodextrin; g-Cyclodextrin
FBI00145	2	Amygdalin; Arbutin; D-Raffinose; Dextrin; Gentiobiose; Lactitol; Salicin; Stachyose; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00151	2	2-Deoxy-D-Ribose; D-Arabinose; D-Fructose; D-Gluconic Acid; D-Glucosamine; D-Mannose; D-Raffinose; Dextrin; Gentiobiose; Glycogen; L-Isoleucine; Maltitol; Maltose; Maltotriose; Mannan; N-Acetyl-D-Glucosamine; Palatinose; Pectin; Stachyose; Sucrose; Turanose; a-Cyclodextrin; a-D-Glucose; b-Cyclodextrin; b-D-Allose; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00152	2	D-Raffinose; Dextrin; Gentiobiose; Glycogen; Laminarin; Stachyose; a-Cyclodextrin; b-Cyclodextrin; g-Cyclodextrin
FBI00175	2	D-Arabinose; D-Arabitol
FBI00197	2	Amygdalin; Arbutin; Chondroitin Sulfate C; D-Arabinose; D-Glucosamine; D-Melezitose; D-Raffinose; Gentiobiose; Lactitol; Laminarin; N-Acetyl-D-Galactosamine; N-Acetyl-Neuraminic Acid; Pectin; Salicin; Stachyose; Turanose; a-Cyclodextrin; b-Cyclodextrin; b-Methyl-D-Galactoside; b-Methyl-D-Glucuronic Acid; b-Methyl-D-Xyloside; g-Cyclodextrin
FBI00206	2	Amygdalin; Arbutin; D-Arabinose; D-Glucosamine; D-Melezitose; D-Raffinose; Dextrin; Gentiobiose; Glycogen; Inulin; Lactitol; Maltitol; N-Acetyl-D-Galactosamine; Palatinose; Pectin; Salicin; Stachyose; Turanose; a-Cyclodextrin; a-Methyl-D-Glucoside; a-Methyl-D-Mannoside; b-Cyclodextrin; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00211	2	Amygdalin; D-Raffinose; Glycogen; Lactitol; Maltitol; Palatinose; Turanose; b-Methyl-D-Galactoside
FBI00212	2	3-Methyl Glucose; 4-Hydroxy Benzoic Acid; Amygdalin; Arbutin; D-Arabinose; D-Arabitol; D-Melezitose; Dextrin; Glycogen; Inulin; L-Isoleucine; L-Lysine; L-Methionine; Lactitol; Maltitol; Palatinose; Turanose; a-Methyl-D-Glucoside; b-D-Allose; b-Methyl-D-Galactoside; g-Cyclodextrin; i-Erythritol
FBI00243	2	Sec-Butylamine
FBI00251	2	D-Raffinose; Dextrin; Glycogen; Lactitol; Palatinose; Salicin; Turanose; b-Methyl-D-Galactoside; g-Cyclodextrin
FBI00255	2	Arbutin; D-Arabinose; D-Melezitose; D-Raffinose; Inulin; Stachyose; b-Cyclodextrin; b-Methyl-D-Glucuronic Acid; b-Methyl-D-Xyloside; g-Cyclodextrin
FBI00267	2	D,L-Octopamine; Sec-Butylamine

FBI00271	2	3-Methyl Glucose; Arbutin; D,L-Carnitine; D-Arabinose; D-Arabitol; D-Raffinose; D-Ribono-1,4-Lactone; D-Tartaric Acid; Gentiobiose; Glycogen; Hydroxy-L-Proline; Itaconic Acid; L-Histidine; L-Isoleucine; L-Valine; Laminarin; Quinic Acid; Sebacic Acid; Sorbic Acid; Stachyose; Succinamic Acid; b-Hydroxy Butyric Acid; b-Methyl-D-Galactoside
FBI00274	2	D-Ribono-1,4-Lactone; L-Histidine; L-Homoserine; Quinic Acid

The single carbon source conditions of Biolog plates are restrictive and not expected to promote growth of strains with more complex growth requirements. This was observed with the 41 strains of FB-001 that do not have a positive growth signature in the Biolog assays performed and the 9 strains that were not tested using Biolog due to insufficient growth. Of these combined 50 strains, 23 were tested with just 2 plates, 18 were tested with both PM1 and 2 plates, and 9 fastidious strains failed to reach the turbidity necessary to conduct a Biolog assay and are characterized in more detail below. The 41 strains that reached sufficient growth OD in complex growth media, but did not show positive growth in the Biolog plates tested, are shown in Table 35. These strains are routinely grown on complex YCFAC media and growth data in this medium are provided as the OD₆₀₀ reached in the time given. Further information on the cultivation of these strains is available in the primary literature and summarized in Table 35 as well. In brief, for each strain we provide known macronutrient utilization, metabolite production and oxalate-formate characters. Macronutrients describe the primary contributors to biomass for a given strain, whereas metabolite production describes excreted small molecules that accumulate during cultivation and oxalate-formate focuses on the ability to degrade or resist the presence of these molecules. In cases where a macronutrient is predicted to be a substrate for growth, but growth was not directly observed in Biolog assays, it is expected that a second nutrient is required such as a vitamin or alternative nitrogen source that can be provided by the YCFAC recipe used for routine growth.

Table 35. Characterization of the 41 strains that did not show positive growth signatures by Biolog assay

Strain	PM	YCFAC OD ₆₀₀	Incubation time (h)	Macronutrient
FBI00068	1,2	0.573	72	mucin o-linked glycans
FBI00012	1,2	0.788	68	indole; mannose; raffinose
FBI00277	1,2	1.097	68	indole; mannose; raffinose
FBI00022	1,2	0.342	72	N/A
FBI00229	1,2	0.186	72	mannose
FBI00061	1,2	0.047	72	mannose; raffinose
FBI00238	1,2	0.251	72	N/A
FBI00288	1,2	0.877	66.6	N/A

FBI00038	1,2	0.512	72	acetate; cellobiose; fructose; glucose; lactose; maltose; mannose; raffinose; starch
FBI00170	1,2	0.067	72	acetate; arginine; secoisolariciresinol diglucoside
FBI00096	1,2	0.068	72	acetate; arginine; secoisolariciresinol diglucoside
FBI00159	1,2	0.063	68	N/A
FBI00018	1,2	0.799	72	acetate; arabinoxylan; arginine; inulin; starch; xos
FBI00099	1,2	0.094	72	arginine; methionine
FBI00081	1,2	0.612	72	N/A
FBI00071	1,2	1.066	70.7	N/A
FBI00097	1,2	0.179	72	N/A
FBI00233	1,2	0.432	72	N/A
FBI00019	2	0.12	72	indole
FBI00208	2	0.768	70	inulin; mannose
FBI00162	2	1.146	70	N/A
FBI00171	2	0.164	72	N/A
FBI00221	2	0.963	70	glucose
FBI00226	2	0.097	72	arabinose; glucose; mannose; xylose
FBI00040	2	0.056	72	N/A
FBI00237	2	0.053	71.8	N/A
FBI00248	2	1.13	71.8	N/A
FBI00260	2	1.153	72	acetate; arabinoxylan; arginine; inulin; starch; xos
FBI00244	2	0.114	71.8	acetate; arginine; chondroitin sulfate; fructose; galacturonate; glucose; inulin; maltose; starch
FBI00132	2	0.154	72	arginine; methionine
FBI00120	2	0.735	72	starch
FBI00092	2	0.15	87.8	arabinose; xylose
FBI00149	2	0.157	87.8	arabinose; xylose
FBI00177	2	0.082	87.8	N/A
FBI00066	2	0.09	87.8	N/A
FBI00093	2	0.896	71.8	starch
FBI00123	2	1.4	71.8	starch
FBI00069	2	0.11	72	starch
FBI00085	2	0.733	72	starch
FBI00224	2	0.047	70	cysteine
FBI00077	2	0.062	72	cysteine

While most strains show a Biolog or YCFAC signature, the nine most fastidious strains require more characterization, which are provided here. Of these nine strains, two are isolates of *Methanobrevibacter smithii* (FBI00270 and FBI00292), the only archaeal strains in FB-001. *M. smithii* grows through methanogenesis (CH₄ production) with utilization of CO₂ + H₂, or formate (HCO₂⁻) as macronutrients. Because of these specific growth conditions and phylogeny,

M. smithii can be challenging to grow, but is readily identifiable. Another two strains are *Oxalobacter formigenes* strains FBI0133 and FBI0289, which can be readily grown with YCFAC supplemented with 20 mM Sodium oxalate.

Strain FBI00258 *Turicibacter sanguinis*, is most easily identified through its distinctive filamentous cell shape, with filamentous growth contributing to a lack of turbidity observed in dispersed culture. For strains FBI00254 *Eubacterium hallii*, FBI00034 *Eubacterium eligens*, FBI00176 *Ruthenibacterium lactatiformans*, and FBI00273 *Barnesiella intestinihominis* identification was conducted with differential plating on four recipes of complex media (Table 36).

Table 36. Seven-day growth scores for strains FBI00176 *Ruthenibacterium lactatiformans* and FBI00273 *Barnesiella intestinihominis*

Strain ID	YCFAC	YCFAC-B	BHI	CBA
FBI00273	+	-	-	+
FBI00176	+	-	+	+
FBI00254	+	+	-	+
FBI00034	+	+	-	+

PM1 plates contained the following molecules: L-Arabinose; N-Acetyl-D- Glucosamine; D-Saccharic Acid; Succinic Acid; D-Galactose; L-Aspartic Acid; L-Proline; D-Alanine; D-Trehalose; D-Mannose; Dulcitol; D-Serine; D-Sorbitol; Glycerol; L-Fucose; D-Glucuronic Acid; D-Gluconic Acid; D,L-a-Glycerol- Phosphate; D-Xylose; L-Lactic Acid; Formic Acid; D-Mannitol; L-Glutamic Acid; D-Glucose-6- Phosphate; D-Galactonic Acid-g-Lactone; D,L-Malic Acid; D-Ribose; Tween 20; L-Rhamnose; D-Fructose; Acetic Acid; a-D; Glucose; Maltose; D-Melibiose; Thymidine; L-Asparagine; D-Aspartic Acid; D-Glucosaminic Acid; 1,2-Propanediol; Tween 40; a-Keto-Glutaric Acid; a-Keto-Butyric Acid; a-Methyl-D- Galactoside; a-D-Lactose; Lactulose; Sucrose; Uridine; L-Glutamine; m-Tartaric Acid; D-Glucose-1- Phosphate; D-Fructose-6- Phosphate; Tween 80; a-Hydroxy Glutaric Acid-g- Lactone; a-Hydroxy Butyric Acid; b-Methyl-D- Glucoside; Adonitol; Maltotriose; 2-Deoxy Adenosine; Adenosine; Glycyl-L-Aspartic Acid; Citric Acid; m-Inositol; D-Threonine; Fumaric Acid; Bromo Succinic Acid; Propionic Acid; Mucic Acid; Glycolic Acid; Glyoxylic Acid; D-Cellobiose; Inosine; Glycyl-L- Glutamic Acid; Tricarballic Acid; L-Serine; L-Threonine; L-Alanine; L-Alanyl-Glycine; Acetoacetic Acid; N-Acetyl-b-D- Mannosamine; Mono Methyl Succinate; Methyl Pyruvate; D-Malic Acid; L-Malic Acid; Glycyl-L-Proline; p-Hydroxy Phenyl Acetic Acid; m-Hydroxy Phenyl Acetic Acid; Tyramine; D-Psicose; L-Lyxose; Glucuronamide; Pyruvic Acid; L-Galactonic Acid-g-Lactone; D; Galacturonic Acid; Phenylethylamine; 2-Aminoethanol.

PM2 plates contained the following molecules: Chondroitin Sulfate C; a-Cyclodextrin; b-Cyclodextrin; g-Cyclodextrin; Dextrin; Gelatin; Glycogen; Inulin; Laminarin; Mannan; Pectin; N-Acetyl-D- Galactosamine; N-Acetyl- Neuraminic Acid; b-D-Allose; Amygdalin; D-Arabinose; D-Arabitol; L-Arabitol; Arbutin; 2-Deoxy-D- Ribose; i-Erythritol; D-Fucose; 3-0-b-D-Galactopyranosyl-D- Arabinose; Gentiobiose; L-Glucose; Lactitol; D-Melezitose; Maltitol; a-Methyl-D-Glucoside; b-Methyl-D- Galactoside; 3-Methyl Glucose; b-Methyl-D- Glucuronic Acid; a-Methyl-D- Mannoside; b-Methyl-D- Xyloside; Palatinose; D-Raffinose; Salicin; Sedoheptulosan; L-Sorbose; Stachyose; D-Tagatose; Turanose; Xylitol; N-Acetyl-D- Glucosaminitol; g-Amino Butyric Acid; d-Amino Valeric Acid; Butyric Acid; Capric Acid; Caproic Acid; Citraconic Acid; Citramalic Acid; D-Glucosamine; 2-Hydroxy Benzoic Acid; 4-Hydroxy Benzoic Acid; b-Hydroxy Butyric Acid; g-Hydroxy Butyric Acid; a-Keto-Valeric Acid; Itaconic Acid; 5-Keto-D- Gluconic Acid; D-Lactic Acid Methyl Ester; Malonic Acid; Melibionc Acid; Oxalic Acid; Oxalomalic Acid; Quinic Acid; D-Ribono-1,4- Lactone; Sebacic Acid; Sorbic Acid; Succinamic Acid; D-Tartaric Acid; L-Tartaric Acid; Acetamide; L-Alaninamide; N-Acetyl-L- Glutamic Acid; L-Arginine; Glycine; L-Histidine; L-Homoserine; Hydroxy-L- Proline; L-Isoleucine; L-Leucine; L-Lysine; L-Methionine; L-Ornithine; L-Phenylalanine; L-Pyroglutamic Acid; L-Valine; D,L-Carnitine; Sec-Butylamine; D,L-Octopamine; Putrescine; Dihydroxy Acetone; 2,3-Butanediol; 2,3-Butanedione; 3-Hydroxy 2-Butanone.

Preparation of cell suspension and PM MicroPlate Inoculation. AN IF-0a Inoculating Fluid (1.2x) was prepared by adding 1.5 ml of 1 M NaHCO₃, 0.15 ml of 0.4 M thioglycolate and 0.15 ml of 1 mM methylene green to a bottle of IF-0a GN/GP base inoculating fluid (1.2x), for a total of 125 ml AN IF-0a Inoculating Fluid (1.2x). The inoculating fluid is confirmed to be fully deoxygenated when colorless as the methylene green indicator changes from the oxidized (green) to the reduced (colorless) form. PM MicroPlates were removed from packaging, placed in an anaerobic chamber. And allowed to equilibrate to the oxygen-free gas mix (5% CO₂, 5%H₂, 90% N₂) for two days to become anaerobic. Preparation of PM inoculating fluids comprised: 1) Prepared a test tube containing 10 ml of 1.2x AN IF-0a, 2) Prepared inoculating fluids as described below, and 3) Dispensed inoculating fluids into vials.

Inoculation of PM MicroPlates. All the following steps were done in a strictly anaerobic atmosphere containing 5% CO₂, 5% H₂, 90% N₂. Step 1: Prepare Cell Suspensions (a. Strains were re-streaked from Research Cell Banks (RCBs) onto four plates of YCFAC media by streaking heavily and allowing the cells to grow 1 – 7 days at 37°C in an atmosphere containing 5% CO₂, 5%H₂, 90% N₂; b. Cells were harvested from agar plates using a sterile swab and transferred into a tube containing 10 ml of 1.2 x AN IF-0a. Cell suspensions were gently stirred with the swab to obtain a uniform

suspension. Turbidity of the suspension was measured in Turbidimeter, and cells added to achieve a density of 40%T (transmittance)). Step 2: Inoculate PMs 1 and 2 (a. MicroPlates were prepped and labeled for each strain; b. 1.5 ml of cell suspension (Mix A) were added to 22.5 ml of AN PM1,2 inoculating fluid (Mix B) to a total of 24.0 ml. The final cell density is a 1:16 dilution of 40%T; c. 5 PM MicroPlates were inoculated anaerobically from the 24 ml AB mixture by multichannel pipettor, with 100 ml aliquots per well).

Incubation and Data Collection. All cultures were maintained at 37 °C and anerobic conditions throughout the incubation. Growth of cells was measure by reading optical density at 600 nm (OD600) every 2 hours for using an Agilent Biostack microplate reader for 50 – 90 hours, 10 depending on when stationary phase was reached across the plate.

* * *

While the present invention has been described at some length and with some particularity 15 with respect to the several described embodiments, it is not intended that it should be limited to any such particulars or embodiments or any particular embodiment, but it is to be construed with references to the appended claims so as to provide the broadest possible interpretation of such claims in view of the prior art and, therefore, to effectively encompass the intended scope of the invention.

20 All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In case of conflict, the present specification, including definitions, will control. In addition, section headings, the materials, methods, and examples are illustrative only and not intended to be limiting.

CLAIMS:

1. A composition comprising a microbial consortia comprising at least 1 oxalate-metabolizing microbial strain, wherein the at least one strain expresses an enzyme selected from a formyl-CoA transferase, an oxalate-formate antiporter, and an oxalyl-CoA decarboxylase.

2. The composition of claim 1, wherein the at least 1 oxalate-metabolizing microbial strain is from the *Oxalobacter* genus.

3. The composition of claim 1 or 2 comprising at least 3 oxalate-metabolizing microbial strains, wherein the at least 3 oxalate-metabolizing microbial strains are different strains of the same species.

4. The composition of claim 1 or 2 comprising at least 3 oxalate-metabolizing microbial strains, wherein the at least 3 oxalate-metabolizing microbial strains are different strains of different species.

5. The composition of any one of claims 3 or 4, wherein the species is *Oxalobacter formigenes* (*O. formigenes*), and optionally wherein the number of oxalate-metabolizing microbial strains is 3 or more.

6. The composition of claims 3-5, wherein:

- a) at least one strain is a low pH tolerance strain;
- b) at least one strain is a high oxalate tolerance strain; and/or
- c) at least one strain is a high growth rate strain.

7. A composition comprising at least 2 *Oxalobacter formigenes* (*O. formigenes*) strains, wherein each of the strains comprises one or more of the following functions:

- a) a low pH tolerance strain;
- b) a high oxalate tolerance strain; and/or
- c) a high growth rate strain.

8. A composition comprising at least 3 *Oxalobacter formigenes* (*O. formigenes*) strains, wherein

- a) at least one strain is a low pH tolerance strain;
- b) at least one strain is a high oxalate tolerance strain; and
- c) at least one strain is a high growth rate strain.

9. The composition of any one of claims 6-8, wherein the low pH tolerance strain can metabolize oxalate at a pH between about 4 and about 6.

10. The composition of claim 9, wherein the low pH tolerance strain can metabolize oxalate at a pH of about 5.

11. The composition of any one of claims 6-10, wherein the high oxalate tolerance strain can metabolize oxalate at a concentration between about 5 mM to about 30 mM.

12. The composition of claim 11, wherein the high oxalate tolerance strain can metabolize oxalate at a concentration of about 15 mM.

13. The composition of any one of claims 1-12, wherein each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

14. The composition of any one of claims 1-13, wherein each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

15. The composition of any one of claims 1-14, wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 42, SEQ ID NO: 79, or SEQ ID NO: 146.

16. The composition of any one of claims 1-15 further comprising one or more microbes metabolizing formate.

17. The composition of any one of claims 1-16 further comprising one or more microbes catalyzing fermentation of polysaccharides.

18. The composition of any one of claims 1-17 further comprising one or more microbes catalyzing fermentation of amino acids.

19. The composition of any one of claims 1-18 further comprising microbes catalyzing the synthesis of at least one molecules selected from the group consisting of methane, acetate, sulfide, propionate, and succinate.

20. The composition of any one of claims 1-19 further comprising microbes catalyzing

a) deconjugation of conjugated bile acids to produce primary bile acids;

b) conversion of cholic acid (CA) to 7-oxocholic acid;

c) conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA);

d) conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid; and/or

e) conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

21. The composition of any one of claims 1-20, wherein the composition comprises:

a) Consortia I or a functional equivalent thereof;

b) Consortia II or a functional equivalent thereof;

- c) Consortia III or a functional equivalent thereof;
- d) Consortia IV or a functional equivalent thereof;
- e) Consortia V or a functional equivalent thereof;
- f) Consortia VI or a functional equivalent thereof;
- g) Consortia VII or a functional equivalent thereof;
- h) Consortia VIII or a functional equivalent thereof;
- i) Consortia IX or a functional equivalent thereof;
- j) Consortia X or a functional equivalent thereof;
- k) Consortia XI or a functional equivalent thereof;
- l) Consortia XII or a functional equivalent thereof;
- m) Consortia XIII or a functional equivalent thereof;
- n) Consortia XIV or a functional equivalent thereof;
- o) Consortia XV or a functional equivalent thereof;
- p) Consortia XVI or a functional equivalent thereof;
- q) Consortia XVII or a functional equivalent thereof;
- r) Consortia XVIII or a functional equivalent thereof; or
- s) Consortia XIX or a functional equivalent thereof.

22. The composition of any one of claims 1-20, further comprising a second composition comprising *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae* sp. FBI00033, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorisoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae* sp. FBI00071, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides finegoldii*, *Clostridiaceae* sp. FBI00191, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*, *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*, *Acidaminococcus intestini*, *Emergencia timonensis*, *Bifidobacterium pseudocatenulatum*, *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, *Lachnospiraceae* sp. FBI00290, or a functional equivalent microbial consortium.

23. The composition of any one of claims 1-20 or 22, further comprising FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, FBI00290, or a functional equivalent thereof.

24. The composition of claim 22 or 23, wherein each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO:

48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

25. The composition of any one of claims 22-24, wherein each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

26. The composition of any one of claims 22-25, wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 5, SEQ ID NO: 8, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 21, SEQ ID NO: 22, SEQ ID NO: 25, SEQ ID NO: 26, SEQ ID NO: 29, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 36, SEQ ID NO: 37, SEQ ID NO: 38, SEQ ID NO: 45, SEQ ID NO: 46, SEQ ID NO: 48, SEQ ID NO: 51, SEQ ID NO: 55, SEQ ID NO: 57, SEQ ID NO: 61, SEQ ID NO: 63, SEQ ID NO: 70, SEQ ID NO: 71, SEQ ID NO: 74, SEQ ID NO: 76, SEQ ID NO: 77, SEQ ID NO: 83, SEQ ID NO: 89, SEQ ID NO: 94, SEQ ID NO: 100, SEQ ID NO: 102, SEQ ID NO: 103, SEQ ID NO: 104, SEQ ID NO: 106, SEQ ID NO: 107, SEQ ID NO: 108, SEQ ID NO: 109, SEQ ID NO: 110, SEQ ID NO: 111, SEQ ID NO: 113, SEQ ID NO: 115, SEQ ID NO: 116, SEQ ID NO: 123, SEQ ID NO: 128, SEQ ID NO: 129, SEQ ID NO: 130, SEQ ID NO: 131, SEQ ID NO: 136, SEQ ID NO: 143, SEQ ID NO: 145, or SEQ ID NO: 147.

27. The composition of any one of claims 1-20 and 22-26, further comprising a third composition comprising *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila*

wadsworthia, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae sp. FBI00097*, *Gordonibacter pamelaee*, *Bacteroides uniformis*, *Gordonibacter pamelaee*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae sp. FBI00233*, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinihominis*, *Alistipes onderdonkii*, *Methanobrevibacter smithii*, or a functional equivalent thereof.

28. The composition of any one of claims 1-20 and 22-27, further comprising FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, FBI00292, or a functional equivalent thereof.

29. The composition of claim 27 or 28, wherein each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

30. The composition of any one of claims 27-29, wherein each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

31. The composition of any one of claims 27-30, wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: SEQ ID NO: 3, SEQ ID NO: 7, SEQ ID NO: 9, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 23, SEQ ID NO: 24, SEQ ID NO: 27, SEQ ID NO: 39, SEQ ID NO: 41, SEQ ID NO: 47, SEQ ID NO: 49, SEQ ID NO: 50, SEQ ID NO: 51, SEQ ID NO: 54, SEQ ID NO: 56, SEQ ID NO: 59, SEQ ID NO: 60, SEQ ID NO: 66, SEQ ID NO: 78, SEQ ID NO: 81, SEQ ID NO: 82, SEQ ID NO: 85, SEQ ID NO: 86, SEQ ID NO: 96, SEQ ID NO: 101, SEQ ID NO: 105, SEQ ID NO: 112, SEQ ID NO: 114, SEQ ID NO: 117, SEQ ID NO: 118, SEQ ID NO: 119, SEQ ID NO: 121, SEQ ID NO: 122, SEQ ID NO: 124, SEQ ID NO: 126, SEQ ID NO: 127, SEQ ID NO: 133, SEQ ID NO: 134, SEQ ID NO: 135, SEQ ID NO: 138, SEQ ID NO: 140, SEQ ID NO: 142, or SEQ ID NO: 148.

32. The composition of any one of claims 1-20 and 22-31, further comprising a fourth composition comprising *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatemulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatemulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, *Bacteroides xylanisolvens*, or a functional equivalent thereof.

33. The composition of any one of claims 1-20 and 22-32, further comprising FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, FBI00271, or a functional equivalent thereof.

34. The composition of claim 32 or 33, wherein each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

35. The composition of any one of claims 32-34, wherein each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

36. The composition of any one of claims 32-35, wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: SEQ ID NO: 4, SEQ ID NO: 6, SEQ ID NO: 10, SEQ ID NO: 13, SEQ ID NO: 16, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 28, SEQ ID NO: 33, SEQ ID NO: 34, SEQ ID NO: 35, SEQ ID NO: 40, SEQ ID NO: 50, SEQ ID NO: 58, SEQ ID NO: 62, SEQ ID NO: 64, SEQ ID NO: 65, SEQ ID NO: 67, SEQ ID NO: 68, SEQ ID NO: 69, SEQ ID NO: 72, SEQ ID NO: 73, SEQ ID NO: 75, SEQ ID NO: 80, SEQ ID NO: 84, SEQ ID NO: 88, SEQ ID NO: 91, SEQ ID NO: 92, SEQ ID NO: 120, SEQ ID NO: 132, or SEQ ID NO: 139.

37. The composition of any one of claims 1-20 and 22-36, further comprising a fifth composition comprising *Alistipes putredinis*, *Dialister succinatiphilus*, *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*, *Bilophila wadsworthia*, *Holdemanella biformis*, *Parasutterella excrementihominis*, *Alistipes sp. FBI00180*, *Bacteroides coprocola*, *Alistipes sp. FBI00238*, *Alistipes putredinis*, *Eubacterium xylanophilum*, *Senegalimassilia anaerobia*, or a functional equivalent thereof.

38. The composition of any one of claims 1-20 and 22-37, further comprising FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, FBI00281, or a functional equivalent thereof.

39. The composition of claim 37 or 38, wherein each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID

NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144.

40. The composition of any one of claims 37-39, wherein each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144.

41. The composition of any one of claims 37-40, wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: SEQ ID NO: 15, SEQ ID NO: 30, SEQ ID NO: 43, SEQ ID NO: 44, SEQ ID NO: 87, SEQ ID NO: 90, SEQ ID NO: 93, SEQ ID NO: 95, SEQ ID NO: 97, SEQ ID NO: 98, SEQ ID NO: 99, SEQ ID NO: 125, SEQ ID NO: 137, SEQ ID NO: 141, or SEQ ID NO: 144

42. A microbial consortium comprising microbial strains set forth in Table 1, Table 2, Table 3, Table 4, Table 5, Table 6, Table 7, Table 8, Table 9, Table 10, Table 11, Table 12, Table 13, Table 14, Table 15, Table 16, Table 17, Table 18, Table 19, or a functional equivalent thereof.

43. A microbial consortium comprising microbial strains set forth in Table 22 or a functional equivalent thereof.

44. The microbial consortium of claim 42 or 43, wherein each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

45. The microbial consortium of any one of claims 42-44, wherein each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

46. The microbial consortium of any one of claims 42-45, wherein each strain comprises a 16s RNA nucleotide sequence that is identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

47. A composition comprising a microbial consortium of any one of claims 42-46.

48. The composition of any one of claims 1-41 and 47, which is a pharmaceutical composition.

49. The composition of any one of claims 1-41, 47, and 48, comprising from about 5×10^{10} to about 5×10^{11} viable cells.

50. The composition of any one of claims 1-41, 47, and 48, comprising from about 5×10^9 to about 5×10^{10} viable cells.

51. The composition of any one of claims 1-41, 47, and 48, comprising from about 5×10^{11} to about 5×10^{12} viable cells.

52. The composition of any one of claims 1-41, 47, and 48, comprising up to about 5×10^{12} viable cells.

53. The composition of any one of claims 1-41 and 47-52, wherein the composition comprises from about 10% to about 50% of oxalate-metabolizing microbial strains.

54. The composition of any one of claims 1-41 and 47-53, wherein the composition comprises from about 10% to about 50% of *O. formigenes* strains on a viable cell count basis.

55. The composition of any one of claims 1-41 and 47-54, wherein the composition comprises about 20% of *O. formigenes* strains on a viable cell count basis.

56. The composition of any one of claims 1-41 and 47-55, wherein the composition comprises about 30% of *O. formigenes* strains on a viable cell count basis.

57. The composition of any one of claims 1-41 and 47-56, wherein the composition comprises about 40% of *O. formigenes* strains on a viable cell count basis.

58. A method of manufacturing the composition of any one of claims 1-41 and 47-57 or the microbial consortium of any one of claims 42-46, the method comprising obtaining and blending:

a) a first composition comprising *Clostridium citroniae*, *Bacteroides salyersiae*, *Blautia obeum*, *Parabacteroides merdae*, *Parabacteroides distasonis*, *Anaerostipes hadrus*, *Lachnospiraceae sp. FBI00033*, *Eubacterium eligens*, *Bifidobacterium dentium*, *Blautia wexlerae*, *Fusicatenibacter saccharivorans*, *Bacteroides nordii*, *Dorea formicigenerans*, *Dorea longicatena*, *Bacteroides stercorisoris*, *Bifidobacterium longum*, *Bacteroides kribbi*, *Lachnospiraceae sp. FBI00071*, *Bacteroides thetaiotaomicron*, *Clostridium clostridioforme*, *Clostridium scindens*, *Roseburia hominis*, *Clostridium fessum*, *Coprococcus comes*, *Blautia faecis*, *Hungatella hathewayi*, *Bacteroides stercoris*, *Collinsella aerofaciens*, *Hungatella effluvii*, *Bifidobacterium adolescentis*, *Bifidobacterium catenulatum*, *Lactobacillus rogosae*, *Bacteroides faecis*, *Bacteroides fingoldii*, *Clostridiaceae sp. FBI00191*, *Ruminococcus faecis*, *Lachnoclostridium pacaense*, *Clostridium bolteae*, *Longicatena caecimuris*, *Eggerthella lenta*, *Blautia massiliensis*, *Bacteroides xylanisolvens*, *Bacteroides vulgatus*, *Megasphaera massiliensis*, *Butyricimonas faecihominis*, *Eisenbergiella tayi*,

Acidaminococcus intestini, *Emergencia timonensis*, *Bifidobacterium pseudocatenulatum*, *Eubacterium hallii*, *Anaerofustis stercorihominis*, *Eubacterium ventriosum*, *Blautia hydrogenotrophica*, and *Lachnospiraceae* sp. FBI00290, or a functional equivalent thereof;

b) a second composition comprising *Acutalibacter timonensis*, *Alistipes onderdonkii*, *Bacteroides uniformis*, *Eubacterium rectale*, *Alistipes timonensis*, *Bacteroides kribbi*, *Coprococcus eutactus*, *Bilophila wadsworthia*, *Bacteroides caccae*, *Alistipes shahii*, *Parasutterella excrementihominis*, *Paraprevotella clara*, *Sutterella wadsworthensis*, *Sutterella massiliensis*, *Porphyromonas asaccharolytica*, *Ruminococcus bromii*, *Monoglobus pectinilyticus*, *Ruminococcaceae* sp. FBI00097, *Gordonibacter pamelaee*, *Bacteroides uniformis*, *Gordonibacter pamelaee*, *Bacteroides fragilis*, *Phascolarctobacterium faecium*, *Monoglobus pectinilyticus*, *Clostridium aldenense*, *Ruthenibacterium lactatiformans*, *Bacteroides ovatus*, *Bifidobacterium bifidum*, *Anaerotruncus massiliensis*, *Clostridium aldenense*, *Sutterella wadsworthensis*, *Catabacter hongkongensis*, *Alistipes senegalensis*, *Ruminococcaceae* sp. FBI00233, *Alistipes shahii*, *Dielma fastidiosa*, *Eubacterium siraeum*, *Faecalibacterium prausnitzii*, *Turicibacter sanguinis*, *Eubacterium rectale*, *Bacteroides caccae*, *Methanobrevibacter smithii*, *Barnesiella intestinhominis*, *Alistipes onderdonkii*, and *Methanobrevibacter smithii*, or a functional equivalent thereof;

c) a third composition comprising *Bifidobacterium adolescentis*, *Bifidobacterium longum*, *Bifidobacterium pseudocatenulatum*, *Bacteroides thetaiotaomicron*, *Coprococcus comes*, *Fusicatenibacter saccharivorans*, *Eggerthella lenta*, *Eubacterium eligens*, *Bacteroides xylanisolvens*, *Lactobacillus rogosae*, *Clostridium citroniae*, *Collinsella aerofaciens*, *Blautia obeum*, *Eggerthella lenta*, *Blautia wexlerae*, *Lachnoclostridium pacaense*, *Bacteroides vulgatus*, *Parabacteroides merdae*, *Dorea formicigenerans*, *Ruminococcus faecis*, *Roseburia hominis*, *Anaerostipes hadrus*, *Bifidobacterium adolescentis*, *Bifidobacterium pseudocatenulatum*, *Clostridium bolteae*, *Eisenbergiella tayi*, *Dorea longicatena*, *Eggerthella lenta*, *Bacteroides stercoris*, *Hungatella hathewayi*, and *Bacteroides xylanisolvens*, or a functional equivalent thereof;

d) a fourth composition comprising *Alistipes putredinis*, *Dialister succinatiphilus*, *Akkermansia muciniphila*, *Ruminococcus bromii*, *Dialister invisus*, *Bacteroides massiliensis*, *Bilophila wadsworthia*, *Holdemanella biformis*, *Parasutterella excrementihominis*, *Alistipes* sp. FBI00180, *Bacteroides coprocola*, *Alistipes* sp. FBI00238, *Alistipes putredinis*, *Eubacterium xylanophilum*, and *Senegalimassilia anaerobia*, or a functional equivalent thereof;

e) a fifth composition comprising a first *O. formigenes* strain;

f) a sixth composition comprising a second *O. formigenes* strain; and/or

g) a seventh composition comprising a third *O. formigenes* strain.

59. A method of manufacturing the composition of any one of claims 1-41 and 47-57 or the microbial consortium of any one of claims 42-46, the method comprising obtaining and blending:

a) a first composition comprising FBI00001, FBI00002, FBI00010, FBI00013, FBI00029, FBI00032, FBI00033, FBI00034, FBI00043, FBI00044, FBI00048, FBI00050, FBI00051, FBI00057, FBI00059, FBI00060, FBI00070, FBI00071, FBI00076, FBI00079, FBI00087, FBI00093, FBI00102, FBI00109, FBI00117, FBI00120, FBI00125, FBI00127, FBI00128, FBI00145, FBI00162, FBI00174, FBI00184, FBI00190, FBI00191, FBI00194, FBI00198, FBI00199, FBI00200, FBI00201, FBI00205, FBI00206, FBI00211, FBI00220, FBI00221, FBI00236, FBI00245, FBI00248, FBI00251, FBI00254, FBI00267, FBI00278, FBI00288, and FBI00290, or a functional equivalent thereof;

b) a second composition comprising FBI00004, FBI00012, FBI00015, FBI00018, FBI00019, FBI00021, FBI00038, FBI00040, FBI00046, FBI00061, FBI00066, FBI00075, FBI00077, FBI00080, FBI00081, FBI00085, FBI00092, FBI00097, FBI00099, FBI00112, FBI00132, FBI00137, FBI00140, FBI00149, FBI00151, FBI00176, FBI00189, FBI00197, FBI00208, FBI00212, FBI00224, FBI00226, FBI00229, FBI00233, FBI00235, FBI00237, FBI00243, FBI00244, FBI00258, FBI00260, FBI00263, FBI00270, FBI00273, FBI00277, and FBI00292, or a functional equivalent thereof;

c) a third composition comprising FBI00009, FBI00011, FBI00016, FBI00020, FBI00025, FBI00027, FBI00030, FBI00047, FBI00052, FBI00053, FBI00056, FBI00062, FBI00078, FBI00096, FBI00104, FBI00110, FBI00111, FBI00113, FBI00115, FBI00116, FBI00123, FBI00124, FBI00126, FBI00135, FBI00147, FBI00159, FBI00167, FBI00170, FBI00232, FBI00255, and FBI00271, or a functional equivalent thereof;

d) a fourth composition comprising FBI00022, FBI00049, FBI00068, FBI00069, FBI00152, FBI00165, FBI00171, FBI00175, FBI00177, FBI00180, FBI00182, FBI00238, FBI00269, FBI00274, and FBI00281, or a functional equivalent thereof;

e) a fifth composition comprising FBI00067 or a functional equivalent thereof;

f) a sixth composition comprising FBI00133 or a functional equivalent thereof; and/or

g) a seventh composition comprising FBI00289 or a functional equivalent thereof.

60. The method of claim 58-59, wherein each strain comprises a 16s RNA nucleotide sequence that is (a) at least about 80% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, (b) at least about 90% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148, or (c) at least about 96% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

61. The method of any one of claims 58-60, wherein each strain comprises a 16s RNA nucleotide sequence that is at least about 97% identical or 98.5% identical to the nucleotide sequence set forth in SEQ ID NOs: 1-148.

62. The method of any one of claims 58-61, wherein each strain comprises a 16s RNA nucleotide sequence identical to the nucleotide sequence set forth in SEQ ID NO: 1-148.

63. The method of any one of claims 58-62, wherein the fourth composition is obtained by growing microbes in presence of threonine.

64. The method of any one of claims 58-63, wherein each composition comprises a lyoprotectant.

65. The method of claim 58-64, wherein each composition comprises maltodextrin, inulin, or a combination thereof.

66. The method of claim 65, wherein the maltodextrin is at a concentration of about 8%.

67. The method of claim 65 or 66, wherein the inulin is at a concentration of about 0.5%.

68. The method of any one of claims 58-67, wherein each composition is separately lyophilized.

69. The method of any one of claims 58-68, wherein the functional equivalent is based on the characteristics set forth in Table 24.

70. The method of any one of claims 58-69, wherein the functional equivalent is based on the characteristics set forth in Table 34.

71. The method of any one of claims 58-70, wherein the functional equivalent is based on the characteristics set forth in Table 35.

72. The method of any one of claims 58-71, wherein the functional equivalent is based on the characteristics set forth in Table 36.

73. The method of any one of claims 58-72, wherein the functional equivalent is based on the characteristics set forth in Tables 34-36.

74. The method of any one of claims 58-73 comprising obtaining and blending microbes comprising a gene regulating oxalate degradation, oxalate resistance, formate metabolism, metabolism of macronutrients, production of microbial metabolites, cross-feeding activity, and/or mucin degradation.

75. The method of any one of claims 68-74 comprising obtaining and blending microbes that are known to protect against diseases and/or that are prevalent in healthy human gut.

76. The method of any one of claims 68-75 comprising obtaining and blending microbes that utilize carbon sources set forth in Table 35.

77. The method of claim 76, wherein each strain can optionally utilize a subset of the carbon sources set forth in Table 35.

78. The method of any one of claims 58-77, wherein each composition is prepared using inoculation density adjustment.

79. The method of any one of claims 58-78, wherein each composition is cultured or has been cultured in presence of gas overlay.

80. The method of any one of claims 58-79, wherein each composition is cultured or has been cultured in absence of gas sparging.

81. A composition prepared by the method of any of claims 58-80.

82. A method of treating hyperoxaluria in a subject in need thereof comprising administering an effective amount of the composition of any one of claims 1-41, 47-57, or 81 or the microbial consortium of any one of claims 42-46.

83. A method of reducing the risk of developing hyperoxaluria in a subject in need thereof comprising administering an effective amount of the composition of any one of claims 1-41, 47-57, or 81 or the microbial consortium of any one of claims 42-46.

84. A method of reducing urinary oxalate in a subject in need thereof comprising administering an effective amount of the composition of any one of claims 1-41, 47-57, or 81 or the microbial consortium of any one of claims 42-46.

85. The method of claim 82 or 83, wherein the hyperoxaluria is a primary hyperoxaluria, a secondary hyperoxaluria, or an enteric hyperoxaluria.

86. The method of claim 85, wherein the secondary hyperoxaluria is associated with bowel resection surgery.

87. The method of any one of claims 82, 83, or 85, wherein the hyperoxaluria is enteric hyperoxaluria.

88. The method of any one of claims 82-87, further comprising administering at least one antibacterial agent, antiviral agent, antifungal agent, anti-inflammatory agent, immunosuppressive agent, prebiotic, or a combination thereof.

89. The method of any one of claims 82-88, further comprising administering NOV-001, SYN8802, OX-1, Lumasiran, Nedosiran, BBP-711, CNK-336, PBGENE-PH1, or a combination thereof.

90. The method of any one of claims 82-89, further comprising administering a low oxalate diet, a high hydration diet, calcium supplements, or a combination thereof.

91. The method of any one of claims 82-90, wherein the composition or the microbial consortium is administered orally.

92. A method of treating hyperoxaluria in a subject in need thereof comprising administering a first dose of the composition of any one of claims 1-41, 47-57, or 81 or the microbial consortium of any one of claims 42-46.

93. A method of reducing the risk of developing hyperoxaluria in a subject in need thereof comprising administering a first dose of the composition of any one of claims 1-41, 47-57, or 81 or the microbial consortium of any one of claims 42-46.

94. A method of reducing urinary oxalate in a subject in need thereof comprising administering a first dose of the composition of any one of claims 1-41, 47-57, or 81 or the microbial consortium of any one of claims 42-46.

95. The method of claim 92 or 93, wherein the hyperoxaluria is a primary hyperoxaluria, a secondary hyperoxaluria, or an enteric hyperoxaluria.

96. The method of claim 95, wherein the secondary hyperoxaluria is associated with bowel resection surgery.

97. The method of any one of claims 92, 93, or 95, wherein the hyperoxaluria is enteric hyperoxaluria.

98. The method of any one of claims 92-97, further comprising administering an antibiotic treatment.

99. The method of claim 98, wherein the antibiotic treatment is administered for about 2 days, about 3 days, about 4 days, about 5 days, about 6 days, or about 7 days.

100. The method of claim 98 or 99, wherein the antibiotic is metronidazole, clarithromycin, or a combination thereof.

101. The method of any one of claims 98-100, wherein the antibiotic treatment is completed 1 day before administering the first dose.

102. The method of any one of claims 98-100, wherein the antibiotic treatment is completed 2 days before administering the first dose.

103. The method of any one of claims 92-102, further comprising administering a bowel preparation treatment.

104. The method of claim 103, wherein the bowel preparation treatment is administered to the subject after the antibiotic treatment.

105. The method of claim 103 or 104, wherein the bowel preparation treatment is administered before the first dose.

106. The method of any one of claims 92-105, wherein the first dose comprises an effective amount of the composition or the microbial consortium.

107. The method of any one of claims 92-106, wherein the first dose comprises about 10^{12} viable cells.
108. The method of any one of claims 92-107, wherein the first dose is administered for about 1 day.
109. The method of any one of claims 92-108, wherein the first dose is administered for about 2 days.
110. The method of any one of claims 92-109 further comprising administering a second dose of the composition of any one of claims 1-41, 47-57, or 81 or the microbial consortium of any one of claims 42-46.
111. The method of claim 110, wherein the second dose comprises an effective amount of the composition or the microbial consortium.
112. The method of claim 110 or 111, wherein the second dose comprises about 10^{11} viable cells.
113. The method of any one of claims 110-112, wherein the second dose is administered up to about 8 days.
114. The method of any one of claims 110-113, wherein the second dose is administered up to about 10 days.
115. The method of claims 92-114, wherein the first dose is administered orally.
116. The method of claims 92-115, wherein the second dose is administered orally.
117. A kit comprising the composition of any one of claims 1-41, 47-57, or 81 or the microbial consortium of any one of claims 42-46.
118. The kit of claim 117, wherein the kit comprises a container comprising a desiccant.
119. The kit of claim 118, wherein the container comprises anaerobic conditions.
120. The kit of claim 119, wherein the container is a blister.
121. The kit of claim 120, further comprising written instructions for administering the composition or microbial consortium.
122. A method of culturing a microbial strain from the *Akkermansia* genus comprising contacting the strain with N-Acetylgalactosamine (GalNAc).
123. The method of claim 122, wherein the strain is *Akkermansia muciniphila*.
124. A microbial consortium comprising the functional properties set forth in Table 23.
125. A microbial consortium comprising the functional properties set forth in Table 24.
126. A microbial consortium comprising the functional properties set forth in Table 34.
127. A microbial consortium comprising the functional properties set forth in Table 35.
128. A microbial consortium comprising the functional properties set forth in Table 36.

129. A microbial consortia comprising FB-001 or a functional equivalent thereof.
130. Any method or composition described herein.