

Novel Co-cultured Microbial Consortia

Cross Reference to Related Applications

[0001] This application claims the benefit of priority to Australian Provisional Patent
5 Application No. 2023902607, filed August 16, 2023, the entire content of which is incorporated
by reference herein.

Incorporation by Reference of Material in Sequence Listing File

[0002] This application incorporates by reference the materials contained in the
10 Sequence Listing XML file being submitted concurrently herewith: File name: SEQ
LIST_WIPO_303386.xml, created on 07 August 2024 and is 433 bytes in size.

Field

[0003] Embodiments of the present invention relates to compositions comprising a
15 microbial consortium for treating or preventing medical disorders and pathologies through
microbiome modulation, including medical disorders associated with a dysbiosis or a loss of
gut microbial function. Embodiments of the present invention also relate to methods of treating
medical disorders and pathologies by administering the composition to a patient in need
thereof.

20

Background

[0004] The following discussion of the background art is intended to facilitate an
understanding of the present disclosure only. The discussion is not an acknowledgement or
admission that any of the material referred to is or was part of the common general knowledge
25 as at the priority date of the application.

[0005] The human intestinal microbiota consists of trillions of microorganisms including
at least 100 prevalent and at least 1000 less common bacterial species, comprising over 100-
fold more genes than those present in the human genome. The intestinal microbiota is
composed predominantly of bacteria, yet also contains fungi, archaea, protozoa, and viruses.
30 The microbiota performs vital functions essential to health maintenance, including food
processing, digestion of complex indigestible polysaccharides and synthesis of vitamins, and
it secretes bioactive metabolites with diverse functions, ranging from inhibition of pathogens,
metabolism of toxic compounds, to modulation of host metabolism.

[0006] There is a need in the art for effective treatments of treating medical disorders and
35 pathologies through microbiome modulation, particularly for disorders associated with a
dysbiosis or a loss of gut microbial function. It is an objective of the invention to overcome one
or more problems foreshadowed by the prior art.

Summary of the Invention

[0007] In several embodiments, a formulation comprising multiple core community microbial strains as well as multiple keystone microbial strains are provided to, for example, restore gut microbiome ecology. Advantageously in several embodiments, the core community and keystone strains are co-cultured together to provide a synergistic consortium with diverse species. When administered to a subject, according to one embodiment, the consortium is capable of providing a beneficially stable microbial ecosystem because the various strains have already been co-cultured together prior to administration.

[0008] In some embodiments, a diverse range of gene families, as described herein, provides the ability to deliver therapies that have broad functional capability as well as highly targeted disease specific function. Oral formulations are provided in several embodiments, which in turn can eliminate the reliance on stool donors and enables production of microbial therapies at scale, to large markets. The formulations are used in some embodiments to treat microbiome dysbiosis. For example, the formulations are used in some embodiments to treat ulcerative colitis, inflammatory bowel disease, Crohn's disease, checkpoint inhibitor colitis, as well as other gastrointestinal diseases and symptoms. The formulations are used in some embodiments to treat liver disorders, including, for example, primary sclerosing cholangitis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, or hepatic encephalopathy. The formulations are used in some embodiments to treat metabolic disorders, including, for example, obesity, insulin resistance, or type 2 diabetes. The formulations are used in some embodiments to treat oncology indications, including, for example, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer, breast cancer, lung cancer, testicular cancer, or sarcoma. The formulations are used in some embodiments to treat cardiovascular disorders, including, for example, dyslipidaemia, atherosclerotic heart disease, or hypertension. The formulations are used in some embodiments to treat immunological diseases, including, for example, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis, psoriasis, systemic lupus erythematosus, or Sjogren's disease. The formulations are used in some embodiments to treat allergic and atopic disorders, including, for example, food allergy, anaphylaxis, atopic dermatitis, or atopic rhinitis or sinusitis. The formulations are used in some embodiments to treat infectious diseases, including, for example, clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory infections, or sepsis. Enhancement of the immune system is provided by several formulations. In some embodiments, the formulations reduce adhesion and/or colonization of pathogenic microbes (such as pathogenic or undesired bacteria, viruses, and/or yeast and other fungi). In some embodiments, restoration of a health gut ecology treats diseases and symptoms that are not considered traditional gastrointestinal

diseases. For example, neurological disorders, including for example, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, or schizophrenia, and other conditions may be treated by restoring a healthier microbiome. In some embodiments, the formulations are formulated to treat one or more of the diseases or disorders described herein, including any combination thereof. In some embodiments, the formulations are used in combination with a therapy to treat any of the diseases or disorders described herein.

[0009] In some embodiments, the formulation comprises or consists essentially of a consortium of core and keystone bacterial strains that replicates at least 90% of the gene families that are found in a healthy microbiome. In other embodiments, replication of 50%-90% of the gene families is provided.

[0010] In several embodiments, a formulation comprises or consists essentially of 5-26 core community microbial strains selected from Table 14 and 5-22 or more keystone microbial strains selected from Table 13. The formulations are co-cultured, lyophilized and provided as an oral formulation (e.g., a capsule, tablet, or powder) in several embodiments. One or more of enteric coatings, pharmaceutically acceptable excipients (e.g., inulin and/or maltodextrin) and fibres are also provided (which may be natural or non-naturally occurring, e.g., partially or fully modified, synthetic, etc.). Agents to balance pH may also be included. For example, the formulation in one embodiment comprises or consists essentially of any 10 or more of *Bifidobacterium longum*, *Faecalibacterium prausnitzii*, *Dysosmobacter welbionis*, *Enterocloster bolteae*, *Alistipes megaguti*, *Parabacteroides goldsteinii*, *Flavonifractor plautii*, *Alistipes communis*, *Ruthenibacterium lactatiformans*, *Vescimonas coprocola*, *Collinsella aerofaciens*, *Coprococcus comes*, *Ruminococcus gnavus*, *Ruminococcus bicirculans*, *Bacteroides caecimuris*, *Coprococcus eutactus*, *Butyricimonas virosa*, *Phocaeicola salanitronis*, *Alistipes dispar*, *Clostridium scindens*, *Parabacteroides merdae*, *Bacteroides salyersiae*, *Pusillimonas faecalis*, *Solibaculum mannosilyticum*, *Akkermansia muciniphila*, or *Christensenella minuta* in combination with any 10 or more of *Bifidobacterium longum*, *Faecalibacterium prausnitzii*, *Bifidobacterium bifidum*, *Alistipes putredinis*, *Alistipes shahii*, *Bacteroides intestinalis*, *Bacteroides stercoris*, *Bifidobacterium adolescentis*, *Coprococcus catus*, *Methonobrevibacter smithii*, *Parabacteroides johnsonii*, *Phocaeicola coprocola*, *Roseburia inulinivorans*, *Ruminococcus bromii*, *Ruminococcus torques*, *Subdoligranulum variabile*, *Bacteroides caccae*, *Bacteroides coprocola*, *Bacteroides eggerthii*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, or *Parabacteroides distasonis*, and one or more of an enteric coating, inulin, or maltodextrin. In some embodiments, 5-10, 10-15, 15-26 core community strains (e.g., from Table 14) and 5-10, 10-15, 15-22 keystone strains (e.g., from Table 13) are co-cultured together and/or in the formulation for administration to a subject. In some embodiments, 90, 92, 95% or all of the core community strains and all of the keystone strains are co-cultured together and/or in the formulation for administration to a subject.

Certain strains may be valuable in the co-culture to support the community as a whole but may not be present in the formulation for administration to a subject. In one embodiment, about 5-20% of strains that are in the co-culture are not significantly present in the formulation for administration to a subject.

5 [0011] In one embodiment, the formulation comprises or consists essentially of (i) 85-90%, 90%-95%, or all of the core community microbial strains in Table 14 and/or (ii) 85-90%, 90%-95% or all of the keystone microbial strains selected from Table 13. In several
10 embodiments, the formulation comprises or consists essentially of 20-26 core community microbial strains selected from Table 14, and keystone strains from Table 13 at a core:keystone strain ratio at 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1. In some
15 embodiments, the formulation comprises or consists essentially of from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage of total number or mass microorganisms in the formulation. In several embodiments, the core and keystone strains have been co-cultured together. With respect to the numbers, amounts
and ratios disclosed herein, the formulation may be the formulation administered to a subject or in the co-culture.

[0012] In some embodiments, the formulations include a microbial consortium having bacteria selected from the phyla Actinomycetota, Bacillota, Bacteroidota, Campylobacterota, Pseudomonadota, Thermodesulfobiota, and Verrucomicrobiota. In some embodiments, the
20 formulations include strains from Actinomycetota, Bacillota, Bacteroidota, and Verrucomicrobiota. In several embodiments, the formulations include strains from no more than two phyla of Actinomycetota, Bacillota, Bacteroidota, and Pseudomonadota. In several
embodiments, the formulation (whether co-cultured or for administration to a subject) does not include bacteria from Pseudomonadota and/or Campylobacterota. In some embodiments,
25 Pseudomonadota or Campylobacterota are completely or significantly excluded or removed from the formulations.

[0013] In some embodiments, the formulations described herein are used with other therapies. For example, the formulations may be used to reduce side effects of other
30 pharmaceuticals (including e.g., biologics) by, for example, reducing the dose or course needed for such pharmaceutical, reducing an inflammatory response, reducing nausea or other undesired effect of such pharmaceutical post administration. The formulations may also
be used to enhance the beneficial effects of other pharmaceuticals by, for example, increasing absorption and/or availability of such pharmaceutical post administration. In some
embodiments, synergistic effects are achieved using the formulations described herein and
35 other therapies such as pharmaceuticals.

[0014] In some embodiments, the formulations are used to restore a healthy microbiome after antibiotic therapy and/or cleanses and may be provided before, together with, or after

antibiotic therapy and/or cleanses. In some embodiments, when treating a specific disease for example, antibiotics and/or cleanses may optionally be administered prior to administration of the formulation to assist in providing a “cleaner slate” for the consortium in the formulation. The cleanse may be associated with medical procedures such as colonoscopies.

5 [0015] In several embodiments, a composition comprising multiple core community microbial strains as well as multiple keystone microbial strains are provided to, for example, restore gut microbiome ecology. Advantageously in several embodiments, the core community and keystone strains are co-cultured together to provide a synergistic consortium with diverse species. When administered to a subject, according to one embodiment, the
10 consortium is capable of providing a beneficially stable microbial ecosystem because the various strains have already been co-cultured together prior to administration.

[0016] In some embodiments, a diverse range of gene families, as described herein, provides the ability to deliver therapies that have broad functional capability as well as highly targeted disease specific function. Oral compositions are provided in several embodiments,
15 which in turn can eliminate the reliance on stool donors and enables production of microbial therapies at scale, to large markets. The compositions are used in some embodiments to treat mycobiome dysbiosis. For example, the compositions are used in some embodiments to treat ulcerative colitis, inflammatory bowel disease, Crohn’s disease, checkpoint inhibitor colitis, as well as other gastrointestinal diseases and symptoms. The compositions are used
20 in some embodiments to treat liver disorders, including, for example, primary sclerosing cholangitis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, or hepatic encephalopathy. The compositions are used in some embodiments to treat metabolic disorders, including, for example, obesity, insulin resistance, or type 2 diabetes. The compositions are used in some embodiments to treat oncology indications,
25 including, for example, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer, breast cancer, lung cancer, testicular cancer, or sarcoma. The compositions are used in some embodiments to treat cardiovascular disorders, including, for example, dyslipidaemia, atherosclerotic heart disease, or hypertension. The compositions are used in some embodiments to treat immunological
30 diseases, including, for example, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis, psoriasis, systemic lupus erythematosus, or Sjogren’s disease. The compositions are used in some embodiments to treat allergic and atopic disorders, including, for example, food allergy, anaphylaxis, atopic dermatitis, or atopic rhinitis or sinusitis. The compositions are used in some embodiments to treat infectious diseases, including, for example, clostridioides difficile
35 infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory infections, or sepsis. Enhancement of the immune system is provided by several compositions. In some embodiments, the compositions reduce

adhesion and/or colonization of pathogenic microbes (such as pathogenic or undesired bacteria, viruses, and/or yeast and other fungi). In some embodiments, restoration of a health gut ecology treats diseases and symptoms that are not considered traditional gastrointestinal diseases. For example, neurological disorders, including for example, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, or schizophrenia, and other conditions may be treated by restoring a healthier microbiome. In some embodiments, the compositions are formulated to treat one or more of the diseases or disorders described herein, including any combination thereof. In some embodiments, the compositions are used in combination with a therapy to treat any of the diseases or disorders described herein.

[0017] In some embodiments, the composition comprises or consists essentially of a consortium of core and keystone bacterial strains that replicates at least 90% of the gene families that are found in a healthy microbiome. In other embodiments, replication of 50%-90% of the gene families is provided.

[0018] In several embodiments, a composition comprises or consists essentially of 5-26 core community microbial strains selected from Table 14 and 5-22 or more keystone microbial strains selected from Table 13. The compositions are co-cultured, lyophilized and provided as an oral composition (e.g., a capsule, tablet, or powder) in several embodiments. One or more of enteric coatings, pharmaceutically acceptable excipients (e.g., inulin and/or maltodextrin) and fibres are also provided (which may be natural or non-naturally occurring, e.g., partially or fully modified, synthetic, etc.). Agents to balance pH may also be included. For example, the composition in one embodiment comprises or consists essentially of any 10 or more of *Bifidobacterium longum*, *Faecalibacterium prausnitzii*, *Dysosmobacter welbionis*, *Enterocloster boltea*, *Alistipes megaguti*, *Parabacteroides goldsteinii*, *Flavonifractor plautii*, *Alistipes communis*, *Ruthenibacterium lactatiformans*, *Vescimonas coprocola*, *Collinsella aerofaciens*, *Coprococcus comes*, *Ruminococcus gnavus*, *Ruminococcus bicirculans*, *Bacteroides caecimuris*, *Coprococcus eutactus*, *Butyricimonas virosa*, *Phocaeicola salanitronis*, *Alistipes dispar*, *Clostridium scindens*, *Parabacteroides merdae*, *Bacteroides salyersiae*, *Pusillimonas faecalis*, *Solibaculum mannosilyticum*, *Akkermansia muciniphila*, or *Christensenella minuta* in combination with any 10 or more of *Bifidobacterium longum*, *Faecalibacterium prausnitzii*, *Bifidobacterium bifidum*, *Alistipes putredinis*, *Alistipes shahii*, *Bacteroides intestinalis*, *Bacteroides stercoris*, *Bifidobacterium adolescentis*, *Coprococcus catus*, *Methonobrevibacter smithii*, *Parabacteroides johnsonii*, *Phocaeicola coprocola*, *Roseburia inulinivorans*, *Ruminococcus bromii*, *Ruminococcus torques*, *Subdoligranulum variabile*, *Bacteroides caccae*, *Bacteroides coprocola*, *Bacteroides eggerthii*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, or *Parabacteroides distasonis*, and one or more of an enteric coating, inulin, or maltodextrin. In some embodiments, 5-10, 10-15, 15-26 core community strains (e.g., from Table 14) and 5-10, 10-15, 15-22 keystone strains (e.g., from

Table 13) are co-cultured together and/or in the composition for administration to a subject. In some embodiments, 90, 92, 95% or all of the core community strains and all of the keystone strains are co-cultured together and/or in the composition for administration to a subject. Certain strains may be valuable in the co-culture to support the community as a whole but may not be present in the composition for administration to a subject. In one embodiment, about 5-20% of strains that are in the co-culture are not significantly present in the composition for administration to a subject.

[0019] In one embodiment, the composition comprises or consists essentially of (i) 85-90%, 90%-95%, or all of the core community microbial strains in Table 14 and/or (ii) 85-90%, 90%-95% or all of the keystone microbial strains selected from Table 13. In several embodiments, the composition comprises or consists essentially of 20-26 core community microbial strains selected from Table 14, and keystone strains from Table 13 at a core:keystone strain ratio at 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1. In some embodiments, the composition comprises or consists essentially of from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage of total number or mass microorganisms in the composition. In several embodiments, the core and keystone strains have been co-cultured together. With respect to the numbers, amounts and ratios disclosed herein, the composition may be the composition administered to a subject or in the co-culture.

[0020] In some embodiments, the compositions include a microbial consortium having bacteria selected from the phyla Actinomycetota, Bacillota, Bacteroidota, Campylobacterota, Pseudomonadota, Thermodesulfobiota, and Verrucomicrobiota. In some embodiments, the compositions include strains from Actinomycetota, Bacillota, Bacteroidota, and Verrucomicrobiota. In several embodiments, the compositions include strains from no more than two phyla of Actinomycetota, Bacillota, Bacteroidota, and Pseudomonadota. In several embodiments, the composition (whether co-cultured or for administration to a subject) does not include bacteria from Pseudomonadota and/or Campylobacterota. In some embodiments, Pseudomonadota or Campylobacterota are completely or significantly excluded or removed from the compositions.

[0021] In some embodiments, the compositions described herein are used with other therapies. For example, the compositions may be used to reduce side effects of other pharmaceuticals (including e.g., biologics) by, for example, reducing the dose or course needed for such pharmaceutical, reducing an inflammatory response, reducing nausea or other undesired effect of such pharmaceutical post administration. The compositions may also be used to enhance the beneficial effects of other pharmaceuticals by, for example, increasing absorption and/or availability of such pharmaceutical post administration. In some

embodiments, synergistic effects are achieved using the compositions described herein and other therapies such as pharmaceuticals.

[0022] In some embodiments, the compositions are used to restore a healthy microbiome after antibiotic therapy and/or cleanses and may be provided before, together with, or after
5 antibiotic therapy and/or cleanses. In some embodiments, when treating a specific disease for example, antibiotics and/or cleanses may optionally be administered prior to administration of the composition to assist in providing a “cleaner slate” for the consortium in the composition. The cleanse may be associated with medical procedures such as colonoscopies.

[0023] In a further embodiment, the invention is a composition comprising a microbial
10 consortium comprising at least one microbe, wherein the at least one microbe is selected from the group consisting of: bacteria and archaea; and wherein the at least one microbe is a member of a phylum, selected from the group consisting of: any one of the phyla listed in Table 1; any one of the phyla listed in Table 2; any one of the phyla listed in Table 3; and any combination, subgroup or multitude thereof.

[0024] In some embodiments, the microbial consortium comprises a plurality of microbes.

[0025] In some embodiments, the microbe is a member of a cladistic group selected from the groups consisting of: the cladistic groups presented in Figure 10 or any combination, subgroup or multitude thereof.

[0026] In some embodiments, the microbe is a member of a family selected from the
20 group consisting of: any one of the families listed in Table 4; any one of the families listed in Table 5; any one of the families listed in Table 6; and any combination, subgroup or multitude thereof.

[0027] In some embodiments, the microbe is a member of a genus selected from the group consisting of: any one of the genera listed in Table 7; any one of the genera listed in
25 Table 8; and any combination, subgroup or multitude thereof.

[0028] In some embodiments, the microbe is a member of a species selected from the group consisting of: any one of the species listed in Table 9; any one of the species listed in Table 10; any one of the species listed in Table 11; any one of the species listed in Table 12; any one of the species listed in Table 13; any one of the species listed in Table 14; any one
30 of the species listed in Table 15; and any one of the species listed in Table 16; and any combination, subgroup or multitude thereof.

[0029] In some embodiments, the microbe is a member of a species selected from the group consisting of: any one of the microbial keystones listed in Table 13; and any combination, subgroup or multitude thereof.

[0030] In some embodiments, the microbe is a member of a species selected from the group consisting of: any one of the core community species listed in Table 14; and any combination, subgroup or multitude thereof.

[0031] In some embodiments, the microbe is a member of a species selected from the group consisting of: any one of the species listed in Table 15; and any combination, subgroup or multitude thereof.

5 [0032] In some embodiments, the microbe is a member of a species selected from the group consisting of: any one of the species listed in Table 16; and any combination, subgroup or multitude thereof.

[0033] In some embodiments, the microbe is selected from the group consisting of: any one of the microbes presented and represented in Figure 6; Figure 7; Figure 9; and any combination, subgroup or multitude thereof.

10 [0034] In some embodiments, the microbial consortium is selected from the group consisting of: the consortium presented in Figure 6; the consortium presented in Figure 7; the consortium presented in Figure 9; and any combination, subgroup or multitude thereof.

[0035] In some embodiments, the microbe has a nucleotide sequence selected from the group consisting of: any one of the Sanger Sequencing 16S ribosomal RNA (rRNA) genes as
15 presented in Figures 6 or 7; and any combination, subgroup or multitude thereof.

[0036] In some embodiments, the microbe comprises a 16S ribosomal RNA (rRNA) gene having a nucleotide sequence selected from the group consisting of: any one of the V3-V4 16S sequences for the 143 isolates presented in Figure 6 (SEQ ID NOs 1 to 143); any one of the full length 16S sequences for the 143 isolates presented in Figure 7 (SEQ ID NOs 144 to
20 286); and any combination, subgroup or multitude thereof.

[0037] In some embodiments, the sequence identity is selected from the any one of the groups consisting of: at least 99.9%; at least 99.5%; at least 99%; at least 98.5%; at least 98%; at least 97.5%; at least 97%; at least 96.5%; at least 96%; at least 95.5%; at least 95%; at least 94.5%; at least 94%; at least 93.5%; at least 93%; at least 92.5%; at least 92%; at
25 least 91.5%; at least 91%; at least 90.5% and at least 90%.

[0038] In some embodiments, the microbial consortium comprises any one of the communities presented in: Table 9; Table 10; Table 11; Table 12; Table 13; Table 14; Table 15; Table 16.

[0039] In some embodiments, the microbial consortium comprises at least the keystones
30 presented in Table 13.

[0040] In some embodiments, the microbial consortium comprises at least the minimum core species presented in Table 14.

[0041] In some embodiments, the microbial consortium is the consortium of 143 members presented in Figure 9 (also known as BB265).

35 [0042] In some embodiments, the microbial consortium is the consortium of 127 members presented in Figure 22.

[0043] In some embodiments, the microbial consortium comprises a supportive community of microbial species, strains or isolates.

[0044] In some embodiments, the composition comprises a plurality of core community microbial species, wherein said core community microbial species comprise members of at least the following genera selected from the group consisting of: *Dysosmobacter*; *Enterocloster*; *Ruthenibacterium*; *Vescimonas*; *Phocaeicola*; *Pusillimonas*; *Solibaculum*; and *Christensenella*, a plurality of keystone microbial species, wherein said keystone microbial species comprise members of at least the genus *Phocaeicola*; and any combination, subgroup or multitude thereof.

[0045] In some embodiments, the composition comprises a plurality of core community microbial species, wherein said core community microbial species comprise at least one of the following species selected from the group consisting of: *Alistipes dispar*; *Bacteroides salyersiae*; *Bifidobacterium bifidum*; *Christensenella minuta*; *Coprococcus catus*; *Coprococcus sp000154245*; *Dysosmobacter faecalis*; *Faecalibacterium duncaniae*; *Gemmiger formicilis*; *Parabacteroides goldsteinii*; *Ruminococcus bicirculans*; *Ruthenibacterium lactatiformans*; *Solibaculum mannosilyticum*; and *Vescimonas coprocola*; and any combination, subgroup or multitude thereof.

[0046] In some embodiments, the plurality of core community microbial species comprises at least one of the following species selected from the group consisting of: *Dysosmobacter welbionis*; *Enterocloster bolteae*; *Ruthenibacterium lactatiformans*; *Vescimonas coprocola*; *Phocaeicola salanitronis*; *Pusillimonas faecalis*; *Solibaculum mannosilyticum*; *Christensenella minuta*; *Alistipes magaguti*; *Parabacteroides goldsteinii*; *Alistipes communis*; *Ruminococcus bicirculans*; *Bacteroides caecimuris*; *Alistipes dispar*, and *Bacteroides salyersiae*; and wherein the plurality of keystone microbial species comprises at least one of the following species: *Phocaeicola coprocola*; *Bifidobacterium bifidum*; and *Coprococcus catus*; and any combination, subgroup or multitude thereof.

[0047] In some embodiments, the plurality of core community microbial species comprises at least the following species: *Dysosmobacter welbionis*; *Enterocloster bolteae*; *Ruthenibacterium lactatiformans*; *Vescimonas coprocola*; *Phocaeicola salanitronis*; *Pusillimonas faecalis*; *Solibaculum mannosilyticum*; *Christensenella minuta*; *Alistipes magaguti*; *Parabacteroides goldsteinii*; *Alistipes communis*; *Ruminococcus bicirculans*; *Bacteroides caecimuris*; *Alistipes dispar*, and *Bacteroides salyersiae*; and any combination, subgroup or multitude thereof.

[0048] In some embodiments, the plurality of keystone microbial species comprises: *Phocaeicola coprocola*; *Bifidobacterium bifidum*; and *Coprococcus catus*; and any combination, subgroup or multitude thereof.

[0049] In some embodiments, the composition comprises a plurality of core community microbial species, wherein said core community microbial species is selected from the group consisting of: *Alistipes dispar*; *Bacteroides salyersiae*; *Bifidobacterium bifidum*; *Christensenella minuta*; *Coprococcus catus*; *Coprococcus sp000154245*; *Dysosmobacter faecalis*; *Faecalibacterium duncaniae*; *Gemmiger formicilis*; *Parabacteroides goldsteinii*; *Ruminococcus bicirculans*; *Ruthenibacterium lactatiformans*; *Solibaculum mannosilyticum*; and *Vescimonas coprocola*; and any combination, subgroup or multitude thereof.

[0050] In some embodiments, the plurality of core community microbial species is selected the group consisting of: *Dysosmobacter welbionis*; *Enterocloster bolteae*; *Ruthenibacterium lactatiformans*; *Vescimonas coprocola*; *Phocaeicola salanitronis*; *Pusillimonas faecalis*; *Solibaculum mannosilyticum*; *Chrstensenella minuta*; *Alistipes magaguti*; *Parabacteroides goldsteinii*, *Alistipes communis*; *Ruminococcus bicirculans*; *Bacteroides caecimuris*; *Alistipes dispar*, and *Bacteroides salversiae*; and wherein the plurality of keystone microbial species is selected from the group consisting of: *Phocaeicola coprocola*; *Bifidobacterium bifidum*; and *Coprococcus catus*; and any combination, subgroup or multitude thereof.

[0051] In some embodiments, the composition comprises a plurality of core community microbial species, wherein said core community microbial species comprises: *Alistipes dispar*; *Bacteroides salyersiae*; *Bifidobacterium bifidum*; *Christensenella minuta*; *Coprococcus catus*; *Coprococcus sp000154245*; *Dysosmobacter faecalis*; *Faecalibacterium duncaniae*; *Gemmiger formicilis*; *Parabacteroides goldsteinii*; *Ruminococcus bicirculans*; *Ruthenibacterium lactatiformans*; *Solibaculum mannosilyticum*; and *Vescimonas coprocola*; and any combination, subgroup or multitude thereof.

[0052] In some embodiments, the plurality of core community microbial species comprises: *Dysosmobacter welbionis*; *Enterocloster bolteae*; *Ruthenibacterium lactatiformans*; *Vescimonas coprocola*; *Phocaeicola salanitronis*; *Pusillimonas faecalis*; *Solibaculum mannosilyticum*; *Chrstensenella minuta*; *Alistipes magaguti*; *Parabacteroides goldsteinii*, *Alistipes communis*; *Ruminococcus bicirculans*; *Bacteroides caecimuris*; *Alistipes dispar*, and *Bacteroides salversiae*; and wherein the plurality of keystone microbial species comprises: *Phocaeicola coprocola*; *Bifidobacterium bifidum*; and *Coprococcus catus*; and any combination, subgroup or multitude thereof.

[0053] In some embodiments, the microbial consortium the does not comprise any bacteria from the phylum Pseudomonadota or Campylobacterota.

[0054] In some embodiments, the microbial consortium the does not comprise one or more species selected from the group consisting of: *Absiella dolichum*; *Acidaminococcus fermentans*; *Acidaminococcus sp.*; *Adlercreutzia equolifaciens*; *Agathobacter rectalis*; *Akkermansia muciniphila*; *Alistipes finegoldii*; *Alistipes indistinctus*; *Alistipes onderdonkii*;

Alistipes putredinis; *Alistipes senegalensis*; *Alistipes shahii*; *Amedibacillus dolichus*;
Anaerobutyricum hallii; *Anaerofustis stercorihominis*; *Anaerostipes caccae*; *Anaerotruncus*
colihominis; *Faecalibacterium prausnitzii*; *Solobacterium moorei*; *Bacteroides*; *Bacteroides*
cacaea; *Bacteroides caccae*; *Bacteroides cellulosilyticus*; *Bacteroides coprocola*; *Bacteroides*
5 *coprophilus*; *Bacteroides dorea*; *Bacteroides dorei*; *Bacteroides eggerthii*; *Bacteroides*
finegoldii; *Bacteroides fragilis*; *Bacteroides intestinalis*; *Bacteroides ovatus*; *Bacteroides*
pectinophilus; *Bacteroides plebeius*; *Bacteroides rodentium*; *Bacteroides stercoris*;
Bacteroides thetaiotaomicron; *Bacteroides uniformis*; *Bacteroides vulgatus*; *Bacteroides*
xylanisolvans; *Bifidobacterium breve*; *Bifidobacterium catenulatum*; *Bifidobacterium*
10 *pseudocatenulatum*; *Bilophila wadsworthia*; *Blautia hansenii*; *Blautia hydrogenotrophica*;
Blautia obeum; *Blautia sp.*; *Blautia wexlerae*; *Butyricimonas virosa*; *Butyrivibrio crossotus*;
Catenibacterium mitsuokai; *Clostridium asparagiforme*; *Clostridium bolteae*; *Clostridium*
hiranonis; *Clostridium hylemonae*; *Clostridium leptum*; *Clostridium methylpentosum*;
Clostridium nexile; *Clostridium orbiscindens*; *Clostridium saccharolyticum*; *Clostridium*
15 *scindens*; *Clostridium sp.*; *Clostridium spiroforme*; *Collinsella aerofaciens*; *Collinsella*
stercoris; *Copracoccus comes*; *Coprococcus eutactus*; *Desulfovibrio piger*; *Dialister invisus*;
Dorea formicigenerans; *Eggerthella lenta*; *Enterocloster asparagiformis*; *Enterocloster*
bolteae; *Ethanoligenens harbinense*; *Eubacterium rectale*; *Eubacterium siraeum*;
Eubacterium ventriosum; *Flavonifractor plautii*; *Granulicatella adiacens*; *Granulicatella*
20 *adiacens adiacens*; *Holdemanella biformis*; *Holdemania filiformis*; *Hoylella buccalis*;
Hungatella hathewayi; *Intestinibacter bartlettii*; *Intestinimonas butyriciproducens*;
Lacrimispora saccharolytica; *Lactobacillus ruminis*; *Ligilactobacillus ruminis*; *Marvinbryantia*
formatexigens; *Mediterraneibacter gnavus*; *Megasphaera sp.*; *Mitsuokella multacida*;
Odoribacter splanchnicus; *Olsenella uli*; *Oscillibacter sp.*; *Parabacteroides distasonis*;
25 *Parabacteroides johnsonii*; *Parabacteroides merdae*; *Parabacteroides sp.*; *Peptacetobacter*
hiranonis; *Phocaeicola coprocola*; *Phocaeicola coprophilus*; *Phocaeicola dorei*; *Phocaeicola*
plebeius; *Phocaeicola vulgatus*; *Prevotella buccalis*; *Prevotella copri*; *Roseburia inulinivorans*;
Ruminococcus gauvreauii; *Ruminococcus gnavus*; *Ruminococcus lactaris*; *Ruminococcus*
torques; *Segatella copri*; *Slackia exigua*; *Slackia heliotrinireducens*; *Streptococcus salivarius*;
30 *Streptococcus salivarius subsp. thermophilus*; *Streptococcus thermophilus*; *Subdoligranulum*
variabile; *Thomasclavelia spiroformis*; *Turicibacter sanguinis*; *Tyzzereella nexilis*; and any
combination, subgroup or multitude thereof. .

[0055] In some embodiments, the microbial consortium is generated by co-culturing the minimum core species and the keystone species in a single bioreactor.

35 [0056] In some embodiments, the microbial consortium comprises a ratio of minimum core species to keystone species of 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1 with respect to number of microbes.

[0057] In some embodiments, the microbial consortium comprises from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage of total microorganisms in the formulation.

[0058] In some embodiments, the microbial consortium comprises from A% to B% minimum core species and from C% to D% keystone species as a percentage of total microorganisms in the formulation, wherein the A% to B% range is selected from the group consisting of: 10% to 99%; 10% to 90%; 20% to 80%; 30% to 70%; 40% to 60%; 50% to 80%; and 20% to 50%; and wherein the C% to D% range is selected from the group consisting of: 10% to 99%; 10% to 90%; 20% to 80%; 30% to 70%; 40% to 60%; 50% to 80%; and 20% to 50%.

[0059] In some embodiments, the microbial consortium comprises 3, 5, 10, 15, 20, or all core community microbial strains selected from Table 14 and 1, 3, 5, 10, 15, 20, or all keystone microbial strains selected from Table 13.

[0060] In some embodiments, the microbial consortium comprises 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25 or all minimum core species selected from Table 14 and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or all keystone species selected from Table 13.

[0061] In some embodiments, the microbial consortium comprises 20 or more minimum core species selected from Table 14 and 10 or more keystone species selected from Table 13.

[0062] In some embodiments, the microbial consortium comprises a plurality of minimum core species and a plurality of keystone species comprising 80-100% of the species identified on Table 9; Table 10; Table 11; Table 12; Table 13; Table 14; Table 15; or Table 16.

[0063] In some embodiments, the microbial consortium comprises between 1 to 1000 microbial species, strains or isolates.

[0064] In some embodiments, the microbial consortium comprises any number between and including 1 to 1000 microbial species, strains or isolates, wherein the number is selected from the group consisting of: 1; 2; 3; 4; 5; 6; 7; 8; 9; 10; 11; 12; 13; 14; 15; 16; 17; 18; 19; 20; 21; 22; 23; 24; 25; 26; 27; 28; 29; 30; 31; 32; 33; 34; 35; 36; 37; 38; 39; 40; 41; 42; 43; 44; 45; 46; 47; 48; 49; 50; 51; 52; 53; 54; 55; 56; 57; 58; 59; 60; 61; 62; 63; 64; 65; 66; 67; 68; 69; 70; 71; 72; 73; 74; 75; 76; 77; 78; 79; 80; 81; 82; 83; 84; 85; 86; 87; 88; 89; 90; 91; 92; 93; 94; 95; 96; 97; 98; 99; 100; 101; 102; 103; 104; 105; 106; 107; 108; 109; 110; 111; 112; 113; 114; 115; 116; 117; 118; 119; 120; 121; 122; 123; 124; 125; 126; 127; 128; 129; 130; 131; 132; 133; 134; 135; 136; 137; 138; 139; 140; 141; 142; 143; 144; 145; 146; 147; 148; 149; 150; 151; 152; 153; 154; 155; 156; 157; 158; 159; 160; 161; 162; 163; 164; 165; 166; 167; 168; 169; 170; 171; 172; 173; 174; 175; 176; 177; 178; 179; 180; 181; 182; 183; 184; 185; 186; 187; 188; 189; 190; 191; 192; 193; 194; 195; 196; 197; 198; 199; 200; 201; 202; 203; 204;

205; 206; 207; 208; 209; 210; 211; 212; 213; 214; 215; 216; 217; 218; 219; 220; 221; 222;
223; 224; 225; 226; 227; 228; 229; 230; 231; 232; 233; 234; 235; 236; 237; 238; 239; 240;
241; 242; 243; 244; 245; 246; 247; 248; 249; 250; 251; 252; 253; 254; 255; 256; 257; 258;
259; 260; 261; 262; 263; 264; 265; 266; 267; 268; 269; 270; 271; 272; 273; 274; 275; 276;
5 277; 278; 279; 280; 281; 282; 283; 284; 285; 286; 287; 288; 289; 290; 291; 292; 293; 294;
295; 296; 297; 298; 299; 300; 301; 302; 303; 304; 305; 306; 307; 308; 309; 310; 311; 312;
313; 314; 315; 316; 317; 318; 319; 320; 321; 322; 323; 324; 325; 326; 327; 328; 329; 330;
331; 332; 333; 334; 335; 336; 337; 338; 339; 340; 341; 342; 343; 344; 345; 346; 347; 348;
349; 350; 351; 352; 353; 354; 355; 356; 357; 358; 359; 360; 361; 362; 363; 364; 365; 366;
10 367; 368; 369; 370; 371; 372; 373; 374; 375; 376; 377; 378; 379; 380; 381; 382; 383; 384;
385; 386; 387; 388; 389; 390; 391; 392; 393; 394; 395; 396; 397; 398; 399; 400; 401; 402;
403; 404; 405; 406; 407; 408; 409; 410; 411; 412; 413; 414; 415; 416; 417; 418; 419; 420;
421; 422; 423; 424; 425; 426; 427; 428; 429; 430; 431; 432; 433; 434; 435; 436; 437; 438;
439; 440; 441; 442; 443; 444; 445; 446; 447; 448; 449; 450; 451; 452; 453; 454; 455; 456;
15 457; 458; 459; 460; 461; 462; 463; 464; 465; 466; 467; 468; 469; 470; 471; 472; 473; 474;
475; 476; 477; 478; 479; 480; 481; 482; 483; 484; 485; 486; 487; 488; 489; 490; 491; 492;
493; 494; 495; 496; 497; 498; 499; 500; 501; 502; 503; 504; 505; 506; 507; 508; 509; 510;
511; 512; 513; 514; 515; 516; 517; 518; 519; 520; 521; 522; 523; 524; 525; 526; 527; 528;
529; 530; 531; 532; 533; 534; 535; 536; 537; 538; 539; 540; 541; 542; 543; 544; 545; 546;
20 547; 548; 549; 550; 551; 552; 553; 554; 555; 556; 557; 558; 559; 560; 561; 562; 563; 564;
565; 566; 567; 568; 569; 570; 571; 572; 573; 574; 575; 576; 577; 578; 579; 580; 581; 582;
583; 584; 585; 586; 587; 588; 589; 590; 591; 592; 593; 594; 595; 596; 597; 598; 599; 600;
601; 602; 603; 604; 605; 606; 607; 608; 609; 610; 611; 612; 613; 614; 615; 616; 617; 618;
619; 620; 621; 622; 623; 624; 625; 626; 627; 628; 629; 630; 631; 632; 633; 634; 635; 636;
25 637; 638; 639; 640; 641; 642; 643; 644; 645; 646; 647; 648; 649; 650; 651; 652; 653; 654;
655; 656; 657; 658; 659; 660; 661; 662; 663; 664; 665; 666; 667; 668; 669; 670; 671; 672;
673; 674; 675; 676; 677; 678; 679; 680; 681; 682; 683; 684; 685; 686; 687; 688; 689; 690;
691; 692; 693; 694; 695; 696; 697; 698; 699; 700; 701; 702; 703; 704; 705; 706; 707; 708;
709; 710; 711; 712; 713; 714; 715; 716; 717; 718; 719; 720; 721; 722; 723; 724; 725; 726;
30 727; 728; 729; 730; 731; 732; 733; 734; 735; 736; 737; 738; 739; 740; 741; 742; 743; 744;
745; 746; 747; 748; 749; 750; 751; 752; 753; 754; 755; 756; 757; 758; 759; 760; 761; 762;
763; 764; 765; 766; 767; 768; 769; 770; 771; 772; 773; 774; 775; 776; 777; 778; 779; 780;
781; 782; 783; 784; 785; 786; 787; 788; 789; 790; 791; 792; 793; 794; 795; 796; 797; 798;
799; 800; 801; 802; 803; 804; 805; 806; 807; 808; 809; 810; 811; 812; 813; 814; 815; 816;
35 817; 818; 819; 820; 821; 822; 823; 824; 825; 826; 827; 828; 829; 830; 831; 832; 833; 834;
835; 836; 837; 838; 839; 840; 841; 842; 843; 844; 845; 846; 847; 848; 849; 850; 851; 852;
853; 854; 855; 856; 857; 858; 859; 860; 861; 862; 863; 864; 865; 866; 867; 868; 869; 870;

- 871; 872; 873; 874; 875; 876; 877; 878; 879; 880; 881; 882; 883; 884; 885; 886; 887; 888; 889; 890; 891; 892; 893; 894; 895; 896; 897; 898; 899; 900; 901; 902; 903; 904; 905; 906; 907; 908; 909; 910; 911; 912; 913; 914; 915; 916; 917; 918; 919; 920; 921; 922; 923; 924; 925; 926; 927; 928; 929; 930; 931; 932; 933; 934; 935; 936; 937; 938; 939; 940; 941; 942; 943; 944; 945; 946; 947; 948; 949; 950; 951; 952; 953; 954; 955; 956; 957; 958; 959; 960; 961; 962; 963; 964; 965; 966; 967; 968; 969; 970; 971; 972; 973; 974; 975; 976; 977; 978; 979; 980; 981; 982; 983; 984; 985; 986; 987; 988; 989; 990; 991; 992; 993; 994; 995; 996; 997; 998; 999; and 1000, or number within a range defined by any two of the aforementioned values.
- 10 [0065] In some embodiments, the microbial consortium comprises between 500 to 1000 microbial species, strains or isolates.
- [0066] In some embodiments, the microbial consortium comprises between 200 to 500 microbial species, strains or isolates.
- [0067] In some embodiments, the microbial consortium comprises between 20 to 200 microbial species, strains or isolates.
- 15 [0068] In some embodiments, the microbial consortium comprises between 130 to 140 microbial species, strains or isolates.
- [0069] In some embodiments, the microbial consortium comprises between 120 to 130 microbial species, strains or isolates.
- 20 [0070] In some embodiments, the microbial consortium comprises between 110 to 120 microbial species, strains or isolates.
- [0071] In some embodiments, the microbial consortium comprises between 100 to 110 microbial species, strains or isolates.
- [0072] In some embodiments, the microbial consortium comprises between 80 to 90 microbial species, strains or isolates.
- 25 [0073] In some embodiments, the microbial consortium comprises between 70 to 80 microbial species, strains or isolates.
- [0074] In some embodiments, the microbial consortium comprises between 10 to 70 microbial species, strains or isolates.
- 30 [0075] In some embodiments, the microbial consortium comprises between 10 to 60 microbial species, strains or isolates.
- [0076] In some embodiments, the microbial consortium comprises between 10 to 50 microbial species, strains or isolates.
- [0077] In some embodiments, the microbial consortium comprises between 5 to 20 microbial species, strains or isolates.
- 35 [0078] In some embodiments, the microbial consortium comprises between 5 to 15 microbial species, strains or isolates.

[0079] In some embodiments, the microbial consortium comprises between 1 to 10 microbial species, strains or isolates.

[0080] In some embodiments, the microbial consortium comprises between 1 to 5 microbial species, strains or isolates.

5 [0081] In some embodiments, the microbial consortium comprises 143 microbial species, strains or isolates.

[0082] In some embodiments, the microbial consortium comprises 127 microbial species, strains or isolates.

[0083] In some embodiments, the number of microbial species, strains or isolates, is a
10 minimum number required to achieve the desired level of functional potential or property.

[0084] In some embodiments, the minimum number is identified by the point on a rarefaction curve where the model's asymptote intersects with the benchmark functional potential or property.

[0085] In some embodiments, the minimum number is identified by a method to estimate
15 the minimum number of isolates required to achieve a desired level of functional potential or property in complex community therapeutics said method comprising the following steps:

[0086] Step 1 - Isolate selection: Selecting a plurality of microbial isolates to comprise a target microbial community, wherein the isolates are representative of the genetic and functional diversity present within the community.

20 [0087] Step 2 - Whole genome sequencing: Subjecting the selected microbial isolates to whole genome sequencing to obtain sequence data.

[0088] Step 3 - Genome assembly and annotation: Assembling the obtained sequence data into complete or draft genomes for each isolate using a genome assembly pipeline, and subsequently annotating these genomes to identify functional gene categories, such as
25 Clusters of Orthologous Genes (COGs) or equivalent functional annotations.

[0089] Step 4 - Functional gene category identification: Identifying and cataloging the presence of functional gene categories within each genome based on the annotation results, wherein non-functional or non-essential categories, such as hypothetical proteins or tRNAs, are excluded from further analysis.

30 [0090] Step 5 - Resampling and subset generation: Performing a resampling procedure on the annotated genomes, wherein subsets of isolates are randomly selected with replacement, covering a range of subset sizes from a single isolate to the total number of isolates in the community, to generate multiple iterations of isolate subsets.

[0091] Step 6 - Functional potential assessment: For each subset generated in the
35 resampling procedure, calculating the total number of unique functional gene categories present, thereby producing a dataset representing the functional potential or property of each subset size.

[0092] Step 7 - Rarefaction curve construction: Constructing a rarefaction curve by plotting the number of unique functional gene categories against the number of isolates in each subset, wherein the curve depicts the relationship between the increasing number of isolates and the cumulative functional potential or property.

- 5 [0093] Step 8 - Model fitting and asymptote determination: Fitting a mathematical model, such as a logistic or polynomial regression, to the rarefaction curve to determine the point at which the curve begins to asymptote, indicating a diminishing return in the discovery of new functional gene categories as additional isolates are added.

- 10 [0094] Step 9 - Minimum viable consortium determination: Estimating the minimum number of isolates required to achieve a functional potential or property that meets or exceeds a predefined benchmark, such as the functional diversity present in a healthy or target microbial community, by identifying the point on the rarefaction curve where the model's asymptote intersects with the benchmark functional potential or property.

- 15 [0095] Step 10 - Application to therapeutic Design: Applying the results of the rarefaction analysis to design a minimal viable microbial consortium that retains the desired level of functional potential or property, ensuring that the consortium is both functionally robust and economically feasible for therapeutic applications.

- 20 [0096] In some embodiments, the microbe or plurality of microbes is a species or strain selected from any one of the species consisting of: any one of the microbes presented in Figure 6; Figure 7; and Figure 9; or any combination, subgroup or multitude thereof; and wherein composition further does not comprise a different microbe or plurality of microbes selected from any one of the species, strains or isolates consisting of: any one of the microbes presented in Figure 6; Figure 7; and Figure 9; or any combination, subgroup or multitude thereof.

- 25 [0097] In some embodiments, the microbe or plurality of microbes is a species or strain selected from any one of the species consisting of: any one of the microbes presented in Table 9; Table 10; Table 11; Table 12; Table 13; Table 14; Table 15; Table 16; or any combination, subgroup or multitude thereof; and wherein composition further does not comprise a different microbe or plurality of microbes selected from any one of the species, strains or isolates consisting of: any one of the microbes presented in Table 9; Table 10; Table 11; Table 12; Table 13; Table 14; Table 15; Table 16; or any combination, subgroup or multitude thereof.

[0098] In some embodiments, the microbe or plurality of microbes is a species or strain and is responsible for a metabolic pathway, wherein the metabolic pathway is selected from any one of the groups consisting of:

- 35 [0099] a. carbohydrate metabolism, including; glycolysis / gluconeogenesis, the citrate cycle, the pentose phosphate pathway, fructose and mannose metabolism, galactose

metabolism, ascorbate and aldarate metabolism, starch and sucrose metabolism, inositol phosphate metabolism, and pyruvate metabolism;

[00100] b. lipid metabolism, including; fatty acid biosynthesis, fatty acid degradation, steroid biosynthesis and bile acid biosynthesis;

5 [00101] c. amino acid metabolism; arginine biosynthesis, alanine, aspartate, and glutamate metabolism, glycine, serine and threonine metabolism, cysteine and methionine metabolism, valine, leucine and isoleucine biosynthesis, lysine biosynthesis and degradation, arginine and proline metabolism, histidine metabolism, tyrosine metabolism, phenylalanine metabolism, tryptophan metabolism, phenylalanine, tyrosine and tryptophan biosynthesis, beta-alanine metabolism, taurine and hypotaurine metabolism, glutathione metabolism; and

10 [00102] d. vitamin / co-factor metabolism, including; riboflavin metabolism, thiamine metabolism, vitamin b6 metabolism, nicotinate and nicotinamide metabolism, pantothenate biosynthesis, biotin metabolism, lipoic acid metabolism, folate biosynthesis, atrazine degradation, retinol metabolism, porphyrin metabolism, and carotenoid biosynthesis; and any combination or multitude thereof.

[00103] In some embodiments, the microbe is a species or strain which contains sulfur metabolic genes, wherein the sulfur metabolic genes are selected from the group consisting of: the sulfur metabolic genes presented in Table 33; and any combination or multitude thereof.

20 [00104] In some embodiments, the microbe is a species or strain which has a reaction/metabolite selected from the group consisting of: the reaction/metabolite presented in Table 33; and any combination or multitude thereof.

[00105] In some embodiments, the microbe is a species or strain which contains acetate metabolic genes, wherein the acetate metabolic genes are selected from the group consisting of: the acetate metabolic genes presented in Table 34; and any combination, subgroup or multitude thereof.

[00106] In some embodiments, the microbe is a species or strain which contains butyrate metabolic genes, wherein the butyrate metabolic genes are selected from the group consisting of: the butyrate metabolic genes presented in Table 35; and any combination, subgroup or multitude thereof.

30 [00107] In some embodiments, the microbe is a species or strain responsible for a metabolic pathway, wherein the metabolic pathway is selected from the group consisting of: the metabolic pathway categories presented in Table 36; and any combination, subgroup or multitude thereof.

35 [00108] In some embodiments, the microbe is a species or strain comprising a gene that is responsible for a phenotype selected from the group consisting of: reducing endogenous sulfide levels in the colon of a patient in need thereof; sulfide consumption; reducing sulfide and nitric oxide load on epithelial cells which affects cellular respiration leading to a metabolic

- lesion; reducing relative abundance and or metabolic activity of sulfidogenic microbiota; reducing sulfide levels in the colon directly through consumption/assimilation; reducing sulfide levels, relative abundance and or metabolic activity of sulfidogenic microbiota in the colon by metabolic substrate competition; reducing sulfide levels, relative abundance and or metabolic activity of sulfidogenic microbiota in the colon by diverting metabolic substrates away from the production of sulfide; reducing sulfide levels, relative abundance and or metabolic activity of sulfidogenic microbiota in the colon by consuming H₂; reducing sulfide levels, relative abundance and or metabolic activity of sulfidogenic microbiota by reducing release of metabolizable sulfur substrates; reducing sulfide levels, relative abundance and or metabolic activity of sulfidogenic microbiota by reducing sulfur amino acid release (methionine, cysteine, homocysteine and/or taurine) into the colon; reducing colonic protein fermentation; reducing nitric oxide production in the colon; reducing nitric oxide levels in the colon; and inducing colonocyte apoptosis in lesions to break an induced stable inflammatory state.
- [00109] In some embodiments, certain strains in the co-culture and/or formulation for administration to a subject are selected based on these phenotypes.
- [00110] In some embodiments, the composition demonstrates a property selected from any one of the groups consisting of:
- [00111] a. emergent metabolic functions;
- [00112] b. emergent metabolic functions relating to: short-chain fatty acids (SCFAs); sulfide homeostasis; energy harvest; tryptophan metabolism; bile acid metabolism; vitamin production; and/or drug metabolism;
- [00113] c. synergistic metabolic functions and wherein the metabolic function of the consortium as a whole is greater than metabolic function of any of the individual isolates;
- [00114] d. synergistic metabolic functions and wherein the sulfide reduction metabolic function of the consortium as a whole is greater than sulfide reduction metabolic function of each of the individual isolates;
- [00115] e. synergistic metabolic functions and wherein the sulfide reduction metabolic function of the consortium as a whole is greater than the sulfide reduction metabolic function of each of the individual isolates (and wherein the sulfide reduction metabolic function is selected from the group consisting of: microbial competition for metabolic substrates (such as volatile fatty acids (acetate, propionate, butyrate), organic acids (lactate, valerate, succinate, pyruvate), amino acids (alanine, glutamate, serine) and ethanol as electron donors in cellular respiration); reduced sulfur substrate release in the colon; removing sulfide from the colon (such as assimilation of sulfide to cysteine));
- [00116] f. synergistic metabolic functions relating to: short-chain fatty acids (SCFAs); sulfide homeostasis; energy harvest; tryptophan metabolism; bile acid metabolism; vitamin production; drug metabolism;

- [00117] g. reduces sulfide and nitric oxide load on epithelial cells which leads to a metabolic lesion via inhibition of cellular respiration;
- [00118] h. reduces relative abundance and or metabolic activity of sulfidogenic microbiota in vitro;
- 5 [00119] i. reduces sulfide levels in vitro either directly or indirectly through consumption/assimilation of sulfide or metabolic substrates and/or a reduction in the production of sulfide;
- [00120] j. reduces sulfide levels in vitro via metabolic substrate competition;
- [00121] k. reduces sulfide levels in vitro by consuming hydrogen;
- 10 [00122] l. reduces relative abundance and or metabolic activity of sulfidogenic microbiota;
- [00123] m. reduce sulfide levels in the colon either directly or indirectly through consumption/assimilation of sulfide or metabolic substrates and/or a reduction in the production of sulfide; reduce sulfide levels in the colon via metabolic substrate competition; and or reduce sulfide levels in the colon by consuming hydrogen;
- 15 [00124] n. reduces the relative abundance and or metabolic activity of sulfidogenic microbiota by reducing metabolizable sulfur substrates; reduce sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by reducing protein fermentation;
- [00125] o. induces colonocyte apoptosis in lesions to break an induced stable inflammatory state driven;
- 20 [00126] p. drives down undesired inflammation;
- [00127] q. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by modulating host protease activity;
- [00128] r. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by reducing host protease activity;
- 25 [00129] s. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by modulating microbial protease activity;
- [00130] t. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by reducing microbial protease activity;
- [00131] u. reduces sulfide (production in the colon by modulating host protease activity);
- 30 [00132] v. reduces sulfide production in the colon by reducing host protease activity;
- [00133] w. reduces sulfide production in the colon by modulating microbial protease activity;
- [00134] x. reduces sulfide production in the colon by reducing microbial protease activity;
- [00135] y. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine)
- 35 into the colon by modulating host antiprotease (protease inhibitor) activity;
- [00136] z. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by reducing host antiprotease (protease inhibitor) activity;

- [00137] aa. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by modulating microbial antiprotease (protease inhibitor) activity;
- [00138] ab. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine)
- 5 [00139] ac. into the colon by reducing microbial antiprotease (protease inhibitor) activity;
- [00140] ad. reduces sulfide production in the colon by modulating host antiprotease (protease inhibitor) activity;
- [00141] ae. reduces sulfide production in the colon by reducing host antiprotease (protease inhibitor) activity;
- 10 [00142] af. reduces sulfide production in the colon by modulating microbial antiprotease (protease inhibitor) activity;
- [00143] ag. reduces sulfide production in the colon by reducing microbial antiprotease (protease inhibitor) activity;
- [00144] ah. prevents or reduces activation of the mucosa immune system in a natural killer
- 15 T-cell driven IL-13 and IL-5 dependent, TH2 mediated, immune response;
- [00145] ai. decreases inflammation in the subject;
- [00146] aj. decreases inflammation in the subject when measured by a parameter selected from the group consisting of: TNF α signaling via NF- κ B; IFN α signaling; IFN γ signaling; IL6 JAK STAT3 signaling; activation of pro-apoptotic pathways; initiation of unfolded protein
- 20 response;
- [00147] ak. down regulates genes associated with pro-apoptotic pathways and the unfolded protein response, including genes selected from the group consisting of: CHAC1, CEBPB, TRIB3, PPP1R15A, DDIT3, ATF4 and XBP1;
- [00148] al. treats and/or prevents dysbiosis;
- 25 [00149] am. treats or prevents a medical disorder or disease associated with dysbiosis;
- [00150] an. treats or prevents a medical disorder or disease associated with mycobiome dysbiosis;
- [00151] ao. treats and/or prevents a gastrointestinal disorder;
- [00152] ap. treats and/or prevents a gastrointestinal disorder; wherein the gastrointestinal
- 30 disorder is selected from the group consisting of: irritable bowel syndrome; an ulcer of the gastrointestinal tract; a cancer of the gastrointestinal tract;
- [00153] aq. treats and/or prevents gastrointestinal tract mucosal inflammation;
- [00154] ar. treats and/or prevents gastrointestinal tract mucosal inflammation, wherein the inflammation is associated with one or more of disorders selected from the group consisting
- 35 of: inflammatory bowel disease (IBD), pouchitis, irritable bowel syndrome (IBS), an enteric bacterial infection, a metabolic disease, a neuropsychiatric disorder, an autoimmune disease, an allergic disorder, hepatic encephalopathy, or a cancer;

[00155] as. treats and/or prevents inflammatory bowel disease;

[00156] at. treats and/or prevents ulcerative colitis; Crohn's disease; gastroenteritis; colitis; checkpoint inhibitor colitis; and pouchitis;

[00157] au. treats and/or prevents one or more of diseases or disorders selected from the
 5 group consisting of: liver disorders; metabolic disorders; neurological disorders; oncology disorders; cardiovascular disorders; immunological disorders; allergy; allergic and atopic disorders; infectious disease; and can affect the efficacy of cancer therapies. In some embodiments, the liver disorder is selected from the group consisting of: Primary sclerosing cholangitis; Non-alcoholic steatohepatitis; Non-alcoholic fatty liver disease; Alcoholic hepatitis;
 10 and Hepatic encephalopathy. In some embodiments, the metabolic disorder is selected from the group consisting of: Obesity; Insulin resistance; and Type 2 diabetes. In some embodiments, the neurological disorder is selected from the group consisting of: Autism; Multiple sclerosis; Parkinson's disease; Depression; Anxiety; Bipolar disorder; Schizophrenia; and Mental health. In some embodiments, the oncology disorder is selected from the group
 15 consisting of: Melanoma; Renal cell carcinoma; Bowel cancer and precancerous polyps; Lymphoma; Leukaemia; Myeloma; Pancreatic cancer; Breast cancer; Lung cancer; Testicular cancer; and Sarcoma. In some embodiments, the cardiovascular disorder is selected from the group consisting of: Dyslipidaemia; Atherosclerotic heart disease; and Hypertension. In some embodiments, the immunological disorder is selected from the group consisting of: Type 1
 20 diabetes; Rheumatoid arthritis; Psoriatic arthritis; Psoriasis; Systemic Lupus Erythematosus; and Sjogren's disease. In some embodiments, the allergic or atopic disorder is selected from the group consisting of: Food allergy; Anaphylaxis; Atopic dermatitis; and Atopic rhinitis or sinusitis. In some embodiments, the infectious disease is selected from the group consisting of: Clostridioides difficile infection; Multidrug resistant infection or colonisation; Renal tract or
 25 urinary tract infections; Blood stream infections; Respiratory infections; and Sepsis. In some embodiments, the disease or disorder is associated with mycobiome dysbiosis; and In some embodiments, the disease or disorder is associated with dysbiosis;

[00158] av. increases the relative abundance of a member of the bacteria genus or colonizes a member of the bacteria genus selected from the group consisting of:
 30 *Acidaminococcaceae* (family), *Acidaminococcus*, *Adlercreutzia*, *Agathobaculum*, *Akkermansia*, *Alistipes*, *Alterileibacterium*, *Amedibacillus*, *Amedibacterium*, *Aminipila*, *Anaerobutyricum*, *Anaerococcus*, *Anaerocolumna*, *Anaerofustis*, *Anaerostipes*, *Anaerotignum*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Barnesiella*, *Bifidobacterium*, *Bilophila*, *Blautia*, *Butyricimonas*, *Butyrivibrio*, *Campylobacter*, *Caproicibacter*, *Caproicibacterium*,
 35 *Caproiciproducens*, *Casaltella*, *Catenibacterium*, *Christensenella*, *Clostridium*, *Collinsella*, *Coprobacillus*, *Coprobacter*, *Coprococcus*, *Desulfovibrio*, *Dorea*, *Duodenibacillus*, *Dysosmobacter*, *Eggerthella*, *Enorma*, *Enterocloster*, *Enterococcus*, *Escherichia*,

Ethanoligenens, Eubacterium, Faecalibacillus, Faecalibacterium, Faecalibaculum, Finegoldia, Flavonifractor, Flintibacter, Fusicatenibacter, Gemmiger, Gordonibacter, Granulicatella, Herbinix, Holdemanella, Holdemania, Hoylesella, Hungatella, Intestinibacter, Intestinibaculum, Intestinimonas, Lachnoanaerobaculum, Lachnoclostridium, Lachnospira,
 5 *Lachnospiraceae incertae sedis (unclassified rank, Lachnospiraceae family), Lacrimispora, Lactococcus, Ligilactobacillus, Longibaculum, Longicatena, Mageeibacillus, Maliibacterium, Marvinbryantia, Massilimicrobiota, Massiliprevotella, Massilistercora, Mediterraneibacter, Megamonas, Megasphaera, Merdibacter, Mesosutterella, Mitsuokella, Mogibacterium, Muribaculum, Negativibacillus, Novisyntrophococcus, Odoribacter, Olsenella, Oscillibacter,*
 10 *Oscillospiraceae (family), Oscillospiraceae incertae sedis (unclassified rank, Oscillospiraceae family), Parabacteroides, Paraclostridium, Paraprevotella, Parolsenella, Peptacetobacter, Peptoniphilus, Peptostreptococcus, Phascolarctobacterium, Phocaeicola, Porphyromonas, Prevotella, Pseudobutyrvibrio, Pusillibacter, Romboutsia, Roseburia, Ruminiclostridium, Ruminococcus, Ruthenibacterium, Schaalia, Segatella, Selenomonas, Sellimonas,*
 15 *Senegalimassilia, Slackia, Sodaliphilus, Solibaculum, Streptococcus, Subdoligranulum, Thomasclavelia, Tyzzerella, Veillonella and Vescimonas or any combination, subgroup or multitude thereof;*

[00159] aw. reduces the relative abundance of a member of the bacteria genus or decolonises a member of the bacteria genus selected from the group consisting of:
 20 *Achromobacter, Acidaminococcus, Aeromonas, Alicyclobacillus, Bacteroides, Bifidobacterium, Blautia, Bosea, Burkholderiales, Clostridium, Cutibacterium, Desulfovibrio, Eggerthella, Enterobacter, Enterococcus, Escherichia, Eubacterium, Flavonifractor, Granulicatella, Hungatella, Klebsiella, Ligilactobacillus, Mediterraneibacter, Minicystis, Oscillibacter, Parabacteroides, Pluralibacter, Prevotella, Prosthecochloris, Pseudomonas,*
 25 *Rhodococcus, Salmonella, Schaalia, Serratia, Shewanella, Staphylococcus, Streptomyces, Sutterella, Veillonella, or any combination, subgroup or multitude thereof; and any combination or multitude thereof; and*

[00160] ax. treats or prevents ulcerative colitis, inflammatory bowel disease, Crohn's disease, checkpoint inhibitor colitis, as well as other gastrointestinal diseases and symptoms,
 30 liver disorders, including, for example, primary sclerosing cholangitis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, or hepatic encephalopathy, metabolic disorders, including, for example, obesity, insulin resistance, or type 2 diabetes, oncology indications, including, for example, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer,
 35 breast cancer, lung cancer, testicular cancer, or sarcoma, cardiovascular disorders, including, for example, dyslipidaemia, atherosclerotic heart disease, or hypertension, immunological diseases, including, for example, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis,

psoriasis, systemic lupus erythematosus, or Sjogren's disease, allergic and atopic disorders, including, for example, food allergy, anaphylaxis, atopic dermatitis, or atopic rhinitis or sinusitis, infectious diseases, including, for example, clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory infections, or sepsis, neurological disorders, including for example, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, or schizophrenia.

[00161] In some embodiments, certain strains in the co-culture and/or formulation for administration to a subject are selected based on these properties.

[00162] In some embodiments, in combination with an therapy or active agent specific to the one or more diseases or disorders.

[00163] In some embodiments, the microbe is a fecal or colonic bacteria.

[00164] In some embodiments, the microbe is non-inflammatory.

[00165] In some embodiments, the microbe is cultured from a fecal or colonic biopsy sample.

[00166] In some embodiments, the microbial consortium comprises a community of microbes derived from a stool or biopsy of one or more human donors.

[00167] In some embodiments, the human donor is a healthy donor.

[00168] In some embodiments, the human donor is not an un-healthy donor.

[00169] In some embodiments, the human donor is not a donor presenting the underlying disease state.

[00170] In some embodiments, the community of microbes is not an inoculum.

[00171] In some embodiments, the community of microbes is cultured microbes produced from a bioreactor.

[00172] In some embodiments, the community of microbes is cultured microbes produced from a single bioreactor.

[00173] In some embodiments, the community of microbes is cultured microbes produced from a single continuous bioreactor.

[00174] In some embodiments, the community of microbes is cultured microbes produced from 1 to 10 bioreactors.

[00175] In some embodiments, the community of microbes is cultured from any number of bioreactors between and including 1 to 10, wherein the number is selected from the group consisting of: 1; 2; 3; 4; 5; 6; 7; 8; 9; 10.

[00176] In some embodiments, the community of microbes is cultured microbes produced from 1 to 10 continuous bioreactors.

[00177] In some embodiments, the community of microbes is cultured from any number of continuous bioreactors between and including 1 to 10, wherein the number is selected from the group consisting of: 1; 2; 3; 4; 5; 6; 7; 8; 9; 10.

- [00178] In some embodiments, the community of microbes has a metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation.
- [00179] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes the production and metabolism of short-chain fatty acids (SCFAs), including but not limited to acetate, propionate, and butyrate.
- 5 [00180] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes the synthesis and metabolism of gases such as hydrogen (H_2), carbon dioxide (CO_2) and methane (CH_4) and may include hydrogen sulfide (H_2S).
- 10 [00181] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes the synthesis and metabolism of organic acids such as lactate and succinate.
- [00182] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes the deamination of amino acids, alongside biogenic amines such as putrescine, cadaverine, and histamine.
- 15 [00183] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes the production and metabolism of ethanol, ammonia and indole.
- [00184] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes carbohydrate metabolism into monosaccharides and oligosaccharides.
- 20 [00185] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes metabolism of monosaccharides and oligosaccharides.
- 25 [00186] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes the synthesis and metabolism of vitamins, particularly B-vitamins.
- [00187] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes metabolism of monosaccharides and oligosaccharides.
- 30 [00188] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes the generation and metabolism of other metabolites and by-products, including but not limited to aromatic compounds, fatty alcohols, or ketones.
- 35 [00189] In some embodiments, the metabolic profile which is indicative of a community of microbes produced from a bioreactor fermentation includes a change in pH of the culture medium.

- [00190] In some embodiments, the community of microbes has a total cell count density (OD) which is indicative of a community of microbes produced from a bioreactor fermentation.
- [00191] In some embodiments, the cell count density (OD) which is indicative of a community of microbes produced from a bioreactor fermentation is from 0.8 to 5.0.
- 5 [00192] In some embodiments, the cell count density (OD) which is indicative of a community of microbes produced from a bioreactor fermentation is preferably from 1.0 to 3.0.
- [00193] In some embodiments, the cell count density (OD) which is indicative of a community of microbes produced from a bioreactor fermentation is from 1.5 to 2.5.
- [00194] In some embodiments, the cell count density (OD) which is indicative of a
10 community of microbes produced from a bioreactor fermentation is from 2.0 to 4.0.
- [00195] In some embodiments, the cell count density (OD) which is indicative of a community of microbes produced from a bioreactor fermentation is 5.0.
- [00196] In some embodiments, the cell count density (OD) which is indicative of a community of microbes produced from a bioreactor fermentation is 0.8 to 1.5.
- 15 [00197] In some embodiments, the cultured microbes are derived from multiple of human donors.
- [00198] In some embodiments, the community of microbes comprises uncultured microbes.
- [00199] In some embodiments, the uncultured microbes are derived from a single human
20 donor.
- [00200] In some embodiments, the composition is a fecal transplant microbiota composition.
- [00201] In some embodiments, the community of microbes comprise microbes which lack lytic phage.
- 25 [00202] In some embodiments, the community of microbes comprises microbes which lack genes selected from the group consisting of: antimicrobial resistant genes encoding resistance to ESBL, tetracycline, efflux, erythromycin, macrolide, trimethoprim, beta-lactamase (not ESBL or carbapenemase), streptomycin, beta-lactamase (unknown spectrum), lincosamide, chloramphenicol, sulfonamide, other aminoglycoside resistance (non-RMT),
30 gentamicin/kanamycin/tobramycin, lincosamide/macrolide/streptogramin, fosfomycin, carbapenemase (MBL), lincosamide/streptogramin, and vancomycin.
- [00203] In some embodiments, the community comprises microbes which lack antimicrobial resistant genes, and the percentage of microbes of the total consortium which lack these genes (by isolate classification or by total cell count) is an "at least percentage" that
35 is selected from the group consisting of: at least 99.9%; at least 99.5%; at least 99%; at least 98.5%; at least 98%; at least 97.5%; at least 97%; at least 96.5%; at least 96%; at least 95.5%; at least 95%; at least 94.5%; at least 94%; at least 93.5%; at least 93%; at least 92.5%; at

least 92%; at least 91.5%; at least 91%; at least 90.5%; at least 90%; at least 89.5%; at least 89%; at least 88.5%; at least 88%; at least 87.5%; at least 87%; at least 86.5%; at least 86%; at least 85.5%; at least 85%; at least 84.5%; at least 84%; at least 83.5%; at least 83%; at least 82.5%; at least 82%; at least 81.5%; at least 81%; at least 80.5%; at least 80%; at least 79.5%; at least 79%; at least 78.5%; at least 78%; at least 77.5%; at least 77%; at least 76.5%; at least 76%; at least 75.5%; at least 75%; at least 74.5%; at least 74%; at least 73.5%; at least 73%; at least 72.5%; at least 72%; at least 71.5%; at least 71%; at least 70.5%; at least 70%; at least 69.5%; at least 69%; at least 68.5%; at least 68%; at least 67.5%; at least 67%; at least 66.5%; at least 66%; at least 65.5%; at least 65%; at least 64.5%; at least 64%; at least 63.5%; at least 63%; at least 62.5%; at least 62%; at least 61.5%; at least 61%; at least 60.5%; at least 60%; at least 59.5%; at least 59%; at least 58.5%; at least 58%; at least 57.5%; at least 57%; at least 56.5%; at least 56%; at least 55.5%; at least 55%; at least 54.5%; at least 54%; at least 53.5%; at least 53%; at least 52.5%; at least 52%; at least 51.5%; at least 51%; at least 50.5%; at least 50%; at least 49.5%; at least 49%; at least 48.5%; at least 48%; at least 47.5%; at least 47%; at least 46.5%; at least 46%; at least 45.5%; at least 45%; at least 44.5%; at least 44%; at least 43.5%; at least 43%; at least 42.5%; at least 42%; at least 41.5%; at least 41%; at least 40.5%; at least 40%; at least 39.5%; at least 39%; at least 38.5%; at least 38%; at least 37.5%; at least 37%; at least 36.5%; at least 36%; at least 35.5%; at least 35%; at least 34.5%; at least 34%; at least 33.5%; at least 33%; at least 32.5%; at least 32%; at least 31.5%; at least 31%; at least 30.5%; at least 30%; at least 29.5%; at least 29%; at least 28.5%; at least 28%; at least 27.5%; at least 27%; at least 26.5%; at least 26%; at least 25.5%; at least 25%; at least 24.5%; at least 24%; at least 23.5%; at least 23%; at least 22.5%; at least 22%; at least 21.5%; at least 21%; at least 20.5%; at least 20%; at least 19.5%; at least 19%; at least 18.5%; at least 18%; at least 17.5%; at least 17%; at least 16.5%; at least 16%; at least 15.5%; at least 15%; at least 14.5%; at least 14%; at least 13.5%; at least 13%; at least 12.5%; at least 12%; at least 11.5%; at least 11%; at least 10.5%; at least 10%; and a value within a range defined by any two of the aforementioned values.

[00204] In some embodiments, the microbes are selected using the following criteria: lack antimicrobial resistant genes; and the percentage of microbes of the total consortium which lack these genes (by isolate classification or by total cell count) is an “at least percentage” that is selected from the group consisting of: at least 99.9%; at least 99.5%; at least 99%; at least 98.5%; at least 98%; at least 97.5%; at least 97%; at least 96.5%; at least 96%; at least 95.5%; at least 95%; at least 94.5%; at least 94%; at least 93.5%; at least 93%; at least 92.5%; at least 92%; at least 91.5%; at least 91%; at least 90.5%; at least 90%; at least 89.5%; at least 89%; at least 88.5%; at least 88%; at least 87.5%; at least 87%; at least 86.5%; at least 86%; at least 85.5%; at least 85%; at least 84.5%; at least 84%; at least 83.5%; at least 83%; at least 82.5%; at least 82%; at least 81.5%; at least 81%; at least 80.5%; at least 80%; at least

79.5%; at least 79%; at least 78.5%; at least 78%; at least 77.5%; at least 77%; at least 76.5%; at least 76%; at least 75.5%; at least 75%; at least 74.5%; at least 74%; at least 73.5%; at least 73%; at least 72.5%; at least 72%; at least 71.5%; at least 71%; at least 70.5%; at least 70%; at least 69.5%; at least 69%; at least 68.5%; at least 68%; at least 67.5%; at least 67%;

5 at least 66.5%; at least 66%; at least 65.5%; at least 65%; at least 64.5%; at least 64%; at least 63.5%; at least 63%; at least 62.5%; at least 62%; at least 61.5%; at least 61%; at least 60.5%; at least 60%; at least 59.5%; at least 59%; at least 58.5%; at least 58%; at least 57.5%; at least 57%; at least 56.5%; at least 56%; at least 55.5%; at least 55%; at least 54.5%; at least 54%; at least 53.5%; at least 53%; at least 52.5%; at least 52%; at least 51.5%; at least

10 51%; at least 50.5%; at least 50%; at least 49.5%; at least 49%; at least 48.5%; at least 48%; at least 47.5%; at least 47%; at least 46.5%; at least 46%; at least 45.5%; at least 45%; at least 44.5%; at least 44%; at least 43.5%; at least 43%; at least 42.5%; at least 42%; at least 41.5%; at least 41%; at least 40.5%; at least 40%; at least 39.5%; at least 39%; at least 38.5%; at least 38%; at least 37.5%; at least 37%; at least 36.5%; at least 36%; at least 35.5%; at

15 least 35%; at least 34.5%; at least 34%; at least 33.5%; at least 33%; at least 32.5%; at least 32%; at least 31.5%; at least 31%; at least 30.5%; at least 30%; at least 29.5%; at least 29%; at least 28.5%; at least 28%; at least 27.5%; at least 27%; at least 26.5%; at least 26%; at least 25.5%; at least 25%; at least 24.5%; at least 24%; at least 23.5%; at least 23%; at least 22.5%; at least 22%; at least 21.5%; at least 21%; at least 20.5%; at least 20%; at least 19.5%;

20 at least 19%; at least 18.5%; at least 18%; at least 17.5%; at least 17%; at least 16.5%; at least 16%; at least 15.5%; at least 15%; at least 14.5%; at least 14%; at least 13.5%; at least 13%; at least 12.5%; at least 12%; at least 11.5%; at least 11%; at least 10.5%; at least 10% and a value within a range defined by any two of the aforementioned values.

[00205] In some embodiments, the composition is lyophilized.

25 [00206] In some embodiments, the composition is a liquid.

[00207] In some embodiments, after at least 4 weeks of storage at room temperature, said composition is capable of maintaining at least 50% cell viability relative to the initial cell viability immediately prior to storage.

[00208] In some embodiments, after at least 4 weeks of storage at room temperature, said

30 composition is capable of maintaining a cell viability relative to the initial cell viability immediately prior to storage selected from the group consisting of: at least 99.9%; at least 99.5%; at least 99%; at least 98.5%; at least 98%; at least 97.5%; at least 97%; at least 96.5%; at least 96%; at least 95.5%; at least 95%; at least 94.5%; at least 94%; at least 93.5%; at least 93%; at least 92.5%; at least 92%; at least 91.5%; at least 91%; at least 90.5%; at least

35 90%; at least 89.5%; at least 89%; at least 88.5%; at least 88%; at least 87.5%; at least 87%; at least 86.5%; at least 86%; at least 85.5%; at least 85%; at least 84.5%; at least 84%; at least 83.5%; at least 83%; at least 82.5%; at least 82%; at least 81.5%; at least 81%; at least

- 80.5%; at least 80%; at least 79.5%; at least 79%; at least 78.5%; at least 78%; at least 77.5%; at least 77%; at least 76.5%; at least 76%; at least 75.5%; at least 75%; at least 74.5%; at least 74%; at least 73.5%; at least 73%; at least 72.5%; at least 72%; at least 71.5%; at least 71%; at least 70.5%; at least 70%; at least 69.5%; at least 69%; at least 68.5%; at least 68%;
- 5 at least 67.5%; at least 67%; at least 66.5%; at least 66%; at least 65.5%; at least 65%; at least 64.5%; at least 64%; at least 63.5%; at least 63%; at least 62.5%; at least 62%; at least 61.5%; at least 61%; at least 60.5%; at least 60%; at least 59.5%; at least 59%; at least 58.5%; at least 58%; at least 57.5%; at least 57%; at least 56.5%; at least 56%; at least 55.5%; at least 55%; at least 54.5%; at least 54%; at least 53.5%; at least 53%; at least 52.5%; at least
- 10 52%; at least 51.5%; at least 51%; at least 50.5%; at least 50%; at least 49.5%; at least 49%; at least 48.5%; at least 48%; at least 47.5%; at least 47%; at least 46.5%; at least 46%; at least 45.5%; at least 45%; at least 44.5%; at least 44%; at least 43.5%; at least 43%; at least 42.5%; at least 42%; at least 41.5%; at least 41%; at least 40.5%; at least 40%; at least 39.5%; at least 39%; at least 38.5%; at least 38%; at least 37.5%; at least 37%; at least 36.5%; at
- 15 least 36%; at least 35.5%; at least 35%; at least 34.5%; at least 34%; at least 33.5%; at least 33%; at least 32.5%; at least 32%; at least 31.5%; at least 31%; at least 30.5%; at least 30%; at least 29.5%; at least 29%; at least 28.5%; at least 28%; at least 27.5%; at least 27%; at least 26.5%; at least 26%; at least 25.5%; at least 25%; at least 24.5%; at least 24%; at least 23.5%; at least 23%; at least 22.5%; at least 22%; at least 21.5%; at least 21%; at least 20.5%;
- 20 at least 20%; at least 19.5%; at least 19%; at least 18.5%; at least 18%; at least 17.5%; at least 17%; at least 16.5%; at least 16%; at least 15.5%; at least 15%; at least 14.5%; at least 14%; at least 13.5%; at least 13%; at least 12.5%; at least 12%; at least 11.5%; at least 11%; at least 10.5%; at least 10%; and a value within a range defined by any two of the aforementioned values.
- 25 [00209] In some embodiments, after at least 4 weeks of storage at room temperature said composition is capable of maintaining about 60% to about 80% cell viability relative to the initial cell viability immediately prior to the start of said storage.
- [00210] In some embodiments, the composition comprises a prebiotic.
- [00211] In some embodiments, the composition comprises a carrier.
- 30 [00212] In some embodiments, the composition comprises an insoluble fibre, a buffer, an osmotic agent, an antifoaming agent, and/or a preservative.
- [00213] In some embodiments, the composition comprises a chemostat medium.
- [00214] In some embodiments, the composition comprises a saline composition.
- [00215] In some embodiments, the composition comprises a resistant starch.
- 35 [00216] In some embodiments, the composition is lyophilized with pharmaceutically acceptable excipients.

[00217] In some embodiments, the composition comprises a stabiliser and/or cryoprotectant.

[00218] In some embodiments, such ingredients (e.g., agents, materials, etc.) are included in the co-culture, the formulation for administration to a subject, or both according to several
5 embodiments. Such ingredients may be natural or non-naturally occurring (e.g., partially or fully modified, synthetic, etc.).

[00219] In some embodiments, the cryoprotectant is selected from the group consisting of: trehalose; inulin; maltodextrin; mannitol; sucrose; glycerol; sorbitol; DMSO; propylene glycol; ethylene glycol; saccharose; galactose-lactose; and any combination or multitude thereof.

10 [00220] In some embodiments, said cryoprotectant further comprises a compound selected from the group consisting of: glycerol; polyethylene glycol (PEG); glycerine; erythritol; arabitol; xylitol; sorbitol; glucose; lactose; ribose; classes of antioxidants; oxygen reducers; and any combination or multitude thereof.

[00221] In some embodiments, said cryoprotectant is trehalose at a concentration of 2%
15 to 15% (e.g., 2-6%, 6-12%, 10-15%, and overlapping ranges therein) in said lyophilized formulation.

[00222] In some embodiments, said cryoprotectant is inulin at a concentration of 2% to 15% (e.g., 2-6%, 6-12%, 10-15%, and overlapping ranges therein) in said lyophilized formulation.

20 [00223] In some embodiments, said cryoprotectant is maltodextrin at a concentration of 2% to 15% (e.g., 2-6%, 6-12%, 10-15%, and overlapping ranges therein) in said lyophilized formulation.

[00224] In some embodiments, said cryoprotectant is trehalose at a concentration of at least 5% in said lyophilized formulation.

25 [00225] In some embodiments, said cryoprotectant is trehalose at a concentration of at least 10% in said lyophilized formulation.

[00226] In some embodiments, said composition is a pharmaceutical composition.

[00227] In some embodiments, the at least one strain of bacteria is diluted with an inert powdered diluent.

30 [00228] In some embodiments, said composition comprises one or more pharmaceutically acceptable carriers or excipients.

[00229] In some embodiments, said composition is formulated as a gellab, pill, enema, microcapsule, capsule, powder, caplet, or tablet.

35 [00230] In some embodiments, the capsule or tablet is enteric-coated, pH dependent, slow-release, and/or gastro-resistant.

[00231] In some embodiments, the composition is adapted for administration orally, colonically or rectally.

[00232] In some embodiments, every 200 mg of the composition comprises a pharmacologically active dose of bacteria cells or spores selected from the group consisting of: 10^3 to 10^{14} ; 10^4 to 10^{14} ; 10^5 to 10^{14} ; 10^6 to 10^{14} ; 10^7 to 10^{14} ; 10^8 to 10^{14} ; 10^4 to 10^{13} ; 10^5 to 10^{12} ; 10^6 to 10^{11} ; 10^7 to 10^{10} ; 10^8 to 10^9 ; 10^3 to 10^{13} ; 10^3 to 10^{12} ; 10^3 to 10^{11} ; 10^3 to 10^{10} ; 10^3 to 10^9 ; 10^3 to 10^8 ; 10^3 to 10^7 ; 10^3 to 10^6 ; 10^3 to 10^5 ; 10^3 to 10^4 colony forming units (cfu) or total cell count; and a value within a range defined by any two of the aforementioned values.

[00233] In some embodiments, the composition comprises a pharmacologically active dose of bacteria cells or spores selected from the group consisting of: from 10 million cfu/mL to 100 billion cfu/mL, from 10 million to 50 million cfu/mL, more preferably from 50 million to 100 million cfu/mL, from 100 million to 500 million cfu/mL, from 500 million to 1 billion cfu/mL, from 1 billion to 5 billion cfu/mL, from 5 billion to 10 billion cfu/mL, from 10 billion to 15 billion cfu/mL, from 15 billion to 20 billion cfu/mL, from 20 billion to 25 billion cfu/mL, from 25 billion to 30 billion cfu/mL, from 30 billion to 35 billion cfu/mL, from 35 billion to 40 billion cfu/mL, from 40 billion to 45 billion cfu/mL, from 45 billion to 50 billion cfu/mL, from 50 billion to 55 billion cfu/mL, from 55 billion to 60 billion cfu/mL, from 60 billion to 65 billion cfu/mL, from 65 billion to 70 billion cfu/mL, from 70 billion to 75 billion cfu/mL, from 75 billion to 80 billion cfu/mL, from 80 billion to 85 billion cfu/mL, from 85 billion to 90 billion cfu/mL, from 90 billion to 95 billion cfu/mL, from 95 billion to 100 billion cfu/mL and a value within a range defined by any two of the aforementioned values.

[00234] In some embodiments, a single dosage form, such as a single capsule, tablet, pill, or powder, includes an amount of bacterial cells ranging from 1 million cfu per dosage form to 100 billion cfu per dosage form, such as 1 million to 50 million cfu per dosage form, 50 million to 100 million cfu per dosage form, 100 million to 500 million cfu per dosage form, 500 million to 1 billion cfu per dosage form, 1 billion to 5 billion cfu per dosage form, 5 billion to 10 billion cfu per dosage form, 10 billion to 15 billion cfu per dosage form, 15 billion to 20 billion cfu per dosage form, 20 billion to 25 billion cfu per dosage form, 25 billion to 30 billion cfu per dosage form, 30 billion to 35 billion cfu per dosage form, 35 billion to 40 billion cfu per dosage form, 40 billion to 45 billion cfu per dosage form, 45 billion to 50 billion cfu per dosage form, 50 billion to 55 billion cfu per dosage form, 55 billion to 60 billion cfu per dosage form, 60 billion to 65 billion cfu per dosage form, 65 billion to 70 billion cfu per dosage form, 70 billion to 75 billion cfu per dosage form, 75 billion to 80 billion cfu per dosage form, 80 billion to 85 billion cfu per dosage form, 85 billion to 90 billion cfu per dosage form, 90 billion to 95 billion cfu per dosage form, 95 billion to 100 billion cfu per dosage form, or an amount within a range defined by any two of the aforementioned values.

[00235] In some embodiments, the dosage form is an amount ranging from about 50 mg to about 1000 mg, such as 50, 100, 200, 300, 400, 500, 600, 700, 800, 900, or 1000 mg, or an amount within a range defined by any two of the aforementioned values.

[00236] In some embodiments, the formulation or composition is administered as a single dosage form or as a multi-dosage form, such as 1, 2, 3, 4, 5, or 6 or more dosages. In some embodiments, the formulations are administered once or multiple times daily, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 times daily in single or multi-dosage form. In some embodiments, a daily dosage of the formulations are administered all at once or are spread out during a the day. wherein the formulations or compositions comprise is administered hourly, or once every 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7, hours, 8 hours, 9 hours, 10 hours, 11 hours, 12 hours, 13 hours, 14 hours, 15 hours, 16 hours, 17 hours, 18 hours, 19 hours, 20 hours, 21 hours, 22 hours, 23 hours, 24 hours, 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 1 year, 2 years, 3 years, 4 years, or 5 years. In some embodiments, the formulations are administered over a period of 1 day, 2 days, 3 days, 4 days, 5 days, 6 days, 7 days, 1 week, 2 weeks, 3 weeks, 4 weeks, 5 weeks, 6 weeks, 1 month, 2 months, 3 months, 4 months, 5 months, 6 months, 7 months, 8 months, 9 months, 10 months, 11 months, 12 months, 1 year, 2 years, 3 years, 4 years, 5 years, 6 years, 7 years, 8 years, 9 years, 10 years, or more, or indefinitely. In some embodiments, the formulations are administered at various dosages and amounts at different periods or stages of health, including, for example, at higher dosages during an induction stage or at lower dosages during maintenance stage.

[00237] In some embodiments, the formulation or composition comprise a plurality of microbial species produced by co-culturing the plurality of microbial species in a single vessel, such as a bioreactor. In some embodiments, the co-culture of the plurality of microbial species includes an amount of bacterial cells ranging from 10 million cfu/mL to 100 billion cfu/mL, from 10 million to 50 million cfu/mL, from 50 million to 100 million cfu/mL, from 100 million to 500 million cfu/mL, from 500 million to 1 billion cfu/mL, from 1 billion to 5 billion cfu/mL, from 5 billion to 10 billion cfu/mL, from 10 billion to 15 billion cfu/mL, from 15 billion to 20 billion cfu/mL, from 20 billion to 25 billion cfu/mL, from 25 billion to 30 billion cfu/mL, from 30 billion to 35 billion cfu/mL, from 35 billion to 40 billion cfu/mL, from 40 billion to 45 billion cfu/mL, from 45 billion to 50 billion cfu/mL, from 50 billion to 55 billion cfu/mL, from 55 billion to 60 billion cfu/mL, from 60 billion to 65 billion cfu/mL, from 65 billion to 70 billion cfu/mL, from 70 billion to 75 billion cfu/mL, from 75 billion to 80 billion cut/mL, from 80 billion to 85 billion cfu/mL, from 85 billion to 90 billion cfu/mL, from 90 billion to 95 billion cfu/mL, or from 95 billion to 100 billion cfu/mL, or a range within any of the aforementioned values. In some embodiments, the vessel or bioreactor has a capacity ranging from about 1 mL to about 10,000 L, such as 1 mL, 5 mL, 10 mL, 100 mL, 0.5 L, 1 L, 2 L, 3 L, 4 L, 5 L, 10 L, 20 L, 50 L, 100 L, 500 L, 1000 L, 2000 L, 3000 L, 4000 L, 5000 L, 6000 L, 7000 L, 8000 L, 9000 L, or 10,000 L, or an amount within a range defined by any two of the aforementioned values.

[00238] In some embodiments, a single formulation (provided for example in a capsule, tablet, powder, or other oral formulation) is capable of treating a particular disease amongst the population suffering from said disease.

5 [00239] In some embodiments, precision therapeutics are provided wherein the formulation is altered based on sex, ethnicity, disease sub-types, diet, age, etc.

[00240] In some embodiments, personalized formulations may also be provided that are individualized to a patient.

[00241] In some embodiments, the types and numbers of core community and keystone
10 strain are selected to deliver a therapeutically effective dose to a subject and/or for the treatment of a disease or its symptoms.

[00242] In some embodiments, other routes of administration may also be used (including but not limited to inhalation, rectal, vaginal, implants (e.g., on a scaffold or substrate), etc.)

[00243] In several embodiments, the types and numbers of core community and keystone
15 strain are selected to deliver a therapeutically effective dose to a subject and/or for the treatment of a disease or its symptoms, such as, for example, ulcerative colitis, inflammatory bowel disease, Crohn's disease, checkpoint inhibitor colitis, primary sclerosing cholangitis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, hepatic encephalopathy, obesity, insulin resistance, type 2 diabetes, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer,
20 breast cancer, lung cancer, testicular cancer, sarcoma, dyslipidaemia, atherosclerotic heart disease, hypertension, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis, psoriasis, systemic lupus erythematosus, Sjogren's disease, food allergy, anaphylaxis, atopic dermatitis, atopic rhinitis or sinusitis, clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory
25 infections, sepsis, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, or schizophrenia, or combinations thereof.

[00244] In some embodiments, the composition comprises a pharmacologically active dose of bacteria cells or spores wherein the concentration of the bacteria cells or spores as a dry microbial body, is selected from the group consisting of: between 5 to 50 w/w %, 1 to 75
30 w/w %, 0.1 to 100 w/w % and 1 to 100 w/w %.

[00245] In some embodiments, the microbial consortium comprises: a plurality of active microbes and an effective amount of a supportive community of microbes, wherein the plurality of active microbes metabolize a first metabolic substrate to produce one or more than one metabolite, wherein the first metabolic substrate causes or contributes to disease in an animal,
35 and the supportive community of microbes comprises between 1 and 1000 microbial strains, wherein for the supportive community of microbes, at least one of the following four conditions is met: 1) the supportive community of microbes metabolizes 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 first metabolic substrate by one or more of the plurality of active microbes, 2) the supportive community of microbes increases 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, 3) the supportive community of microbes enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and 4) the supportive community of microbes catalyzes one or more than one reaction selected from the group consisting of: 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, 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, 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, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[00246] In some embodiments, the microbial consortium: 1) metabolizes 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 first metabolic substrate by one or more of the plurality of active microbes, and 2) increases 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.

[00247] In some embodiments, the microbial consortium: 1) metabolizes 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 first metabolic substrate by one or more of the plurality of active microbes, and 2) enhances one or more than one characteristic of the plurality of active microbes when administered to the animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d)

longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes.

[00248] In some embodiments, the microbial consortium: 1) metabolizes one or more than one metabolite produced by the plurality of active microbes, wherein the one or more than one
5 metabolite inhibits metabolism of the first metabolic substrate by one or more of the plurality of active microbes, and 2) catalyzes one or more than one reaction selected from the group consisting of: 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, fermentation of amino acids
10 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, 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,
15 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, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and
20 conversion of 7- oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[00249] In some embodiments, the microbial consortium: 1) increases 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, and 2) enhances one or more than one characteristic of the plurality of active microbes when administered to the
25 animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes.

[00250] In some embodiments, the microbial consortium: 1) increases 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, and 2) catalyzes one or more than one reaction selected from the group consisting of: 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, fermentation of amino acids to one or more than one of the group
30 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, 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, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).
- 5 [00251] In some embodiments, the microbial consortium: 1) enhances one or more than one characteristic of the plurality of active microbes when administered to the animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and 2)
- 15 catalyzes one or more than one reaction selected from the group consisting of: 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, fermentation of amino acids to one or more than one of the group consisting of acetate, propionate, butanoate, butyrate, isobutyrate,
- 20 2- methylbutyrate, isovalerate, isocaproate, 3-phenylpropanoate, phloretate, 3- (1H-indol-3-yl)propanoate, 5-aminopentanoate, H₂, H₂S, and CO₂, 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,
- 25 deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7- oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).
- 30 [00252] In some embodiments, the microbial consortium: 1) metabolizes 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 first metabolic substrate by one or more of the plurality of active microbes, 2) increases 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
- 35 metabolic substrate, and 3) enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d)

longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes.

[00253] In some embodiments, the microbial consortium: 1) increases 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, and 2) enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and 3) catalyzes one or more than one reaction selected from the group consisting of: 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, 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, 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, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[00254] In some embodiments, the microbial consortium: 1) metabolizes 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 first metabolic substrate by one or more of the plurality of active microbes, 2) increases 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, and 3) catalyzes one or more than one reaction selected from the group consisting of: 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, 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, 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, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[00255] In some embodiments, the microbial consortium: 1) metabolizes 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 first metabolic substrate by one or more of the plurality of active microbes, 2) enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a) gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and 3) catalyzes one or more than one reaction selected from the group consisting of: 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, 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, 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, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[00256] In some embodiments, the microbial consortium: 1) metabolizes 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 first metabolic substrate by one or more of the plurality of active microbes, 2) increases 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, 3) enhances one or more than one characteristic of the plurality of active microbes when administered to an animal selected from the group consisting of: a)

gastrointestinal engraftment, b) biomass, c) first metabolic substrate metabolism, and d) longitudinal stability as compared to administration of the plurality of active microbes in the absence of the supportive community of microbes, and 4) catalyzes one or more than one reaction selected from the group consisting of: 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, 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, 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, deconjugation of conjugated bile acids to produce primary bile acids, conversion of cholic acid (CA) to 7-oxocholic acid, conversion of 7-oxocholic acid to 7-beta-cholic acid (7betaCA), conversion of chenodeoxycholic acid (CDCA) to 7-oxochenodeoxycholic acid, and conversion of 7-oxochenodeoxycholic acid to ursodeoxycholic acid (UDCA).

[00257] In some embodiments, at least one of the two following conditions is met: the first metabolic substrate metabolizing activity of at least one of the plurality of active microbes is significantly different when measured in a standardized substrate metabolization assay at two pH values within a range of 4 to 8, and wherein the difference between the two pH values is at least one pH unit, and the first metabolic substrate metabolizing activity of at least one of the plurality of active microbes is significantly different when measured in a standardized substrate metabolization assay at two first metabolic substrate concentrations within a 100 fold range, and wherein the difference between the two first metabolic substrate concentrations is at least 1.2-fold.

[00258] In some embodiments, the microbial consortium comprises a plurality of between 1 and 1000 defined microbial strains, wherein the defined gut microbial community is capable of: a. metabolizing at least 90% of enumerated substrates selected from the group consisting of: a-mannan (yeast), acetate, agarose, alanine, alginate, anthocyanin, arabinan, arabinogalactan, arabinoxylan, arginine, asparagine, Aspartate, b- glucans, butyrate, carrageenan, chitin, chlorogenic acids, chondroitin sulfate, cinnamic acid, Cysteine, dextran (40), Dihydrochalcones, Enterodiol, flavan-3-ols, flavanones, flavones, flavonols, folate, formate, galactomannan (carob), galacturonan (homo), galacturonate, glucomannan (konjac), glutamate, Glutamine, Glycine, Histidine, hyaluronan, hydrogen, hydroxycinnamic acids, hydroxyproline, inulin, isoflavones/isoflavanones, Isoleucine, lactate, laminarin, Leucine,

levan, Lysine, Methionine, mucin O-linked glycans, Ornithine, Phenylalanine, porphyrin, Proline, propionate, rhamnogalacturonan I, rhamnogalacturonan II, Secoisolariciresinol diglucoside, Serine, starch (potato), starch (structure 1), thiamine, Threonine, tryptophan, Tyrosine, Valine, xyloglucan, and xylooligosaccharides (XOS), and/or b. producing at least
 5 90% of enumerated metabolites selected from the group consisting of: formate, acetate, propionate, butyrate, isobutyrate, valerate, isovalerate, 2-methylbutyrate, caporate, isocaporate, 3-methylvaleric acid, L-phenylalanine, 3-phenylpropionic acid, phenylpyruvate, DL-3-phenyllactic acid, trans-cinnamic acid, phenyllactic acid, phenethylamine, L-tyrosine, 3-(4-hydroxyphenyl)propionic acid, 3-(4-hydroxyphenyl) pyruvic acid, DL-p-hydroxyphenyl
 10 lactic acid, p-coumaric acid, 4-hydroxyphenyl acetic acid, tyramine, phenol, p-cresol, 4-ethylphenol, 4-vinylphenol, 4-hydroxybenzoic acid, L-tryptophan, 3-indolepropionic acid, 3-indolepyruvic acid, DL-indole-3-lactic acid, trans-3-indoleacrylic acid, 3-indoleacetic acid, tryptamine, indole, skatol, indole-3-carboxylic acid, indole-3-carboxyaldehyde, N-acetyl-L-phenylalanine, phenylpropionylglycine, 3-(3-hydroxyphenyl) propionic acid, cinnamoylglycine,
 15 phenylacetylglutamine, hippuric acid, 2-hydroxyhippuric acid, 3-hydroxyhippuric acid, 4-hydroxyhippuric acid, 4-hydroxyphenylacetylglutamine, phenyl sulfate, phenyl glucuronide, p-cresol sulfate, p-cresol glucuronide, 4-ethylphenol sulfate, 4-ethylphenol glucuronide, N-acetyl-L-tryptophan, 5-hydroxy-L-tryptophan, N-acetyl serotonin, 3-indolepropionylglycine, indolyl-3-acryloylglycine, indoxyl sulfate, indoxyl glucuronide, 5-
 20 hydroxyindole-3-acetic acid, indoleacetylglutamine, lithocholic acid, murocholic acid, ursodeoxycholic acid, hyodeoxycholic acid, deoxycholic acid, 7-oxocholic acid, co-muricholic acid, a-muricholic acid, b-muricholic acid, g-muricholic acid, 7Pcholic acid, tauroolithocholic acid, tauroursodeoxycholic acid, taurohyodeoxycholic acid, taurochenodeoxycholic acid, taurodeoxycholic acid, tauro-P-muricholic acid, tauro-co-muricholic acid, and taurocholic acid,
 25 wherein the defined gut microbial community achieves substantial engraftment when administered to a gnotobiotic mouse; and wherein the engrafted defined gut microbial community is stable following a human fecal community microbial challenge.

[00259] In some embodiments, the metabolization of a substrate and/or production of a product can be determined by administering the defined gut microbial community to a
 30 gnotobiotic mouse and measuring whether the substrate is metabolized and/or the product is produced after a defined period of time by liquid chromatography-mass spectrometry analysis of a sample obtained from the mouse.

[00260] In some embodiments, the microbial consortium comprises microbes that comprises a gene that is responsible for a phenotype selected from the group consisting of:
 35 reducing endogenous sulphide levels in the colon of a patient in need thereof; sulphide consumption; reducing sulphide and nitric oxide load on epithelial cells which affects cell respiration leading to a metabolic lesion; reducing relative abundance and or metabolic activity

of sulfidogenic microbiota; reducing sulphide levels in the colon directly through consumption/assimilation; reducing sulphide levels, relative abundance and or metabolic activity of sulfidogenic microbiota in the colon by metabolic substrate competition; reducing sulphide levels, relative abundance and or metabolic activity of sulfidogenic microbiota in the colon by diverting metabolic substrates away from the production of sulphide; reducing sulphide levels, relative abundance and or metabolic activity of sulfidogenic microbiota in the colon by consuming H_2 ; reducing sulphide levels, relative abundance and or metabolic activity of sulfidogenic microbiota by reducing release of metabolizable sulfur substrates; reducing sulphide levels, relative abundance and or metabolic activity of sulfidogenic microbiota by reducing sulfur amino acid release (methionine, cysteine, homocysteine and/or taurine) into the colon; reducing colonic protein fermentation; reducing nitric oxide production in the colon; reducing nitric oxide levels in the colon; and inducing colonocyte apoptosis in lesions to break an induced stable inflammatory state.

[00261] In some embodiments, the microbial consortium comprises microbes that comprise a gene that is responsible for the phenotype of sulfide consumption.

[00262] In some embodiments, the sulfide is present in a form of sulfide selected from the group consisting of: a sulfide ion (S^{2-}); a bisulfide ion (SH^-), an organic compound containing the group R-SH (a thiol); and hydrogen sulphide (H_2S).

[00263] In some embodiments, the microbial consortium comprises microbes that comprises a gene selected from the group consisting of: genes responsible for the use of sulfide in the biosynthesis of methionine and cysteine.

[00264] In some embodiments, the composition comprises a plurality of microbes.

[00265] In some embodiments, the composition is capable of: a. metabolizing at least 85%; 86%; 87%; 88%; 89%; 90%; 91%; 92%; 93%; 94%; 95%; 96%; 97%; 98%; 99%; or 100% of the substrates selected from the group consisting of: glucomannan (konjac); galacturonate; hydroxyproline; rhamnogalacturonan i; galacturonan (homo); aspartate; dextran (40); galactomannan (carob); phenylalanine; leucine; histidine; arabinogalactan; arabinan; chondroitin sulfate; dihydrochalcones; mucin o-linked glycans; alginate; glycine; glutamine; xyloglucan; laminarin; flavonols; proline; anthocyanin; glutamate; folate; asparagine; thiamine; isoflavones/isoflavanones; starch (structure 1); butyrate; cysteine; porphyran; starch (potato); acetate; inulin; enterodiol; xylooligosaccharides (xos); arabinoxylan; cinnamic acid; rhamnogalacturonan ii; flavones; hydroxycinnamic acids; flavanones; flavan-3-ols; arabinose; a-mannan (yeast); methionine; threonine; arginine; flavan-3-ols; tyrosine; propionate; serine; chitin; laminarin; valine; carrageenan; formate; ornithine; alanine; hydrogen; dihydrochalcones; lactate; flavan-3-ols; isoleucine; rhamnogalacturonan i; xylooligosaccharides (xos); enterodiol; secoisolariciresinol diglucoside; hydroxyproline; dextran (40); and levan; and b. producing at least 85%; 86%; 87%; 88%;

- 89%; 90%; 91%; 92%; 93%; 94%; 95%; 96%; 97%; 98%; 99%; or 100% of the metabolites selected from the group consisting of: 3-methylvaleric acid; phenylpropionylglycine; N-acetyl-L-phenylalanine; tauro- co-muricholic acid; N-acetyl serotonin; deoxycholic acid; tyramine; propionate; murocholic acid; phenethylamine; formate; isocaproate; 4-ethylphenol
- 5 glucuronide; isovalerate; DL-3-phenyllactic acid; p-coumaric acid; 4-hydroxyhippuric acid; caporate; 4- hydroxyphenylacetylglutamine; 2-hydroxyhippuric acid; phenylacetylglutamine; trans-3-indoleacrylic acid; 7Pcholic acid; indoleacetylglutamine; DL-indole-3 -lactic acid; 3-indolepyruvic acid; lithocholic acid; 4-hydroxybenzoic acid; cinnamoylglutamine; phenylacetylglutamine; N-acetyl- L-tryptophan; indoxyl glucuronide; phenol;
- 10 taurohyodeoxycholic acid; DL-p- hydroxyphenyl lactic acid; 4-ethylphenol sulfate; p-cresol glucuronide; 3-(4-hydroxyphenyl) pyruvic acid; trans-cinnamic acid; 3-indoleacetic acid; taurochenodeoxycholic acid; L-tryptophan; 5-hydroxyindole-3-acetic acid; acetate; tauroolithocholic acid; 5 -hydroxy -L-typtophan; phenyl sulfate; isobutyrate; phenyllactic acid; tauro-P-muricholic acid; ursodeoxycholic acid; indoxyl sulfate; L- phenylalanine; skatol;
- 15 taurocholic acid; 4-vinylphenol; phyenpyruvate; valerate; phenyl glucuronide; 3-indolepropionic acid; taurodeoxycholic acid; 2-methylbutyrate; indole; 4-hydroxyphenyl acetic acid; 3-(3-hydroxyphenyl) propionic acid; phenylpropionylglycine; phenylacetylglutamine; indolyl-3-acryloylglutamine; tryptamine; co-muricholic acid; b-muricholic acid; hyodeoxycholic acid; cinnamoylglutamine; 3-indolepriopionylglutamine; indole-3 -carboxyaldehyde; a-muricholic acid;
- 20 indole-3 -carboxylic acid; phenylacetylglutamine; phenylacetylglutamine; 4-ethylphenol; phenol; taurocholic acid; 3-(4- hydroxyphenyl)propionic acid; tauro- co-muricholic acid; 3-hydroxyhippuric acid; tauroolithocholic acid; phenyl sulfate; 7-oxocholic acid; tauro-P-muricholic acid; propionate; indoleacetylglutamine; phenyl glucuronide; indoleacetylglutamine; 3-indolepyruvic acid; murocholic acid; tyramine; taurohyodeoxycholic acid; and isobutyrate.
- 25 [00266] In some embodiments, metabolization of a substrate is determined by culturing the community of microbes and measuring whether the substrate is metabolized and/or the metabolite is produced by liquid chromatography-mass spectrometry analysis.
- [00267] In some embodiments, production of a metabolite is determined by culturing the community of microbes and measuring whether the substrate is metabolized and/or the
- 30 metabolite is produced by liquid chromatography-mass spectrometry analysis.
- [00268] In some embodiments, metabolization of a substrate can be determined by administering the community of microbes to a gnotobiotic mouse and measuring whether the substrate is metabolized and/or the product is produced after a defined period of time by liquid chromatography-mass spectrometry analysis.
- 35 [00269] In some embodiments, production of a product can be determined by administering the community of microbes to a gnotobiotic mouse and measuring whether the

substrate is metabolized and/or the product is produced after a defined period of time by liquid chromatography-mass spectrometry analysis.

[00270] In some embodiments, the defined period of time is a time period selected from the group consisting of: 1 hour; 2 hours; 4 hours; 8 hours; 12 hours; 24 hours; 2 days; 7 days; 14 days; 1 month; and 2 months.

[00271] In some embodiments, the composition encodes enzymes catalyzing all reactions at least 85%; at least 86%; at least 87%; at least 88%; at least 89%; at least 90%; at least 91%; at least 92%; at least 93%; at least 94%; at least 95%; at least 96%; at least 97%; at least 98%; at least 99%; or at least 100% of the MetaCyc metabolic pathways selected from the group consisting of: valine-syn-pwy; lysine-deg-1-pwy; pwy-622; trpiacat-pwy; citrulbio-pwy; alanine-syn2-pwy; pwy-7400; serdeg-pwy; pwy-7297; glusyn-iii-pwy; alanine-deg3-pwy; cysts-deg-pwy; beta-ala-degradation-i-pwy; hisdeg-pwy; pro-syn-pwy; arg-degrad-pwy; entbac-syn-pwy; tau-deg-pwy; pwy-7414; pwy-6936; glutde-g-i-pwy; gly-g-syn-ala-pwy; lysine-deg-ii-pwy; his-syn-pwy; pwy-609; pwy-320; ethyl-pwy; pwy-6533; aspasn-pwy; glusyn-pwy; pwy-7104; pwy-426; meth-anal-pwy; pwy-6790; phos-lip-syn-2-pwy; pwy-5739; pwy-6486; pwy-5921; trna-charging-pwy; pwy-7030; pwy-2841; pwy-6045; pwy-748; pwy-5221; pwy-710; pwy-4107; pwy-6130; pwy-8403; arg-deg-v-pwy; pwy-6039; pwy-7147; pwy-7221; arg-glu-pwy; pwy-7101; pwy-6196; pwy-7432; ala-cat-2-pwy; arg-deg-iii-pwy; phenylalanine-deg-i-pwy; cys-syn-pwy; spingolipid-syn-pwy; pwy-5818; trypdeg-pwy; pwy-7000; pwy-5863; homocys-degr-pwy; pwy-6240; pwy-5958; pwy-8102; arg-deg-i-v-pwy; trpkyn-cat-pwy; gly-g-pwy; pwy-5978; pro-ut-pwy; pwy-610; pwy-6818; pwy-8032; glusyn-pwy; pyridnuc-sal-pwy; pwy-5297; homoser-met-syn-pwy; alanine-valine-syn-pwy; threonine-deg-2-pwy; pwy-761; pwy-5913; thr-dlct-cat-pwy; gln-syn-pwy; pwy-6030; pwy-7430; pwy-7304; trpsyn-pwy; meth-acetate-pwy; sam-pwy; pwy-5458; pwy-4031; pwy-1781; pwy-8013; pwy-7025; pwy-5936; arg-ase-deg-pwy; glugln-syn-pwy; glutamin-deg-pwy; pwy-8071; glutamin-fum-pwy; pwy-1121; pwy-3338; pwy-5002; taurine-deg-pwy; hydroxyprodeg-pwy; pwy-840; pwy-7930; pwy-7014; asp-syn-pwy; glusyn-ii-pwy; pwy-402; arg-pro-pwy; pwy-4020; asn-deg-1-pwy; glusyn-pwy; arg-syn-4-pwy; pwy-5188; pwy-5766; asp-syn-pwy; pwy-8045; ala-cat-2-pwy; pwy-3155; pyriod-xsyn-pwy; pwy-5394; arg-synb-sub-pwy; lysine-amino-ad-pwy; beta-ala-degradation-i-pwy; pwy-8007; pwy-7030; pwy-6717; pwy-6263; pwy-5936; glut-deg-pwy; pwy-4070; val-deg-pwy; citrulline-deg-pwy; asp-deg-1-pwy; asparaginesyn-pwy; glut-or-pwy; glusyn-pwy; pwy-5710; pwy-861; pwy-7072; pwy-7986; trpsyn-pwy; pwy-8102; trna-charging-pwy; trpcat-pwy; trpkyn-cat-pwy; trpsyn-pwy; glnsyn-pwy; pwy-3341; pwy-7425; pwy-7432; pwy-7440; pwy-6444; pwy-7688; pwy-6769; pwy-4020; pwy-3004; pwy-4984; pwy-6769; pwy-7160; pwy-6196; pwy-6183; pwy-6181; asp-syn-pwy; pwy-8053; ala-cat-2-pwy; homocys-degr-pwy; pwy-6364; pwy-700; pwy-6790; alanine-syn2-pwy; alanine-valine-syn-pwy; threonine-deg-2-pwy; pwy-761; pwy-5913; thr-dlct-cat-pwy; gln-syn-pwy; pwy-6030; pwy-7430; pwy-7304; trpsyn-

pwy; meth-acetate-pwy; sam-pwy; pwy-5458; pwy-4031; pwy-1781; pwy-8013; pwy-7025;
 pwy-5936; arg-ase-deg-pwy; glugln-syn-pwy; glutamin-deg-pwy; pwy-8071; glutamin-fum-
 pwy; pwy-1121; pwy-3338; pwy-5002; taurine-deg-pwy; hydroxyprodeg-pwy; pwy-840; pwy-
 7930; pwy-7014; asp-syn-pwy; glusyn-ii-pwy; pwy-402; arg-pro-pwy; pwy-4020; asn-deg-1-
 5 pwy; glusyn-pwy; arg-syn-4-pwy; pwy-5188; pwy-5766; asp-syn-pwy; pwy-8045; ala-cat-2-
 pwy; pwy-3155; pyriod-xsyn-pwy; pwy-5394; arg-synb-sub-pwy; lysine-amino-ad-pwy; beta-
 ala-degradation-i-pwy; pwy-8007; pwy-7030; pwy-6717; pwy-6263; pwy-5936; glut-deg-pwy;
 pwy-4070; val-deg-pwy; citrulline-deg-pwy; asp-deg-1-pwy; asparaginesyn-pwy; glut-or-pwy;
 glusyn-pwy; pwy-5710; pwy-861; pwy-7072; pwy-7986; trpsyn-pwy; pwy-8102; trna-charging-
 10 pwy; trpcat-pwy; trpkyn-cat-pwy; trpsyn-pwy; glnsyn-pwy; pwy-3341; pwy-7425; pwy-7432;
 pwy-7440; pwy-6444; pwy-7688; pwy-6769; pwy-4020; pwy-3004; pwy-4984; pwy-6769; pwy-
 7160; pwy-6196; pwy-6183; pwy-6181; asp-syn-pwy; pwy-8053; ala-cat-2-pwy; homocys-
 degr-pwy; pwy-6364; pwy-700; pwy-6790; alanine-syn2-pwy; alanine-valine-syn-pwy;
 threonine-deg-2-pwy; pwy-761; pwy-5913; thr-dlct-cat-pwy; gln-syn-pwy; pwy-6030; pwy-
 15 7430; pwy-7304; trpsyn-pwy; meth-acetate-pwy; sam-pwy; pwy-5458; pwy-4031; pwy-1781;
 pwy-8013; pwy-7025; pwy-5936; arg-ase-deg-pwy; glugln-syn-pwy; glutamin-deg-pwy; pwy-
 8071; glutamin-fum-pwy; pwy-1121; pwy-3338; pwy-5002; taurine-deg-pwy; hydroxyprodeg-
 pwy; pwy-840; pwy-7930; pwy-7014; asp-syn-pwy; glusyn-ii-pwy; pwy-402; arg-pro-pwy; pwy-
 4020; asn-deg-1-pwy; glusyn-pwy; arg-syn-4-pwy; pwy-5188; pwy-5766; and asp-syn (as
 20 defined in WO2021/237162).

[00272] In some embodiments, encoding the enzymes catalyzing all reactions of a
 MetaCyc metabolic pathway can be determined by culturing the community of microbes and
 measuring whether a substrate in the pathway is metabolized, a metabolite in the pathway is
 produced, and/or a reaction intermediate in the pathway is produced by liquid
 25 chromatography-mass spectrometry analysis.

[00273] In some embodiments, encoding the enzymes catalyzing all reactions of a
 MetaCyc metabolic pathway can be determined by administering the community of microbes
 to a gnotobiotic mouse and measuring whether a substrate in the pathway is metabolized, a
 metabolite in the pathway is produced, and/or a reaction intermediate in the pathway is
 30 produced after a defined period of time by liquid chromatography-mass spectrometry analysis
 of a sample obtained from the mouse.

[00274] In some embodiments, the substrates or nutrients metabolized by a metabolic
 pathway are selected from the group consisting of: leucine; arabinan; acetate; chondroitin
 sulfate; dihydrochalcones; folate; laminarin; cinnamic acid; thiamine;
 35 isoflavones/isoflavanones; anthocyanin; arabinoxylan; starch (structure 1); isoleucine;
 butyrate; starch (potato); hydroxyproline; rhamnogalacturonan I; proline; galacturonate;
 galactomannan (carob); flavonols; glucose; arabinogalactan; valine; hydrogen; mucin O-linked

glycans; xyloglucan; formate; flavan-3-ols; tyrosine; threonine; glyc; rhamnogalacturonan II; phenylalanine; xanthan gum; chitin; b-glucans; flavanones; propionate; hydroxycinnamic acids; hyaluronan; asparagine; glutamine; alanine; glutamate; alginate; enterodiol; arabinogalactan; xylooligosaccharides (XOS); seciosolariciresinol diglucoside; histidine; arabinoxylan; mucin O-linked glycans; dextran (40); glucomannan (konjac); and alginate.

[00275] In some embodiments, the substrates or nutrients metabolized by a metabolic pathway comprises at least 85%; at least 86%; at least 87%; at least 88%; at least 89%; at least 90%; at least 91%; at least 92%; at least 93%; at least 94%; at least 95%; at least 96%; at least 97%; at least 98%; at least 99%; or at least 100%; of the substrates described herein.

[00276] In some embodiments, the metabolites synthesized or produced by a metabolic pathway are selected from the group consisting of: acetate; 2-hydroxyhippuric acid; 3-(3-hydroxyphenyl)propionic acid; 3-(4-hydroxyphenyl)propionic acid; 3-(4-hydroxyphenyl)pyruvic acid; 3-indoleacetic acid; 3-indolepropionic acid; 3-indolepropionylglycine; 3-indolepyruvic acid; 3-methyl valeric acid; 4-ethylphenol; 4-ethylphenol glucuronide; 4-ethylphenol sulfate; 4-hydroxybenzoic acid; 4-hydroxyphenyl acetic acid; 4-hydroxyphenylacetylglutamine; 4-hydroxyhippuric acid; 4-vinylphenol; 5-hydroxy-L-tryptophan; β -muricholic acid; α -muricholic acid; γ -muricholic acid; co-muricholic acid; caproate; cinnamoylglycine; DL-3-phenyllactic acid; DL-indole-3-lactic acid; DL-p-hydroxyphenyl lactic acid; deoxycholic acid; formate; hyodeoxycholic acid; indole; indole-3-carboxy aldehyde; indole-3-carboxylic acid; indoleacetylglutamine; indolyl-3-acryloylglycine; indoxyl glucuronide; indoxyl sulfate; isobutyrate; isocaproate; isovalerate; L-phenylalanine; L-tryptophan; lithocholic acid; murocholic acid; N-acetyl-L-phenylalanine; N-acetyl-L-tryptophan; N-acetyl serotonin; phenethylamine; phenol; phenylacetylglutamine; phenylacetylglutamine; phenylpropionylglycine; phenylpyruvate; phenyl sulfate; phenyl glucuronide; propionate; p-coumaric acid; p-cresol; p-cresol sulfate; p-cresol glucuronide; skatol; taurocholic acid; taurodeoxycholic acid; tauro- β -muricholic acid; tauro-co-muricholic acid; taurochenodeoxycholic acid; tauroursodeoxycholic acid; tauroursodeoxycholic acid; taurohyodeoxycholic acid; trans-3-indoleacrylic acid; trans-cinnamic acid; tryptamine; valerate; ursodeoxycholic acid; 7-oxocholic acid; and 7 α -cholic acid.

[00277] In some embodiments, the metabolites synthesized or produced by a metabolic pathway comprise at least 85%; at least 86%; at least 87%; at least 88%; at least 89%; at least 90%; at least 91%; at least 92%; at least 93%; at least 94%; at least 95%; at least 96%; at least 97%; at least 98%; at least 99%; or at least 100%; of the substrates described herein.

[00278] In some embodiments, the microbial communities metabolize at least 85% (e.g., at least 85%; 86%; 87%; 88%; 89%; 90%; 91%; 92%; 93%; 94%; 95%; 96%; 97%; 98%; 99%; or 100%) of the substrates described above and produce at least 85% (e.g., at least 85%;

86%; 87%; 88%; 89%; 90%; 91%; 92%; 93%; 94%; 95%; 96%; 97%; 98%; 99%; or 100%) of the metabolites described herein.

[00279] In some embodiments, the microbial communities metabolize at least 85% (e.g., at least 85%; 86%; 87%; 88%; 89%; 90%; 91%; 92%; 93%; 94%; 95%; 96%; 97%; 98%; 99%;
5 or 100%) of the substrates described above and utilize at least 85% (e.g., at least 85%; 86%; 87%; 88%; 89%; 90%; 91%; 92%; 93%; 94%; 95%; 96%; 97%; 98%; 99%; or 100%) of the MetaCyc metabolic pathways described herein.

[00280] In some embodiments, the composition is assembled to produce at least 85% (e.g., at least 85%; 86%; 87%; 88%; 89%; 90%; 91%; 92%; 93%; 94%; 95%; 96%; 97%; 98%;
10 99%; or 100%) of the metabolites described above and utilize at least 85% (e.g., at least 85%; 86%; 87%; 88%; 89%; 90%; 91%; 92%; 93%; 94%; 95%; 96%; 97%; 98%; 99%; or 100%) of the MetaCyc metabolic pathways described herein.

[00281] In some embodiments, the composition achieves substantial engraftment when administered to a gnotobiotic mouse.

15 [00282] In some embodiments, the community of microbes is stable following a human fecal community microbial challenge.

[00283] In some embodiments, the composition comprises two or more microbial consortiums.

[00284] In some embodiments, the composition is supplemented with a biological active
20 ingredient or agent.

[00285] In some embodiments, biotherapeutic composition comprising the composition of an embodiment of the invention, together with an acceptable diluent or carrier.

[00286] In some embodiments, a pharmaceutical composition comprising the composition of an embodiment of the invention, together with a pharmaceutically acceptable diluent or
25 carrier.

[00287] In some embodiments, a dosage form comprising the composition according to an embodiment of the invention.

[00288] In some embodiments, the dosage form is a unity dosage form.

[00289] In some embodiments, an isolated non-inflammatory strain of bacteria comprising
30 a 16S ribosomal RNA (rRNA) gene having a nucleotide sequence selected from the group consisting of: SEQ ID NO'S 1 to 286.

[00290] In some embodiments, at least one strain of bacteria comprises a 16S ribosomal RNA (rRNA) gene have a sequence identity to one or more SEQ ID NO'S 1 to 286, wherein the sequence identity is selected from the group consisting of: at least 99.9%; at least 99%; at
35 least 98%; at least 97%; at least 96%; at least 95%; at least 94%; at least 93%; at least 92%; at least 91%; and at least 90%.

[00291] In some embodiments, a novel species or strain of microbe, wherein the microbe is selected from the group consisting of: any one of the species selected from a table selected from: Table 9; Table 10; Table 11; Table 12; Table 13; Table 14; Table 15; Table 16.

5 [00292] In some embodiments, the microbe has a less than 97% sequence identity (16S) to the NCBI 16S refSEQ database.

[00293] In some embodiments, a formulation comprising: the composition of an embodiment of the invention, wherein the formulation is formulated as a capsule, tablet, or powder.

10 [00294] In some embodiments, a formulation comprising: a plurality of core community microbial species, wherein said core community microbial species comprise members of at least the following genera: *Dysosmobacter*, *Enterocloster*, *Ruthenibacterium*, *Vescimonas*, *Phocaeicola*, *Pusillimonas*, *Solibaculum*, and *Christensenella*, a plurality of keystone microbial species, wherein said keystone microbial species comprise members of at least the genus *Phocaeicola*, and a non-naturally occurring pharmaceutically acceptable excipient, wherein
15 the formulation is formulated as a capsule, tablet, or powder.

[00295] In some embodiments, the plurality of core community microbial species comprises at least the following species: *Dysosmobacter welbionis*, *Enterocloster bolteae*, *Ruthenibacterium lactatiformans*, *Vescimonas coprocola*, *Phocaeicola salanitronis*, *Pusillimonas faecalis*, *Solibaculum mannosilyticum*, *Christensenella minuta*, *Alistipes magaguti*, *Parabacteroides goldsteinii*, *Alistipes communis*, *Ruminococcus bicirculans*, *Bacteroides caecimuris*, *Alistipes dispar*, and *Bacteroides salyersiae*; and wherein the plurality of keystone microbial species comprises at least the following species: *Phocaeicola coprocola*, *Bifidobacterium bifidum*, and *Coprococcus catus*.

25 [00296] In some embodiments, the plurality of core community microbial species comprises at least the following species: *Alistipes dispar*, *Bacteroides salyersiae*, *Bifidobacterium bifidum*, *Christensenella minuta*, *Coprococcus catus*, *Coprococcus sp000154245*, *Dysosmobacter faecalis*, *Faecalibacterium duncaniae*, *Gemmiger formicilis*, *Parabacteroides goldsteinii*, *Ruminococcus bicirculans*, *Ruthenibacterium lactatiformans*, *Solibaculum mannosilyticum*, and *Vescimonas coprocola*.

30 [00297] In some embodiments, a formulation comprising: a plurality of core community microbial species, wherein said core community microbial species comprise members of at least one of the following genera: *Dysosmobacter*, *Enterocloster*, *Ruthenibacterium*, *Vescimonas*, *Phocaeicola*, *Pusillimonas*, *Solibaculum*, and *Christensenella*, a plurality of keystone microbial species, wherein said keystone microbial species comprise members of at least the genus *Phocaeicola*, and a non-naturally occurring pharmaceutically acceptable
35 excipient, wherein the formulation is formulated as a capsule, tablet, or powder.

- [00298] In some embodiments, the plurality of core community microbial species comprises at least one of the following species: *Dysosmobacter welbionis*, *Enterocloster bolteae*, *Ruthenibacterium lactatiformans*, *Vescimonas coprocola*, *Phocaeicola salanitronis*, *Pusillimonas faecalis*, *Solibaculum mannosilyticum*, *Chrstensenella minuta*, *Alistipes*
5 *magaguti*, *Parabacteroides goldsteinii*, *Alistipes communis*, *Ruminococcus bicirculans*, *Bacteroides caecimuris*, *Alistipes dispar*, and *Bacteroides salversiae*; and wherein the plurality of keystone microbial species comprises at least one of the following species: *Phocaeicola coprocola*, *Bifidobacterium bifidum*, and *Coprococcus catus*.
- [00299] In some embodiments, the plurality of core community microbial species
10 comprises at least one of the following species: *Alistipes dispar*, *Bacteroides salyersiae*, *Bifidobacterium bifidum*, *Christensenella minuta*, *Coprococcus catus*, *Coprococcus sp000154245*, *Dysosmobacter faecalis*, *Faecalibacterium duncaniae*, *Gemmiger formicilis*, *Parabacteroides goldsteinii*, *Ruminococcus bicirculans*, *Ruthenibacterium lactatiformans*, *Solibaculum mannosilyticum*, and *Vescimonas coprocola*.
- 15 [00300] In some embodiments, the formulation is generated by co-culturing the core community microbial species and the keystone microbial species in a single bioreactor.
- [00301] In some embodiments, the formulation is configured to metabolize hydrogen sulphide in the gastrointestinal tract of a subject post administration of the formulation.
- [00302] In some embodiments, the formulation is formulated for oral delivery.
- 20 [00303] In some embodiments, the formulation is lyophilized.
- [00304] In some embodiments, the pharmaceutically acceptable excipient comprises maltodextrin.
- [00305] In some embodiments, the formulation further comprises a prebiotic.
- [00306] In some embodiments, the formulation is encapsulated within an enteric coating.
- 25 [00307] In some embodiments, the plurality of core community microbial species comprises all of the minimum core species in Table 14.
- [00308] In some embodiments, the plurality of keystone microbial species comprises all of the keystone species in Table 13.
- [00309] In some embodiments, a formulation comprising a plurality of microbial species
30 comprising all of the species of Tables 13 and 14.
- [00310] The use of the formulation of an embodiment of the invention for the treatment of dysbiosis.
- [00311] The use of the formulation of an embodiment of the invention for the treatment of ulcerative colitis.
- 35 [00312] The use of the formulation of an embodiment of the invention for the treatment of Crohn's Disease.

[00313] The use of the formulation of an embodiment of the invention for the treatment of one or more diseases or disorders selected from the group consisting of: inflammatory bowel disease, checkpoint inhibitor colitis, primary sclerosing cholangitis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, hepatic encephalopathy, obesity, insulin resistance, type 2 diabetes, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer, breast cancer, lung cancer, testicular cancer, sarcoma, dyslipidaemia, atherosclerotic heart disease, hypertension, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis, psoriasis, systemic lupus erythematosus, Sjogren's disease, food allergy, anaphylaxis, atopic dermatitis, atopic rhinitis or sinusitis, clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory infections, sepsis, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, and schizophrenia.

[00314] In some embodiments, in combination with a therapy specific to the one or more diseases or disorders.

[00315] In some embodiments, the formulation comprises a ratio of core community microbial strains to keystone microbial strains of 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1 with respect to number of bacteria.

[00316] In some embodiments, the formulation comprises from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage of total microorganisms in the formulation.

[00317] In some embodiments, the plurality of core community microbial species comprise minimum core species selected from the strains identified in Table 14; and

[00318] In some embodiments, the plurality of keystone microbial species comprise keystone species selected from the strains identified in Table 13.

[00319] In some embodiments, a formulation for oral administration comprising: a plurality of core community microbial species; and a plurality of keystone microbial species, wherein the plurality of core community microbial species are species of at least the following genera: *Akkermansia*, *Alistipes*, *Bacteroides*, *Bifidobacterium*, *Butyricimonas*, *Christensenella*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dysosmobacter*, *Enterocloster*, *Faecalibacterium*, *Parabacteroides*, *Phocaeicola*, *Pusillimonas*, *Ruminococcus*, *Ruthenibacterium*, *Solibaculum*, and *Vescimonas*; and wherein the plurality of keystone microbial species are species of at least the following genera: *Alistipes*, *Bacteroides*, *Bifidobacterium*, *Coprococcus*, *Faecalibacterium*, *Methanobrevibacter*, *Parabacteroides*, *Phocaeicola*, *Roseburia*, *Ruminococcus*, and *Subdoligranulum*.

[00320] In some embodiments, a formulation comprising: a plurality of core community microbial species, wherein said core community microbial species comprise members of at

least the following genera: *Dysosmobacter*, *Enterocloster*, *Ruthenibacterium*, *Vescimonas*, *Phocaeicola*, *Pusillimonas*, *Solibaculum*, and *Christensenella*, a plurality of keystone microbial species, wherein said keystone microbial species comprise members of at least the genus *Phocaeicola*, and a non-naturally occurring pharmaceutically acceptable excipient, wherein

5 the formulation is formulated as a capsule, tablet, or powder.

[00321] In some embodiments, a formulation comprising: plurality of core community microbial species comprises at least one of the following species: *Dysosmobacter welbionis*, *Enterocloster bolteae*, *Ruthenibacterium lactatiformans*, *Vescimonas coprocola*, *Phocaeicola salanitronis*, *Pusillimonas faecalis*, *Solibaculum mannosilyticum*, *Christensenella minuta*,
10 *Alistipes magaguti*, *Parabacteroides goldsteinii*, *Alistipes communis*, *Ruminococcus bicirculans*, *Bacteroides caecimuris*, *Alistipes dispar*, and *Bacteroides salyersiae*; and wherein the plurality of keystone microbial species comprises at least one of the following species: *Phocaeicola coprocola*, *Bifidobacterium bifidum*, and *Coprococcus catus*.

[00322] In some embodiments, a formulation comprising: a plurality of core community microbial species, wherein said core community microbial species comprise members of at least the following species: *Alistipes dispar*, *Bacteroides salyersiae*, *Bifidobacterium bifidum*, *Christensenella minuta*, *Coprococcus catus*, *Coprococcus sp000154245*, *Dysosmobacter faecalis*, *Faecalibacterium duncaniae*, *Gemmiger formicilis*, *Parabacteroides goldsteinii*, *Ruminococcus bicirculans*, *Ruthenibacterium lactatiformans*, *Solibaculum mannosilyticum*,
20 *Vescimonas coprocola*.

[00323] In some embodiments, a formulation comprising a plurality of core community microbial species and a plurality of keystone microbial species comprising 80-100% of the species identified on Tables 9; Table 10 or Table 11.

[00324] In some embodiments, a formulation comprising: a plurality of core community microbial strains in lyophilized form; a plurality keystone microbial strains in lyophilized form; at least one of a prebiotic, surfactant, a polyester, or a polyvinyl alcohol; and where the formulation is produced by co-culturing the plurality of core community microbial strains with the plurality keystone microbial strains in a single vessel.

[00325] The formulation of an embodiment of the invention, where the formulation does not comprise any bacteria from the phylum Pseudomonadota or Campylobacterota.

[00326] In some embodiments, a method of co-culturing one or more core community microbial strains with one or more keystone microbial strains, comprising selecting one or more core community microbial strains selected from Table 14 and one or more keystone microbial strains selected from Table 13, and co-culturing the strains under suitable culture
35 conditions.

[00327] In some embodiments, the co-culture comprises 3, 5, 10, 15, 20, or all core community microbial strains selected from Table 14 and 1, 3, 5, 10, 15, 20, or all keystone microbial strains selected from Table 13.

5 [00328] In some embodiments, the co-culture comprises 20 or more core community microbial strains selected from Table 14 and 10 or more keystone microbial strains selected from Table 13.

[00329] In some embodiments, a method of decreasing inflammation in a subject in need thereof, said method comprising administering to the subject an effective amount of the composition of an embodiment of the invention.

10 [00330] In some embodiments, a method of decreasing dysbiosis in a subject in need thereof, said method comprising administering to the subject an effective amount of the composition of an embodiment of the invention.

[00331] In some embodiments, wherein the dysbiosis and/or inflammation is associated with one or more of inflammatory bowel disease (IBD), pouchitis, irritable bowel syndrome
15 (IBS), an enteric bacterial infection, a metabolic disease, a neuropsychiatric disorder, an autoimmune disease, an allergic disorder, hepatic encephalopathy, or a cancer.

[00332] In some embodiments, a method of preventing or treating a medical disorder or disease associated with dysbiosis in a subject in need thereof, said method comprising administering to the subject an effective amount of the composition of an embodiment of the
20 invention.

[00333] In some embodiments, the composition is produced from culturing the consortium in a bioreactor.

[00334] In some embodiments, the composition is healthy donor derived.

[00335] In some embodiments, the dysbiosis is an imbalance or perturbation of the
25 microbiota.

[00336] In some embodiments, the dysbiosis is a disruption in the normal balance of microbial communities in the body, particularly the gut.

[00337] In some embodiments, the dysbiosis is an imbalance caused by a variety of reasons, such as antibiotics, certain diets, stress, or diseases.

30 [00338] In some embodiments, the dysbiosis leads to a number of health issues including inflammatory bowel diseases, allergy, irritable bowel syndrome, obesity, mental health and can affect the efficacy of cancer therapies.

[00339] In some embodiments, the dysbiosis is associated with an enteric bacterial infection or dominant strain, such as an infection or proliferation within the gastrointestinal tract
35 of a pathogenic bacterium.

[00340] In some embodiments, said method demonstrates a property selected from the group consisting of:

- [00341] In some embodiments, certain strains in the co-culture and/or formulation for administration to a subject are selected based on these phenotypes.
- [00342] a. emergent metabolic functions;
- [00343] b. emergent metabolic functions relating to: short-chain fatty acids (SCFAs);
5 sulfide homeostasis; energy harvest; tryptophan metabolism; bile acid metabolism; vitamin production; and/or drug metabolism;
- [00344] c. synergistic metabolic functions and wherein the metabolic function of the consortium as a whole is greater than metabolic function of any of the individual isolates;
- [00345] d. synergistic metabolic functions and wherein the sulfide reduction metabolic
10 function of the consortium as a whole is greater than sulfide reduction metabolic function of each of the individual isolates;
- [00346] e. synergistic metabolic functions and wherein the sulfide reduction metabolic function of the consortium as a whole is greater than the sulfide reduction metabolic function of each of the individual isolates (and wherein the sulfide reduction metabolic function is
15 selected from the group consisting of: microbial competition for metabolic substrates (such as volatile fatty acids (acetate, propionate, butyrate), organic acids (lactate, valerate, succinate, pyruvate), amino acids (alanine, glutamate, serine) and ethanol as electron donors in cellular respiration); reduced sulfur substrate release in the colon; removing sulfide from the colon (such as assimilation of sulfide to cysteine));
- [00347] f. synergistic metabolic functions relating to: short-chain fatty acids (SCFAs);
20 sulfide homeostasis; energy harvest; tryptophan metabolism; bile acid metabolism; vitamin production; drug metabolism;
- [00348] g. reduces sulfide and nitric oxide load on epithelial cells which leads to a metabolic lesion via inhibition of cellular respiration;
- [00349] h. reduces relative abundance and or metabolic activity of sulfidogenic microbiota
25 in vitro;
- [00350] i. reduces sulfide levels in vitro either directly or indirectly through consumption/assimilation of sulfide or metabolic substrates and/or a reduction in the production of sulfide;
- [00351] j. reduces sulfide levels in vitro via metabolic substrate competition;
- [00352] k. reduces sulfide levels in vitro by consuming hydrogen;
- [00353] l. reduces relative abundance and or metabolic activity of sulfidogenic microbiota;
- [00354] m. reduce sulfide levels in the colon either directly or indirectly through
30 consumption/assimilation of sulfide or metabolic substrates and/or a reduction in the production of sulfide; reduce sulfide levels in the colon via metabolic substrate competition; and or reduce sulfide levels in the colon by consuming hydrogen;
- 35

- [00355] n. reduces the relative abundance and or metabolic activity of sulfidogenic microbiota by reducing metabolizable sulfur substrates; reduce sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by reducing protein fermentation;
- 5 [00356] o. induces colonocyte apoptosis in lesions to break an induced stable inflammatory state driven;
- [00357] p. drives down undesired inflammation;
- [00358] q. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by modulating host protease activity;
- [00359] r. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine)
- 10 into the colon by reducing host protease activity;
- [00360] s. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by modulating microbial protease activity;
- [00361] t. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by reducing microbial protease activity;
- 15 [00362] u. reduces sulfide (production in the colon by modulating host protease activity;
- [00363] v. reduces sulfide production in the colon by reducing host protease activity;
- [00364] w. reduces sulfide production in the colon by modulating microbial protease activity;
- [00365] x. reduces sulfide production in the colon by reducing microbial protease activity;
- 20 [00366] y. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by modulating host antiprotease (protease inhibitor) activity;
- [00367] z. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine) into the colon by reducing host antiprotease (protease inhibitor) activity;
- [00368] aa. reduces sulfur amino acid release (methionine, cysteine, homocysteine,
- 25 taurine) into the colon by modulating microbial antiprotease (protease inhibitor) activity;
- [00369] ab. reduces sulfur amino acid release (methionine, cysteine, homocysteine, taurine)
- [00370] ac. into the colon by reducing microbial antiprotease (protease inhibitor) activity;
- [00371] ad. reduces sulfide production in the colon by modulating host antiprotease (protease inhibitor) activity;
- 30 [00372] ae. reduces sulfide production in the colon by reducing host antiprotease (protease inhibitor) activity;
- [00373] af. reduces sulfide production in the colon by modulating microbial antiprotease (protease inhibitor) activity;
- 35 [00374] ag. reduces sulfide production in the colon by reducing microbial antiprotease (protease inhibitor) activity;

- [00375] ah. prevents or reduces activation of the mucosa immune system in a natural killer T-cell driven IL-13 and IL-5 dependent, TH2 mediated, immune response;
- [00376] ai. decreases inflammation in the subject;
- [00377] aj. decreases inflammation in the subject when measured by a parameter selected
- 5 from the group consisting of: TNF α signaling via NF- κ B; IFN α signaling; IFN γ signaling; IL6 JAK STAT3 signaling; activation of pro-apoptotic pathways; initiation of unfolded protein response;
- [00378] ak. down regulates genes associated with pro-apoptotic pathways and the unfolded protein response, including genes selected from the group consisting of: CHAC1,
- 10 CEBPB, TRIB3, PPP1R15A, DDIT3, ATF4 and XBP1;
- [00379] al. treats and/or prevents dysbiosis;
- [00380] am. treats or prevents a medical disorder or disease associated with dysbiosis;
- [00381] an. treats or prevents a medical disorder or disease associated with mycobiome dysbiosis;
- 15 [00382] ao. treats and/or prevents a gastrointestinal disorder;
- [00383] ap. treats and/or prevents a gastrointestinal disorder; wherein the gastrointestinal disorder is selected from the group consisting of: irritable bowel syndrome; an ulcer of the gastrointestinal tract; a cancer of the gastrointestinal tract;
- [00384] aq. treats and/or prevents gastrointestinal tract mucosal inflammation;
- 20 [00385] ar. treats and/or prevents gastrointestinal tract mucosal inflammation, wherein the inflammation is associated with one or more of disorders selected from the group consisting of: inflammatory bowel disease (IBD), pouchitis, irritable bowel syndrome (IBS), an enteric bacterial infection, a metabolic disease, a neuropsychiatric disorder, an autoimmune disease, an allergic disorder, hepatic encephalopathy, or a cancer;
- 25 [00386] as. treats and/or prevents inflammatory bowel disease;
- [00387] at. treats and/or prevents ulcerative colitis; Crohn's disease; gastroenteritis; colitis; checkpoint inhibitor colitis; and pouchitis;
- [00388] au. treats and/or prevents one or more of diseases or disorders selected from the group consisting of: liver disorders; metabolic disorders; neurological disorders; oncology
- 30 disorders; cardiovascular disorders; immunological disorders; allergy; allergic and atopic disorders; infectious disease; and can affect the efficacy of cancer therapies. In some embodiments, the liver disorder is selected from the group consisting of: Primary sclerosing cholangitis; Non-alcoholic steatohepatitis; Non-alcoholic fatty liver disease; Alcoholic hepatitis; and Hepatic encephalopathy. In some embodiments, the metabolic disorder is selected from
- 35 the group consisting of: Obesity; Insulin resistance; and Type 2 diabetes. In some embodiments, the neurological disorder is selected from the group consisting of: Autism; Multiple sclerosis; Parkinson's disease; Depression; Anxiety; Bipolar disorder; Schizophrenia;

- and Mental health. In some embodiments, the oncology disorder is selected from the group consisting of: Melanoma; Renal cell carcinoma; Bowel cancer and precancerous polyps; Lymphoma; Leukaemia; Myeloma; Pancreatic cancer; Breast cancer; Lung cancer; Testicular cancer; and Sarcoma. In some embodiments, the cardiovascular disorder is selected from the group consisting of: Dyslipidaemia; Atherosclerotic heart disease; and Hypertension. In some
- 5 embodiments, the immunological disorder is selected from the group consisting of: Type 1 diabetes; Rheumatoid arthritis; Psoriatic arthritis; Psoriasis; Systemic Lupus Erythematosus; and Sjogren's disease. In some embodiments, the allergic or atopic disorder is selected from the group consisting of: Food allergy; Anaphylaxis; Atopic dermatitis; and Atopic rhinitis or
- 10 sinusitis. In some embodiments, the infectious disease is selected from the group consisting of: Clostridioides difficile infection; Multidrug resistant infection or colonisation; Renal tract or urinary tract infections; Blood stream infections; Respiratory infections; and Sepsis. In some embodiments, the disease or disorder is associated with mycobiome dysbiosis; and In some embodiments, the disease or disorder is associated with dysbiosis;
- 15 [00389] av. increases the relative abundance of a member of the bacteria genus or colonizes a member of the bacteria genus selected from the group consisting of: *Acidaminococcaceae* (family), *Acidaminococcus*, *Adlercreutzia*, *Agathobaculum*, *Akkermansia*, *Alistipes*, *Alterileibacterium*, *Amedibacillus*, *Amedibacterium*, *Aminipila*, *Anaerobutyricum*, *Anaerococcus*, *Anaerocolumna*, *Anaerofustis*, *Anaerostipes*,
- 20 *Anaerotignum*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Barnesiella*, *Bifidobacterium*, *Bilophila*, *Blautia*, *Butyricimonas*, *Butyrivibrio*, *Campylobacter*, *Caproicibacter*, *Caproicibacterium*, *Caproiciproducens*, *Casaltella*, *Catenibacterium*, *Christensenella*, *Clostridium*, *Collinsella*, *Coprobacillus*, *Coprobacter*, *Coproccoccus*, *Desulfovibrio*, *Dorea*, *Duodenibacillus*, *Dysosmobacter*, *Eggerthella*, *Enorma*, *Enterocloster*, *Enterococcus*, *Escherichia*,
- 25 *Ethanoligenens*, *Eubacterium*, *Faecalibacillus*, *Faecalibacterium*, *Faecalibaculum*, *Finegoldia*, *Flavonifractor*, *Flintibacter*, *Fusicatenibacter*, *Gemmiger*, *Gordonibacter*, *Granulicatella*, *Herbinix*, *Holdemanella*, *Holdemania*, *Hoylesella*, *Hungatella*, *Intestinibacter*, *Intestinibaculum*, *Intestinimonas*, *Lachnoanaerobaculum*, *Lachnoclostridium*, *Lachnospira*, *Lachnospiraceae incertae sedis* (unclassified rank, *Lachnospiraceae* family), *Lacrimispora*,
- 30 *Lactococcus*, *Ligilactobacillus*, *Longibaculum*, *Longicatena*, *Mageeibacillus*, *Maliibacterium*, *Marvinbryantia*, *Massilimicrobiota*, *Massiliprevotella*, *Massilistercora*, *Mediterraneibacter*, *Megamonas*, *Megasphaera*, *Merdibacter*, *Mesosutterella*, *Mitsuokella*, *Mogibacterium*, *Muribaculum*, *Negativibacillus*, *Novisyntrophococcus*, *Odoribacter*, *Olsenella*, *Oscillibacter*, *Oscillospiraceae* (family), *Oscillospiraceae incertae sedis* (unclassified rank, *Oscillospiraceae*
- 35 family), *Parabacteroides*, *Paraclostridium*, *Paraprevotella*, *Parolsenella*, *Peptacetobacter*, *Peptoniphilus*, *Peptostreptococcus*, *Phascolarctobacterium*, *Phocaeicola*, *Porphyromonas*, *Prevotella*, *Pseudobutyrvibrio*, *Pusillibacter*, *Romboutsia*, *Roseburia*, *Ruminiclostridium*,

Ruminococcus, *Ruthenibacterium*, *Schaalia*, *Segatella*, *Selenomonas*, *Sellimonas*, *Senegalimassilia*, *Slackia*, *Sodaliphilus*, *Solibaculum*, *Streptococcus*, *Subdoligranulum*, *Thomasclavelia*, *Tyzzerella*, *Veillonella* and *Vescimonas* or any combination, subgroup or multitude thereof;

- 5 [00390] aw. reduces the relative abundance of a member of the bacteria genus or decolonises a member of the bacteria genus selected from the group consisting of: *Achromobacter*, *Acidaminococcus*, *Aeromonas*, *Alicyclobacillus*, *Bacteroides*, *Bifidobacterium*, *Blautia*, *Bosea*, *Burkholderiales*, *Clostridium*, *Cutibacterium*, *Desulfovibrio*, *Eggerthella*, *Enterobacter*, *Enterococcus*, *Escherichia*, *Eubacterium*, *Flavonifractor*,
10 *Granulicatella*, *Hungatella*, *Klebsiella*, *Ligilactobacillus*, *Mediterraneibacter*, *Minicystis*, *Oscillibacter*, *Parabacteroides*, *Pluralibacter*, *Prevotella*, *Prosthecochloris*, *Pseudomonas*, *Rhodococcus*, *Salmonella*, *Schaalia*, *Serratia*, *Shewanella*, *Staphylococcus*, *Streptomyces*, *Sutterella*, *Veillonella*, or any combination, subgroup or multitude thereof; and any combination or multitude thereof; and
- 15 [00391] ax. treats or prevents ulcerative colitis, inflammatory bowel disease, Crohn's disease, checkpoint inhibitor colitis, as well as other gastrointestinal diseases and symptoms, liver disorders, including, for example, primary sclerosing cholangitis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, or hepatic encephalopathy, metabolic disorders, including, for example, obesity, insulin resistance, or
20 type 2 diabetes, oncology indications, including, for example, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer, breast cancer, lung cancer, testicular cancer, or sarcoma, cardiovascular disorders, including, for example, dyslipidaemia, atherosclerotic heart disease, or hypertension, immunological diseases, including, for example, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis,
25 psoriasis, systemic lupus erythematosus, or Sjogren's disease, allergic and atopic disorders, including, for example, food allergy, anaphylaxis, atopic dermatitis, or atopic rhinitis or sinusitis, infectious diseases, including, for example, clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory infections, or sepsis, neurological disorders, including for example, autism, multiple
30 sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, or schizophrenia.

[00392] In some embodiments, the composition is administered orally, colonically or rectally.

- [00393] In some embodiments, said composition is administered to the patient using a dosing regimen selected from the group consisting of: hourly; every 2 hours; every 3 hours;
35 every 4 hours; every 5 hours; every 6 hours; every 12 hours; once daily; twice daily; every 2 days; every 3 days; every 4 days; every 5 days; every 6 days; weekly; twice weekly; every 2 weeks; every 3 weeks; every 4 weeks; every 5 weeks; every 6 weeks; once monthly; twice

monthly; every 2 months; every 3 months; every 4 months; every 5 months; every 6 months; yearly; twice yearly; every 2 years; every 3 years; every 4 years; and every 5 years.

[00394] In some embodiments, a method of promoting the growth of a member of a genus selected from the group consisting of: *Acidaminococcaceae* (family), *Acidaminococcus*,
 5 *Adlercreutzia*, *Agathobaculum*, *Akkermansia*, *Alistipes*, *Alterileibacterium*, *Amedibacillus*,
Amedibacterium, *Aminipila*, *Anaerobutyricum*, *Anaerococcus*, *Anaerocolumna*, *Anaerofustis*,
Anaerostipes, *Anaerotignum*, *Anaerotruncus*, *Bacillus*, *Bacteroides*, *Barnesiella*,
Bifidobacterium, *Bilophila*, *Blautia*, *Butyricimonas*, *Butyrivibrio*, *Campylobacter*,
Caproicibacter, *Caproicibacterium*, *Caproiciproducens*, *Casaltella*, *Catenibacterium*,
 10 *Christensenella*, *Clostridium*, *Collinsella*, *Coprobacillus*, *Coprobacter*, *Coprococcus*,
Desulfovibrio, *Dorea*, *Duodenibacillus*, *Dysosmobacter*, *Eggerthella*, *Enorma*, *Enterocloster*,
Enterococcus, *Escherichia*, *Ethanoligenens*, *Eubacterium*, *Faecalibacillus*, *Faecalibacterium*,
Faecalibaculum, *Finegoldia*, *Flavonifractor*, *Flintibacter*, *Fusicatenibacter*, *Gemmiger*,
Gordonibacter, *Granulicatella*, *Herbinix*, *Holdemanella*, *Holdemania*, *Hoylesella*, *Hungatella*,
 15 *Intestinibacter*, *Intestinibaculum*, *Intestinimonas*, *Lachnoanaerobaculum*, *Lachnoclostridium*,
Lachnospira, *Lachnospiraceae incertae sedis* (unclassified rank, *Lachnospiraceae* family),
Lacrimispora, *Lactococcus*, *Ligilactobacillus*, *Longibaculum*, *Longicatena*, *Mageeibacillus*,
Maliibacterium, *Marvinbryantia*, *Massilimicrobiota*, *Massiliprevotella*, *Massilistercora*,
Mediterraneibacter, *Megamonas*, *Megasphaera*, *Merdibacter*, *Mesosutterella*, *Mitsuokella*,
 20 *Mogibacterium*, *Muribaculum*, *Negativibacillus*, *Novisyntrophococcus*, *Odoribacter*, *Olsenella*,
Oscillibacter, *Oscillospiraceae* (family), *Oscillospiraceae incertae sedis* (unclassified rank,
Oscillospiraceae family), *Parabacteroides*, *Paraclostridium*, *Paraprevotella*, *Parolsenella*,
Peptacetobacter, *Peptoniphilus*, *Peptostreptococcus*, *Phascolarctobacterium*, *Phocaeicola*,
Porphyromonas, *Prevotella*, *Pseudobutyrvibrio*, *Pusillibacter*, *Romboutsia*, *Roseburia*,
 25 *Ruminiclostridium*, *Ruminococcus*, *Ruthenibacterium*, *Schaalia*, *Segatella*, *Selenomonas*,
Sellimonas, *Senegalimassilia*, *Slackia*, *Sodaliphilus*, *Solibaculum*, *Streptococcus*,
Subdoligranulum, *Thomasclavelia*, *Tyzzera*, *Veillonella*, *Vescimonas* and any combination
 or multitude thereof, said method comprising the step of administering to a patient in need
 thereof, a composition of an embodiment of the invention.

30 [00395] In some embodiments, a method of decreasing the growth of a member of a genus
 selected from the group consisting of: *Achromobacter*, *Acidaminococcus*, *Aeromonas*,
Alicyclobacillus, *Bacteroides*, *Bifidobacterium*, *Blautia*, *Bosea*, *Burkholderiales*, *Clostridium*,
Cutibacterium, *Desulfovibrio*, *Eggerthella*, *Enterobacter*, *Enterococcus*, *Escherichia*,
Eubacterium, *Flavonifractor*, *Granulicatella*, *Hungatella*, *Klebsiella*, *Ligilactobacillus*,
 35 *Mediterraneibacter*, *Minicystis*, *Oscillibacter*, *Parabacteroides*, *Pluralibacter*, *Prevotella*,
Prosthecochloris, *Pseudomonas*, *Rhodococcus*, *Salmonella*, *Schaalia*, *Serratia*, *Shewanella*,
Staphylococcus, *Streptomyces*, *Sutterella*, *Veillonella*, and any combination or multitude

thereof, said method comprising the step of administering to a patient in need thereof, a composition of an embodiment of the invention.

[00396] In some embodiments, a method of preparing the composition of an embodiment of the invention, the method comprising culturing the microbial consortium of an embodiment
5 of the invention.

[00397] In some embodiments, the consortium is cultured in a bioreactor with a capacity selected from the group consisting of: between 500ml and 1L; between 1L and 10L; between 10L and 100L; between 100L and 1000L; between 1000L and 10,000L; between 10,000L and 100,000L; between 100,000L and 1,000,000L; between 1,000,000L 10,000,000L; and a value
10 within a range defined by any two of the aforementioned values.

[00398] In some embodiments, the bioreactor is adapted for continuous fermentation.

[00399] In some embodiments, a method of preparing the biotherapeutic composition of an embodiment of the invention, the method comprising mixing the composition with a pharmaceutically acceptable carrier.

15 [00400] In some embodiments, a method of preparing the pharmaceutical composition of an embodiment of the invention, the method comprising mixing the composition with a pharmaceutically acceptable carrier.

[00401] In some embodiments, a method of preparing the dosage form of an embodiment of the invention, the method comprising mixing the composition with a pharmaceutically
20 acceptable carrier.

[00402] In some embodiments, a method of co-culturing one or more core community microbial strains with one or more keystone microbial strains, comprising selecting one or more core community microbial strains selected from Table 14 and one or more keystone microbial strains selected from Table 13, and co-culturing the strains under suitable culture
25 conditions.

[00403] In some embodiments, the co-culture comprises 3, 5, 10, 15, 20, or all core community microbial strains selected from Table 14 and 1, 3, 5, 10, 15, 20, or all keystone microbial strains selected from Table 13.

30 [00404] In some embodiments, the co-culture comprises 20 or more core community microbial strains selected from Table 14 and 10 or more keystone microbial strains selected from Table 13.

[00405] In some embodiments, a method of estimating the minimum number of isolates required to achieve a desired level of functional potential or property in a microbial consortium or other complex community, said method comprising identifying the point on a rarefaction
35 curve where the model's asymptote intersects with the benchmark functional potential or property.

[00406] In some embodiments, method comprises the following steps:

- [00407] Step 1 - Isolate selection: Selecting a plurality of microbial isolates to comprise a target microbial community, wherein the isolates are representative of the genetic and functional diversity present within the community.
- 5 [00408] Step 2 - Whole genome sequencing: Subjecting the selected microbial isolates to whole genome sequencing to obtain sequence data.
- [00409] Step 3 - Genome assembly and annotation: Assembling the obtained sequence data into complete or draft genomes for each isolate using a genome assembly pipeline, and subsequently annotating these genomes to identify functional gene categories, such as Clusters of Orthologous Genes (COGs) or equivalent functional annotations.
- 10 [00410] Step 4 - Functional gene category identification: Identifying and cataloging the presence of functional gene categories within each genome based on the annotation results, wherein non-functional or non-essential categories, such as hypothetical proteins or tRNAs, are excluded from further analysis.
- [00411] Step 5 - Resampling and subset generation: Performing a resampling procedure
15 on the annotated genomes, wherein subsets of isolates are randomly selected with replacement, covering a range of subset sizes from a single isolate to the total number of isolates in the community, to generate multiple iterations of isolate subsets.
- [00412] Step 6 - Functional potential assessment: For each subset generated in the resampling procedure, calculating the total number of unique functional gene categories
20 present, thereby producing a dataset representing the functional potential or property of each subset size.
- [00413] Step 7 - Rarefaction curve construction: Constructing a rarefaction curve by plotting the number of unique functional gene categories against the number of isolates in each subset, wherein the curve depicts the relationship between the increasing number of
25 isolates and the cumulative functional potential or property.
- [00414] Step 8 - Model fitting and asymptote determination: Fitting a mathematical model, such as a logistic or polynomial regression, to the rarefaction curve to determine the point at which the curve begins to asymptote, indicating a diminishing return in the discovery of new functional gene categories as additional isolates are added.
- 30 [00415] Step 9 - Minimum viable consortium determination: Estimating the minimum number of isolates required to achieve a functional potential or property that meets or exceeds a predefined benchmark, such as the functional diversity present in a healthy or target microbial community, by identifying the point on the rarefaction curve where the model's asymptote intersects with the benchmark functional potential or property.
- 35 [00416] Step 10 - Application to therapeutic Design: Applying the results of the rarefaction analysis to design a minimal viable microbial consortium that retains the desired level of

functional potential or property, ensuring that the consortium is both functionally robust and economically feasible for therapeutic applications.

[00417] In some embodiments, the use of the composition according to an embodiment of the invention in the manufacture of a medicament for a use selected from the group consisting of: reducing or preventing a medical disorder or disease associated with dysbiosis in a subject in need thereof; decreasing inflammation in a subject in need thereof; and decreasing dysbiosis in a subject.

[00418] In some embodiments, a kit comprising the dosage form of an embodiment of the invention together with instructions for its use.

[00419] In some embodiments, the formulations include one or more microbes selected from one or more of the microbial phyla as set forth in Table 1. In alternative embodiments, any one or more (e.g., 1-5, 5-10, etc.) of the phyla, genera, species or strains identified in the tables provided herein are expressly excluded from the co-culture, the formulation to be administered, or both. One reason for such exclusion may be that such microbe has a deleterious effect on a particular disease state. In some embodiments, 50-95% (50-60, 60-70, 70-80, 80-95% and overlapping ranges therein), of the microbes are included, with the remaining 5-50% excluded.

[00420] Below we present several embodiments of the invention.

[00421] BY PHYLUM

[00422] **Table 1 - By phylum.**

[00423] In some embodiments, the formulations include one or more microbes selected from one or more of the microbial genera as set forth in Table 1. In alternative embodiments, any one or more (e.g., 1-5, 5-10, etc.) of the phyla, genera, species or strains identified in the tables provided herein are expressly excluded from the co-culture, the formulation to be administered, or both. One reason for such exclusion may be that such microbe has a deleterious effect on a particular disease state. In some embodiments, 50-95% (50-60, 60-70, 70-80, 80-95% and overlapping ranges therein), of the microbes are included, with the remaining 5-50% excluded.

Acidobacteriota (NCBI taxid: 57723)	Dictyoglomota (NCBI taxid: 68297)
Actinomycetota (NCBI taxid: 201174)	Elusimicrobiota (NCBI taxid: 74152)
Aquificota (NCBI taxid: 200783)	Euryarchaeota (NCBI taxid: 28890)
Armatimonadota (NCBI taxid: 67819)	Fibrobacterota (NCBI taxid: 65842)
Atribacterota (NCBI taxid: 67818)	Fusobacteriota (NCBI taxid: 32066)
Bacillota (NCBI taxid: 1239)	Gemmatimonadota (NCBI taxid: 142182)
Bacteria candidate phyla (NCBI taxid: 1783234)	Ignavibacteriota (NCBI taxid: 1134404)

Bacteroidota (NCBI taxid: 976)	Kiritimatiellota (NCBI taxid: 134625)
Balneolota (NCBI taxid: 1936987)	Lentisphaerota (NCBI taxid: 256845)
Bdellovibrionota (NCBI taxid: 3018035)	Mycoplasmata (NCBI taxid: 544448)
Caldisericota (NCBI taxid: 67814)	Myxococcota (NCBI taxid: 2818505)
Calditrichota (NCBI taxid: 1930617)	Nitrososphaerota (NCBI taxid: 651137)
Campylobacterota (NCBI taxid: 29547)	Nitrospinota (NCBI taxid: 1293497)
Candidatus Absconditabacteria (NCBI taxid: 221235)	Nitrospirota (NCBI taxid: 40117)
Candidatus Cloacimonadota (NCBI taxid: 456828)	Planctomycetota (NCBI taxid: 203682)
Candidatus Micrarchaeota (NCBI taxid: 1801631)	Pseudomonodota (NCBI taxid: 1224)
Candidatus Nanohalarchaeota (NCBI taxid: 1462430)	Rhodothermota (NCBI taxid: 1853220)
Candidatus Saccharibacteria (NCBI taxid: 95818)	Spirochaetota (NCBI taxid: 203691)
Chlamydiota (NCBI taxid: 204428)	Synergistota (NCBI taxid: 508458)
Chlorobiota (NCBI taxid: 1090)	Thermodesulfobacterota (NCBI taxid: 200940)
Chloroflexota (NCBI taxid: 200795)	Thermodesulfobiota (NCBI taxid: 3002442)
Chrysiogenota (NCBI taxid: 200938)	Thermomicrobiota (NCBI taxid: 3027942)
Coprothermobacterota (NCBI taxid: 2138240)	Thermoproteota (NCBI taxid: 28889)
Cyanobacteriota (NCBI taxid: 1117)	Thermotogota (NCBI taxid: 200918)
Deferribacterota (NCBI taxid: 200930)	Verrucomicrobiota (NCBI taxid: 74201)
Deinococcota (NCBI taxid: 1297)	

[00424] **Table 2 - By Phylum**

[00425] In some embodiments, the formulations include one or more microbes selected from one or more of the microbial genera as set forth in Table 2.

Actinomycetota (NCBI taxid: 201174)
Bacillota (NCBI taxid: 1239)
Bacteroidota (NCBI taxid: 976)
Campylobacterota (NCBI taxid: 29547)
Pseudomonodota (NCBI taxid: 1224)
Thermodesulfobiota (NCBI taxid: 3002442)

Verrucomicrobiota (NCBI taxid: 74201)

[00426] **Table 3 – By Phylum.** In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial phyla as set forth in Table 3.

Actinomycetota (NCBI taxid: 201174)
Bacteroidota (NCBI taxid: 976)
Bacillota (NCBI taxid: 1239)
Verrucomicrobiota (NCBI taxid: 74201)

5

[00427] BY FAMILY

[00428] **Table 4 - By families.** In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial families as set forth in Table 4.

Acanthopleuribacteraceae (NCBI taxid: 533207)	Kosmotogaceae (NCBI taxid: 1643948)
Acaryochloridaceae (NCBI taxid: 1890429)	Kribbellaceae (NCBI taxid: 2726069)
Acetobacteraceae (NCBI taxid: 433)	Ktedonosporobacteraceae (NCBI taxid: 2692416)
Acetomicrobiaceae (NCBI taxid: 3029086)	Kytococcaceae (NCBI taxid: 2805426)
Acholeplasmataceae (NCBI taxid: 2146)	Labilitrichaceae (NCBI taxid: 1524216)
Acidaminococcaceae (NCBI taxid: 909930)	Lachnospiraceae (NCBI taxid: 186803)
Acidiferrobacteraceae (NCBI taxid: 1692041)	Lacipirellulaceae (NCBI taxid: 2691359)
Acidilobaceae (NCBI taxid: 871007)	Lactobacillaceae (NCBI taxid: 33958)
Acidilutibacteraceae (NCBI taxid: 2992717)	Lawsonellaceae (NCBI taxid: 2805586)
Acidimicrobiaceae (NCBI taxid: 84994)	Legionellaceae (NCBI taxid: 444)
Acidithiobacillaceae (NCBI taxid: 225058)	Lentisphaeraceae (NCBI taxid: 566277)
Acidobacteriaceae (NCBI taxid: 204434)	Leptolyngbyaceae (NCBI taxid: 1890438)
Acidothermaceae (NCBI taxid: 85032)	Leptospiraceae (NCBI taxid: 170)
Actinomycetaceae (NCBI taxid: 2049)	Leptotrichiaceae (NCBI taxid: 1129771)
Actinopolymorphaceae (NCBI taxid: 2805400)	Lichenihabitantaceae (NCBI taxid: 2723775)
Actinopolysporaceae (NCBI taxid: 622451)	Limnochordaceae (NCBI taxid: 1676650)
Aerococcaceae (NCBI taxid: 186827)	Listeriaceae (NCBI taxid: 186820)
Aeromonadaceae (NCBI taxid: 84642)	Litoricolaceae (NCBI taxid: 449732)

Akkermansiaceae (NCBI taxid: 1647988)	Litorivicinaceae (NCBI taxid: 449732)
Alcaligenaceae (NCBI taxid: 506)	Magnetococcaceae (NCBI taxid: 1191479)
Alcanivoracaceae (NCBI taxid: 224372)	Maliibacteriaceae (NCBI taxid: 3047432)
Alicyclobacillaceae (NCBI taxid: 186823)	Mangrovivirgaceae (NCBI taxid: 2858885)
Alteromonadaceae (NCBI taxid: 72275)	Maricaulaceae (NCBI taxid: 2800061)
Aminithiophilaceae (NCBI taxid: 3029085)	Marinifilaceae (NCBI taxid: 1573805)
Aminobacteriaceae (NCBI taxid: 3029087)	Marinilabiliaceae (NCBI taxid: 558415)
Amoebophilaceae (NCBI taxid: 1501348)	Marinobacteraceae (NCBI taxid: 2887365)
Amorphaceae (NCBI taxid: 2685818)	Mariprofundaceae (NCBI taxid: 580372)
Anaerohalosphaeraceae (NCBI taxid: 2690158)	Marivirgaceae (NCBI taxid: 2762301)
Anaerolineaceae (NCBI taxid: 292628)	Melioribacteraceae (NCBI taxid: 1334117)
Anaeromyxobacteraceae (NCBI taxid: 1524215)	Merismopediaceae (NCBI taxid: 1890428)
Anaplasmataceae (NCBI taxid: 942)	Mesoaciditogaceae (NCBI taxid: 1769717)
Aphanizomenonaceae (NCBI taxid: 1892259)	Metamycoplasmataceae (NCBI taxid: 2895623)
Aphanothecaceae (NCBI taxid: 1890450)	Methanobacteriaceae (NCBI taxid: 2159)
Aquificaceae (NCBI taxid: 64898)	Methanocaldococcaceae (NCBI taxid: 196117)
Archaeoglobaceae (NCBI taxid: 2232)	Methanocellaceae (NCBI taxid: 570265)
Archangiaceae (NCBI taxid: 39)	Methanococcaceae (NCBI taxid: 2183)
Arcobacteraceae (NCBI taxid: 2808963)	Methanocorpusculaceae (NCBI taxid: 88404)
Ardenticatenaceae (NCBI taxid: 1382930)	Methanomassiliicoccaceae (NCBI taxid: 1577788)
Atopobiaceae (NCBI taxid: 1643824)	Methanomicrobiaceae (NCBI taxid: 2194)
Atribacteraceae (NCBI taxid: 2847776)	Methanopyraceae (NCBI taxid: 183713)
Aurantimonadaceae (NCBI taxid: 255475)	Methanoregulaceae (NCBI taxid: 1198451)
Azonexaceae (NCBI taxid: 2008795)	Methanosarcinaceae (NCBI taxid: 2206)
Azospirillaceae (NCBI taxid: 2829815)	Methanospirillaceae (NCBI taxid: 196137)
Bacillaceae (NCBI taxid: 186817)	Methanothermaceae (NCBI taxid: 2178)
Bacillales Family X. Incertae Sedis (NCBI taxid: 539003)	Methanotrichaceae (NCBI taxid: 143067)
Bacteriovoracaceae (NCBI taxid: 263369)	Methylacidiphilaceae (NCBI taxid: 717964)

Bacteroidaceae (NCBI taxid: 815)	Methylobacteriaceae (NCBI taxid: 119045)
Baekduiaceae (NCBI taxid: 2600303)	Methylococcaceae (NCBI taxid: 403)
Barnesiellaceae (NCBI taxid: 2005519)	Methylocystaceae (NCBI taxid: 31993)
Bartonellaceae (NCBI taxid: 772)	Methylophilaceae (NCBI taxid: 32011)
Bdellovibrionaceae (NCBI taxid: 213483)	Microbacteriaceae (NCBI taxid: 85023)
Beijerinckiaceae (NCBI taxid: 45404)	Microbulbiferaceae (NCBI taxid: 1706373)
Bernardetiaceae (NCBI taxid: 1937968)	Micrococcaceae (NCBI taxid: 1268)
Beutenbergiaceae (NCBI taxid: 125316)	Microcoleaceae (NCBI taxid: 1892252)
Bifidobacteriaceae (NCBI taxid: 31953)	Microcystaceae (NCBI taxid: 1890449)
Blastochloridaceae (NCBI taxid: 2831090)	Micromonosporaceae (NCBI taxid: 28056)
Blattabacteriaceae (NCBI taxid: 39782)	Microvenatoraceae (NCBI taxid: 2946505)
Bogoriellaceae (NCBI taxid: 145358)	Miltoncostaeaceae (NCBI taxid: 2843199)
Borrelliaceae (NCBI taxid: 1643685)	Minwuiaceae (NCBI taxid: 2493628)
Boseaceae (NCBI taxid: 2831100)	Moorellaceae (NCBI taxid: 3039168)
Brachyspiraceae (NCBI taxid: 143786)	Moraxellaceae (NCBI taxid: 468)
Bradymonadaceae (NCBI taxid: 1779135)	Morganellaceae (NCBI taxid: 1903414)
Bradyrhizobiaceae (NCBI taxid: 41294)	Moritellaceae (NCBI taxid: 267891)
Breoghaniaceae (NCBI taxid: 2821832)	Mucispirillaceae (NCBI taxid: 2945020)
Brevibacteriaceae (NCBI taxid: 85019)	Muribaculaceae (NCBI taxid: 2005473)
Breznakiellaceae (NCBI taxid: 2951104)	Mycobacteriaceae (NCBI taxid: 1762)
Brucellaceae (NCBI taxid: 118882)	Mycoplasmataceae (NCBI taxid: 2092)
Bruguierivoracaceae (NCBI taxid: 2812006)	Mycoplasmoidaceae (NCBI taxid: 2790998)
Bryobacteraceae (NCBI taxid: 1962910)	Myxococcaceae (NCBI taxid: 31)
Budviciaceae (NCBI taxid: 1903416)	Nakamurellaceae (NCBI taxid: 85031)
Burkholderiaceae (NCBI taxid: 119060)	Nannocystaceae (NCBI taxid: 224463)
Caedimonadaceae (NCBI taxid: 2100208)	Natranaerobiaceae (NCBI taxid: 485255)
Caldilineaceae (NCBI taxid: 475964)	Natranaerofabaceae (NCBI taxid: 2807496)
Caldiseriaceae (NCBI taxid: 693073)	Natrialbaceae (NCBI taxid: 1644061)
Caldisphaeraceae (NCBI taxid: 255472)	Nautiliaceae (NCBI taxid: 224467)
Calditerrivibrionaceae (NCBI taxid: 2945021)	Neisseriaceae (NCBI taxid: 481)
Calditrichaceae (NCBI taxid: 1962854)	Nitratiruptoraceae (NCBI taxid: 2795691)
Calotrichaceae (NCBI taxid: 2661849)	Nitrobacteraceae (NCBI taxid: 41294)
Campylobacteraceae (NCBI taxid: 72294)	Nitrosomonadaceae (NCBI taxid: 206379)

Candidatus Absconditicoccaceae (NCBI taxid: 2900569)	Nitrosopumilaceae (NCBI taxid: 338190)
Candidatus Babeliaceae (NCBI taxid: 2497645)	Nitrososphaeraceae (NCBI taxid: 1033997)
Candidatus Brocadiaceae (NCBI taxid: 1127830)	Nitrospinaceae (NCBI taxid: 407032)
Candidatus Chazhembacteraceae (NCBI taxid: 2715733)	Nitrospiraceae (NCBI taxid: 189779)
Candidatus Chromulinivoraceae (NCBI taxid: 2953756)	Nocardiaceae (NCBI taxid: 85025)
Candidatus Cloacimonadaceae (NCBI taxid: 3039865)	Nocardioidaceae (NCBI taxid: 85015)
Candidatus Comchoanobacteraceae (NCBI taxid: 2975285)	Nocardiopsaceae (NCBI taxid: 83676)
Candidatus Deianiraeaceae (NCBI taxid: 2603433)	Nostocaceae (NCBI taxid: 1162)
Candidatus Desulfofervidaceae (NCBI taxid: 1902584)	Oceanospirillaceae (NCBI taxid: 135620)
Candidatus Izemoplasmataceae (NCBI taxid: 2975520)	Oculatellaceae (NCBI taxid: 2303507)
Candidatus Methanoliparaceae (NCBI taxid: 2545690)	Odoribacteraceae (NCBI taxid: 1853231)
Candidatus Methanomethylophilaceae (NCBI taxid: 2517203)	Oleiphilaceae (NCBI taxid: 191033)
Candidatus Micrarchaeaceae (NCBI taxid: 2885735)	Opitutaceae (NCBI taxid: 134623)
Candidatus Midichloriaceae (NCBI taxid: 1328881)	Orbaceae (NCBI taxid: 1240483)
Candidatus Nanohalobiaceae (NCBI taxid: 2856054)	Ornithinimicrobiaceae (NCBI taxid: 2805590)
Candidatus Nanopelagicaceae (NCBI taxid: 2162846)	Oscillatoriaceae (NCBI taxid: 1892254)
Candidatus Nanosynbacteraceae (NCBI taxid: 2093822)	Oscillospiraceae (NCBI taxid: 216572)
Candidatus Nitrosocaldaceae (NCBI taxid: 1968910)	Oxalobacteraceae (NCBI taxid: 75682)

Candidatus Paracaedibacteraceae (NCBI taxid: 1777752)	Paenibacillaceae (NCBI taxid: 186822)
Candidatus Saccharimonadaceae (NCBI taxid: 2171986)	Paludibacteraceae (NCBI taxid: 2005523)
Candidatus Uabimicrobiaceae (NCBI taxid: 2897348)	Parachlamydiaceae (NCBI taxid: 92713)
Capillimicrobiaceae (NCBI taxid: 2976758)	Paracoccaceae (NCBI taxid: 31989)
Cardiobacteriaceae (NCBI taxid: 868)	Paraconexibacteraceae (NCBI taxid: 2758916)
Carnobacteriaceae (NCBI taxid: 186828)	Parvibaculaceae (NCBI taxid: 2813035)
Casimicrobiaceae (NCBI taxid: 2705999)	Parvicellaceae (NCBI taxid: 2975259)
Catenulisporaceae (NCBI taxid: 414877)	Parvularculaceae (NCBI taxid: 255474)
Caulobacteraceae (NCBI taxid: 76892)	Pasteurellaceae (NCBI taxid: 712)
Celerinatantimonadaceae (NCBI taxid: 412032)	Pectobacteriaceae (NCBI taxid: 1903410)
Cellulomonadaceae (NCBI taxid: 85016)	Pelagibacteraceae (NCBI taxid: 1655514)
Cellulosilyticaceae (NCBI taxid: 3018741)	Peptococcaceae (NCBI taxid: 186807)
Cellvibrionaceae (NCBI taxid: 1706371)	Peptoniphilaceae (NCBI taxid: 1570339)
Chamaesiphonaceae (NCBI taxid: 1890431)	Peptostreptococcaceae (NCBI taxid: 186804)
Chelatococcaceae (NCBI taxid: 2036754)	Persicobacteraceae (NCBI taxid: 1853234)
Chitinophagaceae (NCBI taxid: 563835)	Petrotogaceae (NCBI taxid: 1643949)
Chlamydiaceae (NCBI taxid: 809)	Phototrophicaceae (NCBI taxid: 2922432)
Chlorobiaceae (NCBI taxid: 191412)	Phreatobacteraceae (NCBI taxid: 2843305)
Chloroflexaceae (NCBI taxid: 1106)	Phycisphaeraceae (NCBI taxid: 666507)
Chloroherpetonaceae (NCBI taxid: 2968741)	Phyllobacteriaceae (NCBI taxid: 69277)
Christensenellaceae (NCBI taxid: 990719)	Picrophilaceae (NCBI taxid: 46630)
Chromatiaceae (NCBI taxid: 1046)	Pirellulaceae (NCBI taxid: 2691357)
Chromobacteriaceae (NCBI taxid: 1499392)	Piscirickettsiaceae (NCBI taxid: 135616)
Chroococcaceae (NCBI taxid: 1890464)	Planctomycetaceae (NCBI taxid: 126)
Chroococcidiopsidaceae (NCBI taxid: 1890528)	Planococcaceae (NCBI taxid: 186818)
Chrysiogenaceae (NCBI taxid: 189770)	Pleomorphomonadaceae (NCBI taxid: 2843308)

Chthonomonadaceae (NCBI taxid: 1077264)	Polyangiaceae (NCBI taxid: 49)
Clostridiaceae (NCBI taxid: 31979)	Porphyromonadaceae (NCBI taxid: 171551)
Clostridiales Family XVI. Incertae Sedis (NCBI taxid: 543347)	Prevotellaceae (NCBI taxid: 171552)
Clostridiales Family XVII. Incertae Sedis (NCBI taxid: 539000)	Prochlorococcaceae (NCBI taxid: 2881426)
Cohaesibacteraceae (NCBI taxid: 655351)	Prochlorotrichaceae (NCBI taxid: 2303730)
Coleofasciculaceae (NCBI taxid: 1892251)	Prolixibacteraceae (NCBI taxid: 1471398)
Colwelliaceae (NCBI taxid: 267889)	Promicromonosporaceae (NCBI taxid: 85017)
Comamonadaceae (NCBI taxid: 80864)	Propionibacteriaceae (NCBI taxid: 31957)
Conexibacteraceae (NCBI taxid: 320583)	Proteinivoraceae (NCBI taxid: 1491775)
Conexivisphaeraceae (NCBI taxid: 2798276)	Pseudanabaenaceae (NCBI taxid: 1890436)
Coprobacillaceae (NCBI taxid: 2810280)	Pseudoalteromonadaceae (NCBI taxid: 267888)
Coprothermobacteraceae (NCBI taxid: 2138247)	Pseudobdellovibrionaceae (NCBI taxid: 213483)
Coriobacteriaceae (NCBI taxid: 84107)	Pseudomonadaceae (NCBI taxid: 135621)
Corynebacteriaceae (NCBI taxid: 1653)	Pseudonocardiaceae (NCBI taxid: 2070)
Coxiellaceae (NCBI taxid: 118968)	Psychromonadaceae (NCBI taxid: 267894)
Crocinitomicaceae (NCBI taxid: 1853230)	Puniceicoccaceae (NCBI taxid: 415002)
Cuniculiplasmataceae (NCBI taxid: 1747776)	Pyrodictiaceae (NCBI taxid: 2307)
Cyclobacteriaceae (NCBI taxid: 563798)	Reichenbachiellaceae (NCBI taxid: 2762302)
Cyclonatronaceae (NCBI taxid: 3024158)	Rhabdochlamydiaceae (NCBI taxid: 689704)
Cytophagaceae (NCBI taxid: 89373)	Rhizobiaceae (NCBI taxid: 82115)
Deferribacteraceae (NCBI taxid: 191394)	Rhodanobacteraceae (NCBI taxid: 1775411)
Dehalococcoidaceae (NCBI taxid: 1202464)	Rhodobacteraceae (NCBI taxid: 31989)
Deinococcaceae (NCBI taxid: 183710)	Rhodocyclaceae (NCBI taxid: 75787)
Demequinaceae (NCBI taxid: 1042322)	Rhodospirillaceae (NCBI taxid: 41295)
Dermabacteraceae (NCBI taxid: 85020)	Rhodothermaceae (NCBI taxid: 563843)

Dermacoccaceae (NCBI taxid: 145357)	Rickettsiaceae (NCBI taxid: 775)
Dermatophilaceae (NCBI taxid: 85018)	Rikenellaceae (NCBI taxid: 171550)
Dermocarpellaceae (NCBI taxid: 1890498)	Rivulariaceae (NCBI taxid: 1185)
Desulfallaceae (NCBI taxid: 2867375)	Roseiflexaceae (NCBI taxid: 1508635)
Desulfarculaceae (NCBI taxid: 453228)	Roseobacteraceae (NCBI taxid: 2854170)
Desulfatibacillaceae (NCBI taxid: 3031627)	Ruaniaceae (NCBI taxid: 1331736)
Desulfotobacteriaceae (NCBI taxid: 2937909)	Rubrobacteraceae (NCBI taxid: 84997)
Desulfobaccaceae (NCBI taxid: 3031656)	Saccharospirillaceae (NCBI taxid: 255527)
Desulfobacteraceae (NCBI taxid: 213119)	Salinibacteraceae (NCBI taxid: 1853225)
Desulfobulbaceae (NCBI taxid: 213121)	Salinisphaeraceae (NCBI taxid: 742031)
Desulfocapsaceae (NCBI taxid: 2886822)	Salinivirgaceae (NCBI taxid: 1970190)
Desulfococcaceae (NCBI taxid: 2931039)	Sandaracinaceae (NCBI taxid: 1055686)
Desulfohalobiaceae (NCBI taxid: 213117)	Sanguibacteraceae (NCBI taxid: 145360)
Desulfolunaceae (NCBI taxid: 3031622)	Saprospiraceae (NCBI taxid: 89374)
Desulfomicrobiaceae (NCBI taxid: 213116)	Schleiferiaceae (NCBI taxid: 1333713)
Desulfomonilaceae (NCBI taxid: 3031658)	Scytonemataceae (NCBI taxid: 1182)
Desulfosarcinaceae (NCBI taxid: 3031624)	Sedimentisphaeraceae (NCBI taxid: 2483367)
Desulfosudaceae (NCBI taxid: 2904715)	Segniliparaceae (NCBI taxid: 316606)
Desulfotomaculaceae (NCBI taxid: 2937910)	Selenomonadaceae (NCBI taxid: 1843491)
Desulfovibrionaceae (NCBI taxid: 194924)	Shewanellaceae (NCBI taxid: 267890)
Desulfurellaceae (NCBI taxid: 117942)	Silvanigrellaceae (NCBI taxid: 2024974)
Desulfurobacteriaceae (NCBI taxid: 558314)	Simkaniaceae (NCBI taxid: 92712)
Desulfurococcaceae (NCBI taxid: 2272)	Sinobacteraceae (NCBI taxid: 568386)
Desulfuromonadaceae (NCBI taxid: 213421)	Sirenicapillariaceae (NCBI taxid: 2934961)
Dethiosulfovibrionaceae (NCBI taxid: 3029088)	Sneathiellaceae (NCBI taxid: 510685)
Devosiaceae (NCBI taxid: 2831106)	Sphaerobacteraceae (NCBI taxid: 85002)
Dictyoglomaceae (NCBI taxid: 203488)	Sphaerochaetaceae (NCBI taxid: 2791015)
Dietziaceae (NCBI taxid: 85029)	Sphaerotilaceae (NCBI taxid: 2975441)
Dissulfurispiraceae (NCBI taxid: 2811505)	Sphingobacteriaceae (NCBI taxid: 84566)

Dysgonomonadaceae (NCBI taxid: 2005520)	Sphingomonadaceae (NCBI taxid: 41297)
Ectothiorhodospiraceae (NCBI taxid: 72276)	Sphingosinicellaceae (NCBI taxid: 2820280)
Eggerthellaceae (NCBI taxid: 1643826)	Spirochaetaceae (NCBI taxid: 137)
Egibacteraceae (NCBI taxid: 1747769)	Spiroplasmataceae (NCBI taxid: 2131)
Egicoccaceae (NCBI taxid: 1755824)	Spirosomaceae (NCBI taxid: 2896860)
Elioraeaceae (NCBI taxid: 2690195)	Spongiibacteraceae (NCBI taxid: 1706375)
Elusimicrobiaceae (NCBI taxid: 641876)	Sporichthyaceae (NCBI taxid: 85033)
Emcibacteraceae (NCBI taxid: 2066491)	Sporolactobacillaceae (NCBI taxid: 186821)
Endomicrobiaceae (NCBI taxid: 1783343)	Sporomusaceae (NCBI taxid: 1843490)
Endozoicomonadaceae (NCBI taxid: 2066474)	Staphylococcaceae (NCBI taxid: 90964)
Enterobacteriaceae (NCBI taxid: 543)	Stappiaceae (NCBI taxid: 2821832)
Enterococcaceae (NCBI taxid: 81852)	Stellaceae (NCBI taxid: 2844601)
Entomoplasmataceae (NCBI taxid: 33925)	Steroidobacteraceae (NCBI taxid: 2689614)
Erwiniaceae (NCBI taxid: 1903409)	Sterolibacteriaceae (NCBI taxid: 2008793)
Erysipelotrichaceae (NCBI taxid: 128827)	Streptococcaceae (NCBI taxid: 1300)
Erythrobacteraceae (NCBI taxid: 335929)	Streptomycetaceae (NCBI taxid: 2062)
Eubacteriaceae (NCBI taxid: 186806)	Streptosporangiaceae (NCBI taxid: 2004)
Eubacteriales Family XIII. Incertae Sedis (NCBI taxid: 543314)	Succinivibrionaceae (NCBI taxid: 83763)
Eubacteriales incertae sedis (NCBI taxid: 538999)	Sulfolobaceae (NCBI taxid: 118883)
Euzebyaceae (NCBI taxid: 908622)	Sulfuricellaceae (NCBI taxid: 2772226)
Fastidiosibacteraceae (NCBI taxid: 2056687)	Sulfurimonadaceae (NCBI taxid: 2771471)
Ferrimonadaceae (NCBI taxid: 267892)	Sulfurospirillaceae (NCBI taxid: 2932623)
Ferropasmaceae (NCBI taxid: 90142)	Sulfurovaceae (NCBI taxid: 2771472)
Ferrovaceae (NCBI taxid: 1442156)	Sutterellaceae (NCBI taxid: 995019)
Fervidicoccaceae (NCBI taxid: 685949)	Symbiobacteriaceae (NCBI taxid: 543349)
Fervidobacteriaceae (NCBI taxid: 1643950)	Synechococcaceae (NCBI taxid: 1890426)
Fibrobacteraceae (NCBI taxid: 204431)	Synergistaceae (NCBI taxid: 649777)
Fimbriimonadaceae (NCBI taxid: 1663426)	Syntrophaceae (NCBI taxid: 213468)

Flammeovirgaceae (NCBI taxid: 200667)	Syntrophobacteraceae (NCBI taxid: 213465)
Flavobacteriaceae (NCBI taxid: 49546)	Syntrophomonadaceae (NCBI taxid: 68298)
Flexistipitaceae (NCBI taxid: 2945022)	Syntrophotaleaceae (NCBI taxid: 2812024)
Fluviibacteraceae (NCBI taxid: 2808923)	Tannerellaceae (NCBI taxid: 2005525)
Fontisphaeraceae (NCBI taxid: 3050006)	Tenuifilaceae (NCBI taxid: 2760872)
Francisellaceae (NCBI taxid: 34064)	Tepidanaerobacteraceae (NCBI taxid: 2770092)
Frankiaceae (NCBI taxid: 74712)	Tepidiformaceae (NCBI taxid: 2682227)
Fulvivirgaceae (NCBI taxid: 2762286)	Tepidimicrobiaceae (NCBI taxid: 2992719)
Fusobacteriaceae (NCBI taxid: 203492)	Tepidisphaeraceae (NCBI taxid: 1771355)
Gallionellaceae (NCBI taxid: 90627)	Terasakiellaceae (NCBI taxid: 2813951)
Geminicoccaceae (NCBI taxid: 2066434)	Thalassobaculaceae (NCBI taxid: 2844864)
Geminocystaceae (NCBI taxid: 2815910)	Thalassospiraceae (NCBI taxid: 2844866)
Gemmataceae (NCBI taxid: 1914233)	Thermaceae (NCBI taxid: 188786)
Gemmatimonadaceae (NCBI taxid: 219687)	Thermincolaceae (NCBI taxid: 2937911)
Geoalkalibacteraceae (NCBI taxid: 3031665)	Thermoactinomycetaceae (NCBI taxid: 186824)
Geobacteraceae (NCBI taxid: 213422)	Thermoanaerobacteraceae (NCBI taxid: 186814)
Geodermatophilaceae (NCBI taxid: 85030)	Thermoanaerobacterales Family III. Incertae Sedis (NCBI taxid: 543371)
Geovibrionaceae (NCBI taxid: 2945019)	Thermoanaerobacterales Family IV. Incertae Sedis (NCBI taxid: 543372)
Gloeobacteraceae (NCBI taxid: 1890422)	Thermococcaceae (NCBI taxid: 2259)
Gloeomargaritaceae (NCBI taxid: 1955043)	Thermodesulfatatoraceae (NCBI taxid: 3031464)
Glycomycetaceae (NCBI taxid: 85034)	Thermodesulfobacteriaceae (NCBI taxid: 188711)
Gomontiellaceae (NCBI taxid: 1892255)	Thermodesulfobiaceae (NCBI taxid: 227387)
Gordoniaceae (NCBI taxid: 85026)	Thermodesulfovibrionaceae (NCBI taxid: 2811504)
Gottschalkiaceae (NCBI taxid: 2042895)	Thermofilaceae (NCBI taxid: 114378)
Granulosicoccaceae (NCBI taxid: 449719)	Thermoguttaceae (NCBI taxid: 2691358)

Hafniaceae (NCBI taxid: 1903412)	Thermohalobacteraceae (NCBI taxid: 2848916)
Hahellaceae (NCBI taxid: 224379)	Thermoleophilaceae (NCBI taxid: 320796)
Halanaerobiaceae (NCBI taxid: 972)	Thermomicrobiaceae (NCBI taxid: 189777)
Halieaceae (NCBI taxid: 1706372)	Thermomonosporaceae (NCBI taxid: 2012)
Haliscomenobacteraceae (NCBI taxid: 1937961)	Thermoplasmataceae (NCBI taxid: 46659)
Haloarculaceae (NCBI taxid: 1963268)	Thermoplasmatales (NCBI taxid: 2301)
Halobacteriaceae (NCBI taxid: 2236)	Thermoproteaceae (NCBI taxid: 2267)
Halobacteriovoraceae (NCBI taxid: 1652132)	Thermosediminibacteraceae (NCBI taxid: 2770093)
Halobacteroidaceae (NCBI taxid: 53434)	Thermospiraceae (NCBI taxid: 3024225)
Haloferacaceae (NCBI taxid: 1644056)	Thermostichaceae (NCBI taxid: 2881384)
Halomonadaceae (NCBI taxid: 28256)	Thermosynechococcaceae (NCBI taxid: 2881378)
Halorubraceae (NCBI taxid: 1644056)	Thermotogaceae (NCBI taxid: 188709)
Halotheotrichaceae (NCBI taxid: 3046412)	Thermotomaculaceae (NCBI taxid: 2562244)
Halothiobacillaceae (NCBI taxid: 255526)	Thermovirgaceae (NCBI taxid: 3029089)
Hapalosiphonaceae (NCBI taxid: 1892263)	Thioalkalibacteraceae (NCBI taxid: 2035710)
Helicobacteraceae (NCBI taxid: 72293)	Thioalkalispiraceae (NCBI taxid: 1096778)
Heliobacteriaceae (NCBI taxid: 31984)	Thiobacillaceae (NCBI taxid: 2008790)
Hippeaceae (NCBI taxid: 3048035)	Thiotrichaceae (NCBI taxid: 135617)
Holosporaceae (NCBI taxid: 44746)	Thiovulaceae (NCBI taxid: 2771471)
Hoyosellaceae (NCBI taxid: 3040680)	Tichowtungiaceae (NCBI taxid: 2907186)
Hydrogenimonaceae (NCBI taxid: 292630)	Tissierellaceae (NCBI taxid: 1737406)
Hydrogenimonadaceae (NCBI taxid: 292630)	Tolypothrichaceae (NCBI taxid: 119859)
Hydrogenophilaceae (NCBI taxid: 206349)	Treponemataceae (NCBI taxid: 137)
Hydrogenothermaceae (NCBI taxid: 224027)	Treponemataceae (NCBI taxid: 2845253)
Hyellaceae (NCBI taxid: 1890500)	Trichocoleusaceae (NCBI taxid: 2303527)
Hymenobacteraceae (NCBI taxid: 1853232)	Tropherymataceae (NCBI taxid: 2805591)
Hyphomicrobiaceae (NCBI taxid: 45401)	Trueperaceae (NCBI taxid: 332247)
Hyphomonadaceae (NCBI taxid: 69657)	Tsukamurellaceae (NCBI taxid: 85028)

lamiaceae (NCBI taxid: 633392)	Turicibacteraceae (NCBI taxid: 2810281)
Ichthyobacteriaceae (NCBI taxid: 1755828)	Usitatibacteraceae (NCBI taxid: 2803844)
Idiomarinaceae (NCBI taxid: 267893)	Vallitaleaceae (NCBI taxid: 2603322)
Ignatzschineriaceae (NCBI taxid: 3018589)	Veillonellaceae (NCBI taxid: 31977)
Ignavibacteriaceae (NCBI taxid: 795749)	Verrucomicrobiaceae (NCBI taxid: 203557)
Ilumatobacteraceae (NCBI taxid: 2448023)	Vibrionaceae (NCBI taxid: 641)
Immundisolibacteraceae (NCBI taxid: 1934946)	Vicinamibacteraceae (NCBI taxid: 2211325)
Intrasporangiaceae (NCBI taxid: 85021)	Vulгатibacteraceae (NCBI taxid: 1524213)
Isosphaeraceae (NCBI taxid: 1763524)	Waddliaceae (NCBI taxid: 92714)
Jatrophihabitantaceae (NCBI taxid: 2805416)	Weeksellaceae (NCBI taxid: 2762318)
Jiangellaceae (NCBI taxid: 1217100)	Wenzhouxiangellaceae (NCBI taxid: 1676141)
Jonesiaceae (NCBI taxid: 85022)	Woeseiaceae (NCBI taxid: 1738654)
Kaistiaceae (NCBI taxid: 2831111)	Xanthobacteraceae (NCBI taxid: 335928)
Kangiellaceae (NCBI taxid: 1920240)	Xanthomonadaceae (NCBI taxid: 32033)
Kiloniellaceae (NCBI taxid: 597359)	Yersiniaceae (NCBI taxid: 1903411)
Kineosporiaceae (NCBI taxid: 83778)	Zhaonellaceae (NCBI taxid: 2748673)
Kiritimatiellaceae (NCBI taxid: 1921783)	Zoogloeaceae (NCBI taxid: 2008794)
Kofleriaceae (NCBI taxid: 224464)	Zooshikellaceae (NCBI taxid: 2898533)
Koleobacteraceae (NCBI taxid: 2786988)	Zymomonadaceae (NCBI taxid: 2844881)
Kordiimonadaceae (NCBI taxid: 1331809)	

[00429] **Table 5 – By Families.**

[00430] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial families as set forth in Table 5.

Acidaminococcaceae (NCBI taxid: 909930)
Akkermansiaceae (NCBI taxid: 1647988)
Bacillaceae (NCBI taxid: 186817)
Bacteroidaceae (NCBI taxid: 815)
Barnesiellaceae (NCBI taxid: 2005519)
Bifidobacteriaceae (NCBI taxid: 31953)
Campylobacteraceae (NCBI taxid: 72294)
Carnobacteriaceae (NCBI taxid: 186828)

Christensenellaceae (NCBI taxid: 990719)
Clostridiaceae (NCBI taxid: 31979)
Coprobacillaceae (NCBI taxid: 2810280)
Coriobacteriaceae (NCBI taxid: 84107)
Desulfovibrionaceae (NCBI taxid: 194924)
Eggerthellaceae (NCBI taxid: 1643826)
Enterobacteriaceae (NCBI taxid: 543)
Enterococcaceae (NCBI taxid: 81852)
Erysipelotrichaceae (NCBI taxid: 128827)
Eubacteriaceae (NCBI taxid: 186806)
Eubacteriales Family XIII. Incertae Sedis (NCBI taxid: 543314)
Eubacteriales incertae sedis (NCBI taxid: 538999)
Lachnospiraceae (NCBI taxid: 186803)
Lactobacillaceae (NCBI taxid: 33958)
Maliibacteriaceae (NCBI taxid: 3047432)
Muribaculaceae (NCBI taxid: 2005473)
Odoribacteraceae (NCBI taxid: 1853231)
Oscillospiraceae (NCBI taxid: 216572)
Peptoniphilaceae (NCBI taxid: 1570339)
Peptostreptococcaceae (NCBI taxid: 186804)
Prevotellaceae (NCBI taxid: 171552)
Rikenellaceae (NCBI taxid: 171550)
Selenomonadaceae (NCBI taxid: 1843491)
Streptococcaceae (NCBI taxid: 1300)
Sutterellaceae (NCBI taxid: 995019)
Veillonellaceae (NCBI taxid: 31977)

[00431] **Table 6 – By Families**

[00432] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial families as set forth in Table 6.

Akkermansiaceae (NCBI taxid: 1647988)
Bacillaceae (NCBI taxid: 186817)
Bacteroidaceae (NCBI taxid: 815)
Barnesiellaceae (NCBI taxid: 2005519)
Bifidobacteriaceae (NCBI taxid: 31953)

Christensenellaceae (NCBI taxid: 990719)
Clostridiaceae (NCBI taxid: 31979)
Coprobacillaceae (NCBI taxid: 2810280)
Coriobacteriaceae (NCBI taxid: 84107)
Erysipelotrichaceae (NCBI taxid: 128827)
Eubacteriaceae (NCBI taxid: 186806)
Eubacteriales incertae sedis (NCBI taxid: 538999)
Lachnospiraceae (NCBI taxid: 186803)
Lactobacillaceae (NCBI taxid: 33958)
Maliibacteriaceae (NCBI taxid: 3047432)
Odoribacteraceae (NCBI taxid: 1853231)
Oscillospiraceae (NCBI taxid: 216572)
Peptoniphilaceae (NCBI taxid: 1570339)
Peptostreptococcaceae (NCBI taxid: 186804)
Porphyromonadaceae (NCBI taxid: 171551)
Prevotellaceae (NCBI taxid: 171552)
Rikenellaceae (NCBI taxid: 171550)
Selenomonadaceae (NCBI taxid: 1843491)
Streptococcaceae (NCBI taxid: 1300)
Tannerellaceae (NCBI taxid: 2005525)

[00433] BY GENUS

[00434] **Table 7 – By Genera.**

[00435] In some embodiments, the composition of the invention includes one or more
5 microbes selected from one or more of the microbial genera as set forth in Table 7.

Acidaminococcaceae (family) (NCBI taxid: 909930)	Intestinibaculum (NCBI taxid: 2679910)
Acidaminococcus (NCBI taxid: 904)	Intestinimonas (NCBI taxid: 1392389)
Adlercreutzia (NCBI taxid: 447020)	Lachnoanaerobaculum (NCBI taxid: 1164882)
Agathobaculum (NCBI taxid: 2048137)	Lachnoclostridium (NCBI taxid: 1506553)
Akkermansia (NCBI taxid: 239934)	Lachnospira (NCBI taxid: 28050)
Alistipes (NCBI taxid: 239759)	Lachnospiraceae incertae sedis (unclassified rank, Lachnospiraceae family) (NCBI taxid: 2840493)
Alterileibacterium (NCBI taxid: 1980680)	Lacrimispora (NCBI taxid: 2719231)

Amedibacillus (NCBI taxid: 2749846)	Lactococcus (NCBI taxid: 1357)
Amedibacterium (NCBI taxid: 2749267)	Ligilactobacillus (NCBI taxid: 2767887)
Aminipila (NCBI taxid: 2060094)	Longibaculum (NCBI taxid: 1918538)
Anaerobutyricum (NCBI taxid: 2569097)	Longicatena (NCBI taxid: 1918536)
Anaerococcus (NCBI taxid: 165779)	Mageeibacillus (NCBI taxid: 1637257)
Anaerocolumna (NCBI taxid: 1843210)	Maliibacterium (NCBI taxid: 3047433)
Anaerofustis (NCBI taxid: 264995)	Marvinbryantia (NCBI taxid: 248744)
Anaerostipes (NCBI taxid: 207244)	Massilimicrobiota (NCBI taxid: 1924110)
Anaerotignum (NCBI taxid: 2039240)	Massiliprevotella (NCBI taxid: 1981037)
Anaerotruncus (NCBI taxid: 244127)	Massilistercora (NCBI taxid: 2717089)
Bacillus (NCBI taxid: 1386)	Mediterraneibacter (NCBI taxid: 2316020)
Bacteroides (NCBI taxid: 816)	Megamonas (NCBI taxid: 158846)
Barnesiella (NCBI taxid: 397864)	Megasphaera (NCBI taxid: 906)
Bifidobacterium (NCBI taxid: 1678)	Merdibacter (NCBI taxid: 1935200)
Bilophila (NCBI taxid: 35832)	Mesosutterella (NCBI taxid: 2494213)
Blautia (NCBI taxid: 572511)	Mitsuokella (NCBI taxid: 52225)
Butyricimonas (NCBI taxid: 574697)	Mogibacterium (NCBI taxid: 86331)
Butyrivibrio (NCBI taxid: 830)	Muribaculum (NCBI taxid: 1918540)
Campylobacter (NCBI taxid: 194)	Negativibacillus (NCBI taxid: 1980693)
Caproicibacter (NCBI taxid: 2576755)	Novisyntrophococcus (NCBI taxid: 2888809)
Caproicibacterium (NCBI taxid: 2834348)	Odoribacter (NCBI taxid: 283168)
Caproiciproducens (NCBI taxid: 1738645)	Olsenella (NCBI taxid: 133925)
Casaltella (NCBI taxid: 1715793)	Oscillibacter (NCBI taxid: 459786)
Catenibacterium (NCBI taxid: 135858)	Oscillospiraceae (family) (NCBI taxid: 216572)
Christensenella (NCBI taxid: 990721)	Oscillospiraceae incertae sedis (unclassified rank, Oscillospiraceae family) (NCBI taxid: 552397)
Clostridium (NCBI taxid: 1485)	Parabacteroides (NCBI taxid: 375288)
Collinsella (NCBI taxid: 102106)	Paraclostridium (NCBI taxid: 1849822)
Coprobacillus (NCBI taxid: 100883)	Paraprevotella (NCBI taxid: 577309)
Coprobacter (NCBI taxid: 1348911)	Parolsenella (NCBI taxid: 2082587)
Coprococcus (NCBI taxid: 33042)	Peptacetobacter (NCBI taxid: 2743582)
Desulfovibrio (NCBI taxid: 872)	Peptoniphilus (NCBI taxid: 162289)

Dorea (NCBI taxid: 189330)	Peptostreptococcus (NCBI taxid: 1257)
Duodenibacillus (NCBI taxid: 1980697)	Phascolarctobacterium (NCBI taxid: 33024)
Dysosmobacter (NCBI taxid: 2591381)	Phocaeicola (NCBI taxid: 909656)
Eggerthella (NCBI taxid: 84111)	Porphyromonas (NCBI taxid: 836)
Enorma (NCBI taxid: 1472762)	Prevotella (NCBI taxid: 838)
Enterocloster (NCBI taxid: 2719313)	Pseudobutyrvibrio (NCBI taxid: 46205)
Enterococcus (NCBI taxid: 1350)	Pusillibacter (NCBI taxid: 2892397)
Erysipelatoclostridium (NCBI taxid: 3025755)	Romboutsia (NCBI taxid: 1501226)
Escherichia (NCBI taxid: 561)	Roseburia (NCBI taxid: 841)
Ethanoligenens (NCBI taxid: 253238)	Ruminiclostridium (NCBI taxid: 1508657)
Eubacterium (NCBI taxid: 1730)	Ruminococcus (NCBI taxid: 1263)
Faecalibacillus (NCBI taxid: 2678885)	Ruthenibacterium (NCBI taxid: 1905344)
Faecalibacterium (NCBI taxid: 216851)	Schaalia (NCBI taxid: 2529408)
Faecalibaculum (NCBI taxid: 1729679)	Segatella (NCBI taxid: 2974251)
Finegoldia (NCBI taxid: 150022)	Selenomonas (NCBI taxid: 970)
Flavonifractor (NCBI taxid: 946234)	Sellimonas (NCBI taxid: 1769710)
Flintibacter (NCBI taxid: 1918454)	Senegalimassilia (NCBI taxid: 1473205)
Fusicatenibacter (NCBI taxid: 1407607)	Slackia (NCBI taxid: 84108)
Gemmiger (NCBI taxid: 204475)	Sodaliphilus (NCBI taxid: 2815786)
Gordonibacter (NCBI taxid: 644652)	Solibaculum (NCBI taxid: 2842531)
Granulicatella (NCBI taxid: 117563)	Streptococcus (NCBI taxid: 1301)
Herbinix (NCBI taxid: 1663717)	Subdoligranulum (NCBI taxid: 292632)
Holdemanella (NCBI taxid: 1573535)	Thomasclavelia (NCBI taxid: 3025755)
Holdemania (NCBI taxid: 61170)	Tyzzereella (NCBI taxid: 1506577)
Hoyleseella (NCBI taxid: 2974257)	Veillonella (NCBI taxid: 29465)
Hungatella (NCBI taxid: 1649459)	Vescimonas (NCBI taxid: 2892396)
Intestinibacter (NCBI taxid: 1505657)	

[00436] **Table 8 – By Genera.**

[00437] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial genera as set forth in Table 8.

Agathobaculum (NCBI taxid: 2048137)	Gemmiger (NCBI taxid: 204475)
Akkermansia (NCBI taxid: 239934)	Holdemanella (NCBI taxid: 1573535)
Alistipes (NCBI taxid: 239759)	Hungatella (NCBI taxid: 1649459)

Amedibacterium (NCBI taxid: 2749267)	Intestinimonas (NCBI taxid: 1392389)
Anaerobutyricum (NCBI taxid: 2569097)	Lachnoanaerobaculum (NCBI taxid: 1164882)
Anaerofustis (NCBI taxid: 264995)	Lachnospira (NCBI taxid: 28050)
Anaerostipes (NCBI taxid: 207244)	Lacrimispora (NCBI taxid: 2719231)
Anaerotignum (NCBI taxid: 2039240)	Lactococcus (NCBI taxid: 1357)
Anaerotruncus (NCBI taxid: 244127)	Ligilactobacillus (NCBI taxid: 2767887)
Bacillus (NCBI taxid: 1386)	Longicatena (NCBI taxid: 1918536)
Bacteroides (NCBI taxid: 816)	Massilimicrobiota (NCBI taxid: 1924110)
Barnesiella (NCBI taxid: 397864)	Megamonas (NCBI taxid: 158846)
Bifidobacterium (NCBI taxid: 1678)	Merdibacter (NCBI taxid: 1935200)
Blautia (NCBI taxid: 572511)	Odoribacter (NCBI taxid: 283168)
Butyricimonas (NCBI taxid: 574697)	Oscillospiraceae (family) (NCBI taxid: 216572)
Christensenella (NCBI taxid: 990721)	Parabacteroides (NCBI taxid: 375288)
Clostridium (NCBI taxid: 1485)	Paraclostridium (NCBI taxid: 1849822)
Collinsella (NCBI taxid: 102106)	Phocaeicola (NCBI taxid: 909656)
Coprobacillus (NCBI taxid: 100883)	Porphyromonas (NCBI taxid: 836)
Coprobacter (NCBI taxid: 1348911)	Prevotella (NCBI taxid: 838)
Coprococcus (NCBI taxid: 33042)	Pusillibacter (NCBI taxid: 2892397)
Dorea (NCBI taxid: 189330)	Romboutsia (NCBI taxid: 1501226)
Enorma (NCBI taxid: 1472762)	Roseburia (NCBI taxid: 841)
Enterocloster (NCBI taxid: 2719313)	Ruminococcus (NCBI taxid: 1263)
Erysipelatoclostridium (NCBI taxid: 3025755)	Ruthenibacterium (NCBI taxid: 1905344)
Eubacterium (NCBI taxid: 1730)	Sellimonas (NCBI taxid: 1769710)
Faecalibacillus (NCBI taxid: 2678885)	Solibaculum (NCBI taxid: 2842531)
Faecalibacterium (NCBI taxid: 216851)	Streptococcus (NCBI taxid: 1301)
Finegoldia (NCBI taxid: 150022)	Thomasclavelia (NCBI taxid: 3025755)
Flintibacter (NCBI taxid: 1918454)	Vescimonas (NCBI taxid: 2892396)

[00438] BY SPECIES

[00439] **Table 9 – By Species.**

[00440] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 9.

5

Absiella dolichum (NCBI taxid: 31971)	Dysosmobacter faecalis
Acidaminococcaceae sp. (NCBI taxid: 909930)	Dysosmobacter welbionis (NCBI taxid: 2093857)
Acidaminococcus fermentans (NCBI taxid: 905)	Eggerthella guodeyinii (NCBI taxid: 2690837)
Acidaminococcus intestini (NCBI taxid: 187327)	Eggerthella lenta (NCBI taxid: 84112)
Adlercreutzia equolifaciens (NCBI taxid: 446660)	Enorma massiliensis (NCBI taxid: 1472761)
Adlercreutzia hattorii (NCBI taxid: 2707299)	Enorma sp. (NCBI taxid: 1920692)
Agathobacter rectalis (NCBI taxid: 39491)	Enterocloster aldenensis (NCBI taxid: 358742)
Agathobaculum sp. (NCBI taxid: 2048138)	Enterocloster bolteae (NCBI taxid: 208479)
Agathobaculum sp003481705	Enterococcus faecium (NCBI taxid: 1352)
Akkermansia muciniphila (NCBI taxid: 239935)	Erysipelatoclostridium ramosum (NCBI taxid: 1547)
Alistipes communis (NCBI taxid: 2585118)	Escherichia coli (NCBI taxid: 562)
Alistipes dispar (NCBI taxid: 2585119)	Ethanoligenens harbinense (NCBI taxid: 253239)
Alistipes finegoldii (NCBI taxid: 214856)	Eubacterium callanderi (NCBI taxid: 53442)
Alistipes ihumii (NCBI taxid: 1470347)	Eubacterium limosum (NCBI taxid: 1736)
Alistipes indistinctus (NCBI taxid: 626932)	Eubacterium maltosivorans (NCBI taxid: 2041044)
Alistipes megaguti (NCBI taxid: 2364787)	Eubacterium rectale (NCBI taxid: 39491)
Alistipes onderdonkii (NCBI taxid: 328813)	Eubacterium siraeum (NCBI taxid: 39492)
Alistipes putredinis (NCBI taxid: 28117)	Eubacterium sp. c-25 (NCBI taxid: 3028070)
Alistipes senegalensis (NCBI taxid: 1288121)	Eubacterium sp. NSJ-61 (NCBI taxid: 2764325)
Alistipes shahii (NCBI taxid: 328814)	Eubacterium ventriosum (NCBI taxid: 39496)
Alistipes sp. dk3624 (NCBI taxid: 2662363)	Extibacter hylemonae
Alterileibacterium massiliense (NCBI taxid: 1870997)	Faecalibacillus intestinalis (NCBI taxid: 1982626)
Alterileibacterium sp. (NCBI taxid: 2046786)	Faecalibacterium duncaniae (NCBI taxid: 411483)

Amedibacterium intestinale (NCBI taxid: 2583452)	Faecalibacterium prausnitzii (NCBI taxid: 853)
Aminipila luticellarii (NCBI taxid: 2507160)	Faecalibaculum rodentium (NCBI taxid: 1702221)
Anaerobutyricum hallii (NCBI taxid: 39488)	Fimivivens sp900113995
Anaerococcus vaginalis (NCBI taxid: 33037)	Finegoldia magna (NCBI taxid: 1260)
Anaerocolumna chitinilytica (NCBI taxid: 1727145)	Flavonifractor plautii (NCBI taxid: 292800)
Anaerocolumna sedimenticola (NCBI taxid: 2696063)	Flintibacter sp. KGMB00164 (NCBI taxid: 2610895)
Anaerofustis sp. (NCBI taxid: 1872517)	Fusicatenibacter sp. (NCBI taxid: 2773922)
Anaerofustis stercorihominis (NCBI taxid: 214853)	Gemmiger formicilis (NCBI taxid: 745368)
Anaerostipes caccae (NCBI taxid: 105841)	Gordonibacter urolithinfaciens (NCBI taxid: 1335613)
Anaerostipes hadrus (NCBI taxid: 649756)	Granulicatella adiacens (NCBI taxid: 46124)
Anaerostipes hominis (NCBI taxid: 2025494)	Herbinix luporum (NCBI taxid: 1679721)
Anaerostipes rhamnosivorans (NCBI taxid: 1229621)	Holdemanella biformis (NCBI taxid: 1735)
Anaerotignum lactatifermentans (NCBI taxid: 160404)	Holdemanella porci (NCBI taxid: 2652276)
Anaerotignum propionicum (NCBI taxid: 28446)	Holdemania filiformis (NCBI taxid: 61171)
Anaerotignum sp. (NCBI taxid: 2039241)	Hungatella effluvii (NCBI taxid: 1096246)
Anaerotignum sp001304995	Hungatella hathewayi (NCBI taxid: 154046)
Anaerotruncus colihominis (NCBI taxid: 169435)	Intestinibaculum porci (NCBI taxid: 2487118)
Anaerotruncus rubiinfantis (NCBI taxid: 1720200)	Intestinimonas butyriciproducens (NCBI taxid: 1297617)
Bacillus bombysepticus (NCBI taxid: 658666)	Lachnoanaerobaculum sp000296385
Bacillus cereus (NCBI taxid: 1396)	Lachnoanaerobaculum umeaense (NCBI taxid: 617123)

Bacteroides caccae (NCBI taxid: 47678)	Lachnoclostridium phocaeense (NCBI taxid: 1871021)
Bacteroides caecimuris (NCBI taxid: 1796613)	Lachnoclostridium phytofermentans (NCBI taxid: 66219)
Bacteroides cellulosilyticus (NCBI taxid: 246787)	Lachnoclostridium sp. YL32 (NCBI taxid: 1834196)
Bacteroides coprocola (NCBI taxid: 310298)	Lachnospira eligens (NCBI taxid: 39485)
Bacteroides coprophilus (NCBI taxid: 387090)	Lachnospira sp003451515
Bacteroides dorei (NCBI taxid: 357276)	Lacrimispora saccharolytica (NCBI taxid: 84030)
Bacteroides eggerthii (NCBI taxid: 28111)	Lactobacillus ruminis (NCBI taxid: 1623)
Bacteroides faecis (NCBI taxid: 674529)	Lactococcus lactis (NCBI taxid: 1358)
Bacteroides finegoldii (NCBI taxid: 338188)	Lactococcus petauri (NCBI taxid: 1940789)
Bacteroides fragilis (NCBI taxid: 817)	Lawsonibacter sp944385665
Bacteroides helcogenes (NCBI taxid: 290053)	Ligilactobacillus ruminis (NCBI taxid: 1623)
Bacteroides heparinolyticus (NCBI taxid: 28113)	Longibaculum sp. KGMB06250 (NCBI taxid: 2584943)
Bacteroides intestinalis (NCBI taxid: 329854)	Longicatena caecimuris (NCBI taxid: 1796635)
Bacteroides luhongzhouii (NCBI taxid: 2650158)	Luoshenia tenuis (NCBI taxid: 2763654)
Bacteroides nordii (NCBI taxid: 291645)	Mageeibacillus indolicus (NCBI taxid: 884684)
Bacteroides ovatus (NCBI taxid: 28116)	Massilimicrobiota merdigallinarum
Bacteroides pectinophilus (NCBI taxid: 384638)	
Bacteroides plebeius (NCBI taxid: 310297)	Massilimicrobiota sp002160865
Bacteroides rodentium (NCBI taxid: 691816)	Massilimicrobiota timonensis (NCBI taxid: 1776392)
Bacteroides salyersiae (NCBI taxid: 291644)	Massilioclostridium methylpentosum
Bacteroides sp. A1C1 (NCBI taxid: 2528203)	Massiliprevotella massiliensis (NCBI taxid: 1816687)

Bacteroides sp. CACC 737 (NCBI taxid: 2755405)	Massilistercora timonensis (NCBI taxid: 2086584)
Bacteroides sp. CBA7301 (NCBI taxid: 2715212)	Mediterraneibacter torques (NCBI taxid: 33039)
Bacteroides sp. HF-162 (NCBI taxid: 2785531)	Megamonas funiformis (NCBI taxid: 437897)
Bacteroides sp. KGMB10229 (NCBI taxid: 2792859)	Megamonas rupellensis (NCBI taxid: 491921)
Bacteroides sp900552405	Megasphaera elsdenii (NCBI taxid: 907)
Bacteroides stercoris (NCBI taxid: 46506)	Megasphaera stantonii (NCBI taxid: 2144175)
Bacteroides thetaiotaomicron (NCBI taxid: 818)	Merdibacter merdigallinarum (NCBI taxid: 2838693)
Bacteroides uniformis (NCBI taxid: 820)	Merdibacter merdipullorum (NCBI taxid: 2838694)
Bacteroides vulgatus (NCBI taxid: 821)	Mesosutterella multiformis (NCBI taxid: 2259133)
Bacteroides xylanisolvens (NCBI taxid: 371601)	Methonobrevibacter sp. (NCBI taxid: 2172)
Bacteroides zhangwenhongii (NCBI taxid: 2650157)	Mitsuokella multacida (NCBI taxid: 52226)
Bacteroides zoogloformans (NCBI taxid: 28119)	Mogibacterium diversum (NCBI taxid: 114527)
Bariatricus comes (NCBI taxid: 410072)	Muribaculum intestinale (NCBI taxid: 1796646)
Barnesiella intestinihominis (NCBI taxid: 487174)	Negativibacillus massiliensis (NCBI taxid: 1871035)
Barnesiella viscericola (NCBI taxid: 397865)	Novisyntrophococcus fermenticellae (NCBI taxid: 2068655)
Bifidobacterium adolescentis (NCBI taxid: 1680)	NSJ-51 sp900549795
Bifidobacterium bifidum (NCBI taxid: 1681)	Odoribacter splanchnicus (NCBI taxid: 28118)
Bifidobacterium breve (NCBI taxid: 1685)	Olsenella sp. GAM18 (NCBI taxid: 2109685)

Bifidobacterium catenulatum (NCBI taxid: 1686)	Olsenella uli (NCBI taxid: 133926)
Bifidobacterium longum (NCBI taxid: 216816)	Oscillibacter sp. PEA192 (NCBI taxid: 2109687)
Bifidobacterium pseudocatenulatum (NCBI taxid: 28026)	Oscillibacter valericigenes (NCBI taxid: 351091)
Bilophila wadsworthia (NCBI taxid: 35833)	Oscillospiraceae sp.
Blautia argi (NCBI taxid: 1912897)	Parabacteroides distasonis (NCBI taxid: 823)
Blautia hansenii (NCBI taxid: 1322)	Parabacteroides goldsteinii (NCBI taxid: 328812)
Blautia hydrogenotrophica (NCBI taxid: 53443)	Parabacteroides johnsonii (NCBI taxid: 387661)
Blautia liquoris (NCBI taxid: 2779518)	Parabacteroides merdae (NCBI taxid: 46503)
Blautia massiliensis (NCBI taxid: 1737424)	Paraclostridium bifermentans (NCBI taxid: 1490)
Blautia obeum (NCBI taxid: 40520)	Paraclostridium dentum (NCBI taxid: 2662455)
Blautia parvula (NCBI taxid: 2877527)	Paraprevotella xylaniphila (NCBI taxid: 454155)
Blautia producta (NCBI taxid: 33035)	Parolsenella catena (NCBI taxid: 2003188)
Blautia pseudococcoides (NCBI taxid: 1796616)	Peptacetobacter hiranonis (NCBI taxid: 89152)
Blautia sp. SC05B48 (NCBI taxid: 2479767)	Peptoniphilus grossensis (NCBI taxid: 1465756)
Blautia stercoris (NCBI taxid: 871664)	Peptoniphilus obesi (NCBI taxid: 1472765)
Blautia wexlerae (NCBI taxid: 418240)	Peptostreptococcus sp. (NCBI taxid: 1262)
Bryantella formatexigens (NCBI taxid: 168384)	Phascolarctobacterium faecium (NCBI taxid: 33025)
Butyricimonas faecalis (NCBI taxid: 2093856)	Phascolarctobacterium sp. (NCBI taxid: 2049039)
Butyricimonas virosa (NCBI taxid: 544645)	Phascolarctobacterium succinatutens (NCBI taxid: 626940)
Butyrivibrio crossotus (NCBI taxid: 45851)	Phocaeicola coprocola (NCBI taxid: 310298)

Butyrivibrio hungatei (NCBI taxid: 185008)	Phocaeicola coprophilus (NCBI taxid: 387090)
Butyrivibrio proteoclasticus (NCBI taxid: 43305)	Phocaeicola dorei (NCBI taxid: 357276)
Campylobacter coli (NCBI taxid: 195)	Phocaeicola salanitronis (NCBI taxid: 376805)
Campylobacter jejuni (NCBI taxid: 197)	Phocaeicola vulgatus (NCBI taxid: 821)
Caproicibacter fermentans (NCBI taxid: 2576756)	Porphyromonas asaccharolytica (NCBI taxid: 28123)
Caproicibacterium amylolyticum (NCBI taxid: 2766537)	Prevotella buccae (NCBI taxid: 28126)
Caproiciproducens sp. NJN-50 (NCBI taxid: 2507162)	Prevotella buccalis (NCBI taxid: 28127)
Casaltella massiliensis (NCBI taxid: 938278)	Prevotella copri (NCBI taxid: 165179)
Catenibacterium mitsuokai (NCBI taxid: 100886)	Prevotella intermedia (NCBI taxid: 28131)
Christensenella minuta (NCBI taxid: 626937)	Prevotella melaninogenica (NCBI taxid: 28132)
Christensenella sp. Marseille-P3954 (NCBI taxid: 2086585)	Pseudobutyrvibrio xylanivorans (NCBI taxid: 185007)
Clostridium asparagiforme (NCBI taxid: 333367)	Pusillimonas faecalis (NCBI taxid: 2714358)
Clostridium bartlettii (NCBI taxid: 261299)	Romboutsia sp. (NCBI taxid: 1965302)
Clostridium beijerinckii (NCBI taxid: 1520)	Romboutsia sp. CE17 (NCBI taxid: 2724150)
Clostridium bolteae (NCBI taxid: 208479)	Romboutsia timonensis (NCBI taxid: 1776391)
Clostridium bornimense (NCBI taxid: 1216932)	Roseburia hominis (NCBI taxid: 301301)
Clostridium botulinum (NCBI taxid: 1491)	Roseburia intestinalis (NCBI taxid: 166486)
Clostridium butyricum (NCBI taxid: 1492)	Roseburia inulinivorans (NCBI taxid: 360807)
Clostridium cadaveris (NCBI taxid: 1529)	Ruminiclostridium cellulolyticum (NCBI taxid: 1521)

Clostridium hathewayi (NCBI taxid: 154046)	Ruminiclostridium siraeum (NCBI taxid: 39492)
Clostridium hylemonae (NCBI taxid: 89153)	Ruminococcus albus (NCBI taxid: 1264)
Clostridium innocuum (NCBI taxid: 1522)	Ruminococcus bicirculans (NCBI taxid: 1160721)
Clostridium leptum (NCBI taxid: 1535)	Ruminococcus bromii (NCBI taxid: 40518)
Clostridium methylpentosum (NCBI taxid: 84026)	Ruminococcus flavefaciens (NCBI taxid: 1265)
Clostridium nexile (NCBI taxid: 29361)	Ruminococcus gauvreauii (NCBI taxid: 438033)
Clostridium paraputrificum (NCBI taxid: 29363)	Ruminococcus gnavus (NCBI taxid: 33038)
Clostridium pasteurianum (NCBI taxid: 1501)	Ruminococcus lactaris (NCBI taxid: 46228)
Clostridium perfringens (NCBI taxid: 1502)	Ruminococcus sp. JE7A12 (NCBI taxid: 2564099)
Clostridium saccharobutylicum (NCBI taxid: 169679)	Ruminococcus torques (NCBI taxid: 33039)
Clostridium saccharoperbutylacetonicum (NCBI taxid: 36745)	Ruthenibacterium lactatiformans (NCBI taxid: 1550024)
Clostridium scindens (NCBI taxid: 29347)	Schaalia odontolytica (NCBI taxid: 1660)
Clostridium sp. (NCBI taxid: 1506)	Selenomonas ruminantium (NCBI taxid: 971)
Clostridium sp. BNL1100 (NCBI taxid: 755731)	Sellimonas intestinalis (NCBI taxid: 1653434)
Clostridium sp. C1 (NCBI taxid: 1155388)	Senegalimassilia anaerobia (NCBI taxid: 1473216)
Clostridium sp. SY8519 (NCBI taxid: 1042156)	Slackia exigua (NCBI taxid: 84109)
Clostridium spiroforme (NCBI taxid: 29348)	Slackia heliotrinireducens (NCBI taxid: 84110)
Clostridium sporogenes (NCBI taxid: 1509)	Slackia isoflavoniconvertens (NCBI taxid: 572010)
Clostridium tetani (NCBI taxid: 1513)	Sodaliphilus pleomorphus (NCBI taxid: 2606626)

Collinsella aerofaciens (NCBI taxid: 74426)	Solibaculum mannosilyticum (NCBI taxid: 2780922)
Collinsella bouchesdurhonensis (NCBI taxid: 1907654)	Solobacterium moorei (NCBI taxid: 102148)
Collinsella sp002232035	Streptococcus infantarius (NCBI taxid: 102684)
Collinsella sp905215835	Streptococcus pasteurianus (NCBI taxid: 197614)
Collinsella stercoris (NCBI taxid: 147206)	Streptococcus salivarius (NCBI taxid: 1304)
Coprobacillus cateniformis (NCBI taxid: 100884)	Streptococcus sanguinis (NCBI taxid: 1305)
Coprobacter fastidiosus (NCBI taxid: 1099853)	Streptococcus suis (NCBI taxid: 1307)
Coprobacter secundus (NCBI taxid: 1501392)	Streptococcus thermophilus (NCBI taxid: 1308)
Coprococcus catus (NCBI taxid: 116085)	Subdoligranulum variabile (NCBI taxid: 214851)
Coprococcus comes (NCBI taxid: 410072)	Thomasclavelia ramosa (NCBI taxid: 1547)
Coprococcus eutactus (NCBI taxid: 33043)	Thomasclavelia spiroformis (NCBI taxid: 29348)
Coprococcus sp000154245	UBA1394 sp900066845
Desulfovibrio piger (NCBI taxid: 901)	Veillonella dispar (NCBI taxid: 39778)
Dorea formicigenerans (NCBI taxid: 39486)	Vescimonas coprocola (NCBI taxid: 2714355)
Dorea longicatena (NCBI taxid: 88431)	Vescimonas fastidiosa (NCBI taxid: 2714353)
Duodenibacillus sp. (NCBI taxid: 1980700)	Vescimonas sp900545585

[00441] **Table 10 – By Species.**

[00442] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 10.

Akkermansia muciniphila (NCBI taxid: 239935)	Lacrimispora saccharolytica (NCBI taxid: 84030)
Alistipes dispar (NCBI taxid: 2585119)	Lactococcus lactis (NCBI taxid: 1358)
Alistipes finegoldii (NCBI taxid: 214856)	Lactococcus petauri (NCBI taxid: 1940789)

Alistipes ihumii (NCBI taxid: 1470347)	Longicatena caecimuris (NCBI taxid: 1796635)
Alistipes indistinctus (NCBI taxid: 626932)	Megamonas funiformis (NCBI taxid: 437897)
Alistipes onderdonkii (NCBI taxid: 328813)	Merdibacter merdipullorum (NCBI taxid: 2838694)
Alistipes putredinis (NCBI taxid: 28117)	Odoribacter splanchnicus (NCBI taxid: 28118)
Alistipes senegalensis (NCBI taxid: 1288121)	Parabacteroides distasonis (NCBI taxid: 823)
Alistipes shahii (NCBI taxid: 328814)	Parabacteroides goldsteinii (NCBI taxid: 328812)
Amedibacterium intestinale (NCBI taxid: 2583452)	Parabacteroides johnsonii (NCBI taxid: 387661)
Anaerobutyricum hallii (NCBI taxid: 39488)	Parabacteroides merdae (NCBI taxid: 46503)
Anaerofustis stercorihominis (NCBI taxid: 214853)	Porphyromonas asaccharolytica (NCBI taxid: 28123)
Anaerostipes caccae (NCBI taxid: 105841)	Prevotella copri (NCBI taxid: 165179)
Anaerostipes hadrus (NCBI taxid: 649756)	Roseburia hominis (NCBI taxid: 301301)
Anaerostipes hominis (NCBI taxid: 2025494)	Roseburia intestinalis (NCBI taxid: 166486)
Anaerotruncus colihominis (NCBI taxid: 169435)	Roseburia inulinivorans (NCBI taxid: 360807)
Anaerotruncus rubiinfantis (NCBI taxid: 1720200)	Ruminococcus bicirculans (NCBI taxid: 1160721)
Bacteroides caccae (NCBI taxid: 47678)	Ruminococcus bromii (NCBI taxid: 40518)
Bacteroides eggerthii (NCBI taxid: 28111)	Ruminococcus gnavus (NCBI taxid: 33038)
Bacteroides faecis (NCBI taxid: 674529)	Ruthenibacterium lactatiformans (NCBI taxid: 1550024)
Bacteroides finegoldii (NCBI taxid: 338188)	Sellimonas intestinalis (NCBI taxid: 1653434)

Bacteroides intestinalis (NCBI taxid: 329854)	Solibaculum mannosilyticum (NCBI taxid: 2780922)
Bacteroides nordii (NCBI taxid: 291645)	Streptococcus infantarius (NCBI taxid: 102684)
Bacteroides ovatus (NCBI taxid: 28116)	Streptococcus salivarius (NCBI taxid: 1304)
Bacteroides salyersiae (NCBI taxid: 291644)	Vescimonas coprocola (NCBI taxid: 2714355)
Bacteroides stercoris (NCBI taxid: 46506)	Agathobacter rectalis (NCBI taxid: 39491)
Bacteroides thetaiotaomicron (NCBI taxid: 818)	Agathobaculum sp003481705
Bacteroides uniformis (NCBI taxid: 820)	Anaerotignum sp001304995
Bacteroides xylanisolvens (NCBI taxid: 371601)	Bacillus bombysepticus (NCBI taxid: 658666)
Barnesiella intestinihominis (NCBI taxid: 487174)	Bacteroides sp900552405
Bifidobacterium adolescentis (NCBI taxid: 1680)	Bariatricus comes (NCBI taxid: 410072)
Bifidobacterium bifidum (NCBI taxid: 1681)	Clostridium sp. (NCBI taxid: 1506)
Bifidobacterium longum (NCBI taxid: 216816)	Collinsella sp002232035
Bifidobacterium pseudocatenulatum (NCBI taxid: 28026)	Collinsella sp905215835
Blautia massiliensis (NCBI taxid: 1737424)	Coprococcus sp000154245
Blautia stercoris (NCBI taxid: 871664)	Dysosmobacter faecalis
Blautia wexlerae (NCBI taxid: 418240)	Extibacter hylemonae
Butyricimonas faecalis (NCBI taxid: 2093856)	Faecalibacterium duncaniae (NCBI taxid: 411483)
Butyricimonas virosa (NCBI taxid: 544645)	Fimivivens sp900113995
Christensenella minuta (NCBI taxid: 626937)	Lachnoanaerobaculum sp000296385

Clostridium butyricum (NCBI taxid: 1492)	Lachnospira sp003451515
Clostridium leptum (NCBI taxid: 1535)	Lawsonibacter sp944385665
Clostridium paraputrificum (NCBI taxid: 29363)	Ligilactobacillus ruminis (NCBI taxid: 1623)
Clostridium scindens (NCBI taxid: 29347)	Luoshenia tenuis (NCBI taxid: 2763654)
Collinsella aerofaciens (NCBI taxid: 74426)	Massilimicrobiota merdigallinarum
Collinsella bouchedurhonensis (NCBI taxid: 1907654)	Massilimicrobiota sp002160865
Coprobacillus cateniformis (NCBI taxid: 100884)	Massilioclostridium methylpentosum
Coprobacter secundus (NCBI taxid: 1501392)	Mediterraneibacter torques (NCBI taxid: 33039)
Coprococcus catus (NCBI taxid: 116085)	Merdibacter merdigallinarum (NCBI taxid: 2838693)
Dorea longicatena (NCBI taxid: 88431)	NSJ-51 sp900549795
Enorma massiliensis (NCBI taxid: 1472761)	Paraclostridium dentum (NCBI taxid: 2662455)
Enterocloster aldenensis (NCBI taxid: 358742)	Phocaeicola coprocola (NCBI taxid: 310298)
Eubacterium callanderi (NCBI taxid: 53442)	Phocaeicola coprophilus (NCBI taxid: 387090)
Eubacterium limosum (NCBI taxid: 1736)	Phocaeicola dorei (NCBI taxid: 357276)
Eubacterium ventriosum (NCBI taxid: 39496)	Phocaeicola vulgatus (NCBI taxid: 821)
Faecalibacillus intestinalis (NCBI taxid: 1982626)	Romboutsia sp. (NCBI taxid: 1965302)
Finegoldia magna (NCBI taxid: 1260)	Ruminiclostridium siraeum (NCBI taxid: 39492)
Gemmiger formicilis (NCBI taxid: 745368)	Thomasclavelia ramosa (NCBI taxid: 1547)
Holdemanella porci (NCBI taxid: 2652276)	Thomasclavelia spiroformis (NCBI taxid: 29348)

Hungatella effluvii (NCBI taxid: 1096246)	UBA1394 sp900066845
	Vescimonas sp900545585

[00443] **Table 11 – By Species.**

[00444] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 11.

Akkermansia muciniphila (NCBI taxid: 239935)	Hungatella hathewayi (NCBI taxid: 154046)
Alistipes communis (NCBI taxid: 2585118)	Intestinimonas butyriciproducens (NCBI taxid: 1297617)
Alistipes dispar (NCBI taxid: 2585119)	Lachnoanaerobaculum umeaense (NCBI taxid: 617123)
Alistipes finegoldii (NCBI taxid: 214856)	Lachnoclostridium phocaeense (NCBI taxid: 1871021)
Alistipes indistinctus (NCBI taxid: 626932)	Lachnoclostridium sp. YL32 (NCBI taxid: 1834196)
Alistipes megaguti (NCBI taxid: 2364787)	Lacrimispora saccharolytica (NCBI taxid: 84030)
Alistipes onderdonkii (NCBI taxid: 328813)	Longibaculum sp. KGMB06250 (NCBI taxid: 2584943)
Alistipes senegalensis (NCBI taxid: 1288121)	Longicatena caecimuris (NCBI taxid: 1796635)
Amedibacterium intestinale (NCBI taxid: 2583452)	Massilistercora timonensis (NCBI taxid: 2086584)
Anaerobutyricum hallii (NCBI taxid: 39488)	Novisyntrophococcus fermenticellae (NCBI taxid: 2068655)
Anaerostipes caccae (NCBI taxid: 105841)	Odoribacter splanchnicus (NCBI taxid: 28118)
Anaerostipes hadrus (NCBI taxid: 649756)	Oscillibacter sp. PEA192 (NCBI taxid: 2109687)
Bacteroides caccae (NCBI taxid: 47678)	Oscillibacter valericigenes (NCBI taxid: 351091)
Bacteroides caecimuris (NCBI taxid: 1796613)	Parabacteroides distasonis (NCBI taxid: 823)

Bacteroides cellulosilyticus (NCBI taxid: 246787)	Parabacteroides goldsteinii (NCBI taxid: 328812)
Bacteroides eggerthii (NCBI taxid: 28111)	Parabacteroides merdae (NCBI taxid: 46503)
Bacteroides fragilis (NCBI taxid: 817)	Phocaeicola dorei (NCBI taxid: 357276)
Bacteroides ovatus (NCBI taxid: 28116)	Phocaeicola salanitronis (NCBI taxid: 376805)
Bacteroides salyersiae (NCBI taxid: 291644)	Phocaeicola vulgatus (NCBI taxid: 821)
Bacteroides thetaiotaomicron (NCBI taxid: 818)	Pseudobutyrvibrio xylanivorans (NCBI taxid: 185007)
Bacteroides uniformis (NCBI taxid: 820)	Pusillimonas faecalis (NCBI taxid: 2714358)
Bacteroides xylanisolvens (NCBI taxid: 371601)	Roseburia hominis (NCBI taxid: 301301)
Bifidobacterium longum (NCBI taxid: 216816)	Roseburia intestinalis (NCBI taxid: 166486)
Blautia argi (NCBI taxid: 1912897)	Ruminococcus bicirculans (NCBI taxid: 1160721)
Blautia hansenii (NCBI taxid: 1322)	Ruminococcus gnavus (NCBI taxid: 33038)
Blautia liquoris (NCBI taxid: 2779518)	Ruthenibacterium lactatiformans (NCBI taxid: 1550024)
Blautia massiliensis (NCBI taxid: 1737424)	Solibaculum mannosilyticum (NCBI taxid: 2780922)
Blautia producta (NCBI taxid: 33035)	Vescimonas coprocola (NCBI taxid: 2714355)
Blautia pseudococcoides (NCBI taxid: 1796616)	Vescimonas fastidiosa (NCBI taxid: 2714353)
Blautia parvula (NCBI taxid: 2877527)	Bacteroides zhangwenhongii (NCBI taxid: 2650157)
Blautia sp. SC05B48 (NCBI taxid: 2479767)	Butyricimonas faecalis (NCBI taxid: 2093856)
Butyrvibrio hungatei (NCBI taxid: 185008)	Butyricimonas virosa (NCBI taxid: 544645)
Butyrvibrio proteoclasticus (NCBI taxid: 43305)	Paraprevotella xylaniphila (NCBI taxid: 454155)
Christensenella minuta (NCBI taxid: 626937)	Phocaeicola coprophilus (NCBI taxid: 387090)

Clostridium hylemonae (NCBI taxid: 89153)	Prevotella melaninogenica (NCBI taxid: 28132)
Clostridium scindens (NCBI taxid: 29347)	Alistipes putredinis (NCBI taxid: 28117)
Clostridium sp. SY8519 (NCBI taxid: 1042156)	Alistipes shahii (NCBI taxid: 328814)
Collinsella aerofaciens (NCBI taxid: 74426)	Bacteroides intestinalis (NCBI taxid: 329854)
Coprococcus comes (NCBI taxid: 410072)	Bacteroides stercoris (NCBI taxid: 46506)
Coprococcus eutactus (NCBI taxid: 33043)	Bifidobacterium adolescentis (NCBI taxid: 1680)
Dysosmobacter welbionis (NCBI taxid: 2093857)	Bifidobacterium bifidum (NCBI taxid: 1681)
Enterocloster bolteae (NCBI taxid: 208479)	Coprococcus catus (NCBI taxid: 116085)
Enterococcus faecium (NCBI taxid: 1352)	Methonobrevibacter sp. (NCBI taxid: 2172)
Erysipelatoclostridium ramosum (NCBI taxid: 1547)	Parabacteroides johnsonii (NCBI taxid: 387661)
Lachnospira eligens (NCBI taxid: 39485)	Phocaeicola coprocola (NCBI taxid: 310298)
Eubacterium sp. c-25 (NCBI taxid: 3028070)	Roseburia inulinivorans (NCBI taxid: 360807)
Eubacterium sp. NSJ-61 (NCBI taxid: 2764325)	Ruminococcus bromii (NCBI taxid: 40518)
Faecalibacterium prausnitzii (NCBI taxid: 853)	Ruminococcus torques (NCBI taxid: 33039)
Flavonifractor plautii (NCBI taxid: 292800)	Subdoligranulum variabile (NCBI taxid: 214851)
Flintibacter sp. KGMB00164 (NCBI taxid: 2610895)	

[00445] **Table 12 – Species of a further embodiment of the invention.**

[00446] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 12.

Agathobacter rectalis (NCBI taxid:39491)	Dorea longicatena (NCBI taxid:88431)
Agathobaculum sp003481705	Dysosmobacter faecalis
Akkermansia muciniphila (NCBI taxid:239935)	Enorma massiliensis (NCBI taxid:1472761)

Alistipes dispar (NCBI taxid:2585119)	Enterocloster aldenensis (NCBI taxid:358742)
Alistipes finegoldii (NCBI taxid:214856)	Eubacterium callanderi (NCBI taxid:53442)
Alistipes ihumii (NCBI taxid:1470347)	Eubacterium limosum (NCBI taxid:1736)
Alistipes indistinctus (NCBI taxid:626932)	Eubacterium ventriosum (NCBI taxid:39496)
Alistipes onderdonkii (NCBI taxid:328813)	Extibacter hylemonae
Alistipes putredinis (NCBI taxid:28117)	Faecalibacillus intestinalis (NCBI taxid:1982626)
Alistipes senegalensis (NCBI taxid:1288121)	Faecalibacterium duncaniae (NCBI taxid:411483)
Alistipes shahii (NCBI taxid:328814)	Fimivivens sp900113995
Amedibacterium intestinale (NCBI taxid:2583452)	Gemmiger formicilis (NCBI taxid:745368)
Anaerobutyricum hallii (NCBI taxid:39488)	Holdemanella porci (NCBI taxid:2652276)
Anaerostipes caccae (NCBI taxid:105841)	Hungatella effluvii (NCBI taxid:1096246)
Anaerostipes hadrus (NCBI taxid:649756)	Lachnoanaerobaculum sp000296385
Anaerostipes hominis (NCBI taxid:2025494)	Lachnospira sp003451515
Anaerotignum sp001304995	Lacrimispora saccharolytica (NCBI taxid:84030)
Anaerotruncus colihominis (NCBI taxid:169435)	Lactococcus petauri (NCBI taxid:1940789)
Anaerotruncus rubiinfantis (NCBI taxid:1720200)	Lawsonibacter sp944385665
Bacteroides eggerthii (NCBI taxid:28111)	Ligilactobacillus ruminis (NCBI taxid:1623)
Bacteroides finegoldii (NCBI taxid:338188)	Longicatena caecimuris (NCBI taxid:1796635)
Bacteroides intestinalis (NCBI taxid:329854)	Luoshenia tenuis (NCBI taxid:2763654)
Bacteroides nordii (NCBI taxid:291645)	Massilimicrobiota merdigallinarum
Bacteroides ovatus (NCBI taxid:28116)	Massilimicrobiota sp002160865
Bacteroides salyersiae (NCBI taxid:291644)	Massilioclostridium methylpentosum
Bacteroides sp900552405	Mediterraneibacter torques (NCBI taxid:33039)
Bacteroides stercoris (NCBI taxid:46506)	Megamonas funiformis (NCBI taxid:437897)

Bacteroides thetaiotaomicron (NCBI taxid:818)	Merdibacter merdigallinarum (NCBI taxid:2838693)
Bacteroides uniformis (NCBI taxid:820)	NSJ-51 sp900549795
Bacteroides xylanisolvens (NCBI taxid:371601)	Odoribacter splanchnicus (NCBI taxid:28118)
Bariatricus comes (NCBI taxid:410072)	Parabacteroides distasonis (NCBI taxid:823)
Barnesiella intestinihominis (NCBI taxid:487174)	Parabacteroides goldsteinii (NCBI taxid:328812)
Bifidobacterium adolescentis (NCBI taxid:1680)	Parabacteroides merdae (NCBI taxid:46503)
Bifidobacterium bifidum (NCBI taxid:1681)	Paraclostridium dentum (NCBI taxid:2662455)
Bifidobacterium longum (NCBI taxid:216816)	Phocaeicola coprocola (NCBI taxid:310298)
Bifidobacterium pseudocatenulatum (NCBI taxid:28026)	Phocaeicola coprophilus (NCBI taxid:387090)
Blautia massiliensis (NCBI taxid:1737424)	Phocaeicola dorei (NCBI taxid:357276)
Blautia stercoris (NCBI taxid:871664)	Phocaeicola vulgatus (NCBI taxid:821)
Butyricimonas faecalis (NCBI taxid:2093856)	Prevotella copri (NCBI taxid:165179)
Butyricimonas virosa (NCBI taxid:544645)	Romboutsia sp. (NCBI taxid:1965302)
Christensenella minuta (NCBI taxid:626937)	Roseburia hominis (NCBI taxid:301301)
Clostridium scindens (NCBI taxid:29347)	Roseburia intestinalis (NCBI taxid:166486)
Clostridium butyricum (NCBI taxid:1492)	Roseburia inulinivorans (NCBI taxid:360807)
Clostridium leptum (NCBI taxid:1535)	Ruminiclostridium siraeum (NCBI taxid:39492)
Clostridium sp. (NCBI taxid:1506)	Ruminococcus bicirculans (NCBI taxid:1160721)
Collinsella aerofaciens (NCBI taxid:74426)	Ruminococcus bromii (NCBI taxid:40518)
Collinsella bouchesdurhonensis (NCBI taxid:1907654)	Ruthenibacterium lactatiformans (NCBI taxid:1550024)
Collinsella sp002232035	Sellimonas intestinalis (NCBI taxid:1653434)

Collinsella sp905215835	Solibaculum mannosilyticum (NCBI taxid:2780922)
Coprobacillus cateniformis (NCBI taxid:100884)	Thomasclavelia ramosa (NCBI taxid:1547)
Coprobacter secundus (NCBI taxid:1501392)	UBA1394 sp900066845
Coprococcus catus (NCBI taxid:116085)	Vescimonas coprocola (NCBI taxid:2714355)
Coprococcus sp000154245	Vescimonas sp900545585

[00447] In some embodiments, the formulations include one or more core community microbial strains and one or more keystone microbial strains. For example, the formulations may include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or 26 core community microbial strains, and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or 22 keystone microbial strains. In some embodiments, the core community microbial strains are selected from the strains as set forth in Table 14. In some embodiments, the keystone microbial strains are selected from the strains as set forth in Table 13.

10 [00448] **Table 13 – Microbial Keystones.**

[00449] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 13.

Phylum	Genus	Species	Strain (NCBI TaxID)
Actinomycetota	Bifidobacterium	Bifidobacterium longum	216816
Bacillota	Faecalibacterium	Faecalibacterium prausnitzii/Faecalibacterium duncaniae	853/411483
Actinomycetota	Bifidobacterium	Bifidobacterium bifidum	1681
Bacteroidota	Alistipes	Alistipes putredinis	28117
Bacteroidota	Alistipes	Alistipes shahii	328814
Bacteroidota	Bacteroides	Bacteroides intestinalis	329854
Bacteroidota	Bacteroides	Bacteroides stercoris	46506
Actinomycetota	Bifidobacterium	Bifidobacterium adolescentis	1680

Bacillota	Coprococcus	Coprococcus catus	116085
Euryarchaeota	Methanobrevibacter	Methanobrevibacter smithii	2173
Bacteroidota	Parabacteroides	Parabacteroides johnsonii	387661
Bacteroidota	Phocaeicola	Phocaeicola coprocola	310298
Bacillota	Roseburia	Roseburia inulinivorans	360807
Bacillota	Ruminococcus	Ruminococcus bromii	40518
Bacillota	Ruminococcus	Ruminococcus torques/Mediterraneibacter torques	33039
Bacillota	Subdoligranulum/Gemmiger	Subdoligranulum variabile/Gemmiger formicilis	214851/745368
Bacteroidota	Bacteroides	Bacteroides caccae	47678
Bacteroidota	Bacteroides	Bacteroides coprocola	310298
Bacteroidota	Bacteroides	Bacteroides eggerthii	28111
Bacteroidota	Bacteroides	Bacteroides thetaiotaomicron	818
Bacteroidota	Bacteroides	Bacteroides uniformis	820
Bacteroidota	Parabacteroides	Parabacteroides distasonis	823

[00450] **Table 14 – Microbial Core Community.**

In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 14.

5

Phylum	Genus	Species	Strain (NCBI TaxID)
Actinomycetota	Bifidobacterium	Bifidobacterium longum	216816
Bacillota	Faecalibacterium	Faecalibacterium prausnitzii/Faecalibacterium duncaniae	853/411483
Bacillota	Dysosmobacter	Dysosmobacter welbionis	2093857
Bacillota	Enterocloster	Enterocloster bolteae/Enterocloster aldensis	208479/358742

Bacteroidota	Alistipes	Alistipes megaguti	2364787
Bacteroidota	Parabacteroides	Parabacteroides goldsteinii	328812
Bacillota	Flavonifractor	Flavonifractor plautii	292800
Bacteroidota	Alistipes	Alistipes communis	2585118
Bacillota	Ruthenibacterium	Ruthenibacterium lactatiformans	1550024
Bacillota	Vescimonas	Vescimonas coprocola	2714355
Actinomycetota	Collinsella	Collinsella aerofaciens	74426
Bacillota	Coprococcus/Bariatricus	Coprococcus comes/Bariatricus comes	410072
Bacillota	Ruminococcus	Ruminococcus gnavus	33038
Bacillota	Ruminococcus	Ruminococcus bicirculans	1160721
Bacteroidota	Bacteroides	Bacteroides caecimuris	1796613
Bacillota	Coprococcus	Coprococcus eutactus/Coprococcus sp000154245	33043/
Bacteroidota	Butyricimonas	Butyricimonas virosa/Butyricimonas phoceensis	544645/1720203
Bacteroidota	Phocaeicola	Phocaeicola salanitronis	376805
Bacteroidota	Alistipes	Alistipes dispar	2585119
Bacillota	Clostridium	Clostridium scindens	29347
Bacteroidota	Parabacteroides	Parabacteroides merdae	46503
Bacteroidota	Bacteroides	Bacteroides salyersiae	291644
Bacillota	Pusillimonas/Dyosmobacter	Pusillimonas faecalis/Dysosmobacter faecalis	2714358/
Bacillota	Solibaculum	Solibaculum mannosilyticum	2780922
Verrucomicrobiota	Akkermansia	Akkermansia muciniphila	239935
Bacillota	Christensenella	Christensenella minuta	626937

[00451] As used herein, the terms “core community microbial strains” or “core community microbial species” refers to a foundational group of microbes that function in synergy with one another, and together with keystone microbial strains, to restore, regenerate, improve, enhance, supplement, protect, stabilize, and/or boost a microbiome, such as a gut microbiome. In some embodiments, the core community microbial strains may maintain its communal synergistic function in the absence of any one strain or any few strains as set forth in Table 14. In some embodiments, a greater synergistic function takes place with the combination of the greatest number of strains as set forth in Table 14. In alternative embodiments, any one or more (e.g., 1-5, 5-10, etc.) of the phyla, genera, species or strains identified in Table 14 are expressly excluded from the co-culture, the formulation to be administered, or both. One reason for such exclusion may be that such microbe has a deleterious effect on a particular disease state

[00452] As used herein, the terms “keystone microbial strains” refers to microbes having a synergistic role in survival, integration, and flourishing of other species in the formulations described herein. For example, a keystone microbial strain may play a role in survival of one or more core community microbial strains during culture of the microbial strains, during preparation of the formulations, during administration of the formulations, and/or during uptake of the microbial strains in a subject following administration. In some embodiments, the keystone microbial strains improve microbial growth, activity, survival, and/or proliferation of a microbial consortium in a bioreactor during culture. In some embodiments, the keystone microbial strains improve growth activity, survival, and/or proliferation of a microbial consortium in the gut of a subject. In some embodiments, the keystone microbial strains improve growth activity, survival, and/or proliferation of a microbial consortium both in a bioreactor and in the gut of a subject. In some embodiments, the keystone strains reduce the growth, activity, survival, and/or proliferation of pathogens or microbes that would otherwise negatively impact the core community strains. In some embodiments, the keystone strains perform one or more of the following: provide nutrients for the core community strains through for example metabolizing compounds into more digestible components, maintain a desired pH, serve as a prebiotic, serve as postbiotic, etc. In alternative embodiments, any one or more (e.g., 1-5, 5-10, etc.) of the phyla, genera, species or strains identified in Table 13 or 8 are expressly excluded from the co-culture, the formulation to be administered, or both. One reason for such exclusion may be that such microbe has a deleterious effect on a particular disease state.

[00453] In some embodiments, the formulations comprise, consist of, or consist essentially of any 1 or more core community microbial strains as set forth in Table 14 and any 1 or more keystone microbial strains as set forth in Table 13; any 2 or more core community microbial strains as set forth in Table 14 and any 1 or more keystone microbial strains as set forth in

Table 13; any 3 or more core community microbial strains as set forth in Table 14 and any 1 or more keystone microbial strains as set forth in Table 13; any 5 or more core community microbial strains as set forth in Table 14 and any 1 or more keystone microbial strains as set forth in Table 13; any 3 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 5 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 5 or more core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; any 10 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 10 or more core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; any 10 or more core community microbial strains as set forth in Table 14 and any 10 or more keystone microbial strains as set forth in Table 13; any 15 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 15 or more core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; any 15 or more core community microbial strains as set forth in Table 14 and any 10 or more keystone microbial strains as set forth in Table 13; any 15 or more core community microbial strains as set forth in Table 14 and any 15 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 10 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 15 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 20 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 10 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 15 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 20 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and all keystone microbial strains as set forth in Table 13, or any number of core community microbial strains and any number of keystone microbial strains within a range described herein. In some embodiments, the formulations include any number

of the core community microbial strains as set forth in Table 14 in combination with any number of the keystone microbial strains as set forth in Table 13.

[00454] In some embodiments, the formulations include a ratio of core community microbial strains to keystone microbial strains. In some embodiments, the ratio of core community microbial strains to keystone microbial strains is in a ratio of 20:1, 15:1, 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, 1:1, 1:2, 1:3, 1:4, 1:5, 1:6, 1:7, 1:8, 1:9, 1:10, 1:15, or 1:20 or at a ratio between any two of the aforementioned ratios. In some embodiments, the microbial strains in the formulations include a majority of core community microbial strains and a minority of keystone microbial strains. In some embodiments, the formulations include the core community microbial strains at a percentage of total microbial strains in an amount of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100% or an amount within a range defined by any two of the aforementioned values. In some embodiments, the formulations include keystone microbial strains at a percentage of total microbial strains in an amount of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100% or an amount within a range defined by any two of the aforementioned values. In some embodiments, the core community microbial strains are present in the formulation in an amount of 80% and the keystone microbial strains are present in the formulation in an amount of 20%. In some embodiments, the core community microbial strains are present in the formulation in an amount of 70% and the keystone microbial strains are present in the formulation in an amount of 30%. In some embodiments, the core community microbial strains are present in the formulation in an amount of 60% and the keystone microbial strains are present in the formulation in an amount of 40%. In some embodiments, the core community microbial strains are present in the formulation in an amount of 50% and the keystone microbial strains are present in the formulation in an amount of 50%. In some embodiments, the core community microbial strains are present in the formulation in an amount of 40% and the keystone microbial strains are present in the formulation in an amount of 60%. In some embodiments, the core community microbial strains are present in the formulation in an amount of 30% and the keystone microbial strains are present in the formulation in an amount of 70%. In some embodiments, the percentage of core community microbial strains and the percentage of keystone microbial strains are present at amounts within the percentages described herein.

[00455] **Table 15 – Microbial Keystones and Core Community currently represented in the 143 isolates comprising BB265.**

[00456] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 15.

Phylum	Genus	Species	Strain (NCBI TaxID)
Verrucomicrobiota	Akkermansia	Akkermansia muciniphila	239935
Bacteroidota	Alistipes	Alistipes dispar	2585119
Bacteroidota	Alistipes	Alistipes putredinis	28117
Bacteroidota	Alistipes	Alistipes shahii	328814
Bacteroidota	Bacteroides	Bacteroides caccae	47678
Bacteroidota	Bacteroides	Bacteroides coprocola	310298
Bacteroidota	Bacteroides	Bacteroides eggerthii	28111
Bacteroidota	Bacteroides	Bacteroides intestinalis	329854
Bacteroidota	Bacteroides	Bacteroides salyersiae	291644
Bacteroidota	Bacteroides	Bacteroides stercoris	46506
Bacteroidota	Bacteroides	Bacteroides thetaiotaomicron	818
Bacteroidota	Bacteroides	Bacteroides uniformis	820
Actinomycetota	Bifidobacterium	Bifidobacterium adolescentis	1680
Actinomycetota	Bifidobacterium	Bifidobacterium bifidum	1681
Actinomycetota	Bifidobacterium	Bifidobacterium longum	216816
Bacteroidota	Butyricimonas	Butyricimonas virosa/Butyricimonas phoceensis	544645/1720203
Bacillota	Christensenella	Christensenella minuta	626937
Bacillota	Clostridium	Clostridium scindens	29347
Actinomycetota	Collinsella	Collinsella aerofaciens	74426
Bacillota	Coprococcus	Coprococcus catus	116085
Bacillota	Coprococcus/Bariatricus	Coprococcus comes/Bariatricus comes	410072
Bacillota	Coprococcus	Coprococcus eutactus/Coprococcus sp000154245	33043/
Bacillota	Enterocloster	Enterocloster bolteae/Enterocloster aldensis	208479/358742

Bacillota	Faecalibacterium	Faecalibacterium prausnitzii/Faecalibacterium duncaniae	853/411483
Bacteroidota	Parabacteroides	Parabacteroides distasonis	823
Bacteroidota	Parabacteroides	Parabacteroides goldsteinii	328812
Bacteroidota	Parabacteroides	Parabacteroides johnsonii	387661
Bacteroidota	Parabacteroides	Parabacteroides merdae	46503
Bacteroidota	Phocaeicola	Phocaeicola coprocola	310298
Bacillota	Pusillimonas/Dyosmobacter	Pusillimonas faecalis/Dysosmobacter faecalis	2714358/
Bacillota	Roseburia	Roseburia inulinivorans	360807
Bacillota	Ruminococcus	Ruminococcus bicirculans	1160721
Bacillota	Ruminococcus	Ruminococcus bromii	40518
Bacillota	Ruminococcus	Ruminococcus gnavus	33038
Bacillota	Ruminococcus	Ruminococcus torques/Mediterraneibacter torques	33039
Bacillota	Ruthenibacterium	Ruthenibacterium lactatiformans	1550024
Bacillota	Solibaculum	Solibaculum mannosilyticum	2780922
Bacillota	Subdoligranulum/Gemmiger	Subdoligranulum variabile/Gemmiger formicilis	214851/745368
Bacillota	Vescimonas	Vescimonas coprocola	2714355

[00457] **Table 16 – Microbial Keystones and Core Community taxa in a further embodiment.**

Phylum	Genus	Species	Strain (NCBI TaxID)
--------	-------	---------	---------------------

Verrucomicrobiota	Akkermansia	Akkermansia muciniphila	239935
Bacteroidota	Alistipes	Alistipes dispar	2585119
Bacteroidota	Alistipes	Alistipes putredinis	28117
Bacteroidota	Alistipes	Alistipes shahii	328814
Bacteroidota	Bacteroides	Bacteroides coprocola	310298
Bacteroidota	Bacteroides	Bacteroides eggerthii	28111
Bacteroidota	Bacteroides	Bacteroides intestinalis	329854
Bacteroidota	Bacteroides	Bacteroides salyersiae	291644
Bacteroidota	Bacteroides	Bacteroides stercoris	46506
Bacteroidota	Bacteroides	Bacteroides thetaiotaomicron	818
Bacteroidota	Bacteroides	Bacteroides uniformis	820
Actinomycetota	Bifidobacterium	Bifidobacterium adolescentis	1680
Actinomycetota	Bifidobacterium	Bifidobacterium bifidum	1681
Actinomycetota	Bifidobacterium	Bifidobacterium longum	216816
Bacteroidota	Butyricimonas	Butyricimonas virosa/Butyricimonas phoceensis	544645/1720203
Bacillota	Christensenella	Christensenella minuta	626937
Bacillota	Clostridium	Clostridium scindens	29347
Actinomycetota	Collinsella	Collinsella aerofaciens	74426
Bacillota	Coprococcus	Coprococcus catus	116085
Bacillota	Coprococcus/Bariatricus	Coprococcus comes/Bariatricus comes	410072
Bacillota	Coprococcus	Coprococcus eutactus/Coprococcus sp000154245	33043/
Bacillota	Enterocloster	Enterocloster bolteae/Enterocloster aldensis	208479/358742
Bacillota	Faecalibacterium	Faecalibacterium prausnitzii/Faecalibacterium duncaniae	853/411483

Bacteroidota	Parabacteroides	Parabacteroides distasonis	823
Bacteroidota	Parabacteroides	Parabacteroides goldsteinii	328812
Bacteroidota	Parabacteroides	Parabacteroides merdae	46503
Bacteroidota	Phocaeicola	Phocaeicola coprocola	310298
Bacillota	Pusillimonas/Dyosmobacter	Pusillimonas faecalis/Dysosmobacter faecalis	2714358/
Bacillota	Roseburia	Roseburia inulinivorans	360807
Bacillota	Ruminococcus	Ruminococcus bicirculans	1160721
Bacillota	Ruminococcus	Ruminococcus bromii	40518
Bacillota	Ruminococcus	Ruminococcus torques/Mediterraneibacter torques	33039
Bacillota	Ruthenibacterium	Ruthenibacterium lactatiformans	1550024
Bacillota	Solibaculum	Solibaculum mannosilyticum	2780922
Bacillota	Subdoligranulum/Gemmiger	Subdoligranulum variabile/Gemmiger formicilis	214851/745368
Bacillota	Vescimonas	Vescimonas coprocola	2714355
Verrucomicrobiota	Akkermansia	Akkermansia muciniphila	239935

[00458] Further features of the present invention are more fully described in the following description of several non-limiting embodiments thereof. This description is included solely for the purposes of exemplifying the present invention. It should not be understood as a restriction on the broad summary, disclosure or description of the invention as set out above.

Brief Description of the Drawings

[00459] Below is a brief description of each of the figures and drawings.

[00460] Figure 1 shows the diagrammatical representation of the processes that lead to ulcerative colitis induced by high levels of sulfide (either as a sulfide ion (S^{2-}), a bisulfide ion (SH^-), or hydrogen sulfide (H_2S)) and nitric oxide (NO).

5 [00461] Figure 2 shows a graphical representation of hydrogen competition between methanogens, acetogens and sulfate-reducing bacteria. Competition for hydrogen by methanogens and acetogens leads to a decrease in the activity and abundance of sulfate-reducing bacteria, resulting in decreased production of hydrogen sulfide.

[00462] Figure 3 shows the cysteine and methionine metabolic pathways which are directly related to sulfide production or consumption phenotype. These pathways were obtained from
10 <https://www.genome.jp/pathway/map00270>.

[00463] Figure 4 shows the BB265 drug discovery process detailing lead selection and validation prior to consortium validation in a phase 1 study.

[00464] Figure 5 shows the taxa identified with the sulfide-consuming phenotype. All taxa listed showed a net decrease in sulfide concentration following incubation when compared to the negative control. Those taxa which showed a statistically significant reduction ($p < 0.05$)
15 in sulfide concentration when compared to the negative control are indicated with an asterisk (*) preceding the Isolate ID.

[00465] Figure 6 shows the V3-V4 hypervariable region of the 16S rRNA gene sequences of the 143 isolates comprising the consortium (SEQ ID NOs 1 to 143). These sequences are
20 used for taxonomic classification of microbial species because the 16S rRNA gene, which is a small ribosomal subunit, is conserved amongst microbial species whilst containing hypervariable regions, such as the V3-V4 region, which provides sufficient variation to determine species-level discrimination between 16 rRNA gene sequences. The sequences presented are DNA sequences encoding the ribosomal RNA.

25 [00466] Figure 7 shows the full-length 16S rRNA gene sequences of the 143 isolates comprising the consortium (SEQ ID NOs 144 to 286). These sequences are used for taxonomic classification of microbial species because the 16S rRNA gene, which is a small ribosomal subunit, is conserved amongst microbial species whilst containing hypervariable regions, such as the V3-V4 region, which provides sufficient variation to determine species-level discrimination between 16 rRNA gene sequences. The sequences presented are DNA
30 sequences encoding the ribosomal RNA.

[00467] Figure 8 (Figure 8A and 8B) shows the average quantity of sulfide (H_2S , S^{2-} , HS^-) consumed by microbial isolates identified to have a statistically significant sulfide consumer phenotype relative to the negative control (medium only). Isolates were assayed in triplicate.
35 Significance was determined by unpaired t-tests with Welch's correction

[00468] Figure 9 shows the taxonomic IDs and lineages for the 143 isolates comprising the consortium. A 'WGS' sequence type infers that taxonomy was derived using Whole

Genome Sequences. Taxonomy was determined by comparison to the Genome Taxonomy Database (release 220).

[00469] Figure 10 shows the clad tree for the cladistic groups comprising the 143 isolate consortium.

5 [00470] Figure 11 shows a pie chart displaying the abundance of annotated genes among metabolic pathway categories identified in the 143 isolate BB265 consortium.

[00471] Figure 12 shows the average reduction in aqueous sulfide (H_2S , S_2^- , HS^-) concentration in an ulcerative proctitis patient stool sample (Patient A) co-incubated with 127 isolates (see also Figure 22) comprising the BB265 complex consortium. Reduction in aqueous sulfide is displayed as change in concentrations (μM) from the negative control, which consists of stool incubated in media only. Individual consumer refers to ulcerative proctitis stool co-incubated with an individual top sulfide consumer isolate, which displayed 670 μM sulfide consumption when phenotyped individually. Significance was determined using Welch's t-test. Mean $\pm$ SD.

15 [00472] Figure 13 shows the average reduction in aqueous sulfide (H_2S , S_2^- , HS^-) concentration in ulcerative proctitis patient stool samples (Patient A and C) co-incubated with the BB265 143-isolate consortium. Reduction in sulfide is displayed as change in concentration (μM) from the negative control, which consists of stool incubated in media only. Individual consumer refers to ulcerative proctitis stool co-incubated with the individual top sulfide consumer isolate, which displayed 670 μM sulfide consumption when phenotyped individually. Significance was determined using a Welch's t-test. Mean $\pm$ SD.

[00473] Figure 14 shows the colony forming units (CFU) determined over time when the 143 isolate BB265 consortium was co-cultured in bioreactors at three difference volumetric scales: 1 L, 4 L and 20 L. CFU was assessed using data pooled from nine 1 L vessels, three 4 L vessels, and three 20 L vessels. Mean $\pm$ SD.

[00474] Figure 15 (Figure 15A and 15B) shows the relative abundances of the 143 isolates comprising BB265 after co-culture in triplicate at 1 L scale.

[00475] Figure 16 (Figure 16A and 16B) shows the relative abundances of the 143 isolates comprising BB265 after co-culture, comparing 1 L, 4 L and 20 L bioreactor scales.

30 [00476] Figure 17 shows a rarefaction analysis used to estimate the functional redundancy within the BB265 consortium via a resampling procedure. The original 143 BB265 isolates were resampled with replacement for each subset of isolates ranging from 1 to 143. For each subset size (n), the total number of unique COG IDs annotated to the sampled isolates was counted. This resampling was repeated 50 times to account for variability. The resampled counts were plotted, resulting in a rarefaction curve. A model ($y \sim \log(x)$) was fitted using polynomial regression, represented by a blue trend line on the plot. A golden horizontal line

was drawn at 1677 COGs, representing the estimated number of COGs expected to be shared among FMT donor samples.

[00477] Figure 18 shows a schematic of the experimental design used to assess successful engraftment of the BB265 co-culture in a germ-free murine model.

5 [00478] Figure 19 shows the CFU determined from the feces of mice 2-weeks post receiving a second dose of the BB265 co-culture.

[00479] Figure 20 (Figure 20A and 20B) shows the relative abundances of the 143 isolates comprising BB265 in the feces of mice at T0 (pre-dose) and T2 (one-week post-dose) after treatment with the BB265 co-culture.

10 [00480] Figure 21 shows a matrix of correlation coefficients (R-sq) among T0 (pre-dose) and T2 (one-week post-dose) post-dose samples of mice having been treated with the BB265 co-culture. Pearson correlations were calculated between the vectors of relative abundances for the included strains for each sample. Cells are color-coded by the strength of the correlation.

15 [00481] Figure 22 shows the taxonomic IDs and lineages for the 127 isolates as outlined in Example 4. A 'WGS' sequence type infers that taxonomy was derived using Whole Genome Sequences. Taxonomy was determined by comparison to the Genome Taxonomy Database (release 220).

[00482] Figure 23 (Figure 23A and 23B) shows the presence of the 143 isolates comprising
20 BB265 in the inoculum used to seed Bioreactor 1, in Bioreactor 1 after fermentation at the time used as inoculum to seed Bioreactor 2, and in Bioreactor 2 after fermentation.

Detailed Description of the Invention

[00483] For convenience, the following sections generally outline the various meanings of
25 the terms used herein. Following this discussion, general aspects regarding compositions, formulations, use of medicaments and methods of the invention are discussed, followed by specific examples demonstrating the properties of various embodiments of the invention and how they can be employed. Headings and titles are for organizational purposes and should not be used to limit the disclosure or claims.

30 [00484] The embodiments described here also include equivalent variations and modifications other than those specifically described.. Several embodiments also include all of the steps, features, formulations and compounds referred to or indicated in the specification, individually or collectively and any and all combinations or any two or more of the steps or features.

35 [00485] Each document, reference, patent application or patent cited in this text is expressly incorporated herein in their entirety by reference, which means that it should be read and considered by the reader as part of this text. That the document, reference, patent

application or patent cited in this text is not repeated in this text is merely for reasons of conciseness. None of the cited material or the information contained in that material should, however, be understood to necessarily be common general knowledge.

5 [00486] Manufacturer's instructions, descriptions, product specifications, and product sheets for any products mentioned herein or in any document incorporated by reference herein, are hereby incorporated herein by reference, and can be employed in the practice of several embodiments of the invention.

10 [00487] The present invention is not to be limited in scope by any of the specific embodiments described herein. These embodiments are intended for the purpose of exemplification only. Functionally equivalent products, formulations and methods are clearly within the scope of the invention as described herein.

1. DEFINITIONS

15 [00488] The meaning of certain terms and phrases used in the specification, examples, and appended claims, are provided below. If there is an apparent discrepancy between the usage of a term in the art and its definition provided herein, the definition provided within the specification shall prevail.

20 [00489] Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about." The term "about" when used in connection with percentages can mean $\pm 1\%$.

25 [00490] "Therapeutically effective amount" as used herein with respect to methods of treatment and in particular drug dosage, shall mean that dosage that provides the specific pharmacological response for which the drug is administered in a significant number of subjects in need of such treatment. It is emphasized that "therapeutically effective amount," administered to a particular subject in a particular instance will not always be effective in treating the diseases described herein, even though such dosage is deemed a "therapeutically effective amount" by those skilled in the art. It is to be further understood that drug dosages are, in particular instances, measured as oral dosages, or with reference to drug levels as measured in blood. Amounts effective for such a use will depend on: the desired therapeutic effect; the potency of the biologically active material; the desired duration of treatment; the stage and severity of the disease being treated; the weight and general state of health of the patient; and the judgment of the prescribing physician. Treatment dosages need to be titrated to optimize safety and efficacy. One skilled in the art will appreciate that the appropriate dosage levels for treatment will thus vary depending, in part, upon the indication for which the active agent is being used, the route of administration, and the size (body weight, body surface or organ size) and condition (the age and general health) of the patient. Accordingly, the clinician may titrate the dosage and modify the route of administration to obtain the optimal

therapeutic effect. A typical dosage may range from about 0.1 mg/kg to up to about 100 mg/kg or more, depending on the factors mentioned above. In other embodiments, the dosage may range from 0.1 mg/kg up to about 100 mg/kg; or 1 mg/kg up to about 100 mg/kg; or 5 mg/kg up to about 100 mg/kg. The microbial concentration in the composition can be, for example,

5 from 1 cfu/mL to 10 cfu/mL, from 100 cfu/mL to 1 thousand cfu/mL, from 10 thousand cfu/mL to 100 thousand cfu/mL, from 10 cfu/mL to 1 million cfu/mL, from 100 cfu/mL to 1 million cfu/mL, from 1 thousand cfu/mL to 1 million cfu/mL, from 10 thousand cfu/mL to 1 million cfu/mL, from 100 thousand cfu/mL to 1 million cfu/mL, from 1 million cfu/mL to 10 million cfu/mL, from 10 million cfu/mL to 100 billion cfu/mL, from 10 million to 50 million cfu/mL, for

10 example from 50 million to 100 million cfu/mL, from 100 million to 500 million cfu/mL, from 500 million to 1 billion cfu/mL, from 1 billion to 5 billion cfu/mL, from 5 billion to 10 billion cfu/mL, from 10 billion to 15 billion cfu/mL, from 15 billion to 20 billion cfu/mL, from 20 billion to 25 billion cfu/mL, from 25 billion to 30 billion cfu/mL, from 30 billion to 35 billion cfu/mL, from 35 billion to 40 billion cfu/mL, from 40 billion to 45 billion cfu/mL, from 45 billion to 50 billion cfu/mL,

15 from 50 billion to 55 billion cfu/mL, from 55 billion to 60 billion cfu/mL, from 60 billion to 65 billion cfu/mL, from 65 billion to 70 billion cfu/mL, from 70 billion to 75 billion cfu/mL, from 75 billion to 80 billion cfu/mL, from 80 billion to 85 billion cfu/mL, from 85 billion to 90 billion cfu/mL, from 90 billion to 95 billion cfu/mL, from 95 billion to 100 billion cfu/mL or an amount within a range defined by any two of the aforementioned values.

20 [00491] The frequency of dosing will depend upon the pharmacokinetic parameters of the active agent and the formulation used. Typically, a clinician will administer the composition until a dosage is reached that achieves the desired effect. The composition may therefore be administered as a single dose, or as two or more doses (which may or may not contain the same amount of the desired molecule or bioactive) over time, or as a continuous infusion via

25 an implantation device, scope or catheter. Further refinement of the appropriate dosage is routinely made by those of ordinary skill in the art and is within the ambit of tasks routinely performed by them. Appropriate dosages may be ascertained through use of appropriate dose-response data.

[00492] As used herein, the term "microbial consortium" component can refer to a plurality

30 of microbes.

[00493] As used herein, a "carrier" can be any solvents, diluents, excipients or other vehicles, dispersion or suspension aids, surface active agents, isotonic agents, thickening or emulsifying agents, preservatives, solid binders, lubricants and the like, as suited to the particular dosage form desired. Such carrier may be natural or non-naturally occurring (e.g.,

35 partially or fully modified, synthetic, etc.).

[00494] As used herein, the term "pharmaceutically acceptable carrier" component can refer to a component that is not biologically or otherwise undesirable, i.e., the component may

be incorporated into a composition of the invention and administered to a subject as described herein without causing any significant undesirable biological effects or interacting in a deleterious manner with any of the other components of the formulation in which it is contained. The component has generally met the required standards of toxicology and manufacturing.

[00495] As used herein the term "subject" generally includes mammals such as: humans; farm animals such as sheep, goats, pigs, cows, horses, llamas; companion animals such as dogs and cats; primates; birds, such as chickens, geese and ducks; fish; and reptiles. The subject is for example human.

[00496] As used herein, the "gastrointestinal tract" refers to the tract from the mouth to the anus which includes all the organs of the digestive system such as the esophagus, stomach, pancreas, liver, gallbladder, small intestine (including the ileum), caecum, large intestine, colon and rectum. Strains of the invention are at least useful for conditions of the terminal ileum, caecum or rectum.

[00497] As used herein, a "non-inflammatory strain" refers to a strain which, when present in the gastrointestinal tract of a subject, for example a human, is associated with a non-inflamed state.

[00498] As used herein, an "inflammatory strain" refers to a strain which, when present in the gastrointestinal tract of a subject, for example a human, is associated with an inflamed state.

[00499] The terms "species" and "strain", as used herein, are not strictly separated from each other, and refer to a microbial entity which reproduces itself while being distinguishable from another species or strain. In some cases, microbial species and strains of the same species are well characterized. In particular in such situations, a strain may be considered as a subcategory of a species. A species is typically considered as a subcategory of a genus. In some cases, species and strains may be at the same taxonomic level, for example, refer to a subcategory of a genus. However, since prokaryotic taxonomy is rather flexible and conflicting, exceptions to those rules are possible. The taxonomic designation of a species or strain, as used herein, refers to all past, present and future taxon names, including all homotypic, heterotypic, subjective, objective, nomenclatural and invalid synonyms, along with misapplied names. In any case, based on common knowledge and state-of-the art taxonomic systems, the person skilled in the art is able to clearly understand the taxonomic terms used herein. Moreover, with help of state-of-the art taxonomic systems and common general knowledge regarding genotypic and phenotypic similarities, such as genotypic similarities, the person skilled in the art can readily judge whether two microbial species or strains are related, or closely related, or not. In particular, two species or strains may be considered to be related, when they share at least 1%, 2%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, or 90%,

e.g. at least 97%, of their 25 genome, and closely related when they share at least 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 96%, 97%, 98% or 99%, for example in several embodiments at least 97%, of their genome. Furthermore, two subpopulations of a microbial species or strain are also considered closely related. The percentage of sharing two genomes refers, in particular, to the sequence similarity between said two genomes. For example, the sequence similarity in the context of two nucleic acid or sequences can refer to the residues in the two 30 sequences which are the same when aligned by methods known in the art, and can take into consideration additions, deletions and substitutions. Moreover, the sequence similarity between microbial species or strains may be also judged as described in Patel (2001), Molecular Diagnosis 6(4) and Nguyen (2016), npj Biofilms and Microbiomes 2.

[00500] As used herein, the term "biotherapeutic" refers to a microorganism, such as bacterial isolate, that is useful for treating or preventing a disease or a condition, or provide a health benefit, in a subject.

[00501] The term "biotherapeutic composition" as used herein, refers to a formulation comprising a biotherapeutic preparation formulated together with one or more additional formulary ingredients to obtain a finished formulation suitable for delivery to a subject.

[00502] As used herein, the terms "treat," "treating," "treatment" and grammatical variations thereof mean subjecting an individual subject to a protocol, regimen, process or remedy, in which it is desired to obtain a physiologic response or outcome in that subject. Since every treated subject may not respond to a particular treatment protocol, regimen, process or remedy, treating does not require that the desired physiologic response or outcome be achieved in each and every subject or subject population. Accordingly, a given subject or subject population may fail to respond or respond inadequately to treatment.

[00503] As used herein, the term "prevent", "prevented", or "preventing" when used with respect to the treatment of mucosal inflammation in the gastrointestinal tract refers to a prophylactic treatment which increases the resistance of a subject to mucosal inflammation in the gastrointestinal tract, in other words, decreases the likelihood that the subject will develop mucosal inflammation in the gastrointestinal tract as well as a treatment after mucosal inflammation in the gastrointestinal tract has begun in order to fight the inflammation, e.g., reduce or eliminate it altogether or prevent it from becoming worse.

[00504] As used herein, the term "reducing", or variations thereof refer to a reduction but not necessarily a complete abolition of gastrointestinal tract mucosal inflammation in a subject.

[00505] As used herein, the term "sample" refers to a collection of biological material obtained from a subject or a subject's surrounding environment. In some embodiments, the sample is obtained directly from the subject. For example, the sample can be a fecal sample or biopsy obtained during a colonoscopy. The sample may be in a form taken directly from the subject or surrounding environment, or it may be at least partially purified to remove at least

some non-nucleic acid material. The purification may be slight, for instance amounting to no more than the concentration of the solids, or cells, of the sample into a smaller volume or the separation of cells from some or all of the remainder of the sample. In some embodiments, nucleic acids are isolated from the sample. Such isolated preparations include reverse

5 transcription products and/or PCR amplification products of the nucleic acids in the sample. In some embodiments, the predominant nucleic acid is DNA or RNA. The nucleic acid preparations can be pure or partially purified nucleic acid preparations. Techniques for the isolation of nucleic acid from samples, including complex samples, are numerous and well known in the art.

10 [00506] The unit "cfu" refers to "colony forming unit", which is the number of bacterial cells as revealed by microbiological counts on agar plates.

[00507] The term "sulfide" refers to molecular hydrogen sulfide (H_2S) and its ions, including a bisulfide (HS^-) ion and sulfide ion (S^{2-}) but may also include polysulfides (S_x^{2-}), thiosulfate ($\text{S}_2\text{O}_3^{2-}$), elemental sulfur (S_8), sulfite (SO_3^{2-}) or sulfate (SO_4^{2-}).

15 [00508] Other definitions for selected terms used herein may be found within the detailed description of the invention and apply throughout. Unless otherwise defined, all other scientific and technical terms used herein have the same meaning as commonly understood to one of ordinary skill in the art to which the invention belongs.

[00509] Where percentages are provided for agents, ingredients and compounds, they can

20 be %m/m, %m/w, %w/w, %m/v, %v/v and variations thereof with respect to the formulation as a whole, unless otherwise indicated.

[00510] As used herein, the terms composition and formulation can be used interchangeably. Salt forms of the acids identified herein may be used instead of or in addition to the acid.

25 [00511] Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about." The term "about" when used in connection with percentages can mean $\pm 1\%$.

[00512] Embodiments of the invention described herein may include one or more range of

30 values (e.g. size, concentration etc.). A range of values will be understood to include all values within the range, including the values defining the range, and values adjacent to the range which lead to the same or substantially the same outcome as the values immediately adjacent to that value which defines the boundary to the range. For example, a 10% variation in upper or lower limits of a range can be totally appropriate and is encompassed by the invention.

35 More particularly, the variation in the upper or lower limits of a range will be 5% or as is commonly recognized in the art, whichever is greater.

[00513] In this application, the use of the singular also includes the plural unless specifically stated otherwise. In this application, the use of "or" means "and/or" unless stated otherwise. Also, terms such as "element" or "component" encompass both elements and components comprising one unit and elements and components that comprise more than one subunit unless specifically stated otherwise. Also, the use of the term "portion" can include part of a moiety or the entire moiety.

[00514] Throughout this specification, unless the context requires otherwise, the word "comprise" or variations such as "comprises" or "comprising", will be understood to imply the inclusion of a stated integer or group of integers but not the exclusion of any other integer or group of integers.

[00515] It will be understood by those within the art that, in general, terms used herein, and especially in the appended claims (for example, bodies of the appended claims) are generally intended as "open" terms (for example, the term "including" should be interpreted as "including but not limited to," the term "having" should be interpreted as "having at least," the term "includes" should be interpreted as "includes but is not limited to," etc.). It will be further understood by those within the art that if a specific number of an introduced claim recitation is intended, such an intent will be explicitly recited in the claim, and in the absence of such recitation no such intent is present. For example, as an aid to understanding, the following appended claims may contain usage of the introductory phrases "at least one" and "one or more" to introduce claim recitations. However, the use of such phrases should not be construed to imply that the introduction of a claim recitation by the indefinite articles "a" or "an" limits any particular claim containing such introduced claim recitation to embodiments containing only one such recitation, even when the same claim includes the introductory phrases "one or more" or "at least one" and indefinite articles such as "a" or "an" (for example, "a" and/or "an" should be interpreted to mean "at least one" or "one or more"); the same holds true for the use of definite articles used to introduce claim recitations. For example, "an" agent can include one, two or several ingredients (and not necessarily a single ingredient). In addition, even if a specific number of an introduced claim recitation is explicitly recited, those skilled in the art will recognize that such recitation should be interpreted to mean at least the recited number (for example, the bare recitation of "two recitations," without other modifiers, means at least two recitations, or two or more recitations). Furthermore, in those instances where a convention analogous to "at least one of A, B, and C, etc." is used, in general such a construction is intended in the sense one having skill in the art would understand the convention (for example, "a system having at least one of A, B, and C" would include but not be limited to systems that have A alone, B alone, C alone, A and B together, A and C together, B and C together, and/or A, B, and C together, etc.). It will be further understood by those within the art that any disjunctive word and/or phrase presenting two or more alternative terms,

whether in the description, claims, or drawings, should be understood to contemplate the possibilities of including one of the terms, either of the terms, or both terms. For example, the phrase “A or B” will be understood to include the possibilities of “A” or “B” or “A and B.”

[00516] In addition, where features or aspects of the disclosure are described in terms of Markush groups, those skilled in the art will recognize that the disclosure is also thereby described in terms of any individual member or subgroup of members of the Markush group.

[00517] As will be understood by one skilled in the art, for any and all purposes, such as in terms of providing a written description, all ranges disclosed herein also encompass any and sub-ranges and combinations of sub-ranges thereof. As will also be understood by one skilled in the art all language such as “up to,” “at least,” “greater than,” “less than,” and the like include the number recited and refer to ranges which can be subsequently broken down into sub-ranges as discussed above. Finally, as will be understood by one skilled in the art, a range includes each individual member. Thus, for example, a group having 1-3 articles refers to groups having 1, 2, or 3 articles. Similarly, a group having 1-5 articles refers to groups having 1, 2, 3, 4, or 5 articles, and so forth. The phrases “and ranges in between” can include ranges that fall in between the numerical values listed. For example, “1, 2, 3, 10, and ranges in between” can include 1-10, 1-3, 2-10, etc.

[00518] While various aspects and embodiments have been disclosed herein, other aspects and embodiments will be apparent to those skilled in the art. The various aspects and embodiments disclosed herein are for purposes of illustration and are not intended to be limiting, with the scope and spirit being indicated by, for example, the following claims.

[00519] For the methods disclosed herein, the functions performed in the processes and methods may be implemented in differing order. The disclosure of methods or uses may also include instructing the method or use (for example, in instructions for use).

[00520] Features of the embodiments of the invention will now be discussed with reference to the following non-limiting description and examples.

2. EMBODIMENTS

Dysbiosis

[00521] The loss of gut microbial ecology, often referred to as gut dysbiosis, is a growing concern in modern medicine. Factors such as the overuse of antibiotics, Western-style diets high in processed foods and sugars, chronic stress, and reduced exposure to environmental microbes have been implicated in disrupting the delicate balance of the gut microbiome. Losing gut microbes results in a loss of the important health-giving functions that they perform, and a loss of these functions leads to disease. When this balance is disturbed, it can lead to a cascade of health issues ranging from digestive disorders like irritable bowel syndrome to systemic problems such as obesity, type 2 diabetes, and even mood disorders. As we continue

to understand the profound impact of the gut microbiome on our health, there is an increasing emphasis on strategies to maintain or restore its ecological balance.

[00522] "Dysbiosis" refers to an imbalance or perturbation of the microbiota and/or microbiome. The term is most often used to describe a disruption in the normal balance of microbial communities in the body, particularly the gut. This imbalance can be due to a variety of reasons, such as antibiotics, certain diets, stress, or diseases.

[00523] In a healthy state, the body's internal microbial communities, including bacteria, fungi, and viruses, are balanced and live in symbiosis, contributing to many physiological processes. Dysbiosis, however, can lead to a number of health issues including inflammatory bowel diseases, allergy, irritable bowel syndrome, obesity and mental illness, and can also affect the efficacy of cancer therapies.

[00524] Network effects within the human gut microbiome play a pivotal role in determining its structure, function, and impact on host health. These effects refer to the intricate web of interactions between different microbial taxa, where the presence or activity of one taxa can influence, and in turn be influenced by, others. Such relationships can be synergistic, where two microbes together exert effects greater than the sum of their individual contributions, or competitive, where they vie for the same resources. For instance, certain bacteria produce compounds that either inhibit harmful microbes or promote the growth of beneficial ones. Additionally, some microbes can modify the gut environment to make it conducive for other species to thrive. This interconnectedness means that a perturbation affecting some microbes can have cascading effects throughout the microbial community. Recognizing these network effects is crucial when considering interventions, as introducing or removing one species might have unforeseen consequences on the broader ecosystem, influencing not just microbial composition but also metabolic outputs and overall gut health. The holistic understanding of these network effects is essential for predicting how changes in the microbiome might impact human health.

Emergent functions of the gut microbiome.

[00525] The gut microbiome's role in human health goes beyond digestion, with increasing evidence pointing to its emergent metabolic functions. Many of these functions require the linkage of the huge number of components of the gut microbial ecosystem.

[00526] Short-Chain Fatty Acids (SCFAs): Some of the most studied metabolic products of the gut microbiota are SCFAs, including butyrate, acetate, and propionate. These compounds are produced when bacteria ferment dietary fibers in the colon. They serve as an energy source for colon cells, help in maintaining the gut barrier function, and play roles in regulating immune responses and inflammation.

[00527] Hydrogen sulfide homeostasis: A healthy gut microbiome balances production and consumption of hydrogen sulfide. Excess production can occur with dysbiosis, leading to diseases such as inflammatory bowel disease.

5 [00528] Energy Harvest: An altered microbiome composition can affect the efficiency of energy extraction from food, which can contribute to obesity and metabolic syndrome. Dysbiosis, or imbalance in the microbiome, has also been linked to other aspects of metabolic syndrome, such as increased inflammation, insulin resistance, and fatty liver disease.

10 [00529] Tryptophan Metabolism: Gut bacteria can influence the metabolism of tryptophan, an essential amino acid, into various bioactive molecules, some of which have roles in brain function and gut barrier maintenance.

[00530] Bile Acid Metabolism: Bile acids aid in fat digestion. After release into the intestine, gut bacteria can convert primary bile acids into secondary bile acids. These bile acid transformations by the microbiome can influence lipid metabolism, glucose regulation, and energy expenditure.

15 [00531] Vitamin Production: Certain gut bacteria are known to synthesize vitamins like vitamin K and several B vitamins, which are essential for various bodily functions.

[00532] Drug Metabolism: The gut microbiome can influence the efficacy and toxicity of some medications by modulating pharmacokinetic and pharmacodynamic properties. This has implications for personalized medicine and drug design.

20 [00533] Link to Cardiovascular Disease: Some gut bacteria can metabolize dietary components like choline and carnitine into trimethylamine (TMA). The liver then converts TMA to trimethylamine N-oxide (TMAO), which has been linked to atherosclerosis and an increased risk of cardiovascular diseases, including, for example, dyslipidaemia, atherosclerotic heart disease, or hypertension.

25 [00534] As our understanding of the gut microbiome expands, it's evident that it acts as a metabolic "organ," influencing and interacting with various physiological systems. Further research promises to yield more insights into these intricate relationships and their implications for human health.

30 [00535] Probiotics or live bacterial therapeutics (LBPs) are preparations of live beneficial bacteria intended to confer health benefits to the host. However, their efficacy and scope have had limitations, especially when compared to fecal microbiota transplantation (FMT). Firstly, probiotics or LBPs have often contained a limited number of bacterial strains, which may not be comprehensive enough to restore a dysbiotic gut microbiome. In contrast, FMT introduces a broad spectrum of microbial taxa from a healthy donor, potentially allowing for a more holistic restoration of the recipient's gut ecosystem. Secondly, the survival and persistence of probiotic strains in the gut environment is limited. There is evidence that many probiotic strains do not colonize the gut long-term and are quickly expelled. FMT, on the other hand, delivers a

35

complete, naturally-occurring microbial community which might have a better chance of successful engraftment. Additionally, while probiotics are often considered safe, there is limited evidence on their efficacy, whereas human donor derived FMT has shown high efficacy, particularly in treating recurrent *Clostridium difficile* infections and ulcerative colitis.

5 The superior efficacy of FMT in these settings is thought to relate to its breadth of function and composition of organisms evolutionarily adapted to the human gut.

[00536] While FMT has emerged as a promising therapeutic approach for various gastrointestinal disorders, especially recurrent *Clostridium difficile* infection, it has a number of limitations. A major concern is scalability; sourcing, screening, and preparing donor material
10 for FMT is labor-intensive and lacks the ease of mass-producing specific bacterial strains. This makes widespread application of FMT particularly challenging. Consistency is another issue. Given that FMT material is derived from individual donors, there can be significant variability in microbial composition between batches, leading to unpredictable therapeutic outcomes. Live bacterial therapeutics, being cultured in controlled environments, offer more consistent
15 and reproducible formulations. Moreover, the specificity of the mechanism of action is clearer with live bacterial therapeutics, as they can be designed to target specific pathways or functions. With FMT, the broad and diverse range of microbes introduced means that the exact mechanisms driving therapeutic effects can be difficult to define, making it challenging to tailor treatments for specific conditions. Live bacterial therapeutics allow for more precision,
20 scalability, and consistency in microbial interventions.

[00537] The field of microbial therapeutics requires a platform solution for manufacturing diverse gut microbial therapies as a single drug substance. By selectively growing multiple beneficial strains together, the inventors have harnessed the collective benefits of a diverse microbial community, much like FMT, but with the precision, consistency, and scalability
25 inherent to modern pharmaceutical practices. This method combines the broad functional benefits of a diverse microbial ecosystem with the specificity of targeted bacterial strains, effectively bridging the gap between FMT's holistic approach and the precise intent of traditional drugs. Moreover, producing these co-cultures in controlled environments ensures a consistent microbial composition across batches, eliminating the variability seen in donor-dependent FMT. By integrating this innovative approach into contemporary pharmaceutical
30 manufacturing, there is potential to realize the full promise of FMT—offering treatments that are both broad-spectrum and condition-specific, all while adhering to stringent industry standards for consistency and scalability.

Compositions and Formulations

35

[00538] The present invention provides a composition for preventing or treating a medical disorder or pathology in a subject in need thereof, said composition comprising at least one

strain of bacteria, archaea or fungi. In some embodiments, the compositions are prepared in formulations for oral, colonic, or rectal delivery.

[00539] In a further embodiment, the composition is selected from the group consisting of: a therapeutic composition; a pharmaceutical composition; a cosmetic composition; and a veterinary composition.

[00540] In several embodiments, compositions are combined with a pharmaceutically acceptable carrier or diluent to produce a pharmaceutical composition (which may be for human or animal use). Suitable carriers and diluents include isotonic saline solutions, for example phosphate-buffered saline. As used herein, "pharmaceutically acceptable carrier" includes any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents and the like. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent that is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. See, e.g., Remington's Pharmaceutical Sciences, 19th Ed. (1995, Mack Publishing Co., Easton, Pa.) and Remington's The Science and Practice of Pharmacy, 23rd Edition. (2020, Mack Publishing Co., Easton, Pa.) which are herein incorporated by reference.

[00541] A pharmaceutically acceptable carrier can be liquid (e.g., saline), gel or solid form of diluents, adjuvant, excipients or an acid resistant encapsulated ingredient. Suitable diluents and excipients include pharmaceutical grades of physiological saline, dextrose, glycerol, mannitol, lactose, starch, magnesium stearate, sodium saccharin, cellulose, magnesium carbonate, and the like, and combinations thereof. In another aspect, a therapeutic composition may contain auxiliary substances such as wetting or emulsifying agents, stabilizing or pH buffering agents. In an aspect, a therapeutic composition contains about 1%-5%, 5%-10%, 10%-15%, 15-20%, 20%-25%, 25-30%, 30-35%, 40-45%, 50%-55%, 1%-95%, 2%-95%, 5%-95%, 10%-95%, 15%-95%, 20%-95%, 25%-95%, 30%-95%, 35%-95%, 40%-95%, 45%-95%, 50%-95%, 55%-95%, 60%-95%, 65%-95%, 70%-95%, 45%-95%, 80%-95%, or 85%-95% of active ingredient, or an amount within a range defined by any two of the aforementioned values. In an aspect, a therapeutic composition contains about 2%-70%, 5%-60%, 10%-50%, 15%-40%, 20%-30%, 25%-60%, 30%-60%, or 35%-60% of active ingredient, or an amount within a range 10 defined by any two of the aforementioned values.

[00542] The composition can contain formulation materials for modifying, maintaining or preserving, for example, the pH, osmolarity, viscosity, clarity, color, isotonicity, odor, sterility, stability, rate of dissolution or release, adsorption or penetration of the composition. Suitable formulation materials include, but are not limited to, amino acids (such as glycine, glutamine, asparagine, arginine or lysine); antimicrobials; antioxidants (such as ascorbic acid, sodium

sulfite or sodium hydrogen-sulfite); buffers (such as borate, bicarbonate, Tris-HCl, citrates, phosphates or other organic acids); bulking agents (such as mannitol or glycine); chelating agents (such as ethylenediamine tetraacetic acid (EDTA)); complexing agents (such as caffeine, polyvinylpyrrolidone, beta-cyclodextrin or hydroxypropyl-beta-cyclodextrin), fillers; 5 monosaccharides, disaccharides; and other carbohydrates (such as glucose, mannose, or dextrans); proteins (such as serum albumin, gelatin or immunoglobulins); coloring, flavoring and diluting agents; emulsifying agents; hydrophilic polymers (such as polyvinylpyrrolidone); low molecular weight polypeptides; salt-forming counterions (such as sodium); preservatives (such as benzalkonium chloride, benzoic acid, salicylic acid, thimerosal, phenethyl alcohol, 10 methylparaben, propylparaben, chlorhexidine, sorbic acid or hydrogen peroxide); solvents (such as glycerin, propylene glycol or polyethylene glycol); sugar alcohols (such as mannitol or sorbitol); suspending agents; surfactants or wetting agents (such as pluronics, PEG, sorbitan esters, polysorbates such as polysorbate 20, polysorbate 80, triton, tromethamine, lecithin, cholesterol, tyloxapol); stability enhancing agents (sucrose or sorbitol); tonicity 15 enhancing agents (such as alkali metal halides, for example sodium or potassium chloride), delivery vehicles, diluents, excipients and/or pharmaceutical adjuvants.

[00543] The optimal composition will be determined by one skilled in the art depending upon, for example, the intended route of administration, delivery format, and desired dosage. Such compositions may influence the physical state, stability, rate of *in vivo* release, and rate 20 of *in vivo* clearance of the biotherapeutic actives of the invention. The form of the pharmaceutical composition depends on the intended mode of administration and therapeutic application.

[00544] The primary vehicle or carrier in a composition is aqueous in nature. For example, a suitable vehicle or carrier may be water for injection, physiological saline solution, possibly 25 supplemented with other materials. Neutral buffered saline or saline mixed with serum albumin are further example vehicles. Other example pharmaceutical compositions comprise Tris buffer of about pH 7.0-8.5, or acetate buffer of about pH 4.0-5.5, which may further include sorbitol or a suitable substitute therefore. In one embodiment of the present invention, pharmaceutical compositions may be prepared for storage by mixing the selected composition 30 having the desired degree of purity with optional formulation agents in the form of an aqueous solution.

[00545] The formulation components are present in concentrations that are acceptable to the site of administration. For example, buffers are used to maintain the composition at physiological pH or at a slightly lower pH, typically within a pH range of from about 5 to about 35 8.

[00546] Additional compositions will be evident to those skilled in the art, including formulations of the invention in sustained- or controlled-delivery formulations. Techniques for

formulating a variety of other sustained- or controlled-delivery means, such as liposome carriers, bio-erodible microparticles or porous beads and depot injections, are also known to those skilled in the art. Additional examples of sustained-sustained-release preparations include semipermeable polymer matrices in the form of shaped articles, for example, films, or
5 microcapsules. Sustained release matrices may include polyesters, hydrogels, polylactides, copolymers of L-glutamic acid and gamma ethyl-L-glutamate, ethylene vinyl acetate or poly-D(-)-3-hydroxybutyric acid. Sustained-release compositions may also include liposomes, which can be prepared by any of several methods known in the art.

[00547] The composition to be used for *in vivo* administration can be filtered to remove
10 undesirable components. This may be accomplished by filtration through filtration membranes. In addition, the compositions generally are placed into a sealed container to reduce exposure to oxygen. Once the pharmaceutical composition has been formulated, it may be stored in sealed containers.

[00548] The term "% sequence identity ", as used here, may for example be calculated as
15 follows. A sequence designated the 'query' sequence is compared to a sequence designated the 'subject', or to a database of subject sequences, using the NCBI-BLAST (Basic Local Alignment Search Tool) toolkit; a speed optimized sequence comparison algorithm that searches for optimal local alignments. The 'blastn' command is used at the Unix command line to call for comparisons among DNA sequences, represented as text in the 'FASTA' format.
20 The program returns a number of statistical metric by which to evaluate the quality of a sequence alignment, of which we rely primarily on the length of the alignment (number of base-pairs) and the 'pident'; this is the percentage of bases in the alignment that are identical among sequences, that we refer to as "% sequence identity". The BLAST program is one of the most widely used programs in bioinformatics and is regularly maintained/updated by the
25 NCBI; we used version v2.13.0

[00549] The bacterial strains for use in several embodiments of the present invention can be cultured using standard microbiology techniques as detailed in, for instance, Handbook of Microbiological Media, Fourth Edition (2010) Ronald Atlas, CRC Press, Maintaining Cultures for Biotechnology and Industry (1996) Jennie C. Hunter-Cevera, Academic Press, as well as
30 how detailed in the Examples using YCFA medium.

[00550] In yet a further embodiment, the composition further comprises water.

[00551] In yet a further embodiment, the composition is a liquid, such as an aqueous solution.

[00552] In yet a further embodiment, further comprises a pharmaceutically acceptable
35 carrier.

[00553] In yet a further embodiment, the composition retains its effective biological activity for a period selected from the group consisting of; greater than 24 hours; greater than 36

hours; and greater than 48 hours. In several embodiments the composition is stable for periods selected from the group consisting of: 6 months, 1 year and 2 years. In one example, the composition is stable at temperatures selected from the group consisting of: -80°C, -20°C, -4°C, 4°C, 18°C and 25°C.

5 [00554] Pharmaceutical and therapeutic compositions are within the scope of the invention.

[00555] The therapeutic composition of the invention may comprise a pharmaceutically acceptable excipient, carrier, buffer, stabilizer or other materials well known to those skilled in the art. Such materials should be non-toxic and should not interfere with the efficacy of the isolated bacteria present in the therapeutic composition. The precise nature of the pharmaceutically acceptable excipient or other material will depend on the route of administration, which may be, for example, oral or rectal. Many methods for the preparation of therapeutic compositions are known to those skilled in the art (see e.g. Robinson ed., Sustained and Controlled Release Drug Delivery Systems, Marcel Dekker, Inc., New York, 15 1978).

[00556] The therapeutic composition of the invention may comprise a prebiotic, a carrier, insoluble fiber, a buffer, an osmotic agent, an anti-foaming agent and/or a preservative.

[00557] The therapeutic composition may be made or provided in chemostat medium. Alternatively, the therapeutic composition may be made or provided in saline, e.g., 0.9% saline. It will be understood that any carrier or solution which does not impair viability of the bacteria present in the therapeutic composition and is compatible with administration to an individual may be used.

[00558] The therapeutic composition may be made or provided under reduced atmosphere, i.e., in the absence of oxygen. A synthetic stool preparation may be made or provided under N₂, CO₂, H₂, or a mixture thereof, optionally with controlled levels of partial pressure of N₂:CO₂:H₂.

[00559] Any pharmaceutical composition (and/or additional therapeutic agents) described herein can take the form of tablets, pills, pellets, capsules, capsules containing liquids, capsules containing multiparticulates, powders, solutions, emulsion, drops, suppositories, emulsions, aerosols, sprays, suspensions, delayed-release formulations, sustained-release formulations, controlled-release formulations, or any other form suitable for use.

[00560] The formulations comprising the pharmaceutical compositions described herein can conveniently be presented in unit dosage forms. For example, the dosage forms can be prepared by methods which include the step of bringing the therapeutic agents into association with a carrier, which constitutes one or more accessory ingredients. For example, the formulations are prepared by uniformly and intimately bringing the therapeutic agent into association with a liquid carrier, a finely divided solid carrier, or both, and then, if necessary,

shaping the product into dosage forms of the desired formulation (e.g., wet or dry granulation, powder blends, etc., followed by press tableting).

[00561] The therapeutic composition may be for oral, rectal or colonic administration to the individual. Where the therapeutic composition is for oral administration, the therapeutic composition may be in the form of a capsule, powder or a tablet. Where the therapeutic composition is for rectal administration, the therapeutic composition may be in the form of an enema. The preparation of suitable capsules, tablets, powders and enema is well-known in the art. The capsule or tablet may comprise a coating to protect the capsule or tablet from stomach acid. For example, the capsule or tablet may be enteric-coated, pH dependent, slow-release, and/or gastro-resistant. Such capsules and tablets are used, for example, to minimize dissolution of the capsule or tablet in the stomach but allow dissolution in the small or large intestine.

[00562] Orally dosed formulations, for example, can, in addition to the viable microorganisms comprise, inert compression aids, such as microcrystalline cellulose or oligosaccharide, flow aids, such as a silica gel, or a lubricant of, for example magnesium stearate (vegetable source) or stearic acid (vegetable source).

[00563] A composition disclosed herein can be used as, for example, a food supplement, an edible product or pharmaceutical product. When it is a food supplement, the composition can further comprise a conventional food supplement filler and/or an extender. The composition disclosed herein can also be included in any edible products, such as dairy products, including for example, a milk product, milk, yogurt, curd, ice-cream, dressing, and cheese, beverage products, meat products, and baked goods.

[00564] Suppository formulations, for example, either for rectal use, can in addition to the compositions, comprise, for example, cocoa butter, polyethylene glycol, glycerin or gelatine.

[00565] The composition may comprise a disintegrant, a glidant, and/or a lubricant. Disintegrants aid in the breakup of the compacted mass when placed in a fluid environment. The disintegrant may be any suitable disintegrant such as for example, a disintegrant selected from the group consisting of sodium croscarmellose, crospovidone, gellan gum, hydroxypropyl cellulose, starch, and sodium starch glycolate. The glidant may be any suitable glidant such as for example, a glidant selected from the group consisting of silicon dioxide, colloidal silicon dioxide, and talc. Lubricants are generally always used in the manufacture of dosage forms by direct compression in order to prevent the compacted powder mass from sticking to the equipment during the tableting or encapsulation process. The lubricant may be any suitable lubricant such as for example, a lubricant selected from the group consisting of calcium stearate, magnesium stearate, stearic acid, sodium stearyl fumarate, and vegetable based fatty acids. In the composition and method of several embodiments present invention, the carrier, may be present in the composition in a range of approximately 30% w/w to

approximately 98% w/w. For example, the carrier may be present in the composition in a range of: 30%; 35%; 40%; 45%; 50%; 55%; 60%; 65%; 70%; 75%; 80%; 85%; 90%; 95%; 96%; 97%; 98%; 99%. This weight percentage is a cumulative weight percentage taking into consideration all ingredients present in the carrier.

5 [00566] Coatings can be used to control the solubility of the composition. Examples of coatings include carrageenan, cellulose acetate phthalate, ethylcellulose, gellan gum, maltodextrin, methacrylates, methylcellulose, microcrystalline cellulose, and shellac.

[00567] The composition may comprise one or more preservatives. Example preservatives include antioxidants, chelating agents, antifungal preservatives, alcohol preservatives, acidic
10 preservatives, and other preservatives.

[00568] Example antioxidants include alpha tocopherol, ascorbic acid, ascorbyl palmitate, butylated hydroxyanisole, butylated hydroxytoluene, monothioglycerol, potassium metabisulfite, propionic acid, propyl gallate, sodium ascorbate, sodium bisulfite, sodium metabisulfite, and sodium sulfite.

15 [00569] Example chelating agents include ethylenediaminetetraacetic acid (EDTA) and salts and hydrates thereof (e.g., sodium edetate, disodium edetate, trisodium edetate, calcium disodium edetate, dipotassium edetate, and the like), citric acid and salts and hydrates thereof (e.g., citric acid monohydrate), fumaric acid and salts and hydrates thereof, malic acid and salts and hydrates thereof, phosphoric acid and salts and hydrates thereof, and tartaric acid
20 and salts and hydrates thereof. Suitable antimicrobial preservatives include benzalkonium chloride, benzethonium chloride, benzyl alcohol, bronopol, cetrimide, cetylpyridinium chloride, chlorhexidine, chlorobutanol, chlorocresol, chloroxylenol, cresol, ethyl alcohol, glycerin, hexetidine, imidurea, phenol, phenoxyethanol, phenylethyl alcohol, phenylmercuric nitrate, propylene glycol, and thimerosal.

25 [00570] Example antifungal preservatives include butyl paraben, methyl paraben, ethyl paraben, propyl paraben, benzoic acid, hydroxybenzoic acid, potassium benzoate, potassium sorbate, sodium benzoate, sodium propionate, and sorbic acid. Suitable alcohol preservatives include ethanol, polyethylene glycol, phenol, phenolic compounds, bisphenol, chlorobutanol, hydroxybenzoate, and phenylethyl alcohol.

30 [00571] Example acidic preservatives include vitamin A, vitamin C, vitamin E, beta-carotene, citric acid, acetic acid, dehydroacetic acid, ascorbic acid, sorbic acid, and phytic acid.

[00572] Other preservatives include tocopherol, tocopherol acetate, deteroxime mesylate, cetrimide, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), ethylenediamine,
35 sodium lauryl sulfate (SLS), sodium lauryl ether sulfate (SLES), sodium bisulfite, sodium metabisulfite, potassium sulfite, potassium metabisulfite, Glydant Plus, Phenonip, methylparaben, Germall 115, Germaben II, Neolone, Kathon, and Euxyl.

[00573] The therapeutic composition may be lyophilized. The lyophilized therapeutic composition may comprise one or more stabilizers, cryoprotectants and/or excipients. The lyophilized therapeutic composition may be reconstituted using a suitable diluent prior to administration to the individual. Example stabilisers, cryoprotectants, and/or excipients include

5 trehalose, inulin, maltodextrin, sucrose and other stabilisers, cryoprotectants, and/or excipients either 20 alone or in combination. In some embodiments, the composition is formulated as a lyophilized powder.

[00574] A therapeutic composition according to several embodiments of the present invention may be administered alone or in combination with other treatments, concurrently or

10 sequentially or as a combined preparation with another therapeutic agent or agents, for the treatment of dysbiosis, or a disease associated with dysbiosis as described herein. For example, a strain of the invention may be used in combination with an existing therapeutic agent for inflammatory bowel disease, irritable bowel syndrome, a metabolic disease, a neuropsychiatric disorder, an autoimmune disease, an allergic disorder, a cancer, or hepatic

15 encephalopathy.

[00575] For example, where the therapeutic composition is for the treatment of a dysbiosis associated with cancer, the therapeutic composition may optionally be administered in combination with a cancer immunotherapy, such as an immune check-point inhibitor, to the individual. Examples of check-point inhibitors which may be employed in this context include

20 Programmed cell death protein 1 (PD-1) inhibitors, Programmed death-ligand 1 (PD-L1) inhibitors, cytotoxic T-lymphocyte-associated protein 4 (CTLA-4) inhibitors. Manipulation of the gut microbiota in combination with immune check-point inhibitor treatment has been shown to improve efficacy of immune check-point inhibitors in treating cancer. In one embodiment, the cancer in this context is colorectal cancer, renal cell carcinoma, lung cancer or melanoma.

[00576] In another embodiment, the composition of the invention further comprises immunomodulating compounds. In other embodiments, the immunomodulating compound is a cytokine, chemokine, or complement component that enhances expression of immune system accessory or adhesion molecules, their receptors, or combinations thereof. In some

25 embodiments, the immunomodulating compound include interleukins, for example interleukins 1 to 15, interferons alpha, beta or gamma, tumour necrosis factor, granulocyte-macrophage colony stimulating factor (GM-CSF), macrophage colony stimulating factor (M-CSF), granulocyte colony stimulating factor (G-CSF), chemokines such as neutrophil activating protein (NAP), macrophage chemoattractant and activating factor (MCAF), RANTES, macrophage inflammatory peptides MIP-1a and MIP-1b, complement components, or

30 combinations thereof. In other embodiments, the immunomodulating compound stimulates expression, or enhanced expression of OX40, OX40L (gp34), lymphotactin, CD40, CD40L, B7.1, B7.2, TRAP, ICAM-1, 2 or 3, cytokine receptors, or combination thereof.

[00577] In another embodiment, the immunomodulatory compound induces or enhances expression of co-stimulatory molecules that participate in the immune response, which include, in some embodiments, CD40 or its ligand, CD28, CTLA-4 or a B7 molecule. In another embodiment, the immunomodulatory compound induces or enhances expression of a heat stable antigen (HSA), chondroitin sulfate-modified MHC invariant chain (Ii-CS), or an intracellular adhesion molecule 1 (ICAM-1).

[00578] The therapeutic compositions of the invention may be administered to an individual, for example a human individual. Administration may be in a "therapeutically effective amount", this being sufficient to show benefit to the individual. Such benefit may be at least amelioration of at least one symptom. Thus "treatment" of a specified disease refers to amelioration of at least one symptom. The actual amount administered, and rate and time-course of administration, will depend on the nature and severity of what is being treated, the particular patient being treated, the clinical condition of the individual patient, the cause of the dysbiosis, the site of delivery of the composition, the type of therapeutic composition, the method of administration, the scheduling of administration and other factors known to medical practitioners. Prescription of treatment, e.g. decisions on dosage etc., is within the responsibility of general practitioners and other medical doctors and may depend on the severity of the symptoms and/or progression of a disease being treated. A therapeutically effective amount or suitable dose of a therapeutic composition of the invention can be determined by comparing its *in vitro* activity and *in vivo* activity in an animal model. Methods for extrapolation of effective dosages in mice and other test animals to humans are known. The precise dose will depend upon a number of factors, including whether the therapeutic composition is for prevention or for treatment.

[00579] Formulary ingredients can be contacted with the preparation and mixed or prepared until a formulation is obtained. As will be clear to those of skill in the art, formulation conditions will generally be such that viable microorganisms are retained. In particular high temperatures, for example temperatures in excess of 40°C are avoided.

[00580] The amount of viable microorganisms included in a composition can vary and can be adjusted and optimized as will be appreciated by those of skill in the art. Such optimization may, for example, be achieved by preparing a series of different doses of a viable microorganism. The bacterial concentration in the composition can be, for example, from 1 cfu/mL to 10 cfu/mL, from 100 cfu/mL to 1 thousand cfu/mL, from 10 thousand cfu/mL to 100 thousand cfu/mL, from 10 cfu/mL to 1 million cfu/mL, from 100 cfu/mL to 1 million cfu/mL, from 1 thousand cfu/mL to 1 million cfu/mL, from 10 thousand cfu/mL to 1 million cfu/mL, from 100 thousand cfu/mL to 1 million cfu/mL, from 1 million cfu/mL to 10 million cfu/mL, from 10 million cfu/mL to 100 billion cfu/mL, from 10 million to 50 million cfu/mL, for example in several embodiments from 50 million to 100 million cfu/mL, from 100 million to 500 million cfu/mL,

from 500 million to 1 billion cfu/mL, from 1 billion to 5 billion cfu/mL, from 5 billion to 10 billion cfu/mL, from 10 billion to 15 billion cfu/mL, from 15 billion to 20 billion cfu/mL, from 20 billion to 25 billion cfu/mL, from 25 billion to 30 billion cfu/mL, from 30 billion to 35 billion cfu/mL, from 35 billion to 40 billion cfu/mL, from 40 billion to 45 billion cfu/mL, from 45 billion to 50 billion cfu/mL, from 50 billion to 55 billion cfu/mL, from 55 billion to 60 billion cfu/mL, from 60 billion to 65 billion cfu/mL, from 65 billion to 70 billion cfu/mL, from 70 billion to 75 billion cfu/mL, from 75 billion to 80 billion cfu/mL, from 80 billion to 85 billion cfu/mL, from 85 billion to 90 billion cfu/mL, from 90 billion to 95 billion cfu/mL, from 95 billion to 100 billion cfu/mL or an amount within a range defined by any two of the aforementioned values.

10 [00581] In an embodiment, the strain of the invention can be administered at, for example, a dosage of 0.01 to 100×10^{11} cells/body, 0.1 to 10×10^{11} cells/body or 0.3 to 5×10^{11} cells/body. Furthermore, for example, the amount ingested per day as the bacteria can be 0.01 to 100×10^{11} cells/60 kg body weight, 0.1 to 10×10^{11} cells/60 kg body weight or 0.3 to 5×10^{11} cells/60 kg body weight or an amount within a range defined by any two of the
15 aforementioned values.

[00582] The content of at least one strain of bacteria, archaea or fungi contained in the orally ingested composition of several embodiments of the present invention may be determined as appropriate depending on its application form. As a dry microbial body it can be, for example, 5 to 50 w/w %, 1 to 75 w/w %, 0.1 to 100 w/w % or 1 to 100 w/w % or an
20 amount within a range defined by any two of the aforementioned values.

[00583] In an embodiment, the composition is a controlled release composition. As used herein, the term "controlled-release" refers to release or administration of a strain of the invention from a given dosage form in a controlled fashion in order to achieve the desired pharmacokinetic profile *in vivo*. An aspect of "controlled" delivery is the ability to manipulate
25 the formulation and/or dosage form in order to establish the desired kinetics of release.

[00584] Procedures for preparing tablets, powders, caplets, capsules and other forms of compositions of the invention are known to those of ordinary skill in the art and include without limitation wet granulation, dry granulation, and direct compression (for tablets and caplets).

[00585] Wet and dry granulation is used to manufacture tablets, caplets, or capsules. With
30 granulation techniques, a chilsonation is used to manufacture the powder for the dosage forms. A chilsonator houses grooved, rotating rollers that are pressed tightly against one another by hydraulic pressure. Raw materials are placed into the hopper of the chilsonator and are fed by a system of horizontal and vertical screws into the rollers. As materials pass through the grooves in the rollers, it is compacted under very high pressure and emerges from
35 the chilsonator as dense sheets. The sheets are milled into a fine granular powder using a Fitz mill and then passed through a screen to produce a uniform free flowing granule. The chilsonation process results in a finished powder that is two to four times denser than the

starting material, a feature that permits the ingredients to be fashioned into the desired dosage form.

[00586] With dry granulation, the powder may be incorporated into a gelatin capsule or it may be mixed with gelatin to form a tablet or caplet. With wet granulation, the powder is moistened thus creating large "chunks" of material that are subsequently dried and milled to convert the chunks to particles of a desired size for the manufacturing process. Once the particles of a desired size are obtained, the particles are incorporated into a gelatin capsule or mixed with gelatin to form a tablet or caplet.

[00587] General considerations in formulation and/or manufacture can be found, for example, in Remington's The Science and Practice of Pharmacy, 23rd Edition. (2020, Mack Publishing Co., Easton, Pa.) which is incorporated by reference.

Prebiotics

[00588] The compositions and methods of several embodiments of the present invention may further comprise one or more prebiotics.

[00589] [00228] A prebiotic is a substrate that is selectively used by a host microorganism to produce a health benefit in a subject. Without wishing to be bound by theory, prebiotics are added to nutritionally supplement bacteria in the microbiome and/or in a microbial composition, e.g., to stimulate the growth or activity of one or more strains of beneficial bacteria. Additionally, the prebiotics may be added to prevent "shock" to bacterial strains subsequent to their isolation or purification, freezing, freeze-drying, spray-drying, reconstitution in solution and the like.

[00590] A composition of the invention can comprise a prebiotic. Because prebiotics have a chemical structure that resists digestion through the alimentary tract, they reach the colon as intact molecules where they are able to elicit systemic physiological functions and act as fermentable substrates for colonic microflora. Where a prebiotic is combined with a biotherapeutic, the resulting composition is sometimes referred to as a "synbiotic."

[00591] Examples of prebiotics include amino acids, ammonium nitrate, amylose, barley, barley mulch, biotin, carbonate, cellulose, chitin, choline, dietary fibres, fermentable polysaccharides, fructooligosaccharides, fructose, glucose, glycerol, 5 heteropolysaccharide, histidine, homopolysaccharide, hydroxyapatite, inulin, isomaltulose, lactic acid, lactose, lactulose, maltodextrins, maltose, mannoooligosaccharides, tagatose, nitrogen, oligodextrose, oligofructoses, oligofructose-enriched inulin, oligosaccharides, pectin, phosphate salts, phosphorus, polydextroses, polyols, potash, potassium, sodium nitrate, starch, resistant starch, sucrose, sulfur, sun fiber, tagatose, thiamine, trans-galactooligosaccharides, trehalose, vitamins, a water-soluble carbohydrate, white navy bean powder, and/or xylooligosaccharides (XOSs), or any combination thereof.

[00592] Additional examples of suitable prebiotics include, but are not limited to, oligosaccharide such as fructooligosaccharides, P95 Nutraflora®, for example, galactooligosaccharides, xylooligosaccharides, isomaltoligosaccharides, human milk oligosaccharides, inulin oligosaccharides, mannan oligosaccharides, pyrodextrin, levan, maltotriose, pectic oligosaccharides, bimuno-galactooligosaccharides, arabinoxylan, fucoidan and resistant starches. Fructooligosaccharides can be extracted from, for example, chicory, artichokes, asparagus, dandelions, dahlias, endive, garlic, leeks, lettuce, and onions.

[00593] In an embodiment, the prebiotic comprises amino acids such as one or more or all of alanine, aspartic acid, glutamic acid, glycine, leucine, isoleucine, proline, serine, threonine and valine.

[00594] In an embodiment, the prebiotic comprises simple sugars which can be a monosaccharide (such as glucose, galactose or fructose) and/or a disaccharide (such as sucrose maltose or lactose).

[00595] In an embodiment, the prebiotic comprises from about 5% (w/w) to about 50% (w/w), about 7.5% (w/w) to about 30% (w/w) or about 10% (w/w) to about 15% (w/w) of the composition. For example, 5% (w/w); 10% (w/w); 15% (w/w); 20% (w/w); 25% (w/w); 30% (w/w); 35% (w/w); 40% (w/w); 45% (w/w); 50% (w/w); 55% (w/w); 60% (w/w); 65% (w/w); 70% (w/w); 75% (w/w); 80% (w/w); 85% (w/w); 90% (w/w); 95% (w/w); 96% (w/w); 97% (w/w); 98% (w/w); 99% (w/w), or an amount within a range defined by any two of the aforementioned values.

[00596] In embodiments, a prebiotic can be added (e.g., in dry or liquid forms) to a microbial composition of the present invention.

[00597] Alternately, or additionally, a prebiotic can be included (e.g., in dry or liquid forms) in a distinct pharmaceutical composition which lacks a microbial composition of several embodiments of the present invention.

[00598] A prebiotic may be provided to a subject before, contemporaneously with, and/or after a pharmaceutical composition comprising a microbial composition of several embodiments of the present invention is administered, either in a pharmaceutical composition comprising the microbial composition or in a pharmaceutical composition lacking a microbial composition.

[00599] A prebiotic may be provided in a single dose or in multiple doses. When provided as a single composition, the single composition may comprise a single prebiotic or a mixture of prebiotics. When provided in multiple compositions, each composition may comprise a single prebiotic or a mixture of prebiotics.

[00600] In some embodiments, the compositions described herein are formulated together with a prebiotic in a single formulation. In some embodiments, the compositions described herein are formulated for administration separately from the prebiotic in a separate

composition. In some embodiments, the compositions of the microbial consortium and the prebiotic may be provided as separate compositions that are co-located in a container. In some embodiments, a kit is provided including the formulations, together or separately along with instructions for use.

5 *Other Microorganisms*

[00601] In order to obtain the desired health benefit to the subject, it may be advantageous to include one or more additional biotherapeutic microorganisms in the composition. Thus, the composition may comprise more than one species/strain of microorganisms in addition to the strain of the invention, such as two, three, four, five or a higher plurality of species/strains of
10 microorganisms. Non-limiting examples of biotherapeutics are suitable strains selected from the genera listed in Tables 7 and 8. Another example of biotherapeutics to add to the composition are strains of the genera selected from the group consisting of: *Acetobacterium*, *Adlercreutzia*, *Aerococcus*, *Akkermansia*, *Alistipes*, *Allobaculum*, *Anaerostipes*, *Blautia*, *Bacillus*, *Bacteroides*, *Bifidobacterium*, *Carnobacterium*, *Clostridium*, *Coprococcus*,
15 *Eubacterium*, *Enterococcus*, *Erysipelatoclostridium*, *Faecalibacterium*, *Lactobacillus*, *Lactococcus*, *Leuconostoc*, *Methanobrevibacter*, *Oenococcus*, *Oscillospira*, *Parabacteroides*, *Pediococcus*, *Prevotella*, *Propionibacterium*, *Roseburia*, *Ruminococcus*, *Sporolactobacillus*, *Sporomusa*, *Staphylococcus*, *Streptococcus*, *Subdoligranulum*, *Tetragenococcus*, *Vagococcus* and *Weisella*. It is to be understood that the foregoing list is intended only to be
20 illustrative and not a limiting representation of the biotherapeutics that may be included. In this respect, any additional biotherapeutic species may also be used in the compositions of the present invention.

[00602] In an embodiment, the *Lactobacillus sp.* is selected from the group consisting of *Lactobacillus rhamnosus* (such as strain GG (ATCC 53103), CGMCC 1.3724 or SP1 (DSM
25 21690)), *Lactococcus lactis*, *Lactococcus cremoris*, *Lactococcus diacetylactis*, *Lactobacillus paracasei*, *Lactobacillus reuteri* (such as strain ATCC 55730 or DSM 17938), *Lactobacillus acidophilus*, *Lactobacillus murinus*, *Lactobacillus helveticus*, *Lactobacillus bulgaricus*, *Lactobacillus casei*, *Lactobacillus salivarius*, *Lactobacillus plantarum*, *Lactobacillus fermentum*, *Lactobacillus taiwanensis*, *Lactobacillus animalis*, *Lactobacillus johnsonii* (such
30 as strain NCC533; CNCM 1-1225) and *Lactobacillus gasseri*.

[00603] In an embodiment, the *Bifidobacterium sp.* is selected from the group consisting of *Bifidobacterium lactis* (such as strain BB-12, BI-04 or CNCM 1-3446 (Bb12)), *Bifidobacterium longum* (such as strain NCC3001, ATCC BAA-999 (BB536)), *Bifidobacterium breve* (such as strain Bb-03, M-16V or R0070), *Bifidobacterium infantis*, *Bifidobacterium animalis*, *Bifidobacterium bifidum* and *Bifidobacterium adolescentis*.
35

[00604] In an embodiment, the *Clostridium sp.* includes or *Clostridium hylemonae* or *Clostridium scindens* or *Flavinofractor plautii*.

[00605] Some yeasts are also useful as biotherapeutics and are sometimes included in the compositions. One non-limiting example of a yeast used in biotherapeutics is *Saccharomyces boulardii*.

[00606] Some archaea are also useful as biotherapeutics and are sometimes included in the compositions. Non-limiting examples of an archaea used in biotherapeutics is *Methanobrevibacter spp*, including *Methanobrevibacter smithii* and *Methanosphaera sp*, including *Methanobrevibacter stadmanae*.

[00607] *Further embodiments in this aspect of the invention*

[00608] In several embodiments, a formulation comprising multiple core community microbial strains as well as multiple keystone microbial strains are provided to, for example, restore gut microbiome ecology. Advantageously in several embodiments, the core community and keystone strains are co-cultured together to provide a synergistic consortium with diverse species. When administered to a subject, according to one embodiment, the consortium is capable of providing a beneficially stable microbial ecosystem because the various strains have already been co-cultured together prior to administration.

[00609] In some embodiments, a diverse range of gene families, as described herein, provides the ability to deliver therapies that have broad functional capability as well as highly targeted disease specific function. Oral formulations are provided in several embodiments, which in turn can eliminate the reliance on stool donors and enables production of microbial therapies at scale, to large markets. The formulations are used in some embodiments to treat mycobiome dysbiosis. For example, the formulations are used in some embodiments to treat ulcerative colitis, inflammatory bowel disease, Crohn's disease, checkpoint inhibitor colitis, as well as other gastrointestinal diseases and symptoms. The formulations are used in some embodiments to treat liver disorders, including, for example, primary sclerosing cholangitis, primary biliary cirrhosis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, or hepatic encephalopathy. The formulations are used in some embodiments to treat metabolic disorders, including, for example, obesity, insulin resistance, or type 2 diabetes. The formulations are used in some embodiments to treat oncology indications, including, for example, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer, breast cancer, lung cancer, testicular cancer, or sarcoma. The formulations are used in some embodiments to treat cardiovascular disorders, including, for example, dyslipidaemia, atherosclerotic heart disease, or hypertension. The formulations are used in some embodiments to treat immunological diseases, including, for example, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis, psoriasis, systemic lupus erythematosus, or Sjogren's disease. The formulations are used in some embodiments to treat allergic and atopic disorders, including, for example, food allergy, anaphylaxis, atopic dermatitis, or atopic rhinitis or sinusitis. The formulations are used

in some embodiments to treat infectious diseases, including, for example, clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory infections, or sepsis. Enhancement of the immune system is provided by several formulations. In some embodiments, the formulations
5 reduce adhesion and/or colonization of pathogenic microbes (such as pathogenic or undesired bacteria, viruses, and/or yeast and other fungi). In some embodiments, restoration of a healthy gut ecology treats diseases and symptoms that are not considered traditional gastrointestinal diseases. For example, neurological disorders, including for example, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, or schizophrenia, and
10 other conditions may be treated by restoring a healthier microbiome. In some embodiments, the formulations are formulated to treat one or more of the diseases or disorders described herein, including any combination thereof. In some embodiments, the formulations are used in combination with a therapy to treat any of the diseases or disorders described herein.

[00610] In some embodiments, the formulation comprises or consists essentially of a
15 consortium of core and keystone bacterial strains that replicates at least 90% of the gene families that are found in a healthy microbiome. In other embodiments, replication of 50%-90% of the gene families is provided.

[00611] In some embodiments, the microbial consortium includes at least one microbe of the phylum selected from the group consisting of Actinomycetota, Bacillota, Bacteroidota,
20 Campylobacterota, Pseudomonodota, Thermodesulfobiota, and Verrocomicrobiota. In some embodiments, the microbial consortium includes a microbe from any one of these phyla, any combination of two of these phyla, any combination of three of these phyla, any combination of four of these phyla, any combination of five of these phyla, any combination of six of these phyla, or all seven of these phyla.

[00612] In some embodiments, the microbial consortium includes at least one microbe of the phylum selected from the group consisting of Actinomycetota, Bacillota, Bacteroidota, and Verrocomicrobiota. In some embodiments, the microbial consortium includes a bacteria selected from: Actinomycetota; Bacillota; Bacteroidota; Verrocomicrobiota; Actinomycetota and Bacillota; Actinomycetota and Bacteroidota; Actinomycetota and Verrocomicrobiota;
30 Bacillota and Bacteroidota; Bacillota and Verrocomicrobiota; Bacteroidota and Verrocomicrobiota; Actinomycetota, Bacillota, and Bacteroidota; Actinomycetota, Bacillota, and Verrocomicrobiota; Actinomycetota, Bacteroidota, and Verrocomicrobiota; Bacillota, Bacteroidota, and Verrocomicrobiota; or Actinomycetota, Bacillota, Bacteroidota, and Verrocomicrobiota.

[00613] In some embodiments, the formulations include one or more microbes selected from one or more of the following microbial families: Acidaminococcaceae, Akkermansiaceae, Bacillaceae, Bacteroidaceae, Barnisiellaceae, Bifidobacteriaceae, Campylobacteraceae,

Carnobacteriaceae, Christensenellaceae, Clostridiaceae, Coprobacillaceae, Coriobacteriaceae, Desulfovibrionaceae, Eggerthellaceae, Enterobacteriaceae, Enterococcaceae, Erysipelotrichaceae, Eubacteriaceae, Eubacteriales Family XIII. Incertae Sedis, Eubacteriales incertae sedis, Lachnospiraceae, Lactobacillaceae, Maliobacteriaceae, Muribaculaceae, Odoribacteraceae, Oscillospiraceae, Peptoniphilaceae, Peptostreptococcaceae, Prevotellaceae, Rikenellaceae, Selenomonadaceae, Streptococcaceae, Sutterellaceae, and Veillonellaceae. In some embodiments, the formulations include one or more microbes selected from any one of the aforementioned families, or from any combination of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, or 33 of the aforementioned bacterial families, or from all 34 of the aforementioned bacterial families.

[00614] In several embodiments, a formulation comprises or consists essentially of 5-26 core community microbial strains selected from Table 14 and 5-22 or more keystone microbial strains selected from Table 13. The formulations are co-cultured, lyophilized and provided as an oral formulation (e.g., a capsule, tablet, or powder) in several embodiments. One or more of enteric coatings, pharmaceutically acceptable excipients (e.g., inulin and/or maltodextrin) and fibres are also provided (which may be natural or non-naturally occurring, e.g., partially or fully modified, synthetic, etc.). Agents to balance pH may also be included. For example, the formulation in one embodiment comprises or consists essentially of any 10 or more of *Bifidobacterium longum*, *Faecalibacterium prausnitzii*, *Dysosmobacter welbionis*, *Enterocloster bolteae*, *Alistipes megaguti*, *Parabacteroides goldsteinii*, *Flavonifractor plautii*, *Alistipes communis*, *Ruthenibacterium lactatiformans*, *Vescimonas coprocola*, *Collinsella aerofaciens*, *Coprococcus comes*, *Ruminococcus gnavus*, *Ruminococcus bicirculans*, *Bacteroides caecimuris*, *Coprococcus eutactus*, *Butyricimonas virosa*, *Phocaeicola salanitronis*, *Alistipes dispar*, *Clostridium scindens*, *Parabacteroides merdae*, *Bacteroides salyersiae*, *Pusillimonas faecalis*, *Solibaculum mannosilyticum*, *Akkermansia muciniphila*, or *Christensenella minuta* in combination with any 10 or more of *Bifidobacterium longum*, *Faecalibacterium prausnitzii*, *Bifidobacterium bifidum*, *Alistipes putredinis*, *Alistipes shahii*, *Bacteroides intestinalis*, *Bacteroides stercoris*, *Bifidobacterium adolescentis*, *Coprococcus catus*, *Methonobrevibacter smithii*, *Parabacteroides johnsonii*, *Phocaeicola coprocola*, *Roseburia inulinivorans*, *Ruminococcus bromii*, *Ruminococcus torques*, *Subdoligranulum variabile*, *Bacteroides caccae*, *Bacteroides coprocola*, *Bacteroides eggerthii*, *Bacteroides thetaiotaomicron*, *Bacteroides uniformis*, or *Parabacteroides distasonis*, and one or more of an enteric coating, inulin, or maltodextrin. In some embodiments, 5-10, 10-15, 15-26 core community strains (e.g., from Table 14) and 5-10, 10-15, 15-22 keystone strains (e.g., from Table 13) are co-cultured together and/or in the formulation for administration to a subject. In some embodiments, 90, 92, 95% or all of the core community strains and all of the keystones

strains are co-cultured together and/or in the formulation for administration to a subject. Certain strains may be valuable in the co-culture to support the community as a whole but may not be present in the formulation for administration to a subject. In one embodiment, about 5-20% of strains that are in the co-culture are not significantly present in the formulation

5 for administration to a subject.

[00615] In one embodiment, the formulation comprises or consists essentially of (i) 85-90%, 90%-95%, or all of the core community microbial strains in Table 14 and/or (ii) 85-90%, 90%-95% or all of the keystone microbial strains selected from Table 13. In several embodiments, the formulation comprises or consists essentially of 20-26 core community
10 microbial strains selected from Table 14, and keystone strains from Table 13 at a core:keystone strain ratio at 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1. In some embodiments, the formulation comprises or consists essentially of from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage of total number or mass microorganisms in the formulation. In several embodiments, the core
15 and keystone strains have been co-cultured together. With respect to the numbers, amounts and ratios disclosed herein, the formulation may be the formulation administered to a subject or in the co-culture.

[00616] In some embodiments, the formulations include a microbial consortium having bacteria selected from the phyla Actinomycetota, Bacillota, Bacteroidota, Campylobacterota,
20 Pseudomonadota, Thermodesulfobiota, and Verrucomicrobiota. In some embodiments, the formulations include strains from Actinomycetota, Bacillota, Bacteroidota, and Verrucomicrobiota. In several embodiments, the formulations include strains from no more than two phyla of Actinomycetota, Bacillota, Bacteroidota, and Pseudomonadota. In several embodiments, the formulation (whether co-cultured or for administration to a subject) does not
25 include bacteria from Pseudomonadota and/or Campylobacterota. In some embodiments, Pseudomonadota or Campylobacterota are completely or significantly excluded or removed from the formulations.

[00617] In some embodiments, the formulation (whether co-cultured or for administration to a subject) does not include bacteria of the species *Acidaminococcus intestini*, *Bacillus bombysepticus*, *Bacillus cereus*, *Bacteroides fragilis*, *Blautia pseudococcoides*,
30 *Burkholderiales bacterium 1 1 47*, *Campylobacter coli*, *Campylobacter jejuni*, *Clostridium botulinum*, *Clostridium paraputrificum*, *Clostridium perfringens*, *Clostridium perfringens*, *Clostridium tetani*, *Desulfovibrio piger*, *Eggerthella lenta*, *Enterococcus faecium*, *Erysipelatoclostridium ramosum*, *Escherichia coli*, *Escherichia marmotae*, *Fingoldia magna*, *Flavonifractor plautii*, *Klebsiella pneumoniae*, *Klebsiella variicola*, *Lactococcus lactis*,
35 *Paraclostridium bifermentans*, *Pluralibacter gergoviae*, *Porphyromonas asaccharolytica*, *Ruminococcus gnavus*, *Salmonella enterica*, *Staphylococcus aureus*,

Streptococcus infantarius, *Streptococcus salivarius*, *Sutterella wadsworthensis*, *Thomasclavelia spiroformis*, *Veillonella parvula*, and in some embodiments are completely or significantly excluded or removed. In some embodiments, the formulation (whether co-cultured or for administration to a subject) does not include bacteria of the species *Bacillus*

5 *bombysepticus*, *Bacillus cereus*, *Bacteroides fragilis*, *Campylobacter coli*, *Campylobacter jejuni*, *Clostridium botulinum*, *Clostridium perfringens*, *Clostridium perfringens*, *Clostridium tetani*, *Klebsiella pneumoniae*, *Klebsiella variicola*, *Pluralibacter gergoviae*, *Salmonella enterica*, *Staphylococcus aureus*, and in some embodiments are completely or significantly excluded or removed. In some embodiments, the formulation (whether co-cultured or for

10 administration to a subject) does not include bacteria from of the species *Burkholderiales bacterium 1 1 47*, *Clostridium paraputrificum*, *Enterococcus faecium*, *Erysipelatoclostridium ramosum*, *Finegoldia magna*, *Lactococcus lactis*, *Paraclostridium bifermentans*, *Porphyromonas asaccharolytica*, *Ruminococcus gnavus*, *Streptococcus infantarius*, *Streptococcus salivarius*, *Sutterella wadsworthensis*, *Thomasclavelia spiroformis*, and in

15 some embodiments are completely or significantly excluded or removed. In some embodiments, the formulation (whether co-cultured or for administration to a subject) does not include bacteria from of the species *Acidaminococcus intestini*, *Blautia pseudococcoides*, *Desulfovibrio piger*, *Eggerthella lenta*, *Escherichia coli*, *Escherichia marmotae*, *Flavonifractor plautii*, *Veillonella parvula*, and in some embodiments are completely or

20 significantly excluded or removed. In several embodiments, the formulation (whether co-cultured or for administration to a subject) does not include bacteria from of the species.

[00618] In some embodiments, the formulations described herein are used with other therapies. For example, the formulations may be used to reduce side effects of other pharmaceuticals (including e.g., biologics) by, for example, reducing the dose or course

25 needed for such pharmaceutical, reducing an inflammatory response, reducing nausea or other undesired effect of such pharmaceutical post administration. The formulations may also be used to enhance the beneficial effects of other pharmaceuticals by, for example, increasing absorption and/or availability of such pharmaceutical post administration. In some embodiments, synergistic effects are achieved using the formulations described herein and

30 other therapies such as pharmaceuticals.

[00619] In some embodiments, the formulations are used to restore a healthy microbiome after antibiotic therapy and/or cleanses and may be provided before, together with, or after antibiotic therapy and/or cleanses. In some embodiments, when treating a specific disease for example, antibiotics and/or cleanses may optionally be administered prior to administration

35 of the formulation to assist in providing a "cleaner slate" for the consortium in the formulation. The cleanse may be associated with medical procedures such as colonoscopies.

[00620] Methods of co-culturing one or more core community microbial strains with one or more keystone microbial strains are also provided. In some embodiments, the method comprises selecting a plurality of core community microbial strains selected from Table 14 and a plurality of keystone microbial strains selected from Table 13, and co-culturing the strains under suitable culture conditions (e.g., in a single bioreactor). In some embodiments, the method comprises or consists essentially of co-culturing (i) 85-90%, 90%-95%, or all of the core community microbial strains in Table 14 and/or (ii) 85-90%, 90%-95% or all of the keystone microbial strains selected from Table 13. In several embodiments, the co-culture comprises or consists essentially of 20-26 core community microbial strains selected from Table 14, and keystone strains from Table 13 at a core:keystone strain ratio at 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1. In some embodiments, the co-culture comprises or consists essentially of from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage of total number or mass microorganisms in the co-culture. Co-culturing occurs in a single bioreactor in several embodiments, and the keystone strains may facilitate the growth, activity, and/or survival of the core community strains. In one embodiment, about 5-20% of strains that are in the co-culture are not significantly present in the formulation for administration to a subject. In one embodiment, the method further comprises excluding certain bacteria or other microorganisms. In several embodiments, the co-culturing method includes the use of a medium, which contains the following components in varying concentrations per liter: (-)-riboflavin ranges broadly from 10 µg to 100 µg, optionally from 20 µg to 75 µg, preferably from 40 µg to 60 µg, and most preferably about 50 µg. 4-aminobenzoic acid ranges broadly from 5 µg to 50 µg, optionally from 10 µg to 30 µg, preferably from 10 µg to 20 µg, and most preferably about 15 µg. Acetic acid ranges broadly from 2 mL to 10 mL, optionally from 3 mL to 6 mL, preferably from 3.5 mL to 5 mL, and most preferably about 4.05 mL. Ammonium sulfate ranges broadly from 0.5 g to 2 g, optionally from 0.75 g to 1.25 g, preferably from 0.8 g to 1 g, and most preferably about 0.9 g. Biotin ranges broadly from 1 µg to 15 µg, optionally from 3 µg to 10 µg, preferably from 4 µg to 6 µg, and most preferably about 5 µg. Calcium chloride ranges broadly from 0.05 g to 0.2 g, optionally from 0.07 g to 0.15 g, preferably from 0.08 g to 0.1 g, and most preferably about 0.09 g. Cyanocobalamin (B12) ranges broadly from 2 µg to 15 µg, optionally from 4 µg to 10 µg, preferably from 4.5 µg to 6 µg, and most preferably about 5 µg. D-(+)-cellobiose, D-(+)-glucose, and D-(+)-maltose each range broadly from 1 g to 5 g, optionally from 1.5 g to 3.5 g, preferably from 1.8 g to 2.2 g, and most preferably about 2 g. Ethanol ranges broadly from 1 mL to 5 mL, optionally from 2 mL to 4 mL, preferably from 2.3 mL to 2.7 mL, and most preferably about 2.5 mL. Folic acid ranges broadly from 10 µg to 100 µg, optionally from 20 µg to 50 µg, preferably from 20 µg to 30 µg, and most preferably about 25 µg. Haemin chloride ranges broadly from 5 mg to 30 mg, optionally from 7 mg to 15 mg, preferably from 9 mg to

12 mg, and most preferably about 10 mg. Isobutyric acid and isovaleric acid each range broadly from 0.1 mL to 1 mL, optionally from 0.15 mL to 0.5 mL, preferably from 0.2 mL to 0.3 mL, and most preferably about 0.24 mL. L-cysteine ranges broadly from 0.5 g to 2 g, optionally from 0.75 g to 1.5 g, preferably from 0.9 g to 1.1 g, and most preferably about 1 g. Magnesium sulfate ranges broadly from 0.05 g to 0.15 g, optionally from 0.07 g to 0.1 g, preferably from 0.08 g to 0.1 g, and most preferably about 0.09 g. Potassium hydroxide ranges broadly from 10 mg to 50 mg, optionally from 20 mg to 40 mg, preferably from 25 mg to 30 mg, and most preferably about 28 mg. Potassium phosphate dibasic and potassium phosphate monobasic each range broadly from 0.2 g to 1 g, optionally from 0.35 g to 0.75 g, preferably from 0.4 g to 0.5 g, and most preferably about 0.45 g. Propionic acid ranges broadly from 0.5 mL to 3 mL, optionally from 1 mL to 2 mL, preferably from 1.3 mL to 1.6 mL, and most preferably about 1.43 mL. Pyridoxine ranges broadly from 25 µg to 100 µg, optionally from 50 µg to 80 µg, preferably from 60 µg to 70 µg, and most preferably about 75 µg. Resazurin ranges broadly from 0.5 mg to 2 mg, optionally from 0.75 mg to 1.5 mg, preferably from 0.9 mg to 1.1 mg, and most preferably about 1 mg. Sodium chloride ranges broadly from 0.5 g to 2 g, optionally from 0.75 g to 1.5 g, preferably from 0.8 g to 1 g, and most preferably about 0.9 g. Sodium hydrogen carbonate (sodium bicarbonate) ranges broadly from 2 g to 8 g, optionally from 3 g to 6 g, preferably from 3.5 g to 4.5 g, and most preferably about 4 g. Thiamine hydrochloride ranges broadly from 10 µg to 100 µg, optionally from 25 µg to 75 µg, preferably from 40 µg to 60 µg, and most preferably about 50 µg. Tryptone ranges broadly from 5 g to 20 g, optionally from 8 g to 15 g, preferably from 9 g to 11 g, and most preferably about 10 g. Valeric acid ranges broadly from 0.1 mL to 1 mL, optionally from 0.15 mL to 0.5 mL, preferably from 0.2 mL to 0.3 mL, and most preferably about 0.24 mL. Yeast extract ranges broadly from 1.5 g to 5 g, optionally from 2 g to 4 g, preferably from 2.3 g to 2.7 g, and most preferably about 2.5 g. The culture is incubated at 37°C in a stirred reactor under anaerobic conditions, with purged gas at a flow rate of 0.5 to 5 normal liters per minute, more preferably from 1 to 4 normal liters per minute, and most preferably from 2 to 3 normal liters per minute. The gas mixture can be selected from 10% H₂, 10% CO₂, 80% N₂; 5% H₂, 10% CO₂, 85% N₂; 5% H₂, 5% CO₂, 90% N₂; or other similar combinations that facilitate the desired anaerobic conditions. The pH of the medium ranges broadly from 5 to 9, optionally from 6 to 8, preferably from 6.5 to 7.5, and most preferably about 7.

Dosage Form

[00621] Dosage forms are within the scope of the invention. In an embodiment, the invention provides a dosage form comprising the composition as described in the first aspect of this invention. For example, the dosage form is stored in a sealed and sterile container.

Methods of making

[00622] Some embodiments provided herein relate to methods of culturing the microbial consortium described herein. In some embodiments, the methods include co-culturing any 1 or more core community microbial strains as set forth in Table 14 and any 1 or more keystone microbial strains as set forth in Table 13; any 2 or more core community microbial strains as set forth in Table 14 and any 1 or more keystone microbial strains as set forth in Table 13; any 3 or more core community microbial strains as set forth in Table 14 and any 1 or more keystone microbial strains as set forth in Table 13; any 5 or more core community microbial strains as set forth in Table 14 and any 1 or more keystone microbial strains as set forth in Table 13; any 3 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 5 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 5 or more core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; any 10 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 10 or more core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; any 10 or more core community microbial strains as set forth in Table 14 and any 10 or more keystone microbial strains as set forth in Table 13; any 15 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 15 or more core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; any 15 or more core community microbial strains as set forth in Table 14 and any 10 or more keystone microbial strains as set forth in Table 13; any 15 or more core community microbial strains as set forth in Table 14 and any 15 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 10 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 15 or more keystone microbial strains as set forth in Table 13; any 20 or more core community microbial strains as set forth in Table 14 and any 20 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 3 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 5 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 10 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and any 15 or more keystone microbial strains as set forth in Table 13; all core community

microbial strains as set forth in Table 14 and any 20 or more keystone microbial strains as set forth in Table 13; all core community microbial strains as set forth in Table 14 and all keystone microbial strains as set forth in Table 13, or co-culturing any number of core community microbial strains with any number of keystone microbial strains within a range described
5 herein. In some embodiments, the methods include co-culturing any number of the core community microbial strains as set forth in Table 14 with any number of the keystone microbial strains as set forth in Table 13. In several embodiments, the number and/or type of strains are selected to achieve a formulation for administration to a subject that provides a therapeutic benefit (e.g., are therapeutically effective).

10 [00623] In some embodiments, the microbial consortium is co-cultured under conditions that synergistically enhance growth and proliferation of the core community microbial strains with the keystone microbial strains.

[00624] Although a single bioreactor is used for co-culturing the core community and keystone strains in several embodiments and has advantages, multiple bioreactors may be
15 used in one embodiment.

Method for treating

[00625] Methods for preventing or treating a medical disorder, disease or pathology associated with dysbiosis or a loss of gut microbial function are within the scope of the invention. In an embodiment, the invention provides a method for treating a medical disorder,
20 disease or pathology associated with dysbiosis, wherein said method comprises the administration to a patient in need thereof a therapeutically effective amount of the composition as described in the first aspect of this invention.

[00626] In a further embodiment, the dosage form is administered at an amount to treat, or at least partially treat a medical disorder or disease associated with dysbiosis or a loss of
25 gut microbial function.

[00627] A subject that can be treated with the invention will include humans as well as other mammals and animals.

[00628] The effect of the administered therapeutic composition can be monitored by standard diagnostic procedures.

30 [00629] Methods of the invention can be used to treat or prevent a dysbiosis of the gastrointestinal tract in a subject. "Dysbiosis" in the context of the present invention refers to a state in which the normal diversity and/or function of the microbiota or microbiome, in particular the human gastrointestinal microbiota, is disrupted. Any disruption from the normal state of the microbiota in a healthy individual can be considered a dysbiosis, even if the
35 dysbiosis does not result in a detectable decrease in health in the individual. In an embodiment, the dysbiosis may be associated with one or more pathological symptoms. For example, "dysbiosis" may refer to a decrease in the microbial diversity of the microbiota. In

addition, or alternatively, "dysbiosis" may refer to an increase in the abundance of one or more bacteria, e.g. one or more pathogenic bacteria, in the microbiota of an individual relative to the abundance of said bacterium or bacteria in the microbiota of a healthy individual, i.e. an individual without a dysbiosis. The pathogenic bacteria present during dysbiosis are often

5 Proteobacteria and resistant to one or more antibiotics. Examples of Proteobacteria include *Escherichia*, *Salmonella*, *Campylobacter*, *Vibrio*, *Helicobacter*, and *Yersinia* species. In some embodiments, administration of the compositions described herein synergistically improve dysbiosis, for example, by improving or restoring beneficial microbiome organisms, reducing growth of harmful microorganisms, or improving or enhancing overall microbial diversity.

10 [00630] The dysbiosis may be a dysbiosis associated with an enteric bacterial infection or dominant strain, such as an infection or proliferation within the gastrointestinal tract of a pathogenic bacterium. Many bacteria capable of causing infections of the gastrointestinal tract or dysbiosis in humans are known and include: gram-positive bacteria, and gram-negative bacteria. The pathogenic bacterium is a pathogenic species of the genus *Blautia*, *Clostridium*,

15 *Escherichia*, *Enterococcus*, *Klebsiella*, *Enterobacter*, *Hungatella*, *Proteus*, *Salmonella*, *Shigella*, *Staphylococcus*, *Vibrio*, *Aeromonas*, *Campylobacter*, *Plesiomonas*, *Bacillus*, *Helicobacter*, *Listeria*, *Veillonella* or *Yersinia*. Examples of such pathogenic bacteria include *Clostridium difficile*, *Clostridium perfringens*, *Clostridium botulinum*, *Escherichia coli*, *Salmonella typhi*, *Staphylococcus aureus*, *Vibrio cholerae*, *Vibrio parahaemolyticus*, *Vibrio vulnificus*, *Campylobacter fetus*, *Campylobacter jejuni*, *Aeromonas hydrophila*, *Plesiomonas shigelloides*, *Bacillus cereus*, *Helicobacter pylori*, *Listeria monocytogenes*, and *Yersinia enterocolitica*. For example, the pathogenic bacterium is a pathogenic species of the genus *Blautia*, *Bacteroides*, *Bifidobacterium*, *Clostridium*, *Escherichia*, *Enterobacter*, *Enterococcus*,

20 *Hungatella*, *Klebsiella*, *Parabacteroides*, *Phocaeicola*, and *Veillonella*. For example, the pathogenic bacterium is *Clostridium difficile*, *Enterococcus avium*, *Enterococcus gilvus* or *Escherichia coli*. *Escherichia*, *Hungatella*, *Klebsiella*, *Ligilactobacillus*, *Mediterraneibacter*, *Parabacteroides*, *Prevotella*, *Veillonella*,

[00631] Methods of the invention can be used to reduce or prevent gastrointestinal tract mucosal inflammation in a subject using compositions of the invention.

30 [00632] In an embodiment, the subject has, or is susceptible to having, an inflammatory bowel disease (IBD), periodontal disease, chronic fatigue syndrome, obesity, diabetes mellitus, cardiovascular disease, acne vulgaris, cancer, bacterial vaginosis, or other disease associated with or resulting from dysbiosis. In some embodiments, the subject has or is susceptible to having IBD, such as Crohn's disease, ulcerative colitis and pouchitis.

35 [00633] As used herein, the term "inflammatory bowel diseases (IBD)" has its general meaning in the art and refers to a group of inflammatory diseases of the colon and small intestine such as revised in the World Health Organisation Classification K20-K93 (ICD-10)

- such as Crohn disease (such as granulomatous enteritis; Crohn disease of small intestine; Crohn disease of large intestine; granulomatous and regional Colitis; Crohn disease of colon, large bowel and rectum; Crohn disease of both small and large intestine), Ulcerative colitis (such as Ulcerative (chronic) pancolitis; backwash ileitis; Ulcerative (chronic) proctitis;
- 5 Ulcerative (chronic) rectosigmoiditis; Inflammatory polyps; Left sided colitis; left hemicolitis) and noninfective gastroenteritis and colitis (Gastroenteritis and colitis due to radiation; Toxic gastroenteritis and colitis; Allergic and dietetic gastroenteritis and colitis; Food hypersensitivity gastroenteritis or colitis; indeterminate colitis; specified noninfective gastroenteritis and colitis such as Collagenous colitis; Eosinophilic gastritis or gastroenteritis; Lymphocytic colitis
- 10 Microscopic colitis (collagenous colitis or lymphocytic colitis); Noninfective gastroenteritis and colitis such as Diarrhoea; Enteritis; Ileitis; Jejunitis; Sigmoiditis) and postprocedural disorders of digestive system such as pouchitis. In an embodiment, the IBD is paediatric IBD.
- [00634] In an embodiment, the subject has, or is susceptible to having, checkpoint inhibitor colitis, liver disorders, including, for example, primary sclerosing cholangitis, primary biliary
- 15 cirrhosis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, or hepatic encephalopathy, metabolic disorders, including, for example, obesity, insulin resistance, or type 2 diabetes, oncology indications, including, for example, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer, breast cancer, lung cancer, testicular cancer, or sarcoma, cardiovascular
- 20 disorders, including, for example, dyslipidaemia, atherosclerotic heart disease, or hypertension, immunological diseases, including, for example, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis, psoriasis, systemic lupus erythematosus, or Sjogren's disease, allergic and atopic disorders, including, for example, food allergy, anaphylaxis, atopic dermatitis, or atopic rhinitis or sinusitis, infectious diseases, including, for example,
- 25 clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory infections, or sepsis, neurological disorders, including for example, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, and/or schizophrenia.
- [00635] Administration to humans includes administration by a medical professional and
- 30 self-administration. In general, in order to achieve a health benefit, multiple doses of the composition are administered, for example daily for a period of at least one week, at least two weeks, at least three weeks, at least six weeks, at least nine weeks, or at least twelve weeks. In one embodiment, the compositions can be administered for the remaining duration of a subject's life.
- 35 [00636] In some embodiments, the formulations described herein are administered to a subject before, along with and/or after another therapy to increase the efficacy of or reduce side effects from the additional therapy. For example, the formulations may be used to reduce

side effects of other pharmaceuticals (including e.g., biologics) by, for example, reducing the dose or course needed for such pharmaceutical, reducing an inflammatory response, reducing nausea or other undesired effect of such pharmaceutical post administration. The formulations may also be used to enhance the beneficial effects of other pharmaceuticals by, for example, increasing absorption and/or availability of such pharmaceutical post administration. In some embodiments, synergistic effects are achieved using the formulations described herein and other therapies such as pharmaceuticals.

Device

[00637] Devices are within the scope of the invention. In an embodiment, the invention provides a device, wherein the device comprises: (1) the composition as described in the first aspect of this invention; and (2) an applicator, container or material.

Use of a composition in the manufacture of a medicament

[00638] Uses are within the scope of this invention. In an embodiment, the invention provides the use of a composition in the manufacture of a medicament for treating or preventing a medical disorder associated with a dysbiosis or a loss of gut microbial function.

Method for Stabilising

[00639] Methods for stabilizing the compositions of the invention are within the scope of the invention.

[00640] In a further embodiment, the said method protects the compositions of the invention against degradation.

[00641] In yet a further embodiment, the compositions of the invention retain its effective biological activity for a period selected from the group consisting of; greater than 24 hours; greater than 36 hours; greater than 48 hours.

[00642] The addition of approved pharmaceutical excipients to stabilize the compositions of the invention solutions in several embodiments is preferred from a safety standpoint, as the simpler methodology may produce a less variable outcome and the choice of excipient can be limited to those with Generally Regarded as Safe (GRAS) status. Embodiments described herein may use the simpler or different methodology. Excipients for the stabilization of protein solutions can be classified into four broad categories, and one or more categories may be included in the formulations described herein: salts, sugars, polymers or protein/amino acids, based on their chemical properties and mechanism of action. Salts (e.g. chlorides, nitrates) stabilize the tertiary structure of proteins by shielding charges through ionic interactions. Sugars (e.g. glycerol, sorbitol, fructose, trehalose) increase the surface tension and viscosity of the solution to prevent protein aggregation. Similarly, polymers (e.g. polyethylene glycol, cellulose derivatives) stabilize the protein tertiary structure by increasing the viscosity of the solution to prevent protein aggregation and intra- and inter-molecular electrostatic interactions

between amino acids in the protein. Proteins (e.g. human serum albumin) are able to stabilize the structure of other proteins through ionic, electrostatic and hydrophobic interactions. Similarly, small amino acids with no net charge, such as alanine and glycine, stabilize proteins through the formation of weak electrostatic interactions.

- 5 [00643] As discussed above, the medicaments of the present invention may include one or more pharmaceutically acceptable carriers. The use of such media and agents for the manufacture of medicaments is well known in the art. Except insofar as any conventional media or agent is incompatible with the pharmaceutically acceptable material, use thereof in the manufacture of a pharmaceutical composition according to the invention is contemplated.
- 10 Pharmaceutical acceptable carriers according to several embodiments of the invention may include one or more of the following examples:
- a. surfactants and polymers, including, however not limited to polyethylene glycol (PEG), polyvinylpyrrolidone, polyvinylalcohol, crospovidone, polyvinylpyrrolidone-polyvinylacrylate copolymer, cellulose derivatives, HPMC, hydroxypropyl cellulose,
 - 15 carboxymethylethyl cellulose, hydroxypropylmethyl cellulose phthalate, polyacrylates and polymethacrylates, urea, sugars, polyols, and their polymers, emulsifiers, sugar gum, starch, organic acids and their salts, vinyl pyrrolidone and vinyl acetate; and/or
 - b. binding agents such as various celluloses and cross-linked polyvinylpyrrolidone,
 - 20 microcrystalline cellulose; and/or (3) filling agents such as lactose monohydrate, lactose anhydrous, microcrystalline cellulose and various starches; and/or
 - c. filling agents such as lactose monohydrate, lactose anhydrous, mannitol, microcrystalline cellulose and various starches; and/or
 - d. lubricating agents such as agents that act on the increased ability of the dosage
 - 25 form to be ejected from the packaging cavity, and/or
 - e. sweeteners such as any natural or artificial sweetener including sucrose, xylitol, sodium saccharin, cyclamate, aspartame, and acesulfame K; and/or
 - f. flavoring agents; and/or
 - g. preservatives such as potassium sorbate, methylparaben, propylparaben, benzoic acid and its salts, other esters of parahydroxybenzoic acid such as butylparaben,
 - 30 alcohols such as ethyl or benzyl alcohol, phenolic chemicals such as phenol, or quarternary compounds such as benzalkonium chloride; and/or
 - h. buffers; and/or
 - i. diluents such as pharmaceutically acceptable inert fillers, such as microcrystalline cellulose, lactose, dibasic calcium phosphate, saccharides, and/or mixtures of any
 - 35 of the foregoing; and/or
 - j. absorption enhancer such as glyceryl trinitrate; and/or

k. other pharmaceutically acceptable excipients.

[00644] Medicaments of the invention suitable for use in animals and in particular in human beings typically must be sterile and stable under the conditions of manufacture and storage.

Methods for Detection

5 [00645] A strain of the invention can be detected using a wide variety of known techniques. Conveniently the strain is detected using quantifiable methods, such as flow cytometry or microscopy, and a nucleic acid-based detection system, such as Propidium Monoazide-based PCR Assay (PMA) or quantitative PCR (qPCR).

10 [00646] In an embodiment, nucleic acid sequencing is used. Illustrative non-limiting examples of nucleic acid sequencing techniques include, but are not limited to, chain terminator (Sanger) sequencing and dye terminator sequencing. In some embodiments, the technology provided herein finds use in a Second Generation (a.k.a. Next Generation or Next-Gen), Third Generation (a.k.a. Next-Next-Gen), or Fourth Generation (a.k.a. N3-Gen) sequencing technology including, but not limited to, pyrosequencing, sequencing-by-ligation, 15 single molecule sequencing, sequence-by-synthesis (SBS), massive parallel clonal, massive parallel single molecule SBS, massive parallel single molecule real-time, massive parallel single molecule real-time nanopore technology.

[00647] In some embodiments, hybridization is employed in a detection method of the invention. Illustrative non-limiting examples of nucleic acid hybridization techniques include, 20 but are not limited to, *in situ* hybridization (ISH), microarray, and Southern or Northern blot. In one embodiment, a FISH assay is used. In other embodiments, nucleic acid amplification is used. Nucleic acids may be amplified prior to or simultaneous with detection. Conducting one or more amplification reactions may comprise one or more PCR-based amplifications, non-PCR based amplifications, or a combination thereof. Illustrative non-limiting examples of 25 nucleic acid amplification techniques include, but are not limited to, polymerase chain reaction (PCR), reverse transcription polymerase chain reaction (RT-PCR), nested PCR, linear amplification, multiple displacement amplification (MDA), real-time SDA, rolling circle amplification, circle-to-circle amplification transcription-mediated amplification (TMA), ligase chain reaction (LCR), strand displacement amplification (SDA), and nucleic acid sequence 30 based amplification (NASBA). Those of ordinary skill in the art will recognize that certain amplification techniques (e.g., PCR) require that RNA be reversed transcribed to DNA prior to amplification (e.g., RT-PCR), whereas other amplification techniques directly amplify RNA (e.g., TMA and NASBA).

[00648] Non-amplified or amplified nucleic acids can be detected by any conventional 35 means. For example, the nucleic acids can be detected by hybridization with a detectably labelled probe and measurement of the resulting hybrids. In another example, the nucleic

acids are detected by sequencing. Illustrative non-limiting examples of detection methods are described herein.

[00649] Evaluation of an amplification process in "real-time" involves determining the amount of amplicon in the reaction mixture either continuously or periodically during the amplification reaction and using the determined values to calculate the amount of target sequence initially present in the sample. A variety of methods for determining the amount of initial target sequence present in a sample based on real-time amplification are well known in the art. These include methods disclosed in U.S. Pat. Nos. 6,303,305 and 6,541,205. Another method for determining the quantity of target sequence initially present in a sample, but which is not based on a real-time amplification, is disclosed in U.S. Pat. No. 5,710,029.

[00650] Amplification products may be detected in real-time through the use of various self-hybridizing probes, most of which have a stem-loop structure. Such self-hybridizing probes are labeled so that they emit differently detectable signals, depending on whether the probes are in a self-hybridized state or an altered state through hybridization to a target sequence. By way of non-limiting example, "molecular torches" are a type of self-hybridizing probe that includes distinct regions of self-complementarity (referred to as "the target binding domain" and "the target closing domain") which are connected by a joining region (e.g., non-nucleotide linker) and which hybridize to each other under predetermined hybridization assay conditions. In an embodiment, molecular torches contain single-stranded base regions in the target binding domain that are from 1 to about 20 bases in length and are accessible for hybridization to a target sequence present in an amplification reaction under strand displacement conditions. Under strand displacement conditions, hybridization of the two complementary regions, which may be fully or partially complementary, of the molecular torch is favored, except in the presence of the target sequence, which will bind to the single-stranded region present in the target binding domain and displace all or a portion of the target closing domain. The target binding domain and the target closing domain of a molecular torch include a detectable label or a pair of interacting labels (e.g., luminescent/quencher) positioned so that a different signal is produced when the molecular torch is self-hybridized than when the molecular torch is hybridized to the target sequence, thereby permitting detection of probe:target duplexes in a test sample in the presence of unhybridized molecular torches. Molecular torches and a variety of types of interacting label pairs are disclosed in U.S. Pat. No. 6,534,274, herein incorporated by reference in its entirety.

[00651] Amplification products may be detected in real time through a combination of primers specific to the region of interest and a non-specific fluorescent DNA binding dye. Such primers are designed so that they specifically target a region unique to the microbe of interest, leading to amplification of only the designed target. The primer design incorporates two individual primers that complementarily bind up and downstream of the targeted DNA site.

During amplification the primers will bind up and downstream of the target of interest, generate an additional copy through polymerase chain reaction and the DNA binding dye is incorporated into the newly generated amplicon. Post amplification, the DNA binding dye is excited via a specific wavelength of light and the emission at a different wavelength is measured. Binding of the fluorescent DNA binding dye to the exponentially increasing amplicon of interest can be correlated with standards of known concentration through linear regression to determine the original copy number of the target region amplified. The methodology of using DNA binding dyes is disclosed in U.S. Pat. No. 6,174,670. The specific use of the fluorescent DNA binding dye SYBR green I is disclosed in U.S. Pat. No. 5,338,671 and 5,587,287.

[00652] Another example of a detection probe having self-complementarity is a "molecular beacon." Molecular beacons include nucleic acid molecules having a target complementary sequence, an affinity pair (or nucleic acid arms) holding the probe in a closed conformation in the absence of a target sequence present in an amplification reaction, and a label pair that interacts when the probe is in a closed conformation. Hybridization of the target sequence and the target complementary sequence separates the members of the affinity pair, thereby shifting the probe to an open conformation. The shift to the open conformation is detectable due to reduced interaction of the label pair, which may be, for example, a fluorophore and a quencher (e.g., DABCYL and 25 EDANS). Molecular beacons are disclosed in U.S. Pat. Nos. 5,925,517 and 6,150,097.

[00653] In an embodiment, the method includes quantifying the amount of strain present in the sample.

[00654] The present invention will now be described with reference to the following non-limiting Examples. The description of the Examples is in no way limiting on the preceding paragraphs of this specification, however, is provided for exemplification of the methods and compositions of the invention.

Examples

[00655] It will be apparent to persons skilled in the milling and pharmaceutical arts that numerous enhancements and modifications can be made to the above-described processes without departing from the basic inventive concepts. For example, in some applications the biologically active material may be pretreated and supplied to the process in the pretreated form. All such modifications and enhancements are considered to be within the scope of the present invention, the nature of which is to be determined from the foregoing description and the appended claims. Furthermore, the following Examples are provided for illustrative purposes only, and are not intended to limit the scope of the processes or compositions of the invention. In several embodiments, one or more (e.g., 1-5, 5-10, etc.) of the phyla, genera, species or strains identified in the Examples below are expressly excluded from the co-culture,

the formulation to be administered, or both. One reason for such exclusion may be that such microbe has a deleterious or otherwise undesired effect (e.g., in a particular disease). In some embodiments, 50-95% (50-60, 60-70, 70-80, 80-95% and overlapping ranges therein), of the microbes are included, with the remaining 5-50% excluded.

- 5 [00656] In several embodiments, the compositions and formulations described in the Examples below treat or prevent ulcerative colitis, inflammatory bowel disease, Crohn's disease, checkpoint inhibitor colitis, as well as other gastrointestinal diseases and symptoms, liver disorders, including, for example, primary sclerosing cholangitis, primary biliary cirrhosis, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, or hepatic
- 10 encephalopathy, metabolic disorders, including, for example, obesity, insulin resistance, or type 2 diabetes, oncology indications, including, for example, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer, breast cancer, lung cancer, testicular cancer, or sarcoma, cardiovascular disorders, including, for example, dyslipidaemia, atherosclerotic heart disease, or hypertension, immunological
- 15 diseases, including, for example, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis, psoriasis, systemic lupus erythematosus, or Sjogren's disease, allergic and atopic disorders, including, for example, food allergy, anaphylaxis, atopic dermatitis, or atopic rhinitis or sinusitis, infectious diseases, including, for example, clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections,
- 20 respiratory infections, or sepsis, neurological disorders, including for example, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, and/or schizophrenia

A EXAMPLE 1 – THE BB265 COMPLEX COMMUNITY LIVE BIOTHERAPEUTIC PRODUCT: AN OVERVIEW

25 A.1 STUDY AIM

[00657] The aim of the therapy, in this embodiment, is to induce and maintain remission by targeting dysbiosis to reduce sulfide levels in the colon of patients with ulcerative colitis

A.2 MATERIALS, METHODS AND RESULTS

A.2.1 THE COMPOSITIONS OF THIS INVENTION, INCLUDING THE BB265

- 30 [00658] The compositions of this invention, including the BB265 live biotherapeutic product, targets the proximal cause of colonocyte barrier disruption that results in immune activation in ulcerative colitis.

A.2.2 SUMMARY OF THE METABOLIC LESION INCITING INFLAMMATION IN ULCERATIVE COLITIS

- 35 [00659] Ulcerative colitis results from an energy deficiency state in colonocytes induced by sulfide and nitric oxide, which depletes Coenzyme A (CoA) and inhibits β -oxidation of butyrate. Without energy in the form of adenosine triphosphate (ATP), colonocytes are unable

to maintain the normal mucosal barrier that separates the luminal contents of the colon from the mucosal immune system. The loss of the mucus and tight junction barrier allows for translocation of microbes into the bowel wall, whereby a natural killer T-cell driven IL-13 and IL-5-dependent, TH2-mediated, immune response is initiated. Refer to Figure 1 for a diagrammatical representation of the processes that lead to ulcerative colitis induced by high levels of sulfide and nitric oxide.

A.2.3 REDUCING LUMINAL SULFIDE BY 'TURNING OFF THE TAP' FOR PRODUCTION

[00660] Reducing luminal sulfide can be accomplished by "turning off the tap" of production or by removing sulfide from the colon. Each of these mechanisms can be targeted using a live biotherapeutic product.

[00661] *Microbial competition for metabolic substrates*

[00662] Sulfidogenic microbiota use specific substrates for metabolism. As an example, sulphate reducing bacteria (SRB) preferentially use volatile fatty acids (acetate, propionate, butyrate), organic acids (lactate, valerate, succinate, pyruvate), amino acids (alanine, glutamate, serine) and ethanol as electron donors in cellular respiration. Non sulfidogenic microbiota which utilize these substrates compete with sulfidogenic microbiota; such competition would limit the growth of sulfidogenic microbiota and lessen the production of luminal sulfide. Microbiota also compete with sulfidogenic organisms for electron acceptors. Please refer to Figure 2 that shows a diagrammatic representation of hydrogen uptake by acetogens and methanogens that reduce SRB sulfide production. Competition for metabolic substrates necessary for the growth and metabolism of sulfidogenic microbiota offers a therapeutic target to reduce endogenous sulfide in the colon.

[00663] *Reduced sulfur substrate release in the colon*

[00664] Sulfidogenic microbiota require sulfur substrates (such as inorganic sulfate, sulfite, thiosulfate, and tetrathionate, and organic cysteine, methionine, and taurine) to produce sulfide. In the colon, these substrates come from but are not limited to dietary sulfur sources, such as meat and cruciferous vegetables, host mucin, bile acids, and endogenous proteins. Though sulfur is ubiquitously present in the colon, much of it is bound in complex molecules inaccessible to sulfidogenic microbiota. For sulfidogenic microbiota to access sulfur to produce sulfide, other organisms are often required to biotransform these compounds into accessible forms.

[00665] Colonic protein fermentation by bacteria is a major source of microbial sulfide. Low protein, high resistant starch diets have been demonstrated to induce remission in ulcerative colitis. In a published study where 28 patients with ulcerative colitis were given a diet high in fiber and low in sulfated protein that was designed to reduce sulfide production in the colon, a clinical response (defined as a reduction in partial Mayo ≥ 2 , in 13/28 (46%) ($p < 0.0001$)) and endoscopic improvement (defined as a reduction in Mayo endoscopic sub score ≥ 1 , in 10/28

(36%) ($p=0.02$)) was observed (Day AS, Yao CK, Costello SP, Ruszkiewicz A, Andrews JM, Gibson PR, Bryant RV. Therapeutic Potential of the 4 Strategies to Sulfide-Reduction (4-SURE) Diet in Adults with Mild to Moderately Active Ulcerative Colitis: An Open-Label Feasibility Study. J Nutr. 2022 Jul 6;152(7):1690-1701). Histological improvement occurred in 43% and median fecal inflammatory marker levels of fecal calprotectin reduced by 131ug/g ($p=0.02$) at week 8.

[00666] *Removing sulfide from the colon*

[00667] Bacterial species can consume sulfide thereby reducing colonic sulfide levels.

A.2.4 PHASE 1B/2A HUMAN CLINICAL TRIAL

[00668] The final BB265 drug product will initially be evaluated in a phase 1b/2a human clinical trial. The final BB265 drug product will contain the enriched bacterial strains which target the underlying cause of the metabolic lesions in ulcerative colitis, further supported by a community comprising the most prevalent bacteria in healthy humans globally in addition to known keystone species that sustain important synergistic links in the colonic ecosystem. The phase 1b/2a human trial will primarily assess clinical outcomes (endoscopy, histology, disease scores, biomarkers), but will also be conducted to observe changes related to the two mechanisms of action incorporated into BB265.

B EXAMPLE 2 – THE DISCOVERY AND DEVELOPMENT OF BB265 AS A COMPLEX COMMUNITY LIVE BIOTHERAPEUTIC PRODUCT TO ADDRESS METABOLIC LESIONS IN ULCERATIVE COLITIS

B.1 STUDY AIM

[00669] To develop BB265 (as one embodiment of the invention) as a complex community live biotherapeutic product to address metabolic lesions in ulcerative colitis.

B.2 MATERIALS, METHODS AND RESULTS

B.2.1 BACKGROUND

[00670] *Summary of the BB265 live biotherapeutic product*

[00671] BB265 is an encapsulated bioreactor-derived microbial consortium comprising specific microbial strains that reduce colonic sulfide which drives the onset of the chemical lesion seen in ulcerative colitis and can optionally include a collection of the globally most prevalent taxa or isolates (global core microbiome), taxa or isolates which best discriminate between health and ulcerative colitis (Leads), keystone taxa or isolates (literature and informatic based), and taxa or isolates to add additional phylogenetic and functional diversity. The BB265 drug discovery process detailing lead selection and validation prior to consortium validation in a phase 1B/2A trial is presented in Figure 4.

[00672] *Microbial complexity as a therapeutic modality*

[00673] Current treatments for ulcerative colitis are hampered by incomplete efficacy and have the potential for unacceptable side effects including allergy, intolerance, serious infection, and malignancy due to long-term immunosuppression. The inventors posit that the current immune-targeted therapies for UC are inadequate because they do not address the primary drivers of the disease, only the secondary immune response.

[00674] The inventors are developing a defined microbial therapy to address the primary metabolic lesion that instigates the inflammatory process in ulcerative colitis, driven by excess microbial production of sulfide. This therapy, BB265, consists of a complex consortium of phylogenetically diverse bacteria derived from screened healthy donors that aims to: (1) restore those microbes lost in ulcerative colitis, (2) restore those functions lost in ulcerative colitis, and (3) target excess sulfide in ulcerative colitis.

[00675] This therapeutic approach acknowledges the intricate and multifaceted mechanisms governing health and disease, recognizing that microbial diversity is a critical feature of a robust microbiome. It accounts for the ecological dynamics within the human-microbe relationship, which have co-evolved over hundreds of thousands of years. By developing complex consortia, such therapies can more closely replicate natural microbial ecosystems, target multiple known and unknown functional pathways, and foster greater resilience within the microbial community. This comprehensive approach to therapy is designed to restore the ecological balance and adaptability required for optimal health outcomes.

B.2.2 IDENTIFYING TAXA CONSIDERED FOR INCLUSION IN BB265

[00676] *Global prevalence analysis*

[00677] The widespread presence of microbial species commonly found in healthy human faecal microbiomes, regardless of differences in diet, lifestyle, and environmental conditions across various populations, indicates their importance as integral components of the human gut microbiota. Global prevalence of such taxa suggests they have co-evolved with humans, forming a mutualistic relationship necessary for human health. To this effect, the inventors embarked to define this 'core' community structure for inclusion in BB265. A global metagenomic analysis of 882 publicly available metagenomes from healthy individuals from the European Nucleotide Archive (ENA) (Leinonen R, Akhtar R, Birney E, Bower L, Cerdeno-Tárraga A, Cheng Y, et al. The European Nucleotide Archive. Nucleic Acids Res. 2011 Jan;39(Database issue):D28-31) was performed to identify the most prevalent species shared across different geographical regions (Africa, South America, North America, Europe and Asia-Pacific). Microbial species comprising greater than 0.001% of total reads and present within > 90% of samples across all geographies were considered as 'core' species for inclusion in BB265.

[00678] *Identification of targets and leads*

[00679] The inventors aimed to define taxa that discern between ulcerative colitis and non-inflammatory bowel disease (non-IBD) controls from a diverse array of publicly available fecal metagenomes, with the purpose to identify candidate therapeutic taxa (Leads) and to exclude taxa for inclusion in BB265 associated with the disease state (Targets).

- 5 [00680] To this effect, the inventors used differential abundance analyses to identify Lead and Target taxa which best discriminate between health (281) and ulcerative colitis (283) metagenomes downloaded from the ENA (Leinonen R, Akhtar R, Birney E, Bower L, Cerdeno-Tárraga A, Cheng Y, et al. The European Nucleotide Archive. Nucleic Acids Res. 2011 Jan;39(Database issue):D28-31). Lead and Target taxa were determined by consensus analysis between the tools ALDEx2 v1.29.1 (215), ANCOM-BC v1.6.4 (216), and Selbal v0.1.0 (217). Consensus taxa identified as associated with ulcerative colitis and anticorrelated with health were considered Targets and considered for removal from BB265, whereas Leads, which showed a polar trend, were considered for inclusion.

[00681] *Identification of keystone taxa*

- 15 [00682] In addition to common and highly abundant microbial species, and those that best discriminate between health and disease, the inventors also considered taxa that may be less abundant but functionally critical to the microbial ecosystem. These keystone species have outsized importance on the ecosystem often through uniquely held functions or functions that have limited redundancy within the system. Here, keystone species are also those linked with clinical efficacy, identified by their presence as a predictive factor for whole community recovery post-antibiotic treatment, as well as those identified as 'hub' taxa informatically.

- [00683] Literature searches were performed to identify these important microbes. The researched literature detailed a meta-analysis of post-antibiotic recovery, revealing the presence of organisms that facilitate recovery of the gut microbial ecosystem following broad antibiotic loss thus identifying them as key players in recovery (Chng KR, Ghosh TS, Tan YH, Nandi T, Lee IR, Ng AHQ, et al. Metagenome-wide association analysis identifies microbial determinants of post-antibiotic ecological recovery in the gut. Nature Ecology & Evolution. 2020 Jul 6;4(9):1256–64). These keystone species were considered for inclusion in BB265.

- [00684] The inventors employed network analysis as a strategic tool to pinpoint hub taxa. Using SpiecEasi Kurtz ZD, Müller CL, Miraldi ER, Littman DR, Blaser MJ, Bonneau RA. Sparse and compositionally robust inference of microbial ecological networks. PLoS Comput Biol. 2015 May;11(5):e1004226) and NetCOMI Peschel S, Müller CL, von Mutius E, Boulesteix A-L, Depner M. NetCoMi: network construction and comparison for microbiome data in R. Brief Bioinform [Internet]. 2021 Jul 20;22(4). Available from: <http://dx.doi.org/10.1093/bib/bbaa290>), the inventors identified taxa with highest degrees of centrality, suggesting these taxa may contribute more to community functioning and stability than others; these taxa were considered for inclusion in the BB265.

B.2.3 SULFIDE PHENOTYPING

[00685] The inventors have developed unique phenotypic assays that identify sulfide producing and consuming (assimilating) microbial isolates. Isolates considered for inclusion in BB265 with the ability to consume sulfide were considered candidate therapeutic organisms, whereas those identified with a phenotype for sulfide production were optionally excluded from the consortium. Isolates identified as putative H₂ consuming organisms via taxonomic and genomic means, such as methanogenic archaea and homoacetogenic bacteria, were also considered candidate therapeutic organisms.

[00686] A total of 21,728 microbial isolates were screened for a phenotype of sulfide production from the inventors microbial culture collection. Where possible, the inventors selected isolates for inclusion in the BB265 consortium that showed a negative phenotype for sulfide production. However, where this could not occur, rather than dismissing these isolates outright, the inventors considered their potential role in ulcerative colitis management due to their prevalence in healthy individuals, keystone characteristics and anti-correlation with ulcerative colitis datasets (i.e., Leads).

[00687] The inventors identified 155 isolates with a net sulfide consumption phenotype compared to the negative control (Figure 5), 89 of which demonstrated statistically significant sulfide consumption (Figure 8A and 8B). These isolates were considered as candidate therapeutic organisms for inclusion in BB265.

B.2.4 ISOLATE SCREENING FOR ANTIBIOTIC RESISTANCE, PHAGE ELEMENTS, AND VIRULENCE FACTORS

[00688] As the consortium is to be used as a microbial therapy, safety is paramount. Screening microbial isolates intended for use as a microbial therapy for antibiotic resistance, phage elements, and virulence factors is vital to ensure patient safety and effectiveness.

[00689] To ensure each isolate meets the regulatory safety profile, the following were considered:

- a. only isolates sourced from healthy individuals with complete passage history were included.
- b. all isolates were phenotypically screened for antibiotic-resistance and phage presence, genomically screened for anti-microbial resistance, virulence and phage elements, and phenotypically screened for detrimental products, e.g., sulfide production.
- c. pathogen searches were performed via literature reviews to ensure known pathogens or species linked with disease were removed.
- d. redundancy was considered, with at least three strains from the same species assessed to overcome knockout from above processes.

- e. redundant strains were removed, with preference given to isolates with lowest risk profile from above screening.

B.2.5 SELECTION OF ISOLATES COMPRISING BB265

[00690] In one embodiment, the selection process for the BB25 consortium aimed at treating ulcerative colitis involved a meticulous approach integrating globally prevalent taxa, literature and informatic based keystones and phenotypic data to maximize functional diversity and bolster the mechanism of action of sulfide reduction. In total, 143 isolates were selected to comprise the consortium. The V3-V4 16S sequences for the 143 isolates are presented in Figure 6 (SEQ ID NOs 1 to 143) and the full length 16S sequences are presented in Figure 7 (SEQ ID NOs 144 to 286). The isolate lineages are presented in Figure 9. The 143 isolates are made up of members comprising the Actinomycetota, Bacillota, Bacteroidota, and Verrucomicrobiota phyla (Figure 10). This selection strategy aims to create a robust microbial ecosystem that mirrors natural microbiomes while targeting specific mechanisms implicated in ulcerative colitis.

[00691] The final complex consortium, including the co-cultured microbial species or the formulations of microbial species, consisted of a list of 274 species, of which, via extensive microbial culturing from healthy donor fecal samples, followed by phenotypic and genomic screening, resulted in 143 isolates, comprising 116 species, being in the final complex consortium according to one embodiment. In other embodiments, the final complex consortium will consist essentially of 25-300 species (e.g., 25-50, 50-75, 75-100, 100-200, 200-300, and overlapping ranges therein) and/or 25-200 isolates (e.g., 25-50, 50-75, 75-100, 100-200, and overlapping ranges therein).

B.2.6 CLASSIFICATION OF THE BB265 CONSORTIUM

[00692] Below we present lists of taxa by taxonomic rank.

[00693] **BY PHYLUM**

[00694] **Table 17 - By phylum.**

[00695] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial phyla as set forth in Table 1. In alternative embodiments, any one or more (e.g., 1-5, 5-10, etc.) of the phyla, genera, species or strains identified in the tables provided herein are expressly excluded from the co-culture, the formulation to be administered, or both. One reason for such exclusion may be that such microbe has a deleterious effect on a particular disease state. In some embodiments, 50-95% (50-60, 60-70, 70-80, 80-95% and overlapping ranges therein), of the microbes are included, with the remaining 5-50% excluded.

Acidobacteriota (NCBI taxid: 57723)	Dictyoglomota (NCBI taxid: 68297)
Actinomycetota (NCBI taxid: 201174)	Elusimicrobiota (NCBI taxid: 74152)

Aquificota (NCBI taxid: 200783)	Euryarchaeota (NCBI taxid: 28890)
Armatimonadota (NCBI taxid: 67819)	Fibrobacterota (NCBI taxid: 65842)
Atribacterota (NCBI taxid: 67818)	Fusobacteriota (NCBI taxid: 32066)
Bacillota (NCBI taxid: 1239)	Gemmatimonadota (NCBI taxid: 142182)
Bacteria candidate phyla (NCBI taxid: 1783234)	Ignavibacteriota (NCBI taxid: 1134404)
Bacteroidota (NCBI taxid: 976)	Kiritimatiellota (NCBI taxid: 134625)
Balneolota (NCBI taxid: 1936987)	Lentisphaerota (NCBI taxid: 256845)
Bdellovibrionota (NCBI taxid: 3018035)	Mycoplasmata (NCBI taxid: 544448)
Caldisericota (NCBI taxid: 67814)	Myxococcota (NCBI taxid: 2818505)
Calditrichota (NCBI taxid: 1930617)	Nitrososphaerota (NCBI taxid: 651137)
Campylobacterota (NCBI taxid: 29547)	Nitrospinota (NCBI taxid: 1293497)
Candidatus Absconditabacteria (NCBI taxid: 221235)	Nitrospirota (NCBI taxid: 40117)
Candidatus Cloacimonadota (NCBI taxid: 456828)	Planctomycetota (NCBI taxid: 203682)
Candidatus Micrarchaeota (NCBI taxid: 1801631)	Pseudomonodota (NCBI taxid: 1224)
Candidatus Nanohalarchaeota (NCBI taxid: 1462430)	Rhodothermota (NCBI taxid: 1853220)
Candidatus Saccharibacteria (NCBI taxid: 95818)	Spirochaetota (NCBI taxid: 203691)
Chlamydiota (NCBI taxid: 204428)	Synergistota (NCBI taxid: 508458)
Chlorobiota (NCBI taxid: 1090)	Thermodesulfobacteriota (NCBI taxid: 200940)
Chloroflexota (NCBI taxid: 200795)	Thermodesulfobiota (NCBI taxid: 3002442)
Chrysiogenota (NCBI taxid: 200938)	Thermomicrobiota (NCBI taxid: 3027942)
Coprothermobacterota (NCBI taxid: 2138240)	Thermoproteota (NCBI taxid: 28889)
Cyanobacteriota (NCBI taxid: 1117)	Thermotogota (NCBI taxid: 200918)
Deferribacterota (NCBI taxid: 200930)	Verrucomicrobiota (NCBI taxid: 74201)
Deinococcota (NCBI taxid: 1297)	

[00696] **Table 18 - By Phylum**

[00697] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial phyla as set forth in Table 18.

Actinomycetota (NCBI taxid: 201174)
Bacillota (NCBI taxid: 1239)
Bacteroidota (NCBI taxid: 976)
Campylobacterota (NCBI taxid: 29547)
Pseudomonodota (NCBI taxid: 1224)
Thermodesulfobiota (NCBI taxid: 3002442)
Verrucomicrobiota (NCBI taxid: 74201)

[00698] **Table 19 – By Phylum.** In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial phyla as set forth in Table 19.

Actinomycetota (NCBI taxid: 201174)
Bacteroidota (NCBI taxid: 976)
Bacillota (NCBI taxid: 1239)
Verrucomicrobiota (NCBI taxid: 74201)

5

[00699] **BY FAMILY**

[00700] **Table 20 - By families.** In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial families as set forth in Table 20.

Acanthopleuribacteraceae (NCBI taxid: 533207)	Kosmotogaceae (NCBI taxid: 1643948)
Acaryochloridaceae (NCBI taxid: 1890429)	Kribbellaceae (NCBI taxid: 2726069)
Acetobacteraceae (NCBI taxid: 433)	Ktedonospiraceae (NCBI taxid: 2692416)
Acetomicrobiaceae (NCBI taxid: 3029086)	Kytococcaceae (NCBI taxid: 2805426)
Acholeplasmataceae (NCBI taxid: 2146)	Labilitrichaceae (NCBI taxid: 1524216)
Acidaminococcaceae (NCBI taxid: 909930)	Lachnospiraceae (NCBI taxid: 186803)
Acidiferrobacteraceae (NCBI taxid: 1692041)	Lacipirellulaceae (NCBI taxid: 2691359)
Acidilobaceae (NCBI taxid: 871007)	Lactobacillaceae (NCBI taxid: 33958)
Acidilutibacteraceae (NCBI taxid: 2992717)	Lawsonellaceae (NCBI taxid: 2805586)
Acidimicrobiaceae (NCBI taxid: 84994)	Legionellaceae (NCBI taxid: 444)
Acidithiobacillaceae (NCBI taxid: 225058)	Lentisphaeraceae (NCBI taxid: 566277)
Acidobacteriaceae (NCBI taxid: 204434)	Leptolyngbyaceae (NCBI taxid: 1890438)
Acidothermaceae (NCBI taxid: 85032)	Leptospiraceae (NCBI taxid: 170)

Actinomycetaceae (NCBI taxid: 2049)	Leptotrichiaceae (NCBI taxid: 1129771)
Actinopolymorphaceae (NCBI taxid: 2805400)	Lichenihibitantaceae (NCBI taxid: 2723775)
Actinopolysporaceae (NCBI taxid: 622451)	Limnochordaceae (NCBI taxid: 1676650)
Aerococcaceae (NCBI taxid: 186827)	Listeriaceae (NCBI taxid: 186820)
Aeromonadaceae (NCBI taxid: 84642)	Litoricolaceae (NCBI taxid: 449732)
Akkermansiaceae (NCBI taxid: 1647988)	Litorivicinaceae (NCBI taxid: 449732)
Alcaligenaceae (NCBI taxid: 506)	Magnetococcaceae (NCBI taxid: 1191479)
Alcanivoracaceae (NCBI taxid: 224372)	Maliibacteriaceae (NCBI taxid: 3047432)
Alicyclobacillaceae (NCBI taxid: 186823)	Mangrovivirgaceae (NCBI taxid: 2858885)
Alteromonadaceae (NCBI taxid: 72275)	Maricaulaceae (NCBI taxid: 2800061)
Aminithiophilaceae (NCBI taxid: 3029085)	Marinifilaceae (NCBI taxid: 1573805)
Aminobacteriaceae (NCBI taxid: 3029087)	Marinilabiliaceae (NCBI taxid: 558415)
Amoebophilaceae (NCBI taxid: 1501348)	Marinobacteraceae (NCBI taxid: 2887365)
Amorphaceae (NCBI taxid: 2685818)	Mariprofundaceae (NCBI taxid: 580372)
Anaerohalosphaeraceae (NCBI taxid: 2690158)	Marivirgaceae (NCBI taxid: 2762301)
Anaerolineaceae (NCBI taxid: 292628)	Melioribacteraceae (NCBI taxid: 1334117)
Anaeromyxobacteraceae (NCBI taxid: 1524215)	Merismopediaceae (NCBI taxid: 1890428)
Anaplasmataceae (NCBI taxid: 942)	Mesoaciditogaceae (NCBI taxid: 1769717)
Aphanizomenonaceae (NCBI taxid: 1892259)	Metamycoplasmataceae (NCBI taxid: 2895623)
Aphanothecaceae (NCBI taxid: 1890450)	Methanobacteriaceae (NCBI taxid: 2159)
Aquificaceae (NCBI taxid: 64898)	Methanocaldococcaceae (NCBI taxid: 196117)
Archaeoglobaceae (NCBI taxid: 2232)	Methanocellaceae (NCBI taxid: 570265)
Archangiaceae (NCBI taxid: 39)	Methanococcaceae (NCBI taxid: 2183)
Arcobacteraceae (NCBI taxid: 2808963)	Methanocorpusculaceae (NCBI taxid: 88404)
Ardenticatenaceae (NCBI taxid: 1382930)	Methanomassiliicoccaceae (NCBI taxid: 1577788)
Atopobiaceae (NCBI taxid: 1643824)	Methanomicrobiaceae (NCBI taxid: 2194)
Atribacteraceae (NCBI taxid: 2847776)	Methanopyraceae (NCBI taxid: 183713)
Aurantimonadaceae (NCBI taxid: 255475)	Methanoregulaceae (NCBI taxid: 1198451)

Azonexaceae (NCBI taxid: 2008795)	Methanosarcinaceae (NCBI taxid: 2206)
Azospirillaceae (NCBI taxid: 2829815)	Methanospirillaceae (NCBI taxid: 196137)
Bacillaceae (NCBI taxid: 186817)	Methanothermaceae (NCBI taxid: 2178)
Bacillales Family X. Incertae Sedis (NCBI taxid: 539003)	Methanotrichaceae (NCBI taxid: 143067)
Bacteriovoracaceae (NCBI taxid: 263369)	Methylacidiphilaceae (NCBI taxid: 717964)
Bacteroidaceae (NCBI taxid: 815)	Methylobacteriaceae (NCBI taxid: 119045)
Baekduiaceae (NCBI taxid: 2600303)	Methylococcaceae (NCBI taxid: 403)
Barnesiellaceae (NCBI taxid: 2005519)	Methylocystaceae (NCBI taxid: 31993)
Bartonellaceae (NCBI taxid: 772)	Methylophilaceae (NCBI taxid: 32011)
Bdellovibrionaceae (NCBI taxid: 213483)	Microbacteriaceae (NCBI taxid: 85023)
Beijerinckiaceae (NCBI taxid: 45404)	Microbulbiferaceae (NCBI taxid: 1706373)
Bernardetiaceae (NCBI taxid: 1937968)	Micrococcaceae (NCBI taxid: 1268)
Beutenbergiaceae (NCBI taxid: 125316)	Microcoleaceae (NCBI taxid: 1892252)
Bifidobacteriaceae (NCBI taxid: 31953)	Microcystaceae (NCBI taxid: 1890449)
Blastochloridaceae (NCBI taxid: 2831090)	Micromonosporaceae (NCBI taxid: 28056)
Blattabacteriaceae (NCBI taxid: 39782)	Microvenatoraceae (NCBI taxid: 2946505)
Bogoriellaceae (NCBI taxid: 145358)	Miltoncostaceae (NCBI taxid: 2843199)
Borrelliaceae (NCBI taxid: 1643685)	Minwuiaceae (NCBI taxid: 2493628)
Boseaceae (NCBI taxid: 2831100)	Moorellaceae (NCBI taxid: 3039168)
Brachyspiraceae (NCBI taxid: 143786)	Moraxellaceae (NCBI taxid: 468)
Bradymonadaceae (NCBI taxid: 1779135)	Morganellaceae (NCBI taxid: 1903414)
Bradyrhizobiaceae (NCBI taxid: 41294)	Moritellaceae (NCBI taxid: 267891)
Breoghaniaceae (NCBI taxid: 2821832)	Mucispirillaceae (NCBI taxid: 2945020)
Brevibacteriaceae (NCBI taxid: 85019)	Muribaculaceae (NCBI taxid: 2005473)
Breznakiellaceae (NCBI taxid: 2951104)	Mycobacteriaceae (NCBI taxid: 1762)
Brucellaceae (NCBI taxid: 118882)	Mycoplasmataceae (NCBI taxid: 2092)
Bruguierivoracaceae (NCBI taxid: 2812006)	Mycoplasmoidaceae (NCBI taxid: 2790998)
Bryobacteraceae (NCBI taxid: 1962910)	Myxococcaceae (NCBI taxid: 31)
Budviciaceae (NCBI taxid: 1903416)	Nakamurellaceae (NCBI taxid: 85031)
Burkholderiaceae (NCBI taxid: 119060)	Nannocystaceae (NCBI taxid: 224463)
Caedimonadaceae (NCBI taxid: 2100208)	Natranaerobiaceae (NCBI taxid: 485255)
Caldilineaceae (NCBI taxid: 475964)	Natranaerofabaceae (NCBI taxid: 2807496)
Caldiseriaceae (NCBI taxid: 693073)	Natrialbaceae (NCBI taxid: 1644061)
Caldiisphaeraceae (NCBI taxid: 255472)	Nautiliaceae (NCBI taxid: 224467)

Calditerrivibrionaceae (NCBI taxid: 2945021)	Neisseriaceae (NCBI taxid: 481)
Calditrichaceae (NCBI taxid: 1962854)	Nitratiruptoraceae (NCBI taxid: 2795691)
Calotrichaceae (NCBI taxid: 2661849)	Nitrobacteraceae (NCBI taxid: 41294)
Campylobacteraceae (NCBI taxid: 72294)	Nitrosomonadaceae (NCBI taxid: 206379)
Candidatus Absconditicoccaceae (NCBI taxid: 2900569)	Nitrosopumilaceae (NCBI taxid: 338190)
Candidatus Babeliaceae (NCBI taxid: 2497645)	Nitrososphaeraceae (NCBI taxid: 1033997)
Candidatus Brocadiaceae (NCBI taxid: 1127830)	Nitrospinaceae (NCBI taxid: 407032)
Candidatus Chazhembtobacteraceae (NCBI taxid: 2715733)	Nitrospiraceae (NCBI taxid: 189779)
Candidatus Chromulinivoraceae (NCBI taxid: 2953756)	Nocardiaceae (NCBI taxid: 85025)
Candidatus Cloacimonadaceae (NCBI taxid: 3039865)	Nocardioidaceae (NCBI taxid: 85015)
Candidatus Comchoanobacteraceae (NCBI taxid: 2975285)	Nocardiopsaceae (NCBI taxid: 83676)
Candidatus Deianiraeaceae (NCBI taxid: 2603433)	Nostocaceae (NCBI taxid: 1162)
Candidatus Desulfofervidaceae (NCBI taxid: 1902584)	Oceanospirillaceae (NCBI taxid: 135620)
Candidatus Izemoplasmataceae (NCBI taxid: 2975520)	Oculatellaceae (NCBI taxid: 2303507)
Candidatus Methanoliparaceae (NCBI taxid: 2545690)	Odoribacteraceae (NCBI taxid: 1853231)
Candidatus Methanomethylophilaceae (NCBI taxid: 2517203)	Oleiphilaceae (NCBI taxid: 191033)
Candidatus Micrarchaeaceae (NCBI taxid: 2885735)	Opitutaceae (NCBI taxid: 134623)
Candidatus Midichloriaceae (NCBI taxid: 1328881)	Orbaceae (NCBI taxid: 1240483)
Candidatus Nanohalobiaceae (NCBI taxid: 2856054)	Ornithinimicrobiaceae (NCBI taxid: 2805590)

Candidatus Nanopelagicaceae (NCBI taxid: 2162846)	Oscillatoriaceae (NCBI taxid: 1892254)
Candidatus Nanosynbacteraceae (NCBI taxid: 2093822)	Oscillospiraceae (NCBI taxid: 216572)
Candidatus Nitrosocaldaceae (NCBI taxid: 1968910)	Oxalobacteraceae (NCBI taxid: 75682)
Candidatus Paracaedibacteraceae (NCBI taxid: 1777752)	Paenibacillaceae (NCBI taxid: 186822)
Candidatus Saccharimonadaceae (NCBI taxid: 2171986)	Paludibacteraceae (NCBI taxid: 2005523)
Candidatus Uabimicrobiaceae (NCBI taxid: 2897348)	Parachlamydiaceae (NCBI taxid: 92713)
Capillimicrobiaceae (NCBI taxid: 2976758)	Paracoccaceae (NCBI taxid: 31989)
Cardiobacteriaceae (NCBI taxid: 868)	Paraconexibacteraceae (NCBI taxid: 2758916)
Carnobacteriaceae (NCBI taxid: 186828)	Parvibaculaceae (NCBI taxid: 2813035)
Casimicrobiaceae (NCBI taxid: 2705999)	Parvicellaceae (NCBI taxid: 2975259)
Catenulisporaceae (NCBI taxid: 414877)	Parvularculaceae (NCBI taxid: 255474)
Caulobacteraceae (NCBI taxid: 76892)	Pasteurellaceae (NCBI taxid: 712)
Celerinatantimonadaceae (NCBI taxid: 412032)	Pectobacteriaceae (NCBI taxid: 1903410)
Cellulomonadaceae (NCBI taxid: 85016)	Pelagibacteraceae (NCBI taxid: 1655514)
Cellulosilyticaceae (NCBI taxid: 3018741)	Peptococcaceae (NCBI taxid: 186807)
Cellvibrionaceae (NCBI taxid: 1706371)	Peptoniphilaceae (NCBI taxid: 1570339)
Chamaesiphonaceae (NCBI taxid: 1890431)	Peptostreptococcaceae (NCBI taxid: 186804)
Chelatococcaceae (NCBI taxid: 2036754)	Persicobacteraceae (NCBI taxid: 1853234)
Chitinophagaceae (NCBI taxid: 563835)	Petrotogaceae (NCBI taxid: 1643949)
Chlamydiaceae (NCBI taxid: 809)	Phototrophicaceae (NCBI taxid: 2922432)
Chlorobiaceae (NCBI taxid: 191412)	Phreatobacteraceae (NCBI taxid: 2843305)
Chloroflexaceae (NCBI taxid: 1106)	Phycisphaeraceae (NCBI taxid: 666507)
Chloroherpetonaceae (NCBI taxid: 2968741)	Phyllobacteriaceae (NCBI taxid: 69277)
Christensenellaceae (NCBI taxid: 990719)	Picrophilaceae (NCBI taxid: 46630)
Chromatiaceae (NCBI taxid: 1046)	Pirellulaceae (NCBI taxid: 2691357)
Chromobacteriaceae (NCBI taxid: 1499392)	Piscirickettsiaceae (NCBI taxid: 135616)

Chroococcaceae (NCBI taxid: 1890464)	Planctomycetaceae (NCBI taxid: 126)
Chroococcidiopsidaceae (NCBI taxid: 1890528)	Planococcaceae (NCBI taxid: 186818)
Chrysiogenaceae (NCBI taxid: 189770)	Pleomorphomonadaceae (NCBI taxid: 2843308)
Chthonomonadaceae (NCBI taxid: 1077264)	Polyangiaceae (NCBI taxid: 49)
Clostridiaceae (NCBI taxid: 31979)	Porphyromonadaceae (NCBI taxid: 171551)
Clostridiales Family XVI. Incertae Sedis (NCBI taxid: 543347)	Prevotellaceae (NCBI taxid: 171552)
Clostridiales Family XVII. Incertae Sedis (NCBI taxid: 539000)	Prochlorococcaceae (NCBI taxid: 2881426)
Cohaesibacteraceae (NCBI taxid: 655351)	Prochlorotrichaceae (NCBI taxid: 2303730)
Coleofasciculaceae (NCBI taxid: 1892251)	Prolixibacteraceae (NCBI taxid: 1471398)
Colwelliaceae (NCBI taxid: 267889)	Promicromonosporaceae (NCBI taxid: 85017)
Comamonadaceae (NCBI taxid: 80864)	Propionibacteriaceae (NCBI taxid: 31957)
Conexibacteraceae (NCBI taxid: 320583)	Proteinivoraceae (NCBI taxid: 1491775)
Conexivisphaeraceae (NCBI taxid: 2798276)	Pseudanabaenaceae (NCBI taxid: 1890436)
Coprobacillaceae (NCBI taxid: 2810280)	Pseudoalteromonadaceae (NCBI taxid: 267888)
Coprothermobacteraceae (NCBI taxid: 2138247)	Pseudobdellovibrionaceae (NCBI taxid: 213483)
Coriobacteriaceae (NCBI taxid: 84107)	Pseudomonadaceae (NCBI taxid: 135621)
Corynebacteriaceae (NCBI taxid: 1653)	Pseudonocardiaceae (NCBI taxid: 2070)
Coxiellaceae (NCBI taxid: 118968)	Psychromonadaceae (NCBI taxid: 267894)
Crocinitomicaceae (NCBI taxid: 1853230)	Puniceicoccaceae (NCBI taxid: 415002)
Cuniculiplasmataceae (NCBI taxid: 1747776)	Pyrodictiaceae (NCBI taxid: 2307)
Cyclobacteriaceae (NCBI taxid: 563798)	Reichenbachiellaceae (NCBI taxid: 2762302)
Cyclonatronaceae (NCBI taxid: 3024158)	Rhabdochlamydiaceae (NCBI taxid: 689704)
Cytophagaceae (NCBI taxid: 89373)	Rhizobiaceae (NCBI taxid: 82115)

Deferribacteraceae (NCBI taxid: 191394)	Rhodanobacteraceae (NCBI taxid: 1775411)
Dehalococcoidaceae (NCBI taxid: 1202464)	Rhodobacteraceae (NCBI taxid: 31989)
Deinococcaceae (NCBI taxid: 183710)	Rhodocyclaceae (NCBI taxid: 75787)
Demequinaceae (NCBI taxid: 1042322)	Rhodospirillaceae (NCBI taxid: 41295)
Dermabacteraceae (NCBI taxid: 85020)	Rhodothermaceae (NCBI taxid: 563843)
Dermacoccaceae (NCBI taxid: 145357)	Rickettsiaceae (NCBI taxid: 775)
Dermatophilaceae (NCBI taxid: 85018)	Rikenellaceae (NCBI taxid: 171550)
Dermocarpellaceae (NCBI taxid: 1890498)	Rivulariaceae (NCBI taxid: 1185)
Desulfallaceae (NCBI taxid: 2867375)	Roseiflexaceae (NCBI taxid: 1508635)
Desulfarculaceae (NCBI taxid: 453228)	Roseobacteraceae (NCBI taxid: 2854170)
Desulfatibacillaceae (NCBI taxid: 3031627)	Ruaniaceae (NCBI taxid: 1331736)
Desulfitobacteriaceae (NCBI taxid: 2937909)	Rubrobacteraceae (NCBI taxid: 84997)
Desulfobaccaceae (NCBI taxid: 3031656)	Saccharospirillaceae (NCBI taxid: 255527)
Desulfobacteraceae (NCBI taxid: 213119)	Salinibacteraceae (NCBI taxid: 1853225)
Desulfobulbaceae (NCBI taxid: 213121)	Salinisphaeraceae (NCBI taxid: 742031)
Desulfocapsaceae (NCBI taxid: 2886822)	Salinivirgaceae (NCBI taxid: 1970190)
Desulfococcaceae (NCBI taxid: 2931039)	Sandaracinaceae (NCBI taxid: 1055686)
Desulfohalobiaceae (NCBI taxid: 213117)	Sanguibacteraceae (NCBI taxid: 145360)
Desulfolunaceae (NCBI taxid: 3031622)	Saprospiraceae (NCBI taxid: 89374)
Desulfomicrobiaceae (NCBI taxid: 213116)	Schleiferiaceae (NCBI taxid: 1333713)
Desulfomonilaceae (NCBI taxid: 3031658)	Scytonemataceae (NCBI taxid: 1182)
Desulfosarcinaceae (NCBI taxid: 3031624)	Sedimentisphaeraceae (NCBI taxid: 2483367)
Desulfosudaceae (NCBI taxid: 2904715)	Segniliparaceae (NCBI taxid: 316606)
Desulfotomaculaceae (NCBI taxid: 2937910)	Selenomonadaceae (NCBI taxid: 1843491)
Desulfovibrionaceae (NCBI taxid: 194924)	Shewanellaceae (NCBI taxid: 267890)
Desulfurellaceae (NCBI taxid: 117942)	Silvanigrellaceae (NCBI taxid: 2024974)
Desulfurobacteriaceae (NCBI taxid: 558314)	Simkaniaceae (NCBI taxid: 92712)
Desulfurococcaceae (NCBI taxid: 2272)	Sinobacteraceae (NCBI taxid: 568386)
Desulfuromonadaceae (NCBI taxid: 213421)	Sirenicapillariaceae (NCBI taxid: 2934961)

Dethiosulfovibrionaceae (NCBI taxid: 3029088)	Sneathiellaceae (NCBI taxid: 510685)
Devosiaceae (NCBI taxid: 2831106)	Sphaerobacteraceae (NCBI taxid: 85002)
Dictyoglomaceae (NCBI taxid: 203488)	Sphaerochaetaceae (NCBI taxid: 2791015)
Dietziaceae (NCBI taxid: 85029)	Sphaerotilaceae (NCBI taxid: 2975441)
Dissulfurispiraceae (NCBI taxid: 2811505)	Sphingobacteriaceae (NCBI taxid: 84566)
Dysgonomonadaceae (NCBI taxid: 2005520)	Sphingomonadaceae (NCBI taxid: 41297)
Ectothiorhodospiraceae (NCBI taxid: 72276)	Sphingosinicellaceae (NCBI taxid: 2820280)
Eggerthellaceae (NCBI taxid: 1643826)	Spirochaetaceae (NCBI taxid: 137)
Egibacteraceae (NCBI taxid: 1747769)	Spiroplasmataceae (NCBI taxid: 2131)
Egicoccaceae (NCBI taxid: 1755824)	Spirosomaceae (NCBI taxid: 2896860)
Elioraeaceae (NCBI taxid: 2690195)	Spongiibacteraceae (NCBI taxid: 1706375)
Elusimicrobiaceae (NCBI taxid: 641876)	Sporichthyaceae (NCBI taxid: 85033)
Emcibacteraceae (NCBI taxid: 2066491)	Sporolactobacillaceae (NCBI taxid: 186821)
Endomicrobiaceae (NCBI taxid: 1783343)	Sporomusaceae (NCBI taxid: 1843490)
Endozoicomonadaceae (NCBI taxid: 2066474)	Staphylococcaceae (NCBI taxid: 90964)
Enterobacteriaceae (NCBI taxid: 543)	Stappiaceae (NCBI taxid: 2821832)
Enterococcaceae (NCBI taxid: 81852)	Stellaceae (NCBI taxid: 2844601)
Entomoplasmataceae (NCBI taxid: 33925)	Steroidobacteraceae (NCBI taxid: 2689614)
Erwiniaceae (NCBI taxid: 1903409)	Sterolibacteriaceae (NCBI taxid: 2008793)
Erysipelotrichaceae (NCBI taxid: 128827)	Streptococcaceae (NCBI taxid: 1300)
Erythrobacteraceae (NCBI taxid: 335929)	Streptomycetaceae (NCBI taxid: 2062)
Eubacteriaceae (NCBI taxid: 186806)	Streptosporangiaceae (NCBI taxid: 2004)
Eubacteriales Family XIII. Incertae Sedis (NCBI taxid: 543314)	Succinivibrionaceae (NCBI taxid: 83763)
Eubacteriales incertae sedis (NCBI taxid: 538999)	Sulfolobaceae (NCBI taxid: 118883)
Euzebyaceae (NCBI taxid: 908622)	Sulfuricellaceae (NCBI taxid: 2772226)
Fastidiosibacteraceae (NCBI taxid: 2056687)	Sulfurimonadaceae (NCBI taxid: 2771471)
Ferrimonadaceae (NCBI taxid: 267892)	Sulfurospirillaceae (NCBI taxid: 2932623)
Ferropasmaceae (NCBI taxid: 90142)	Sulfurovaceae (NCBI taxid: 2771472)

Ferrovaceae (NCBI taxid: 1442156)	Sutterellaceae (NCBI taxid: 995019)
Fervidicoccaceae (NCBI taxid: 685949)	Symbiobacteriaceae (NCBI taxid: 543349)
Fervidobacteriaceae (NCBI taxid: 1643950)	Synechococcaceae (NCBI taxid: 1890426)
Fibrobacteraceae (NCBI taxid: 204431)	Synergistaceae (NCBI taxid: 649777)
Fimbriimonadaceae (NCBI taxid: 1663426)	Syntrophaceae (NCBI taxid: 213468)
Flammeovirgaceae (NCBI taxid: 200667)	Syntrophobacteraceae (NCBI taxid: 213465)
Flavobacteriaceae (NCBI taxid: 49546)	Syntrophomonadaceae (NCBI taxid: 68298)
Flexistipitaceae (NCBI taxid: 2945022)	Syntrophotaleaceae (NCBI taxid: 2812024)
Fluviibacteraceae (NCBI taxid: 2808923)	Tannerellaceae (NCBI taxid: 2005525)
Fontisphaeraceae (NCBI taxid: 3050006)	Tenuifilaceae (NCBI taxid: 2760872)
Francisellaceae (NCBI taxid: 34064)	Tepidanaerobacteraceae (NCBI taxid: 2770092)
Frankiaceae (NCBI taxid: 74712)	Tepidiformaceae (NCBI taxid: 2682227)
Fulvivirgaceae (NCBI taxid: 2762286)	Tepidimicrobiaceae (NCBI taxid: 2992719)
Fusobacteriaceae (NCBI taxid: 203492)	Tepidisphaeraceae (NCBI taxid: 1771355)
Gallionellaceae (NCBI taxid: 90627)	Terasakiellaceae (NCBI taxid: 2813951)
Geminicoccaceae (NCBI taxid: 2066434)	Thalassobaculaceae (NCBI taxid: 2844864)
Geminocystaceae (NCBI taxid: 2815910)	Thalassospiraceae (NCBI taxid: 2844866)
Gemmataceae (NCBI taxid: 1914233)	Thermaceae (NCBI taxid: 188786)
Gemmatimonadaceae (NCBI taxid: 219687)	Thermincolaceae (NCBI taxid: 2937911)
Geoalkalibacteraceae (NCBI taxid: 3031665)	Thermoactinomycetaceae (NCBI taxid: 186824)
Geobacteraceae (NCBI taxid: 213422)	Thermoanaerobacteraceae (NCBI taxid: 186814)
Geodermatophilaceae (NCBI taxid: 85030)	Thermoanaerobacterales Family III. Incertae Sedis (NCBI taxid: 543371)
Geovibrionaceae (NCBI taxid: 2945019)	Thermoanaerobacterales Family IV. Incertae Sedis (NCBI taxid: 543372)
Gloeobacteraceae (NCBI taxid: 1890422)	Thermococcaceae (NCBI taxid: 2259)
Gloeomargaritaceae (NCBI taxid: 1955043)	Thermodesulfatatoraceae (NCBI taxid: 3031464)
Glycomycetaceae (NCBI taxid: 85034)	Thermodesulfobacteriaceae (NCBI taxid: 188711)
Gomontiellaceae (NCBI taxid: 1892255)	Thermodesulfobiaceae (NCBI taxid: 227387)

Gordoniaceae (NCBI taxid: 85026)	Thermodesulfovibrionaceae (NCBI taxid: 2811504)
Gottschalkiaceae (NCBI taxid: 2042895)	Thermofilaceae (NCBI taxid: 114378)
Granulosicoccaceae (NCBI taxid: 449719)	Thermoguttaceae (NCBI taxid: 2691358)
Hafniaceae (NCBI taxid: 1903412)	Thermohalobacteraceae (NCBI taxid: 2848916)
Hahellaceae (NCBI taxid: 224379)	Thermoleophilaceae (NCBI taxid: 320796)
Halanaerobiaceae (NCBI taxid: 972)	Thermomicrobiaceae (NCBI taxid: 189777)
Halieaceae (NCBI taxid: 1706372)	Thermomonosporaceae (NCBI taxid: 2012)
Haliscomenobacteraceae (NCBI taxid: 1937961)	Thermoplasmataceae (NCBI taxid: 46659)
Haloarculaceae (NCBI taxid: 1963268)	Thermoplasmatales (NCBI taxid: 2301)
Halobacteriaceae (NCBI taxid: 2236)	Thermoproteaceae (NCBI taxid: 2267)
Halobacteriovoraceae (NCBI taxid: 1652132)	Thermosediminibacteraceae (NCBI taxid: 2770093)
Halobacteroidaceae (NCBI taxid: 53434)	Thermospiraceae (NCBI taxid: 3024225)
Haloferacaceae (NCBI taxid: 1644056)	Thermostichaceae (NCBI taxid: 2881384)
Halomonadaceae (NCBI taxid: 28256)	Thermosynechococcaceae (NCBI taxid: 2881378)
Halorubraceae (NCBI taxid: 1644056)	Thermotogaceae (NCBI taxid: 188709)
Halothermotrichaceae (NCBI taxid: 3046412)	Thermotomaculaceae (NCBI taxid: 2562244)
Halothiobacillaceae (NCBI taxid: 255526)	Thermovirgaceae (NCBI taxid: 3029089)
Hapalosiphonaceae (NCBI taxid: 1892263)	Thioalkalibacteraceae (NCBI taxid: 2035710)
Helicobacteraceae (NCBI taxid: 72293)	Thioalkalispiraceae (NCBI taxid: 1096778)
Heliobacteriaceae (NCBI taxid: 31984)	Thiobacillaceae (NCBI taxid: 2008790)
Hippeaceae (NCBI taxid: 3048035)	Thiotrichaceae (NCBI taxid: 135617)
Holosporaceae (NCBI taxid: 44746)	Thiovulaceae (NCBI taxid: 2771471)
Hoyosellaceae (NCBI taxid: 3040680)	Tichowtungiaceae (NCBI taxid: 2907186)
Hydrogenimonaceae (NCBI taxid: 292630)	Tissierellaceae (NCBI taxid: 1737406)
Hydrogenimonadaceae (NCBI taxid: 292630)	Tolypothrichaceae (NCBI taxid: 119859)
Hydrogenophilaceae (NCBI taxid: 206349)	Treponemataceae (NCBI taxid: 137)
Hydrogenothermaceae (NCBI taxid: 224027)	Treponemataceae (NCBI taxid: 2845253)

Hyellaceae (NCBI taxid: 1890500)	Trichocoleusaceae (NCBI taxid: 2303527)
Hymenobacteraceae (NCBI taxid: 1853232)	Tropherymataceae (NCBI taxid: 2805591)
Hyphomicrobiaceae (NCBI taxid: 45401)	Trueperaceae (NCBI taxid: 332247)
Hyphomonadaceae (NCBI taxid: 69657)	Tsukamurellaceae (NCBI taxid: 85028)
Iamiaceae (NCBI taxid: 633392)	Turcibacteraceae (NCBI taxid: 2810281)
Ichthyobacteriaceae (NCBI taxid: 1755828)	Usitatibacteraceae (NCBI taxid: 2803844)
Idiomarinaceae (NCBI taxid: 267893)	Vallitaleaceae (NCBI taxid: 2603322)
Ignatzschineriaceae (NCBI taxid: 3018589)	Veillonellaceae (NCBI taxid: 31977)
Ignavibacteriaceae (NCBI taxid: 795749)	Verrucomicrobiaceae (NCBI taxid: 203557)
Ilumatobacteraceae (NCBI taxid: 2448023)	Vibrionaceae (NCBI taxid: 641)
Immundisolibacteraceae (NCBI taxid: 1934946)	Vicinamibacteraceae (NCBI taxid: 2211325)
Intrasporangiaceae (NCBI taxid: 85021)	Vulgatibacteraceae (NCBI taxid: 1524213)
Isosphaeraceae (NCBI taxid: 1763524)	Waddliaceae (NCBI taxid: 92714)
Jatrophihabitantaceae (NCBI taxid: 2805416)	Weeksellaceae (NCBI taxid: 2762318)
Jiangellaceae (NCBI taxid: 1217100)	Wenzhouxiangellaceae (NCBI taxid: 1676141)
Jonesiaceae (NCBI taxid: 85022)	Woeseiaceae (NCBI taxid: 1738654)
Kaistiaceae (NCBI taxid: 2831111)	Xanthobacteraceae (NCBI taxid: 335928)
Kangiellaceae (NCBI taxid: 1920240)	Xanthomonadaceae (NCBI taxid: 32033)
Kiloniellaceae (NCBI taxid: 597359)	Yersiniaceae (NCBI taxid: 1903411)
Kineosporiaceae (NCBI taxid: 83778)	Zhaonellaceae (NCBI taxid: 2748673)
Kiritimatiellaceae (NCBI taxid: 1921783)	Zoogloeaceae (NCBI taxid: 2008794)
Kofleriaceae (NCBI taxid: 224464)	Zooshikellaceae (NCBI taxid: 2898533)
Koleobacteraceae (NCBI taxid: 2786988)	Zymomonadaceae (NCBI taxid: 2844881)
Kordiimonadaceae (NCBI taxid: 1331809)	

[00701] **Table 21 – By Families.**

[00702] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial families as set forth in Table 21.

Acidaminococcaceae (NCBI taxid: 909930)
Akkermansiaceae (NCBI taxid: 1647988)
Bacillaceae (NCBI taxid: 186817)
Bacteroidaceae (NCBI taxid: 815)

Barnesiellaceae (NCBI taxid: 2005519)
Bifidobacteriaceae (NCBI taxid: 31953)
Campylobacteraceae (NCBI taxid: 72294)
Carnobacteriaceae (NCBI taxid: 186828)
Christensenellaceae (NCBI taxid: 990719)
Clostridiaceae (NCBI taxid: 31979)
Coprobacillaceae (NCBI taxid: 2810280)
Coriobacteriaceae (NCBI taxid: 84107)
Desulfovibrionaceae (NCBI taxid: 194924)
Eggerthellaceae (NCBI taxid: 1643826)
Enterobacteriaceae (NCBI taxid: 543)
Enterococcaceae (NCBI taxid: 81852)
Erysipelotrichaceae (NCBI taxid: 128827)
Eubacteriaceae (NCBI taxid: 186806)
Eubacteriales Family XIII. Incertae Sedis (NCBI taxid: 543314)
Eubacteriales incertae sedis (NCBI taxid: 538999)
Lachnospiraceae (NCBI taxid: 186803)
Lactobacillaceae (NCBI taxid: 33958)
Maliibacteriaceae (NCBI taxid: 3047432)
Muribaculaceae (NCBI taxid: 2005473)
Odoribacteraceae (NCBI taxid: 1853231)
Oscillospiraceae (NCBI taxid: 216572)
Peptoniphilaceae (NCBI taxid: 1570339)
Peptostreptococcaceae (NCBI taxid: 186804)
Prevotellaceae (NCBI taxid: 171552)
Rikenellaceae (NCBI taxid: 171550)
Selenomonadaceae (NCBI taxid: 1843491)
Streptococcaceae (NCBI taxid: 1300)
Sutterellaceae (NCBI taxid: 995019)
Veillonellaceae (NCBI taxid: 31977)

[00703] **Table 22 – By Families**

[00704] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial families as set forth in Table 22.

Akkermansiaceae (NCBI taxid: 1647988)

Bacillaceae (NCBI taxid: 186817)
Bacteroidaceae (NCBI taxid: 815)
Barnesiellaceae (NCBI taxid: 2005519)
Bifidobacteriaceae (NCBI taxid: 31953)
Christensenellaceae (NCBI taxid: 990719)
Clostridiaceae (NCBI taxid: 31979)
Coprobacillaceae (NCBI taxid: 2810280)
Coriobacteriaceae (NCBI taxid: 84107)
Erysipelotrichaceae (NCBI taxid: 128827)
Eubacteriaceae (NCBI taxid: 186806)
Eubacteriales incertae sedis (NCBI taxid: 538999)
Lachnospiraceae (NCBI taxid: 186803)
Lactobacillaceae (NCBI taxid: 33958)
Maliibacteriaceae (NCBI taxid: 3047432)
Odoribacteraceae (NCBI taxid: 1853231)
Oscillospiraceae (NCBI taxid: 216572)
Peptoniphilaceae (NCBI taxid: 1570339)
Peptostreptococcaceae (NCBI taxid: 186804)
Porphyromonadaceae (NCBI taxid: 171551)
Prevotellaceae (NCBI taxid: 171552)
Rikenellaceae (NCBI taxid: 171550)
Selenomonadaceae (NCBI taxid: 1843491)
Streptococcaceae (NCBI taxid: 1300)
Tannerellaceae (NCBI taxid: 2005525)

[00705] **BY GENUS**

[00706] **Table 23 – By Genera.**

[00707] In some embodiments, the composition of the invention includes one or more

- 5 microbes selected from one or more of the microbial genera as set forth in Table 23.

Acidaminococcaceae (family) (NCBI taxid: 909930)	Intestinibaculum (NCBI taxid: 2679910)
Acidaminococcus (NCBI taxid: 904)	Intestinimonas (NCBI taxid: 1392389)
Adlercreutzia (NCBI taxid: 447020)	Lachnoanaerobaculum (NCBI taxid: 1164882)
Agathobaculum (NCBI taxid: 2048137)	Lachnoclostridium (NCBI taxid: 1506553)

Akkermansia (NCBI taxid: 239934)	Lachnospira (NCBI taxid: 28050)
Alistipes (NCBI taxid: 239759)	Lachnospiraceae incertae sedis (unclassified rank, Lachnospiraceae family) (NCBI taxid: 2840493)
Alterileibacterium (NCBI taxid: 1980680)	Lacrimispora (NCBI taxid: 2719231)
Amedibacillus (NCBI taxid: 2749846)	Lactococcus (NCBI taxid: 1357)
Amedibacterium (NCBI taxid: 2749267)	Ligilactobacillus (NCBI taxid: 2767887)
Aminipila (NCBI taxid: 2060094)	Longibaculum (NCBI taxid: 1918538)
Anaerobutyricum (NCBI taxid: 2569097)	Longicatena (NCBI taxid: 1918536)
Anaerococcus (NCBI taxid: 165779)	Mageebacillus (NCBI taxid: 1637257)
Anaerocolumna (NCBI taxid: 1843210)	Maliibacterium (NCBI taxid: 3047433)
Anaerofustis (NCBI taxid: 264995)	Marvinbryantia (NCBI taxid: 248744)
Anaerostipes (NCBI taxid: 207244)	Massilimicrobiota (NCBI taxid: 1924110)
Anaerotignum (NCBI taxid: 2039240)	Massiliprevotella (NCBI taxid: 1981037)
Anaerotruncus (NCBI taxid: 244127)	Massilistercora (NCBI taxid: 2717089)
Bacillus (NCBI taxid: 1386)	Mediterraneibacter (NCBI taxid: 2316020)
Bacteroides (NCBI taxid: 816)	Megamonas (NCBI taxid: 158846)
Barnesiella (NCBI taxid: 397864)	Megasphaera (NCBI taxid: 906)
Bifidobacterium (NCBI taxid: 1678)	Merdibacter (NCBI taxid: 1935200)
Bilophila (NCBI taxid: 35832)	Mesosutterella (NCBI taxid: 2494213)
Blautia (NCBI taxid: 572511)	Mitsuokella (NCBI taxid: 52225)
Butyricimonas (NCBI taxid: 574697)	Mogibacterium (NCBI taxid: 86331)
Butyrivibrio (NCBI taxid: 830)	Muribaculum (NCBI taxid: 1918540)
Campylobacter (NCBI taxid: 194)	Negativibacillus (NCBI taxid: 1980693)
Caproicibacter (NCBI taxid: 2576755)	Novisyntrophococcus (NCBI taxid: 2888809)
Caproicibacterium (NCBI taxid: 2834348)	Odoribacter (NCBI taxid: 283168)
Caproiciproducens (NCBI taxid: 1738645)	Olsenella (NCBI taxid: 133925)
Casaltella (NCBI taxid: 1715793)	Oscillibacter (NCBI taxid: 459786)
Catenibacterium (NCBI taxid: 135858)	Oscillospiraceae (family) (NCBI taxid: 216572)
Christensenella (NCBI taxid: 990721)	Oscillospiraceae incertae sedis (unclassified rank, Oscillospiraceae family) (NCBI taxid: 552397)
Clostridium (NCBI taxid: 1485)	Parabacteroides (NCBI taxid: 375288)

Collinsella (NCBI taxid: 102106)	Paraclostridium (NCBI taxid: 1849822)
Coprobacillus (NCBI taxid: 100883)	Paraprevotella (NCBI taxid: 577309)
Coprobacter (NCBI taxid: 1348911)	Parolsenella (NCBI taxid: 2082587)
Coprococcus (NCBI taxid: 33042)	Peptacetobacter (NCBI taxid: 2743582)
Desulfovibrio (NCBI taxid: 872)	Peptoniphilus (NCBI taxid: 162289)
Dorea (NCBI taxid: 189330)	Peptostreptococcus (NCBI taxid: 1257)
Duodenibacillus (NCBI taxid: 1980697)	Phascolarctobacterium (NCBI taxid: 33024)
Dysosmobacter (NCBI taxid: 2591381)	Phocaeicola (NCBI taxid: 909656)
Eggerthella (NCBI taxid: 84111)	Porphyromonas (NCBI taxid: 836)
Enorma (NCBI taxid: 1472762)	Prevotella (NCBI taxid: 838)
Enterocloster (NCBI taxid: 2719313)	Pseudobutyrvibrio (NCBI taxid: 46205)
Enterococcus (NCBI taxid: 1350)	Pusillibacter (NCBI taxid: 2892397)
Erysipelatoclostridium (NCBI taxid: 3025755)	Romboutsia (NCBI taxid: 1501226)
Escherichia (NCBI taxid: 561)	Roseburia (NCBI taxid: 841)
Ethanoligenens (NCBI taxid: 253238)	Ruminiclostridium (NCBI taxid: 1508657)
Eubacterium (NCBI taxid: 1730)	Ruminococcus (NCBI taxid: 1263)
Faecalibacillus (NCBI taxid: 2678885)	Ruthenibacterium (NCBI taxid: 1905344)
Faecalibacterium (NCBI taxid: 216851)	Schaalia (NCBI taxid: 2529408)
Faecalibaculum (NCBI taxid: 1729679)	Segatella (NCBI taxid: 2974251)
Finegoldia (NCBI taxid: 150022)	Selenomonas (NCBI taxid: 970)
Flavonifractor (NCBI taxid: 946234)	Sellimonas (NCBI taxid: 1769710)
Flintibacter (NCBI taxid: 1918454)	Senegalimassilia (NCBI taxid: 1473205)
Fusicatenibacter (NCBI taxid: 1407607)	Slackia (NCBI taxid: 84108)
Gemmiger (NCBI taxid: 204475)	Sodaphilus (NCBI taxid: 2815786)
Gordonibacter (NCBI taxid: 644652)	Solibaculum (NCBI taxid: 2842531)
Granulicatella (NCBI taxid: 117563)	Streptococcus (NCBI taxid: 1301)
Herbinix (NCBI taxid: 1663717)	Subdoligranulum (NCBI taxid: 292632)
Holdemanella (NCBI taxid: 1573535)	Thomasclavelia (NCBI taxid: 3025755)
Holdemania (NCBI taxid: 61170)	Tyzzerella (NCBI taxid: 1506577)
Hoyleseella (NCBI taxid: 2974257)	Veillonella (NCBI taxid: 29465)
Hungatella (NCBI taxid: 1649459)	Vescimonas (NCBI taxid: 2892396)
Intestinibacter (NCBI taxid: 1505657)	

[00708] Table 24 – By Genera.

[00709] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial genera as set forth in Table 24.

Agathobaculum (NCBI taxid: 2048137)	Gemmiger (NCBI taxid: 204475)
Akkermansia (NCBI taxid: 239934)	Holdemanella (NCBI taxid: 1573535)
Alistipes (NCBI taxid: 239759)	Hungatella (NCBI taxid: 1649459)
Amedibacterium (NCBI taxid: 2749267)	Intestinimonas (NCBI taxid: 1392389)
Anaerobutyricum (NCBI taxid: 2569097)	Lachnoanaerobaculum (NCBI taxid: 1164882)
Anaerofustis (NCBI taxid: 264995)	Lachnospira (NCBI taxid: 28050)
Anaerostipes (NCBI taxid: 207244)	Lacrimispora (NCBI taxid: 2719231)
Anaerotignum (NCBI taxid: 2039240)	Lactococcus (NCBI taxid: 1357)
Anaerotruncus (NCBI taxid: 244127)	Ligilactobacillus (NCBI taxid: 2767887)
Bacillus (NCBI taxid: 1386)	Longicatena (NCBI taxid: 1918536)
Bacteroides (NCBI taxid: 816)	Massilimicrobiota (NCBI taxid: 1924110)
Barnesiella (NCBI taxid: 397864)	Megamonas (NCBI taxid: 158846)
Bifidobacterium (NCBI taxid: 1678)	Merdibacter (NCBI taxid: 1935200)
Blautia (NCBI taxid: 572511)	Odoribacter (NCBI taxid: 283168)
Butyricimonas (NCBI taxid: 574697)	Oscillospiraceae (family) (NCBI taxid: 216572)
Christensenella (NCBI taxid: 990721)	Parabacteroides (NCBI taxid: 375288)
Clostridium (NCBI taxid: 1485)	Paraclostridium (NCBI taxid: 1849822)
Collinsella (NCBI taxid: 102106)	Phocaeicola (NCBI taxid: 909656)
Coprobacillus (NCBI taxid: 100883)	Porphyromonas (NCBI taxid: 836)
Coprobacter (NCBI taxid: 1348911)	Prevotella (NCBI taxid: 838)
Coprococcus (NCBI taxid: 33042)	Pusillibacter (NCBI taxid: 2892397)
Dorea (NCBI taxid: 189330)	Romboutsia (NCBI taxid: 1501226)
Enorma (NCBI taxid: 1472762)	Roseburia (NCBI taxid: 841)
Enterocloster (NCBI taxid: 2719313)	Ruminococcus (NCBI taxid: 1263)
Erysipelatoclostridium (NCBI taxid: 3025755)	Ruthenibacterium (NCBI taxid: 1905344)
Eubacterium (NCBI taxid: 1730)	Sellimonas (NCBI taxid: 1769710)
Faecalibacillus (NCBI taxid: 2678885)	Solibaculum (NCBI taxid: 2842531)
Faecalibacterium (NCBI taxid: 216851)	Streptococcus (NCBI taxid: 1301)
Finegoldia (NCBI taxid: 150022)	Thomasclavelia (NCBI taxid: 3025755)
Flintibacter (NCBI taxid: 1918454)	Vescimonas (NCBI taxid: 2892396)

[00710] **BY SPECIES**

[00711] **Table 25 – By Species.**

[00712] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 25.

Absiella dolichum (NCBI taxid: 31971)	Dysosmobacter faecalis
Acidaminococcaceae sp. (NCBI taxid: 909930)	Dysosmobacter welbionis (NCBI taxid: 2093857)
Acidaminococcus fermentans (NCBI taxid: 905)	Eggerthella guodeyinii (NCBI taxid: 2690837)
Acidaminococcus intestini (NCBI taxid: 187327)	Eggerthella lenta (NCBI taxid: 84112)
Adlercreutzia equolifaciens (NCBI taxid: 446660)	Enorma massiliensis (NCBI taxid: 1472761)
Adlercreutzia hattorii (NCBI taxid: 2707299)	Enorma sp. (NCBI taxid: 1920692)
Agathobacter rectalis (NCBI taxid: 39491)	Enterocloster aldenensis (NCBI taxid: 358742)
Agathobaculum sp. (NCBI taxid: 2048138)	Enterocloster bolteae (NCBI taxid: 208479)
Agathobaculum sp003481705	Enterococcus faecium (NCBI taxid: 1352)
Akkermansia muciniphila (NCBI taxid: 239935)	Erysipelatoclostridium ramosum (NCBI taxid: 1547)
Alistipes communis (NCBI taxid: 2585118)	Escherichia coli (NCBI taxid: 562)
Alistipes dispar (NCBI taxid: 2585119)	Ethanoligenens harbinense (NCBI taxid: 253239)
Alistipes finegoldii (NCBI taxid: 214856)	Eubacterium callanderi (NCBI taxid: 53442)
Alistipes ihumii (NCBI taxid: 1470347)	Eubacterium limosum (NCBI taxid: 1736)
Alistipes indistinctus (NCBI taxid: 626932)	Eubacterium maltosivorans (NCBI taxid: 2041044)
Alistipes megaguti (NCBI taxid: 2364787)	Eubacterium rectale (NCBI taxid: 39491)
Alistipes onderdonkii (NCBI taxid: 328813)	Eubacterium siraeum (NCBI taxid: 39492)
Alistipes putredinis (NCBI taxid: 28117)	Eubacterium sp. c-25 (NCBI taxid: 3028070)
Alistipes senegalensis (NCBI taxid: 1288121)	Eubacterium sp. NSJ-61 (NCBI taxid: 2764325)
Alistipes shahii (NCBI taxid: 328814)	Eubacterium ventriosum (NCBI taxid: 39496)
Alistipes sp. dk3624 (NCBI taxid: 2662363)	Extibacter hylemonae

Alterileibacterium massiliense (NCBI taxid: 1870997)	Faecalibacillus intestinalis (NCBI taxid: 1982626)
Alterileibacterium sp. (NCBI taxid: 2046786)	Faecalibacterium duncaniae (NCBI taxid: 411483)
Amedibacterium intestinale (NCBI taxid: 2583452)	Faecalibacterium prausnitzii (NCBI taxid: 853)
Aminipila luticellarii (NCBI taxid: 2507160)	Faecalibaculum rodentium (NCBI taxid: 1702221)
Anaerobutyricum hallii (NCBI taxid: 39488)	Fimivivens sp900113995
Anaerococcus vaginalis (NCBI taxid: 33037)	Finegoldia magna (NCBI taxid: 1260)
Anaerocolumna chitinilytica (NCBI taxid: 1727145)	Flavonifractor plautii (NCBI taxid: 292800)
Anaerocolumna sedimenticola (NCBI taxid: 2696063)	Flintibacter sp. KGMB00164 (NCBI taxid: 2610895)
Anaerofustis sp. (NCBI taxid: 1872517)	Fusicatenibacter sp. (NCBI taxid: 2773922)
Anaerofustis stercorihominis (NCBI taxid: 214853)	Gemmiger formicilis (NCBI taxid: 745368)
Anaerostipes caccae (NCBI taxid: 105841)	Gordonibacter urolithinfaciens (NCBI taxid: 1335613)
Anaerostipes hadrus (NCBI taxid: 649756)	Granulicatella adiacens (NCBI taxid: 46124)
Anaerostipes hominis (NCBI taxid: 2025494)	Herbinix luporum (NCBI taxid: 1679721)
Anaerostipes rhamnosivorans (NCBI taxid: 1229621)	Holdemanella biformis (NCBI taxid: 1735)
Anaerotignum lactatifermentans (NCBI taxid: 160404)	Holdemanella porci (NCBI taxid: 2652276)
Anaerotignum propionicum (NCBI taxid: 28446)	Holdemania filiformis (NCBI taxid: 61171)
Anaerotignum sp. (NCBI taxid: 2039241)	Hungatella effluvii (NCBI taxid: 1096246)
Anaerotignum sp001304995	Hungatella hathewayi (NCBI taxid: 154046)
Anaerotruncus colihominis (NCBI taxid: 169435)	Intestinibaculum porci (NCBI taxid: 2487118)
Anaerotruncus rubiinfantis (NCBI taxid: 1720200)	Intestinimonas butyriciproducens (NCBI taxid: 1297617)

Bacillus bombysepticus (NCBI taxid: 658666)	Lachnoanaerobaculum sp000296385
Bacillus cereus (NCBI taxid: 1396)	Lachnoanaerobaculum umeaense (NCBI taxid: 617123)
Bacteroides caccae (NCBI taxid: 47678)	Lachnoclostridium phocaeense (NCBI taxid: 1871021)
Bacteroides caecimuris (NCBI taxid: 1796613)	Lachnoclostridium phytofermentans (NCBI taxid: 66219)
Bacteroides cellulosilyticus (NCBI taxid: 246787)	Lachnoclostridium sp. YL32 (NCBI taxid: 1834196)
Bacteroides coprocola (NCBI taxid: 310298)	Lachnospira eligens (NCBI taxid: 39485)
Bacteroides coprophilus (NCBI taxid: 387090)	Lachnospira sp003451515
Bacteroides dorei (NCBI taxid: 357276)	Lacrimispora saccharolytica (NCBI taxid: 84030)
Bacteroides eggerthii (NCBI taxid: 28111)	Lactobacillus ruminis (NCBI taxid: 1623)
Bacteroides faecis (NCBI taxid: 674529)	Lactococcus lactis (NCBI taxid: 1358)
Bacteroides finegoldii (NCBI taxid: 338188)	Lactococcus petauri (NCBI taxid: 1940789)
Bacteroides fragilis (NCBI taxid: 817)	Lawsonibacter sp944385665
Bacteroides helcogenes (NCBI taxid: 290053)	Ligilactobacillus ruminis (NCBI taxid: 1623)
Bacteroides heparinolyticus (NCBI taxid: 28113)	Longibaculum sp. KGMB06250 (NCBI taxid: 2584943)
Bacteroides intestinalis (NCBI taxid: 329854)	Longicatena caecimuris (NCBI taxid: 1796635)
Bacteroides luhongzhouii (NCBI taxid: 2650158)	Luoshenia tenuis (NCBI taxid: 2763654)
Bacteroides nordii (NCBI taxid: 291645)	Mageeibacillus indolicus (NCBI taxid: 884684)
Bacteroides ovatus (NCBI taxid: 28116)	Massilimicrobiota merdigallinarum
Bacteroides pectinophilus (NCBI taxid: 384638)	
Bacteroides plebeius (NCBI taxid: 310297)	Massilimicrobiota sp002160865
Bacteroides rodentium (NCBI taxid: 691816)	Massilimicrobiota timonensis (NCBI taxid: 1776392)

Bacteroides salyersiae (NCBI taxid: 291644)	Massilioclostridium methylpentosum
Bacteroides sp. A1C1 (NCBI taxid: 2528203)	Massiliprevotella massiliensis (NCBI taxid: 1816687)
Bacteroides sp. CACC 737 (NCBI taxid: 2755405)	Massilistercora timonensis (NCBI taxid: 2086584)
Bacteroides sp. CBA7301 (NCBI taxid: 2715212)	Mediterraneibacter torques (NCBI taxid: 33039)
Bacteroides sp. HF-162 (NCBI taxid: 2785531)	Megamonas funiformis (NCBI taxid: 437897)
Bacteroides sp. KGMB10229 (NCBI taxid: 2792859)	Megamonas rupellensis (NCBI taxid: 491921)
Bacteroides sp900552405	Megasphaera elsdenii (NCBI taxid: 907)
Bacteroides stercoris (NCBI taxid: 46506)	Megasphaera stantonii (NCBI taxid: 2144175)
Bacteroides thetaiotaomicron (NCBI taxid: 818)	Merdibacter merdigallinarum (NCBI taxid: 2838693)
Bacteroides uniformis (NCBI taxid: 820)	Merdibacter merdipullorum (NCBI taxid: 2838694)
Bacteroides vulgatus (NCBI taxid: 821)	Mesosutterella multiformis (NCBI taxid: 2259133)
Bacteroides xylanisolvens (NCBI taxid: 371601)	Methonobrevibacter sp. (NCBI taxid: 2172)
Bacteroides zhangwenhongii (NCBI taxid: 2650157)	Mitsuokella multacida (NCBI taxid: 52226)
Bacteroides zoogloformans (NCBI taxid: 28119)	Mogibacterium diversum (NCBI taxid: 114527)
Bariatricus comes (NCBI taxid: 410072)	Muribaculum intestinale (NCBI taxid: 1796646)
Barnesiella intestinihominis (NCBI taxid: 487174)	Negativibacillus massiliensis (NCBI taxid: 1871035)
Barnesiella viscericola (NCBI taxid: 397865)	Novisyntrophococcus fermenticellae (NCBI taxid: 2068655)
Bifidobacterium adolescentis (NCBI taxid: 1680)	NSJ-51 sp900549795

Bifidobacterium bifidum (NCBI taxid: 1681)	Odoribacter splanchnicus (NCBI taxid: 28118)
Bifidobacterium breve (NCBI taxid: 1685)	Olsenella sp. GAM18 (NCBI taxid: 2109685)
Bifidobacterium catenulatum (NCBI taxid: 1686)	Olsenella uli (NCBI taxid: 133926)
Bifidobacterium longum (NCBI taxid: 216816)	Oscillibacter sp. PEA192 (NCBI taxid: 2109687)
Bifidobacterium pseudocatenulatum (NCBI taxid: 28026)	Oscillibacter valericigenes (NCBI taxid: 351091)
Bilophila wadsworthia (NCBI taxid: 35833)	Oscillospiraceae sp.
Blautia argi (NCBI taxid: 1912897)	Parabacteroides distasonis (NCBI taxid: 823)
Blautia hansenii (NCBI taxid: 1322)	Parabacteroides goldsteinii (NCBI taxid: 328812)
Blautia hydrogenotrophica (NCBI taxid: 53443)	Parabacteroides johnsonii (NCBI taxid: 387661)
Blautia liquoris (NCBI taxid: 2779518)	Parabacteroides merdae (NCBI taxid: 46503)
Blautia massiliensis (NCBI taxid: 1737424)	Paraclostridium bifermentans (NCBI taxid: 1490)
Blautia obeum (NCBI taxid: 40520)	Paraclostridium dentum (NCBI taxid: 2662455)
Blautia parvula (NCBI taxid: 2877527)	Paraprevotella xylaniphila (NCBI taxid: 454155)
Blautia producta (NCBI taxid: 33035)	Parolsenella catena (NCBI taxid: 2003188)
Blautia pseudococcoides (NCBI taxid: 1796616)	Peptacetobacter hiranonis (NCBI taxid: 89152)
Blautia sp. SC05B48 (NCBI taxid: 2479767)	Peptoniphilus grossensis (NCBI taxid: 1465756)
Blautia stercoris (NCBI taxid: 871664)	Peptoniphilus obesi (NCBI taxid: 1472765)
Blautia wexlerae (NCBI taxid: 418240)	Peptostreptococcus sp. (NCBI taxid: 1262)
Bryantella formatexigens (NCBI taxid: 168384)	Phascolarctobacterium faecium (NCBI taxid: 33025)
Butyricimonas faecalis (NCBI taxid: 2093856)	Phascolarctobacterium sp. (NCBI taxid: 2049039)

Butyricimonas virosa (NCBI taxid: 544645)	Phascolarctobacterium succinatutens (NCBI taxid: 626940)
Butyrivibrio crossotus (NCBI taxid: 45851)	Phocaeicola coprocola (NCBI taxid: 310298)
Butyrivibrio hungatei (NCBI taxid: 185008)	Phocaeicola coprophilus (NCBI taxid: 387090)
Butyrivibrio proteoclasticus (NCBI taxid: 43305)	Phocaeicola dorei (NCBI taxid: 357276)
Campylobacter coli (NCBI taxid: 195)	Phocaeicola salanitronis (NCBI taxid: 376805)
Campylobacter jejuni (NCBI taxid: 197)	Phocaeicola vulgatus (NCBI taxid: 821)
Caproicibacter fermentans (NCBI taxid: 2576756)	Porphyromonas asaccharolytica (NCBI taxid: 28123)
Caproicibacterium amylolyticum (NCBI taxid: 2766537)	Prevotella buccae (NCBI taxid: 28126)
Caproiciproducens sp. NJN-50 (NCBI taxid: 2507162)	Prevotella buccalis (NCBI taxid: 28127)
Casaltella massiliensis (NCBI taxid: 938278)	Prevotella copri (NCBI taxid: 165179)
Catenibacterium mitsuokai (NCBI taxid: 100886)	Prevotella intermedia (NCBI taxid: 28131)
Christensenella minuta (NCBI taxid: 626937)	Prevotella melaninogenica (NCBI taxid: 28132)
Christensenella sp. Marseille-P3954 (NCBI taxid: 2086585)	Pseudobutyrvibrio xylanivorans (NCBI taxid: 185007)
Clostridium asparagiforme (NCBI taxid: 333367)	Pusillimonas faecalis (NCBI taxid: 2714358)
Clostridium bartlettii (NCBI taxid: 261299)	Romboutsia sp. (NCBI taxid: 1965302)
Clostridium beijerinckii (NCBI taxid: 1520)	Romboutsia sp. CE17 (NCBI taxid: 2724150)
Clostridium bolteae (NCBI taxid: 208479)	Romboutsia timonensis (NCBI taxid: 1776391)
Clostridium bornimense (NCBI taxid: 1216932)	Roseburia hominis (NCBI taxid: 301301)
Clostridium botulinum (NCBI taxid: 1491)	Roseburia intestinalis (NCBI taxid: 166486)

Clostridium butyricum (NCBI taxid: 1492)	Roseburia inulinivorans (NCBI taxid: 360807)
Clostridium cadaveris (NCBI taxid: 1529)	Ruminiclostridium cellulolyticum (NCBI taxid: 1521)
Clostridium hathewayi (NCBI taxid: 154046)	Ruminiclostridium siraeum (NCBI taxid: 39492)
Clostridium hylemonae (NCBI taxid: 89153)	Ruminococcus albus (NCBI taxid: 1264)
Clostridium innocuum (NCBI taxid: 1522)	Ruminococcus bicirculans (NCBI taxid: 1160721)
Clostridium leptum (NCBI taxid: 1535)	Ruminococcus bromii (NCBI taxid: 40518)
Clostridium methylpentosum (NCBI taxid: 84026)	Ruminococcus flavefaciens (NCBI taxid: 1265)
Clostridium nexile (NCBI taxid: 29361)	Ruminococcus gauvreauii (NCBI taxid: 438033)
Clostridium paraputrificum (NCBI taxid: 29363)	Ruminococcus gnavus (NCBI taxid: 33038)
Clostridium pasteurianum (NCBI taxid: 1501)	Ruminococcus lactaris (NCBI taxid: 46228)
Clostridium perfringens (NCBI taxid: 1502)	Ruminococcus sp. JE7A12 (NCBI taxid: 2564099)
Clostridium saccharobutylicum (NCBI taxid: 169679)	Ruminococcus torques (NCBI taxid: 33039)
Clostridium saccharoperbutylacetonicum (NCBI taxid: 36745)	Ruthenibacterium lactatiformans (NCBI taxid: 1550024)
Clostridium scindens (NCBI taxid: 29347)	Schaalia odontolytica (NCBI taxid: 1660)
Clostridium sp. (NCBI taxid: 1506)	Selenomonas ruminantium (NCBI taxid: 971)
Clostridium sp. BNL1100 (NCBI taxid: 755731)	Sellimonas intestinalis (NCBI taxid: 1653434)
Clostridium sp. C1 (NCBI taxid: 1155388)	Senegalimassilia anaerobia (NCBI taxid: 1473216)
Clostridium sp. SY8519 (NCBI taxid: 1042156)	Slackia exigua (NCBI taxid: 84109)
Clostridium spiroforme (NCBI taxid: 29348)	Slackia heliotrinireducens (NCBI taxid: 84110)

Clostridium sporogenes (NCBI taxid: 1509)	Slackia isoflavoniconvertens (NCBI taxid: 572010)
Clostridium tetani (NCBI taxid: 1513)	Sodaliophilus pleomorphus (NCBI taxid: 2606626)
Collinsella aerofaciens (NCBI taxid: 74426)	Solibaculum mannosilyticum (NCBI taxid: 2780922)
Collinsella bouchesdurhonensis (NCBI taxid: 1907654)	Solobacterium moorei (NCBI taxid: 102148)
Collinsella sp002232035	Streptococcus infantarius (NCBI taxid: 102684)
Collinsella sp905215835	Streptococcus pasteurianus (NCBI taxid: 197614)
Collinsella stercoris (NCBI taxid: 147206)	Streptococcus salivarius (NCBI taxid: 1304)
Coprobacillus cateniformis (NCBI taxid: 100884)	Streptococcus sanguinis (NCBI taxid: 1305)
Coprobacter fastidiosus (NCBI taxid: 1099853)	Streptococcus suis (NCBI taxid: 1307)
Coprobacter secundus (NCBI taxid: 1501392)	Streptococcus thermophilus (NCBI taxid: 1308)
Coprococcus catus (NCBI taxid: 116085)	Subdoligranulum variabile (NCBI taxid: 214851)
Coprococcus comes (NCBI taxid: 410072)	Thomasclavelia ramosa (NCBI taxid: 1547)
Coprococcus eutactus (NCBI taxid: 33043)	Thomasclavelia spiroformis (NCBI taxid: 29348)
Coprococcus sp000154245	UBA1394 sp900066845
Desulfovibrio piger (NCBI taxid: 901)	Veillonella dispar (NCBI taxid: 39778)
Dorea formicigenerans (NCBI taxid: 39486)	Vescimonas coprocola (NCBI taxid: 2714355)
Dorea longicatena (NCBI taxid: 88431)	Vescimonas fastidiosa (NCBI taxid: 2714353)
Duodenibacillus sp. (NCBI taxid: 1980700)	Vescimonas sp900545585

[00713] **Table 26 – By Species.**

[00714] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 26.

Akkermansia muciniphila (NCBI taxid: 239935)	Lacrimispora saccharolytica (NCBI taxid: 84030)
Alistipes dispar (NCBI taxid: 2585119)	Lactococcus lactis (NCBI taxid: 1358)
Alistipes finegoldii (NCBI taxid: 214856)	Lactococcus petauri (NCBI taxid: 1940789)
Alistipes ihumii (NCBI taxid: 1470347)	Longicatena caecimuris (NCBI taxid: 1796635)
Alistipes indistinctus (NCBI taxid: 626932)	Megamonas funiformis (NCBI taxid: 437897)
Alistipes onderdonkii (NCBI taxid: 328813)	Merdibacter merdipullorum (NCBI taxid: 2838694)
Alistipes putredinis (NCBI taxid: 28117)	Odoribacter splanchnicus (NCBI taxid: 28118)
Alistipes senegalensis (NCBI taxid: 1288121)	Parabacteroides distasonis (NCBI taxid: 823)
Alistipes shahii (NCBI taxid: 328814)	Parabacteroides goldsteinii (NCBI taxid: 328812)
Amedibacterium intestinale (NCBI taxid: 2583452)	Parabacteroides johnsonii (NCBI taxid: 387661)
Anaerobutyricum hallii (NCBI taxid: 39488)	Parabacteroides merdae (NCBI taxid: 46503)
Anaerofustis stercorihominis (NCBI taxid: 214853)	Porphyromonas asaccharolytica (NCBI taxid: 28123)
Anaerostipes caccae (NCBI taxid: 105841)	Prevotella copri (NCBI taxid: 165179)
Anaerostipes hadrus (NCBI taxid: 649756)	Roseburia hominis (NCBI taxid: 301301)
Anaerostipes hominis (NCBI taxid: 2025494)	Roseburia intestinalis (NCBI taxid: 166486)
Anaerotruncus colihominis (NCBI taxid: 169435)	Roseburia inulinivorans (NCBI taxid: 360807)
Anaerotruncus rubiinfantis (NCBI taxid: 1720200)	Ruminococcus bicirculans (NCBI taxid: 1160721)
Bacteroides caccae (NCBI taxid: 47678)	Ruminococcus bromii (NCBI taxid: 40518)

Bacteroides eggerthii (NCBI taxid: 28111)	Ruminococcus gnavus (NCBI taxid: 33038)
Bacteroides faecis (NCBI taxid: 674529)	Ruthenibacterium lactatiformans (NCBI taxid: 1550024)
Bacteroides finegoldii (NCBI taxid: 338188)	Sellimonas intestinalis (NCBI taxid: 1653434)
Bacteroides intestinalis (NCBI taxid: 329854)	Solibaculum mannosilyticum (NCBI taxid: 2780922)
Bacteroides nordii (NCBI taxid: 291645)	Streptococcus infantarius (NCBI taxid: 102684)
Bacteroides ovatus (NCBI taxid: 28116)	Streptococcus salivarius (NCBI taxid: 1304)
Bacteroides salyersiae (NCBI taxid: 291644)	Vescimonas coprocola (NCBI taxid: 2714355)
Bacteroides stercoris (NCBI taxid: 46506)	Agathobacter rectalis (NCBI taxid: 39491)
Bacteroides thetaiotaomicron (NCBI taxid: 818)	Agathobaculum sp003481705
Bacteroides uniformis (NCBI taxid: 820)	Anaerotignum sp001304995
Bacteroides xylanisolvens (NCBI taxid: 371601)	Bacillus bombysepticus (NCBI taxid: 658666)
Barnesiella intestinihominis (NCBI taxid: 487174)	Bacteroides sp900552405
Bifidobacterium adolescentis (NCBI taxid: 1680)	Bariatricus comes (NCBI taxid: 410072)
Bifidobacterium bifidum (NCBI taxid: 1681)	Clostridium sp. (NCBI taxid: 1506)
Bifidobacterium longum (NCBI taxid: 216816)	Collinsella sp002232035
Bifidobacterium pseudocatenulatum (NCBI taxid: 28026)	Collinsella sp905215835
Blautia massiliensis (NCBI taxid: 1737424)	Coprococcus sp000154245
Blautia stercoris (NCBI taxid: 871664)	Dysosmobacter faecalis
Blautia wexlerae (NCBI taxid: 418240)	Extibacter hylemonae

Butyricimonas faecalis (NCBI taxid: 2093856)	Faecalibacterium duncaniae (NCBI taxid: 411483)
Butyricimonas virosa (NCBI taxid: 544645)	Fimivivens sp900113995
Christensenella minuta (NCBI taxid: 626937)	Lachnoanaerobaculum sp000296385
Clostridium butyricum (NCBI taxid: 1492)	Lachnospira sp003451515
Clostridium leptum (NCBI taxid: 1535)	Lawsonibacter sp944385665
Clostridium paraputrificum (NCBI taxid: 29363)	Ligilactobacillus ruminis (NCBI taxid: 1623)
Clostridium scindens (NCBI taxid: 29347)	Luoshenia tenuis (NCBI taxid: 2763654)
Collinsella aerofaciens (NCBI taxid: 74426)	Massilimicrobiota merdigallinarum
Collinsella bouchesdurhonensis (NCBI taxid: 1907654)	Massilimicrobiota sp002160865
Coprobacillus cateniformis (NCBI taxid: 100884)	Massilioclostridium methylpentosum
Coprobacter secundus (NCBI taxid: 1501392)	Mediterraneibacter torques (NCBI taxid: 33039)
Coprococcus catus (NCBI taxid: 116085)	Merdibacter merdigallinarum (NCBI taxid: 2838693)
Dorea longicatena (NCBI taxid: 88431)	NSJ-51 sp900549795
Enorma massiliensis (NCBI taxid: 1472761)	Paraclostridium dentum (NCBI taxid: 2662455)
Enterocloster aldenensis (NCBI taxid: 358742)	Phocaeicola coprocola (NCBI taxid: 310298)
Eubacterium callanderi (NCBI taxid: 53442)	Phocaeicola coprophilus (NCBI taxid: 387090)
Eubacterium limosum (NCBI taxid: 1736)	Phocaeicola dorei (NCBI taxid: 357276)
Eubacterium ventriosum (NCBI taxid: 39496)	Phocaeicola vulgatus (NCBI taxid: 821)
Faecalibacillus intestinalis (NCBI taxid: 1982626)	Romboutsia sp. (NCBI taxid: 1965302)

Finnegoldia magna (NCBI taxid: 1260)	Ruminiclostridium siraeum (NCBI taxid: 39492)
Gemmiger formicilis (NCBI taxid: 745368)	Thomasclavelia ramosa (NCBI taxid: 1547)
Holdemanella porci (NCBI taxid: 2652276)	Thomasclavelia spiroformis (NCBI taxid: 29348)
Hungatella effluvii (NCBI taxid: 1096246)	UBA1394 sp900066845
	Vescimonas sp900545585

[00715] **Table 27 – By Species.**

[00716] In some embodiments, the composition of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 27.

Akkermansia muciniphila (NCBI taxid: 239935)	Hungatella hathewayi (NCBI taxid: 154046)
Alistipes communis (NCBI taxid: 2585118)	Intestinimonas butyriciproducens (NCBI taxid: 1297617)
Alistipes dispar (NCBI taxid: 2585119)	Lachnoanaerobaculum umeaense (NCBI taxid: 617123)
Alistipes finegoldii (NCBI taxid: 214856)	Lachnoclostridium phocaeense (NCBI taxid: 1871021)
Alistipes indistinctus (NCBI taxid: 626932)	Lachnoclostridium sp. YL32 (NCBI taxid: 1834196)
Alistipes megaguti (NCBI taxid: 2364787)	Lacrimispora saccharolytica (NCBI taxid: 84030)
Alistipes onderdonkii (NCBI taxid: 328813)	Longibaculum sp. KGMB06250 (NCBI taxid: 2584943)
Alistipes senegalensis (NCBI taxid: 1288121)	Longicatena caecimuris (NCBI taxid: 1796635)
Amedibacterium intestinale (NCBI taxid: 2583452)	Massilistercora timonensis (NCBI taxid: 2086584)
Anaerobutyricum hallii (NCBI taxid: 39488)	Novisyntrophococcus fermenticellae (NCBI taxid: 2068655)
Anaerostipes caccae (NCBI taxid: 105841)	Odoribacter splanchnicus (NCBI taxid: 28118)

Anaerostipes hadrus (NCBI taxid: 649756)	Oscillibacter sp. PEA192 (NCBI taxid: 2109687)
Bacteroides caccae (NCBI taxid: 47678)	Oscillibacter valericigenes (NCBI taxid: 351091)
Bacteroides caecimuris (NCBI taxid: 1796613)	Parabacteroides distasonis (NCBI taxid: 823)
Bacteroides cellulosilyticus (NCBI taxid: 246787)	Parabacteroides goldsteinii (NCBI taxid: 328812)
Bacteroides eggerthii (NCBI taxid: 28111)	Parabacteroides merdae (NCBI taxid: 46503)
Bacteroides fragilis (NCBI taxid: 817)	Phocaeicola dorei (NCBI taxid: 357276)
Bacteroides ovatus (NCBI taxid: 28116)	Phocaeicola salanitronis (NCBI taxid: 376805)
Bacteroides salyersiae (NCBI taxid: 291644)	Phocaeicola vulgatus (NCBI taxid: 821)
Bacteroides thetaiotaomicron (NCBI taxid: 818)	Pseudobutyrvibrio xylanivorans (NCBI taxid: 185007)
Bacteroides uniformis (NCBI taxid: 820)	Pusillimonas faecalis (NCBI taxid: 2714358)
Bacteroides xylanisolvens (NCBI taxid: 371601)	Roseburia hominis (NCBI taxid: 301301)
Bifidobacterium longum (NCBI taxid: 216816)	Roseburia intestinalis (NCBI taxid: 166486)
Blautia argi (NCBI taxid: 1912897)	Ruminococcus bicirculans (NCBI taxid: 1160721)
Blautia hansenii (NCBI taxid: 1322)	Ruminococcus gnavus (NCBI taxid: 33038)
Blautia liquoris (NCBI taxid: 2779518)	Ruthenibacterium lactatiformans (NCBI taxid: 1550024)
Blautia massiliensis (NCBI taxid: 1737424)	Solibaculum mannosilyticum (NCBI taxid: 2780922)
Blautia producta (NCBI taxid: 33035)	Vescimonas coprocola (NCBI taxid: 2714355)
Blautia pseudococcoides (NCBI taxid: 1796616)	Vescimonas fastidiosa (NCBI taxid: 2714353)
Blautia parvula (NCBI taxid: 2877527)	Bacteroides zhangwenhongii (NCBI taxid: 2650157)

Blautia sp. SC05B48 (NCBI taxid: 2479767)	Butyricimonas faecalis (NCBI taxid: 2093856)
Butyrivibrio hungatei (NCBI taxid: 185008)	Butyricimonas virosa (NCBI taxid: 544645)
Butyrivibrio proteoclasticus (NCBI taxid: 43305)	Paraprevotella xylaniphila (NCBI taxid: 454155)
Christensenella minuta (NCBI taxid: 626937)	Phocaeicola coprophilus (NCBI taxid: 387090)
Clostridium hylemonae (NCBI taxid: 89153)	Prevotella melaninogenica (NCBI taxid: 28132)
Clostridium scindens (NCBI taxid: 29347)	Alistipes putredinis (NCBI taxid: 28117)
Clostridium sp. SY8519 (NCBI taxid: 1042156)	Alistipes shahii (NCBI taxid: 328814)
Collinsella aerofaciens (NCBI taxid: 74426)	Bacteroides intestinalis (NCBI taxid: 329854)
Coprococcus comes (NCBI taxid: 410072)	Bacteroides stercoris (NCBI taxid: 46506)
Coprococcus eutactus (NCBI taxid: 33043)	Bifidobacterium adolescentis (NCBI taxid: 1680)
Dysosmobacter welbionis (NCBI taxid: 2093857)	Bifidobacterium bifidum (NCBI taxid: 1681)
Enterocloster bolteae (NCBI taxid: 208479)	Coprococcus catus (NCBI taxid: 116085)
Enterococcus faecium (NCBI taxid: 1352)	Methonobrevibacter sp. (NCBI taxid: 2172)
Erysipelatoclostridium ramosum (NCBI taxid: 1547)	Parabacteroides johnsonii (NCBI taxid: 387661)
Lachnospira eligens (NCBI taxid: 39485)	Phocaeicola coprocola (NCBI taxid: 310298)
Eubacterium sp. c-25 (NCBI taxid: 3028070)	Roseburia inulinivorans (NCBI taxid: 360807)
Eubacterium sp. NSJ-61 (NCBI taxid: 2764325)	Ruminococcus bromii (NCBI taxid: 40518)
Faecalibacterium prausnitzii (NCBI taxid: 853)	Ruminococcus torques (NCBI taxid: 33039)
Flavonifractor plautii (NCBI taxid: 292800)	Subdoligranulum variabile (NCBI taxid: 214851)
Flintibacter sp. KGMB00164 (NCBI taxid: 2610895)	

[00717] Table 28 – Species of a further embodiment of the invention.

Agathobacter rectalis (NCBI taxid:39491)	Dorea longicatena (NCBI taxid:88431)
Agathobaculum sp003481705	Dysosmobacter faecalis
Akkermansia muciniphila (NCBI taxid:239935)	Enorma massiliensis (NCBI taxid:1472761)
Alistipes dispar (NCBI taxid:2585119)	Enterocloster aldenensis (NCBI taxid:358742)
Alistipes finegoldii (NCBI taxid:214856)	Eubacterium callanderi (NCBI taxid:53442)
Alistipes ihumii (NCBI taxid:1470347)	Eubacterium limosum (NCBI taxid:1736)
Alistipes indistinctus (NCBI taxid:626932)	Eubacterium ventriosum (NCBI taxid:39496)
Alistipes onderdonkii (NCBI taxid:328813)	Extibacter hylemonae
Alistipes putredinis (NCBI taxid:28117)	Faecalibacillus intestinalis (NCBI taxid:1982626)
Alistipes senegalensis (NCBI taxid:1288121)	Faecalibacterium duncaniae (NCBI taxid:411483)
Alistipes shahii (NCBI taxid:328814)	Fimivivens sp900113995
Amedibacterium intestinale (NCBI taxid:2583452)	Gemmiger formicilis (NCBI taxid:745368)
Anaerobutyricum hallii (NCBI taxid:39488)	Holdemanella porci (NCBI taxid:2652276)
Anaerostipes caccae (NCBI taxid:105841)	Hungatella effluvii (NCBI taxid:1096246)
Anaerostipes hadrus (NCBI taxid:649756)	Lachnoanaerobaculum sp000296385
Anaerostipes hominis (NCBI taxid:2025494)	Lachnospira sp003451515
Anaerotignum sp001304995	Lacrimispora saccharolytica (NCBI taxid:84030)
Anaerotruncus colihominis (NCBI taxid:169435)	Lactococcus petauri (NCBI taxid:1940789)
Anaerotruncus rubiinfantis (NCBI taxid:1720200)	Lawsonibacter sp944385665
Bacteroides eggerthii (NCBI taxid:28111)	Ligilactobacillus ruminis (NCBI taxid:1623)
Bacteroides finegoldii (NCBI taxid:338188)	Longicatena caecimuris (NCBI taxid:1796635)
Bacteroides intestinalis (NCBI taxid:329854)	Luoshenia tenuis (NCBI taxid:2763654)
Bacteroides nordii (NCBI taxid:291645)	Massilimicrobiota merdigallinarum
Bacteroides ovatus (NCBI taxid:28116)	Massilimicrobiota sp002160865

Bacteroides salyersiae (NCBI taxid:291644)	Massilioclostridium methylpentosum
Bacteroides sp900552405	Mediterraneibacter torques (NCBI taxid:33039)
Bacteroides stercoris (NCBI taxid:46506)	Megamonas funiformis (NCBI taxid:437897)
Bacteroides thetaiotaomicron (NCBI taxid:818)	Merdibacter merdigallinarum (NCBI taxid:2838693)
Bacteroides uniformis (NCBI taxid:820)	NSJ-51 sp900549795
Bacteroides xylanisolvens (NCBI taxid:371601)	Odoribacter splanchnicus (NCBI taxid:28118)
Bariatricus comes (NCBI taxid:410072)	Parabacteroides distasonis (NCBI taxid:823)
Barnesiella intestinihominis (NCBI taxid:487174)	Parabacteroides goldsteinii (NCBI taxid:328812)
Bifidobacterium adolescentis (NCBI taxid:1680)	Parabacteroides merdae (NCBI taxid:46503)
Bifidobacterium bifidum (NCBI taxid:1681)	Paraclostridium dentum (NCBI taxid:2662455)
Bifidobacterium longum (NCBI taxid:216816)	Phocaeicola coprocola (NCBI taxid:310298)
Bifidobacterium pseudocatenulatum (NCBI taxid:28026)	Phocaeicola coprophilus (NCBI taxid:387090)
Blautia massiliensis (NCBI taxid:1737424)	Phocaeicola dorei (NCBI taxid:357276)
Blautia stercoris (NCBI taxid:871664)	Phocaeicola vulgatus (NCBI taxid:821)
Butyricimonas faecalis (NCBI taxid:2093856)	Prevotella copri (NCBI taxid:165179)
Butyricimonas virosa (NCBI taxid:544645)	Romboutsia sp. (NCBI taxid:1965302)
Christensenella minuta (NCBI taxid:626937)	Roseburia hominis (NCBI taxid:301301)
Clostridium scindens (NCBI taxid:29347)	Roseburia intestinalis (NCBI taxid:166486)
Clostridium butyricum (NCBI taxid:1492)	Roseburia inulinivorans (NCBI taxid:360807)
Clostridium leptum (NCBI taxid:1535)	Ruminiclostridium siraeum (NCBI taxid:39492)
Clostridium sp. (NCBI taxid:1506)	Ruminococcus bicirculans (NCBI taxid:1160721)
Collinsella aerofaciens (NCBI taxid:74426)	Ruminococcus bromii (NCBI taxid:40518)

Collinsella bouchesdurhonensis (NCBI taxid:1907654)	Ruthenibacterium lactatiformans (NCBI taxid:1550024)
Collinsella sp002232035	Sellimonas intestinalis (NCBI taxid:1653434)
Collinsella sp905215835	Solibaculum mannosilyticum (NCBI taxid:2780922)
Coprobacillus cateniformis (NCBI taxid:100884)	Thomasclavelia ramosa (NCBI taxid:1547)
Coprobacter secundus (NCBI taxid:1501392)	UBA1394 sp900066845
Coprococcus catus (NCBI taxid:116085)	Vescimonas coprocola (NCBI taxid:2714355)
Coprococcus sp000154245	Vescimonas sp900545585

[00718] In some embodiments, the compositions or formulations of the invention includes one or more microbes selected from one or more of the microbial species as set forth in Table 27 or 28.

- 5 [00719] “Keystone”, as discussed already above, refers to taxa identified in the literature which predicts microbiome recovery post antibiotic intervention. As used herein, the terms “keystone microbial strains” or “keystone species” refers to microbes having a synergistic role in survival, integration, and flourishing of other species in the formulations described herein. For example, a keystone microbial strain may play a role in survival of one or more core
- 10 community microbial strains during culture of the microbial strains, during preparation of the formulations, during administration of the formulations, and/or during uptake of the microbial strains in a subject following administration. In some embodiments, the keystone microbial strains improve microbial growth, activity, survival, and/or proliferation of a microbial consortium in a bioreactor during culture. In some embodiments, the keystone microbial
- 15 strains improve growth activity, survival, and/or and proliferation of a microbial consortium in the gut of a subject. In some embodiments, the keystone microbial strains improve growth activity, survival, and/or and proliferation of a microbial consortium both in a bioreactor and in the gut of a subject. In some embodiments, the keystone strains reduce the growth, activity, survival, and/or proliferation of pathogens or microbes that would otherwise negatively impact
- 20 the core community strains. In some embodiments, the keystone strains perform one or more of the following: provide nutrients for the core community strains through for example metabolizing compounds into more digestible components, maintain a desired pH, serve as a prebiotic, serve as postbiotic, etc. In alternative embodiments, any one or more (e.g., 1-5, 5-

10, etc.) of the phyla, genera, species or strains identified in Table 29 or 14 are expressly excluded from the co-culture, the formulation to be administered, or both. One reason for such exclusion may be that such microbe has a deleterious effect on a particular disease state.

[00720] “Minimum core”, as discussed already above, refers to remaining taxa identified

5 as preferentially important through the inventor’s analyses. For example, using the methods described in Example 6. As used herein, the terms “minimum core species”, “core community microbial strains” or “core community microbial species” refers to a foundational group of microbes that function in synergy with one another, and together with keystone microbial strains, restore, regenerate, improve, enhance, supplement, protect, stabilize, and/or boost a
10 microbiome, such as a gut microbiome. In some embodiments, the core community microbial strains may maintain its communal synergistic function in the absence of any one strain or any few strains as set forth in Tables 29 and 30. In some embodiments, a greater synergistic function takes place with the combination of the greatest number of strains as set forth in Table 30. In alternative embodiments, any one or more (e.g., 1-5, 5-10, etc.) of the phyla, genera,
15 species or strains identified in Table 30 are expressly excluded from the co-culture, the formulation to be administered, or both. One reason for such exclusion may be that such microbe has a deleterious effect on a particular disease state.

[00721] In some embodiments, the compositions of the invention include one or more core community microbial strains and one or more keystone microbial strains. For example, the
20 formulations may include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, or 26 core community microbial strains, and 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, or 22 keystone microbial strains. In some embodiments, the core community microbial strains are selected from the strains as set forth in Table 30. In some embodiments, the 5 keystone microbial strains are selected from the strains as set forth
25 in Table 29.

[00722] **Table 29 – Microbial Keystones.**

Phylum	Genus	Species	Strain (NCBI TaxID)
Actinomycetota	Bifidobacterium	Bifidobacterium longum	216816
Bacillota	Faecalibacterium	Faecalibacterium prausnitzii/Faecalibacterium duncaniae	853/411483
Actinomycetota	Bifidobacterium	Bifidobacterium bifidum	1681
Bacteroidota	Alistipes	Alistipes putredinis	28117

Bacteroidota	Alistipes	Alistipes shahii	328814
Bacteroidota	Bacteroides	Bacteroides intestinalis	329854
Bacteroidota	Bacteroides	Bacteroides stercoris	46506
Actinomycetota	Bifidobacterium	Bifidobacterium adolescentis	1680
Bacillota	Coprococcus	Coprococcus catus	116085
Euryarchaeota	Methanobrevibacter	Methanobrevibacter smithii	2173
Bacteroidota	Parabacteroides	Parabacteroides johnsonii	387661
Bacteroidota	Phocaeicola	Phocaeicola coprocola	310298
Bacillota	Roseburia	Roseburia inulinivorans	360807
Bacillota	Ruminococcus	Ruminococcus bromii	40518
Bacillota	Ruminococcus	Ruminococcus torques/Mediterraneibacter torques	33039
Bacillota	Subdoligranulum/Gemmiger	Subdoligranulum variable/Gemmiger formicilis	214851/745368
Bacteroidota	Bacteroides	Bacteroides caccae	47678
Bacteroidota	Bacteroides	Bacteroides coprocola	310298
Bacteroidota	Bacteroides	Bacteroides eggerthii	28111
Bacteroidota	Bacteroides	Bacteroides thetaiotaomicron	818
Bacteroidota	Bacteroides	Bacteroides uniformis	820
Bacteroidota	Parabacteroides	Parabacteroides distasonis	823

[00723] Table 30 – Microbial Core Community.

Phylum	Genus	Species	Strain (NCBI TaxID)
Actinomycetota	Bifidobacterium	Bifidobacterium longum	216816
Bacillota	Faecalibacterium	Faecalibacterium prausnitzii/Faecalibacterium duncaniae	853/411483
Bacillota	Dysosmobacter	Dysosmobacter welbionis	2093857

Bacillota	Enterocloster	Enterocloster bolteae/Enterocloster aldensis	208479/35874 2
Bacteroidota	Alistipes	Alistipes megaguti	2364787
Bacteroidota	Parabacteroides	Parabacteroides goldsteinii	328812
Bacillota	Flavonifractor	Flavonifractor plautii	292800
Bacteroidota	Alistipes	Alistipes communis	2585118
Bacillota	Ruthenibacterium	Ruthenibacterium lactatiformans	1550024
Bacillota	Vescimonas	Vescimonas coprocola	2714355
Actinomycetota	Collinsella	Collinsella aerofaciens	74426
Bacillota	Coprococcus/Bariatricus	Coprococcus comes/Bariatricus comes	410072
Bacillota	Ruminococcus	Ruminococcus gnavus	33038
Bacillota	Ruminococcus	Ruminococcus bicirculans	1160721
Bacteroidota	Bacteroides	Bacteroides caecimuris	1796613
Bacillota	Coprococcus	Coprococcus eutactus/Coprococcus sp000154245	33043/
Bacteroidota	Butyricimonas	Butyricimonas virosa/Butyricimonas phoceensis	544645/17202 03
Bacteroidota	Phocaeicola	Phocaeicola salanitronis	376805
Bacteroidota	Alistipes	Alistipes dispar	2585119
Bacillota	Clostridium	Clostridium scindens	29347
Bacteroidota	Parabacteroides	Parabacteroides merdae	46503
Bacteroidota	Bacteroides	Bacteroides salyersiae	291644
Bacillota	Pusillimonas/Dyosmobacter	Pusillimonas faecalis/Dysosmobacter faecalis	2714358/
Bacillota	Solibaculum	Solibaculum mannosilyticum	2780922
Verrucomicrobiota	Akkermansia	Akkermansia muciniphila	239935

Bacillota	Christensenella	Christensenella minuta	626937
-----------	-----------------	------------------------	--------

T

[00724] **Table 31 – Microbial Keystones and Core Community currently represented in the 143 isolates comprising BB265.**

Phylum	Genus	Species	Strain (NCBI TaxID)
Verrucomicrobiota	Akkermansia	Akkermansia muciniphila	239935
Bacteroidota	Alistipes	Alistipes dispar	2585119
Bacteroidota	Alistipes	Alistipes putredinis	28117
Bacteroidota	Alistipes	Alistipes shahii	328814
Bacteroidota	Bacteroides	Bacteroides caccae	47678
Bacteroidota	Bacteroides	Bacteroides coprocola	310298
Bacteroidota	Bacteroides	Bacteroides eggerthii	28111
Bacteroidota	Bacteroides	Bacteroides intestinalis	329854
Bacteroidota	Bacteroides	Bacteroides salyersiae	291644
Bacteroidota	Bacteroides	Bacteroides stercoris	46506
Bacteroidota	Bacteroides	Bacteroides thetaiotaomicron	818
Bacteroidota	Bacteroides	Bacteroides uniformis	820
Actinomycetota	Bifidobacterium	Bifidobacterium adolescentis	1680
Actinomycetota	Bifidobacterium	Bifidobacterium bifidum	1681
Actinomycetota	Bifidobacterium	Bifidobacterium longum	216816
Bacteroidota	Butyricimonas	Butyricimonas virosa/Butyricimonas phoceensis	544645/1720203
Bacillota	Christensenella	Christensenella minuta	626937
Bacillota	Clostridium	Clostridium scindens	29347
Actinomycetota	Collinsella	Collinsella aerofaciens	74426
Bacillota	Coprococcus	Coprococcus catus	116085
Bacillota	Coprococcus/Bariatricus	Coprococcus comes/Bariatricus comes	410072
Bacillota	Coprococcus	Coprococcus eutactus/Coprococcus sp000154245	33043/

Bacillota	Enterocloster	Enterocloster bolteae/Enterocloster aldensis	208479/35874 2
Bacillota	Faecalibacterium	Faecalibacterium prausnitzii/Faecalibacterium duncaniae	853/411483
Bacteroidota	Parabacteroides	Parabacteroides distasonis	823
Bacteroidota	Parabacteroides	Parabacteroides goldsteinii	328812
Bacteroidota	Parabacteroides	Parabacteroides johnsonii	387661
Bacteroidota	Parabacteroides	Parabacteroides merdae	46503
Bacteroidota	Phocaeicola	Phocaeicola coprocola	310298
Bacillota	Pusillimonas/Dyosmobacter	Pusillimonas faecalis/Dysosmobacter faecalis	2714358/
Bacillota	Roseburia	Roseburia inulinivorans	360807
Bacillota	Ruminococcus	Ruminococcus bicirculans	1160721
Bacillota	Ruminococcus	Ruminococcus bromii	40518
Bacillota	Ruminococcus	Ruminococcus gnavus	33038
Bacillota	Ruminococcus	Ruminococcus torques/Mediterraneibacter torques	33039
Bacillota	Ruthenibacterium	Ruthenibacterium lactatiformans	1550024
Bacillota	Solibaculum	Solibaculum mannosilyticum	2780922
Bacillota	Subdoligranulum/Gemmiger	Subdoligranulum variabile/Gemmiger formicilis	214851/74536 8
Bacillota	Vescimonas	Vescimonas coprocola	2714355

[00725] **Table 32 – Microbial Keystones and Core Community taxa in a further embodiment.**

Phylum	Genus	Species	Strain (NCBI TaxID)
Verrucomicrobiota	Akkermansia	Akkermansia muciniphila	239935
Bacteroidota	Alistipes	Alistipes dispar	2585119
Bacteroidota	Alistipes	Alistipes putredinis	28117
Bacteroidota	Alistipes	Alistipes shahii	328814
Bacteroidota	Bacteroides	Bacteroides coprocola	310298
Bacteroidota	Bacteroides	Bacteroides eggerthii	28111
Bacteroidota	Bacteroides	Bacteroides intestinalis	329854
Bacteroidota	Bacteroides	Bacteroides salyersiae	291644
Bacteroidota	Bacteroides	Bacteroides stercoris	46506
Bacteroidota	Bacteroides	Bacteroides thetaiotaomicron	818
Bacteroidota	Bacteroides	Bacteroides uniformis	820
Actinomycetota	Bifidobacterium	Bifidobacterium adolescentis	1680
Actinomycetota	Bifidobacterium	Bifidobacterium bifidum	1681
Actinomycetota	Bifidobacterium	Bifidobacterium longum	216816
Bacteroidota	Butyricimonas	Butyricimonas virosa/Butyricimonas phoceensis	544645/1720203
Bacillota	Christensenella	Christensenella minuta	626937
Bacillota	Clostridium	Clostridium scindens	29347
Actinomycetota	Collinsella	Collinsella aerofaciens	74426
Bacillota	Coprococcus	Coprococcus catus	116085
Bacillota	Coprococcus/Bariatricus	Coprococcus comes/Bariatricus comes	410072
Bacillota	Coprococcus	Coprococcus eutactus/Coprococcus sp000154245	33043/
Bacillota	Enterocloster	Enterocloster bolteae/Enterocloster aldensis	208479/358742

Bacillota	Faecalibacterium	Faecalibacterium prausnitzii/Faecalibacterium duncaniae	853/411483
Bacteroidota	Parabacteroides	Parabacteroides distasonis	823
Bacteroidota	Parabacteroides	Parabacteroides goldsteinii	328812
Bacteroidota	Parabacteroides	Parabacteroides merdae	46503
Bacteroidota	Phocaeicola	Phocaeicola coprocola	310298
Bacillota	Pusillimonas/Dyosmobacter	Pusillimonas faecalis/Dysosmobacter faecalis	2714358/
Bacillota	Roseburia	Roseburia inulinivorans	360807
Bacillota	Ruminococcus	Ruminococcus bicirculans	1160721
Bacillota	Ruminococcus	Ruminococcus bromii	40518
Bacillota	Ruminococcus	Ruminococcus torques/Mediterraneibacter torques	33039
Bacillota	Ruthenibacterium	Ruthenibacterium lactatiformans	1550024
Bacillota	Solibaculum	Solibaculum mannosilyticum	2780922
Bacillota	Subdoligranulum/Gemmiger	Subdoligranulum variabile/Gemmiger formicilis	214851/745368
Bacillota	Vescimonas	Vescimonas coprocola	2714355
Verrucomicrobiota	Akkermansia	Akkermansia muciniphila	239935

[00726] In some embodiments, the compositions or formulations of the invention comprise, consist of, or consist essentially of any 1 or more core community microbial strains as set forth in Table 30 and any 1 or more keystone microbial strains as set forth in Table 29; any 2 or

5 more core community microbial strains as set forth in Table 30 and any 1 or more keystone microbial strains as set forth in Table 29; any 3 or more core community microbial strains as set forth in Table 30 and any 1 or more keystone microbial strains as set forth in Table 29; any

5 or more core community microbial strains as set forth in Table 30 and any 1 or more keystone microbial strains as set forth in Table 29; any 3 or more core community microbial strains as set forth in Table 30 and any 3 or more keystone microbial strains as set forth in Table 29; any 5 or more core community microbial strains as set forth in Table 30 and any 3 or more keystone microbial strains as set forth in Table 29; any 5 or more core community microbial strains as set forth in Table 30 and any 5 or more keystone microbial strains as set forth in Table 29; any 10 or more core community microbial strains as set forth in Table 30 and any 3 or more keystone microbial strains as set forth in Table 29; any 10 or more core community microbial strains as set forth in Table 30 and any 5 or more keystone microbial strains as set forth in Table 29; any 10 or more core community microbial strains as set forth in Table 30 and any 10 or more keystone microbial strains as set forth in Table 29; any 15 or more core community microbial strains as set forth in Table 30 and any 3 or more keystone microbial strains as set forth in Table 29; any 15 or more core community microbial strains as set forth in Table 30 and any 5 or more keystone microbial strains as set forth in Table 29; any 15 or more core community microbial strains as set forth in Table 30 and any 10 or more keystone microbial strains as set forth in Table 29; any 15 or more core community microbial strains as set forth in Table 30 and any 15 or more keystone microbial strains as set forth in Table 29; any 20 or more core community microbial strains as set forth in Table 30 and any 3 or more keystone microbial strains as set forth in Table 29; any 20 or more core community microbial strains as set forth in Table 30 and any 5 or more keystone microbial strains as set forth in Table 29; any 20 or more core community microbial strains as set forth in Table 30 and any 10 or more keystone microbial strains as set forth in Table 29; any 20 or more core community microbial strains as set forth in Table 30 and any 15 or more keystone microbial strains as set forth in Table 29; any 20 or more core community microbial strains as set forth in Table 30 and any 20 or more keystone microbial strains as set forth in Table 29; all core community microbial strains as set forth in Table 30 and any 3 or more keystone microbial strains as set forth in Table 29; all core community microbial strains as set forth in Table 30 and any 5 or more keystone microbial strains as set forth in Table 29; all core community microbial strains as set forth in Table 30 and any 10 or more keystone microbial strains as set forth in Table 29; all core community microbial strains as set forth in Table 30 and any 15 or more keystone microbial strains as set forth in Table 29; all core community microbial strains as set forth in Table 30 and any 20 or more keystone microbial strains as set forth in Table 29; all core community microbial strains as set forth in Table 30 and all keystone microbial strains as set forth in Table 29, or any number of core community microbial strains and any number of keystone microbial strains within a range described herein. In some embodiments, the compositions or formulations of the invention include any number of the core community

microbial strains as set forth in Table 30 in combination with any number of the keystone microbial strains as set forth in Table 29.

[00727] In some embodiments, compositions or formulations of the invention include a ratio of core community microbial strains to keystone microbial strains. In some embodiments, the ratio of core community microbial strains to keystone microbial strains is in a ratio of 20:1, 15:1, 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, 1:1, 1:2, 1:3, 1:4, 1:5, 1:6, 1:7, 1:8, 1:9, 1:10, 1:15, or 1:20 or at a ratio between any two of the aforementioned ratios. In some embodiments, the microbial strains in the composition or formulation of the invention include a majority of core community microbial strains and a minority of keystone microbial strains. In some embodiments, the compositions or formulations of the invention include the core community microbial strains at a percentage of total microbial strains in an amount of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100% or an amount within a range defined by any two of the aforementioned values. In some embodiments, the compositions or formulations of the invention include keystone microbial strains at a percentage of total microbial strains in an amount of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 99%, or 100% or an amount within a range defined by any two of the aforementioned values. In some embodiments, the core community microbial strains are present in the composition or formulation of the invention in an amount of 80% and the keystone microbial strains are present in the composition or formulation of the invention in an amount of 20%. In some embodiments, the core community microbial strains are present in the composition or formulation of the invention in an amount of 70% and the keystone microbial strains are present in the formulation in an amount of 30%. In some embodiments, the core community microbial strains are present in the composition or formulation of the invention in an amount of 60% and the keystone microbial strains are present in the formulation in an amount of 40%. In some embodiments, the core community microbial strains are present in the composition or formulation of the invention in an amount of 50% and the keystone microbial strains are present in the composition or formulation of the invention in an amount of 50%. In some embodiments, the core community microbial strains are present in the composition or formulation of the invention in an amount of 40% and the keystone microbial strains are present in the composition or formulation of the invention in an amount of 60%. In some embodiments, the core community microbial strains are present in the composition or formulation of the invention in an amount of 30% and the keystone microbial strains are present in the composition or formulation of the invention in an amount of 70%. In some embodiments, the percentage of core community microbial strains and the percentage of keystone microbial strains are present at amounts within the percentages described herein.

C EXAMPLE 3 – CHARACTERIZING THE BB265 COMPLEX COMMUNITY LIVE BIOTHERAPEUTIC PRODUCT

C.1 STUDY AIM

[00728] The aim of this study was to characterize the predicted functional metabolic
5 capacity of isolates comprising, in one embodiment, the BB265 complex community live
biotherapeutic product.

C.2 MATERIALS, METHODS AND RESULTS

C.2.1 SUBSTRATE METABOLISM

[00729] The sulfur-related metabolic genes, their reactions, and metabolites functionally
10 predicted in the genomes of isolates comprising the BB265 complex community live
biotherapeutic product are presented in Table 33.

Table 33 – The sulfur-related metabolic genes, reactions, and metabolites functionally predicted in the genomes of isolates comprising the BB265 complex community live biotherapeutic product.

Gene	Gene name	Reaction/Metabolites	No. annotations
ahcY	adenosylhomocysteinase	S-Adenosyl-L-homocysteine + H ₂ O $\rightleftharpoons$ Adenosine + L-Homocysteine	31
apr	adenylyl-sulfate reductase	AMP + Sulfite + Glutathione disulfide $\rightleftharpoons$ Adenylyl sulphate + 2 Glutathione	1097
asrA	anaerobic sulfide reductase A	Hydrogen sulfide + 3 NADP ⁺ + 3 H ₂ O $\rightleftharpoons$ Sulfite + 3 NADPH + 3 H ⁺	15
aspB	aspartate aminotransferase	L-Aspartate + 2-Oxoglutarate $\rightleftharpoons$ Oxaloacetate + L-Glutamate	4
aspC	aspartate aminotransferase	L-Aspartate + 2-Oxoglutarate $\rightleftharpoons$ Oxaloacetate + L-Glutamate	74
asrB	anaerobic sulfide reductase B	Hydrogen sulfide + 3 NADP ⁺ + 3 H ₂ O $\rightleftharpoons$ Sulfite + 3 NADPH + 3 H ⁺	15
asrC	anaerobic sulfide reductase C	Hydrogen sulfide + 3 NADP ⁺ + 3 H ₂ O $\rightleftharpoons$ Sulfite + 3 NADPH + 3 H ⁺	11
bsh	bile salt hydrolase	Taurocholate + H ₂ O $\rightleftharpoons$ Cholic acid + Taurine	18
CAT	cysteine aminotransferase	L-Cysteine + 2-Oxoglutarate $\rightleftharpoons$ Mercaptopyruvate + L-Glutamate	33608

CBS	cystathionine beta-synthase	L-Serine + Hydrogen sulfide $\rightleftharpoons$ L-Cysteine + H ₂ O	7
CTH	cystathionine gamma-lyase	L-Cysteine + H ₂ O $\rightleftharpoons$ Hydrogen sulfide + Pyruvate + Ammonia	30
cysJ	sulfite reductase (NADPH) flavoprotein alpha-component	Hydrogen sulfide + 3 NADP ⁺ + 3 H ₂ O $\rightleftharpoons$ Sulfite + 3 NADPH + 3 H ⁺	4
cysK	cysteine synthase A	O-Acetyl-L-serine + Hydrogen sulfide $\rightleftharpoons$ L-Cysteine + Acetate	96
cysM	cysteine synthase B	O-Acetyl-L-serine + Hydrogen sulfide $\rightleftharpoons$ L-Cysteine + Acetate	4
dcm	(cytosine-5)-methyltransferase 1	S-Adenosyl-L-methionine + DNA $\rightleftharpoons$ S-Adenosyl-L-homocysteine + DNA 5-methylcytosine	0
dcyD	D-cysteine desulfhydrase	D-Cysteine + H ₂ O $\rightleftharpoons$ Hydrogen sulfide + Ammonia + Pyruvate	9
ddh	dimethylsulfide dehydrogenase	Dimethyl sulfide + 2 Ferricytochrome c ₂ + H ₂ O $\rightleftharpoons$ Dimethyl sulfoxide + 2 Ferrocyclochrome c ₂ + 2 H ⁺	43
dmsA	DSMO reductase A	Dimethyl sulfide + Menaquinone + H ₂ O $\rightleftharpoons$ Dimethyl sulfoxide + Menaquinol	4
dmsB	DSMO reductase B	Dimethyl sulfide + Menaquinone + H ₂ O $\rightleftharpoons$ Dimethyl sulfoxide + Menaquinol	10
dmsC	DSMO reductase C	Dimethyl sulfide + Menaquinone + H ₂ O $\rightleftharpoons$ Dimethyl sulfoxide + Menaquinol	0
doxA	thiosulfate dehydrogenase (quinone) small subunit	2 Thiosulfate + Decylubiquinone $\rightleftharpoons$ Tetrathionate + Decylubiquinol	286
iscS	cysteine desulfurase	L-Cysteine + [Protein]-L-cysteine $\rightleftharpoons$ L-Alanine + [Protein]-S-sulfanyl-L-cysteine	105
isfD	sulfoacetaldehyde reductase	Sulphoacetaldehyde + NADPH + H ⁺ $\rightleftharpoons$ 2-	2

		Hydroxyethanesulphonate + NADP+	
lcd	L-cysteine desulfhydrase	L-Cysteine + H ₂ O $\rightleftharpoons$ Hydrogen sulfide + Pyruvate + Ammonia	9
luxS	S-ribosylhomocysteine lyase	S-Ribosyl-L-homocysteine $\rightleftharpoons$ (S)-4,5-Dihydroxypentane-2,3-dione + L-Homocysteine	48
malY	cystathionine beta-lyase	L-Cysteine + H ₂ O $\rightleftharpoons$ Hydrogen sulfide + Pyruvate + Ammonia	2
mccB	cystathionine gamma lyase	L-Cystathionine + H ₂ O $\rightleftharpoons$ L-Cysteine + Ammonia + 2-Oxobutanoate	4
metB	cystathionine gamma-synthase	O-Succinyl-L-homoserine + L-Cysteine $\rightleftharpoons$ L-Cystathionine + Succinate	8
metC	cystathionine beta-lyase	L-Cysteine + H ₂ O $\rightleftharpoons$ Hydrogen sulfide + Pyruvate + Ammonia	10
metE	5-methyltetrahydropteroyltriglutamate-homocysteine methyltransferase	5-Methyltetrahydropteroyltri-L-glutamate + L-Homocysteine $\rightleftharpoons$ Tetrahydropteroyltri-L-glutamate + L-Methionine	24
metH	5-methyltetrahydrofolate--homocysteine methyltransferase	5-Methyltetrahydrofolate + L-Homocysteine $\rightleftharpoons$ Tetrahydrofolate + L-Methionine	6208
metK	S-adenosylmethionine synthetase	Orthophosphate + Diphosphate + S-Adenosyl-L-methionine $\rightleftharpoons$ ATP + L-Methionine + H ₂ O	93
mgl	methionine gamma lyase	L-Methionine + H ₂ O $\rightleftharpoons$ Methanethiol + Ammonia + 2-Oxobutanoate	139
msrC	L-methionine (R)-S-oxide reductase	L-Methionine + Thioredoxin disulfide + H ₂ O $\rightleftharpoons$ L-Methionine S-oxide + Thioredoxin	31
mtnN	adenosylhomocysteine nucleosidase	S-Adenosyl-L-homocysteine + H ₂ O $\rightleftharpoons$ S-Ribosyl-L-homocysteine + Adenine	69

phsA	thiosulfate reductase A	Sulfite + Hydrogen sulfide + Quinone $\rightleftharpoons$ Thiosulphate + Hydroquinone	1
sat	sulfate adenylyltransferase	ATP + Sulfate $\rightleftharpoons$ Diphosphate + Adenylyl sulfate	321
sqr	sulfide quinone reductase	n Hydrogen sulfide + n Quinone $\rightleftharpoons$ Polysulfide + n Hydroquinone	0
sufS	cysteine desulfurase	L-Cysteine + [Protein]-L-cysteine $\rightleftharpoons$ L-Alanine + [Protein]-S-sulfanyl-L-cysteine	82
toa	taurine:2-oxoglutarate aminotransferase	Taurine + 2-Oxoglutarate $\rightleftharpoons$ Sulfoacetaldehyde + L-Glutamate	55
tpa	taurine pyruvate aminotransferase	Taurine + Pyruvate $\rightleftharpoons$ Sulfoacetaldehyde + L-Alanine	1826
ttrA	tetrathionate reductase A	Tetrathionate + 2 e- $\rightleftharpoons$ 2 Thiosulfate	0
ttrB	tetrathionate reductase B	Tetrathionate + 2 e- $\rightleftharpoons$ 2 Thiosulfate	0
xsc	Sulfoacetaldehyde acetyltransferase	Sulfoacetaldehyde + Orthophosphate $\rightleftharpoons$ Acetyl phosphate + Sulfite	0

[00730] The acetate-related metabolic genes predicted in the genomes of isolates comprising the BB265 complex community live biotherapeutic product are presented in Table 34.

5 **Table 34 – Acetate-related metabolic genes predicted in the genomes isolates comprising the BB265 complex community live biotherapeutic product**

Gene	Gene Name	No. annotations
C1-hpah	4-hydroxyphenylacetate 3-hydroxylase, reductase component	2
C2-hpah	4-hydroxyphenylacetate 3-monooxygenase	1
maeB	malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+)	105
maeA	malate dehydrogenase (oxaloacetate-decarboxylating)	62
cat1	succinyl-CoA:acetate CoA-transferase	3
acdAB	acetate Coligase (ADP-forming)	8

acdB	acetate Coligase (ADP-forming) subunit bet 8	
ackA	acetate kinase	415
acmB	methyl acetate hydrolase	2
atoA	acetate CoA/acetoacetate CoA-transferase beta-subunit	36
atoD	acetate CoA/acetoacetate CoA-transferase alpha-subunit	36
bcpA	oxaloacetate decarboxylase	1
dehH	haloacetate dehalogenase	3
hpcB	3,4-dihydroxyphenylacetate 2,3-dioxygenase	1
iacA	indole-3-acetate monooxygenase	1
maiA	maleylacetoacetate isomerase	2
oadA	oxaloacetate decarboxylase (Na ⁺ extruding) subunit alpha	54
oadG	oxaloacetate decarboxylase (Na ⁺ extruding) subunit gamma	46
paaK	phenylacetate-Coligase	108
phnA	phosphonoacetate hydrolase	1

[00731] The butyrate-related metabolic genes predicted in isolates comprising the BB265 complex community live biotherapeutic product are presented in Table 35.

Table 35 – The butyrate-related metabolic genes predicted in isolates comprising the BB265 complex community live biotherapeutic product.

5

Gene	Gene Name	No. annotations
abfH	4-hydroxybutyrate dehydrogenase	6
bdhA	3-hydroxybutyrate dehydrogenase	2
mmsB	3-hydroxyisobutyrate dehydrogenase	15
buk	butyrate kinase	43
abfT	4-hydroxybutyrate CoA-transferase	25
gabT	5-aminovalerate/4-aminobutyrate aminotransferase	4
doeD	L-2,4-diaminobutyrate transaminase	1
dat	diaminobutyrate-2-oxoglutarate transaminase	6
gabT	4-aminobutyrate aminotransferase	21
lpqC	polyhydroxybutyrate depolymerase	4
puuE	4-aminobutyrate aminotransferase	15

[00732] The BB265 complex community live biotherapeutic product contains a list of diverse microbial species with equally diverse metabolic functions. For example, many metabolic pathways directly linked to sulfide-related genes, which is the key mechanism of

action for ulcerative colitis therapy, are present in the complex consortium. Gene annotation with PROKKA and gene ontology analysis using KEGG confirm the presence of many of these genes already (and in most cases many copies; see 'no. annotations' column in the tables) with this number expected to rise as genome assemblies representing the members of the consortium improve.

[00733] Homo-acetogens, which are known to produce acetate are included in the complex consortium, as well as butyrate producers, both of which are linked to gut health. We have also been able to use gene annotation (as above) to confirm the presence of a number of genes involved in acetate and butyrate metabolism (see Tables 34 and 35, respectively).

[00734] Bioinformatic analyses determining the functional capacity of the complex consortium compared to a healthy donor metagenome indicate substantial overlap in gene families. Annotation using the NCBI COG database ('Clusters of Orthologous Genes') identified members of 1,775 gene families from a healthy donor metagenome, of which 1,735 gene families (97%) were represented in the consortium metagenome. Therefore, this complex consortium enables the replacement of a wide range of lost functions in diversity-depleted recipients.

C.2.2 INFLAMMATORY MARKERS

[00735] Inflammatory markers expected to be influenced by the complex consortium include: TNF α signalling via NF- κ B; IFN α signaling; IFN γ signaling; IL6 JAK STAT3 signaling; activation of pro-apoptotic pathways; initiation of unfolded protein response.

C.2.3 METABOLIC PATHWAYS

[00736] A summary of the metabolic pathways is presented in Figure 11. This is a pie chart showing abundance of annotated genes among metabolic pathway categories (counts provided in Table 36 below).

Table 36 – The number of annotated genes responsible for each metabolic pathway.

Category	No. Annotated Genes
Carbohydrate metabolism	22879
Amino acid metabolism	17203
Energy metabolism	8590
Metabolism of cofactors / vitamins	8498
Glycan biosynthesis / metabolism	7165
Nucleotide metabolism	5285
Lipid metabolism	4420
Biosynthesis of secondary metabolites	4191
Xenobiotics biodegradation	1998
Metabolism of terpenoids / polyketides	1812

C.2.4 METABOLIC GENES

[00737] With the current state of the inventor's consortium genome assemblies, 2633 uniquely named genes, comprising 1752 known metabolic genes, can be annotated. This list includes but is not limited to the following:

[00738] Carbohydrate metabolism, including; Glycolysis / Gluconeogenesis, the Citrate cycle, the Pentose phosphate pathway, Fructose & mannose metabolism, Galactose metabolism, Ascorbate & aldarate metabolism, Starch & sucrose metabolism, Inositol phosphate metabolism, and Pyruvate metabolism.

10 [00739] Lipid metabolism, including Fatty acid biosynthesis, Fatty acid degradation, Steroid biosynthesis and bile acid biosynthesis.

[00740] Amino acid metabolism; Arginine biosynthesis, Alanine, aspartate, & glutamate metabolism, Glycine, serine & threonine metabolism, Cysteine methionine metabolism, valine, leucine & isoleucine biosynthesis, Lysine biosynthesis & degradation, Arginine & proline metabolism, Histidine metabolism, Tyrosine metabolism, Phenylalanine metabolism, Tryptophan metabolism, Phenylalanine, tyrosine & tryptophan biosynthesis, beta-Alanine metabolism, Taurine & hypotaurine metabolism, Glutathione metabolism.

15 [00741] Vitamin / co-factor metabolism, including: Riboflavin metabolism, Thiamine metabolism, Vitamin B6 metabolism, Nicotinate & nicotinamide metabolism, Pantothenate biosynthesis, Biotin metabolism, Lipoic acid metabolism, Folate biosynthesis, Atrazine degradation, Retinol metabolism, Porphyrin metabolism, and Carotenoid biosynthesis

D EXAMPLE 4 – EMERGENT EFFECT: 127 ISOLATE SUBSET OF BB265 OUTPERFORMS TOP SULFIDE CONSUMER ALONE

25 **D.1 STUDY AIM**

[00742] To support the premise that community complexity may bolster the effect of sulfide reduction in ulcerative colitis, the inventors compared the effectiveness of a 127 isolate subset of the BB265 consortium with that of the top individual sulfide-consuming isolate alone when co-incubated with ulcerative colitis stool. By examining both the consortium and the individual isolate, the inventors sought to determine whether complex consortia offer significant advantages over single-strain approaches in modulating sulfide levels in the context of ulcerative colitis.

D.2 MATERIALS AND METHODS

[00743] *Sample collection*

35 [00744] Baseline feces was collected from one patient (Patient A) with active ulcerative proctitis.

[00745] *Sample preparation*

[00746] Feces from Patient A was thawed at 37 °C in and processed in an anaerobic chamber where it was homogenized in a minimal medium to form a fecal slurry. The 127 isolate mix was co-cultured in a single bioreactor with the co-culture harvest used as inoculum. The co-cultured 127 isolate mix and a separately cultured individual top sulfide consumer isolate were spiked into the fecal slurry in equal concentrations, with five replicates per treatment. A negative control consisting of sterile media-spiked fecal slurry was run in parallel. Samples were then left to incubate at 37 °C for 24 h after which sulfide concentration was determined.

D.3 RESULTS

[00747] When the fecal slurry from Patient A was incubated with the top sulfide consumer alone, an average net reduction in sulfide compared to the negative control (stool only) of 7.4 μM ($\pm$ 8.4 SD) sulfide was observed (Figure 12). When incubated with the 127 isolate co-culture mix and average net reduction in sulfide of 18.7 μM ($\pm$ 3.2 SD) was observed, significantly greater than the single consumer alone (Figure 12).

D.4 DISCUSSION

[00748] These results demonstrate that, in this embodiment, a rationally designed complex co-cultured microbial community exhibited superior sulfide reduction in ulcerative proctitis stool when compared to a top sulfide consumer alone in the same context (Figure 12). This substantiates the notion that the microorganisms within the complex consortium engage in cooperative ecological interactions, effectively bolstering the reduction of sulfide in ulcerative proctitis stool when contrasted with individual strong sulfide consumers in the same environment. Consequently, in this case, the utilization of a 127 isolate subset of BB265 demonstrates a greater phenotype for sulfide reduction, than a top sulfide consumer alone.

E EXAMPLE 5 – EMERGENT EFFECT: BB265 OUTPERFORMS TOP SULFIDE CONSUMER ALONE

E.1 STUDY AIM

[00749] In Example 4, the inventors determined that a co-culture harvest comprising 127 microbial isolated had elevated capacity for sulfide consumption when compared to an individually phenotypically identified strong sulfide consumer. Consequently, the inventors expanded the investigation to assess how the BB265 complex consortium, comprised of 143 genomically and phenotypically screened healthy gut bacteria, supports sulfide reduction in ulcerative colitis. This complex consortium displays extended taxonomic and metabolic diversity beyond that of the 127 isolate mix. Here, the inventors assessed the effectiveness of the BB265 consortium with that of the top individual sulfide consuming strain in reducing sulfide in ulcerative proctitis stool.

E.2 MATERIALS AND METHODS

[00750] *Sample collection*

[00751] Baseline feces were collected from two patients (Patients A and C) with active ulcerative proctitis.

5 [00752] *Sample preparation*

[00753] Two ulcerative proctitis stool samples (Patient A and C) were used in this study. Feces from both patients were thawed at 37 °C and processed in an anaerobic chamber where they were homogenized in a minimal medium to form a fecal slurry. The BB265 consortium was co-cultured in a single bioreactor with the co-culture harvest used as inoculum. The co-cultured BB265 consortium and an individual top sulfide consumer isolate (average net reduction in sulfide of 670 µM when phenotyped alone) were spiked into the fecal slurry in equal concentrations, with five replicates per treatment. A negative control consisting of sterile media-spiked fecal slurry was run in parallel. Samples were then left to incubate at 37 °C for 24 h after which sulfide concentration was determined.

15 **E.3 RESULTS**

[00754] Post incubation, when incubated with the BB265 consortium, Patients A and C fecal slurries showed an average net reduction in sulfide of 10.5 µM (± 8.1 SD) and 12.7 µM (± 3.6 SD), respectively (Figure 13). This was a significant reduction when compared to the negative control (stool only). There was a significant reduction in sulfide concentration for Patient C when comparing stool co-incubated with the BB265 consortium to the individual strong sulfide consumer ($p < 0.05$) and when co-cultured with top sulfide consumer isolate; however, no significant difference was found in this regard for Patient A ($p = 0.079$), though stool co-incubated with the BB265 consortium did, on average, reduce sulfide to a greater extent than when co-incubated with the individual top sulfide consumer (Figure 13). No significant reduction in sulfide was observed for both patients when stool was co-cultured with the individual strong sulfide consumer, with average net reduction of 1.0 µM (± 9.8 SD) and 1.7×10^{-14} µM (± 4.8 SD) sulfide for Patient A and C samples, respectively (Figure 13).

E.4 DISCUSSION

[00755] This embodiment of the invention reveals that the BB265 complex consortium, comprised of 143 genomically and phenotypically diverse gut bacteria, outperforms a single top sulfide consumer strain in reducing sulfide levels in ulcerative proctitis stool when inoculated at the same concentration (Figure 13). This result aligns with the initial hypothesis that a more diverse microbial community could exert enhanced metabolic functions through synergistic interactions among its members.

35 [00756] For Patient C, the significant reduction in sulfide concentration when using the BB265 consortium compared to the individual sulfide consumer highlights the potential of the consortium to drive more effective sulfide metabolism in ulcerative colitis (Figure 13). The

trend towards greater sulfide reduction with the BB265 consortium suggests that the diversity and cooperative interactions within the consortium play a crucial role in achieving this outcome (Figure 13).

[00757] Interestingly, the negligible sulfide reduction observed when using the individual strong sulfide consumer alone underscores the importance of microbial diversity in achieving optimal metabolic outcomes (Figure 13). The complex consortium appears to engage in multifaceted interactions that enhance its overall capacity to reduce sulfide, an outcome that is not achievable by the individual strain alone.

[00758] These results underscore the advantage of employing a rationally designed, diverse microbial consortium over a single, phenotypically strong isolate for therapeutic applications aimed at modifying the gut microbiome, particularly in conditions like ulcerative colitis where metabolic interventions may be crucial for disease management. These data suggests that leveraging the cooperative interactions within a complex microbial community could be a more effective strategy in reducing harmful metabolites such as sulfide in the gut environment.

F EXAMPLE 6 – SCALABLE AND REPRODUCIBLE CO-CULTURE OF THE BB265 COMPLEX COMMUNITY LIVE BIOTHERAPEUTIC PRODUCT

F.1 STUDY AIM

[00759] The inventors aimed to optimize and validate the reproducibility and scalability of a microbial co-culture system for BB265 from 1 L to 20 L, ensuring consistent viability and diversity across different scales. This study assessed the impact of scale-up on co-culture performance by evaluating:

[00760] Reproducibility: comparing the reproducibility of co-culture outcomes across triplicate bioreactor runs at each scale (1 L, 4 L, 20 L).

[00761] Viability and diversity: measuring the consistency of microbial viability (CFU) and diversity at various bioreactor volumes and timepoints.

[00762] Scale-up effects: analyzing the effects of scaling on co-culture abundance and strain-specific viability over time to confirm that high reproducibility and consistent co-culture characteristics are maintained as the bioreactor volume increases.

[00763] Seed train approach: assessing the viability and reproducibility of fermentation using an initial bioreactor to inoculate subsequent bioreactors, demonstrating scalability and maintaining consistent microbial viability and diversity across increasing volumes.

F.2 MATERIALS AND METHODS

[00764] *Bioreactor setup and experimental design*

[00765] To evaluate the reproducibility and scalability of a microbial co-culture system, bioreactor experiments were conducted at three different scales: 1 L, 4 L, and 20 L, with each scale tested in triplicate to ensure reproducibility.

[00766] *Inoculation and incubation*

- 5 [00767] Bioreactors were inoculated with a standardized microbial co-culture comprising BB265 at the beginning of the experiment. All bioreactors were maintained under identical conditions (atmosphere, temperature, pH, agitation) to minimize external variability.

[00768] *Sampling and analysis*

- [00769] Samples were collected from each bioreactor at regular intervals up to 48 hours
10 post-inoculation. Due to practical constraints, not all timepoints were sampled for all bioreactors; however, a minimum of three datapoints were collected per bioreactor size and timepoint.

- [00770] Microbial viability was assessed using the spread plate method to determine colony-forming units (CFU) at each timepoint. Data were averaged across triplicate
15 bioreactors for each scale.

[00771] Diversity was assessed using shotgun metagenomic sequencing on samples collected from each bioreactor to evaluate microbial diversity and strain-specific viability. Sequencing data were analyzed to determine the presence and abundance of specific strains within the co-culture.

- 20 [00772] *Data analysis*

[00773] The consistency of co-culture viability and diversity across different bioreactor scales was evaluated by comparing CFU counts and metagenomic sequencing results.

- [00774] Reproducibility was assessed by comparing variability in CFU counts and microbial diversity across replicate bioreactors at each scale. Scale-up effects were analyzed
25 to ensure that reproducibility and co-culture characteristics remained stable as bioreactor volume increased.

[00775] Data were pooled from all bioreactor runs for each scale, and trends in co-culture abundance and viability over time were examined. The impact of scaling on these parameters was evaluated by comparing results across the different bioreactor sizes.

- 30 [00776] *Seed train*

- [00777] To assess scalability and maintain microbial consistency, a seed train approach was employed. Initially, the BB265 co-culture was fermented in a 1 L bioreactor. The fermentation product was then harvested and used to inoculate another 1 L bioreactor. Throughout the process, microbial viability (measured as CFU) and diversity were monitored
35 to ensure consistent performance and reproducibility. This approach enabled the evaluation of the co-culture system's scalability from small to large commercial volumes while preserving the integrity of microbial characteristics.

F.3 RESULTS

[00778] *Reproducibility of CFU with co-culture scale-up*

[00779] Microbial growth was assessed across bioreactor scales of 1 L, 4 L, and 20 L using data pooled from nine 1 L vessels, three 4 L vessels, and three 20 L vessels. At each scale, samples were collected at regular intervals up to 48 hours post-inoculation, and CFU were measured using the spread plate method.

[00780] The data demonstrated a consistent increase in CFU counts up to 48 hours across all bioreactor scales, with growth patterns showing high reproducibility (Figure 14). The co-culture abundance remained steady after 24 hours, indicating that scaling up from 1L to 20L did not adversely impact microbial growth rates or overall abundance (Figure 14).

[00781] *Reproducible growth of strains in replicate 1L bioreactors*

[00782] Bioinformatic analysis was performed on a 1 L bioreactor run, with three separate bioreactors each inoculated with the BB265 consortium. Samples were harvested post-fermentation, and microbial abundance was assessed through DNA extraction followed by shotgun metagenomic sequencing.

[00783] The analysis revealed that the relative abundance of strains was generally highly reproducible across the replicate bioreactor vessels (Figure 15A and 15B). Most isolates exhibited similar levels of abundance and recovery, indicating that the microbial community composition and strain representation were consistent across the different bioreactors (Figure 15A and 15B). These results underscore the reliability of the co-culture system in achieving reproducible strain abundance in a 1 L bioreactor setup.

[00784] *Reproducible growth of strains in scaling bioreactor volumes*

[00785] Bioinformatic analysis of microbial diversity and abundance across 1 L, 4 L, and 20 L bioreactors, revealed primarily consistent patterns (Figure 16A and 16B). Although some variability was observed between vessel sizes, the data demonstrated strong reproducibility in microbial diversity and abundance during volumetric scaling.

[00786] *Reproducible fermentation using a seed train approach*

[00787] Metagenomic sequencing was conducted on samples from the inoculum, the initial bioreactor, and the seed train bioreactor (Bioreactor 2) to assess the persistence and viability of microbial strains through the seed train process (Figure 23 A and B). The results demonstrated that the majority of strains identified in the inoculum were consistently present in both the initial bioreactor and Bioreactor 2 (Figure 23 A and B). This finding suggests that these strains not only remained viable following the initial fermentation but were also capable of sustained growth and proliferation during the subsequent seed fermentation. The consistency in microbial composition between the initial and seed train bioreactors supports the robustness of the seed train approach in maintaining the integrity and diversity of the co-culture system across successive fermentations

F.4 DISCUSSION

[00788] This study underscores, in this embodiment, the robust performance and scalability of the inventor's co-culture system across 1 L, 4 L, and 20 L bioreactors. The consistent microbial growth and diversity observed confirm the system's reliability at different
5 scales.

[00789] Culturing each individual isolate separately would be both impractical and economically prohibitive, particularly at larger volumes. The inventors co-culture system represents a novel and inventive approach, providing a feasible and cost-effective solution for simultaneous cultivation of multiple strains. This system not only addresses the challenges
10 associated with scaling but also optimizes resource use, making it a valuable tool for large-scale applications.

[00790] The seed train approach demonstrated a robust method for maintaining microbial viability and diversity across successive fermentations (Figure 23 A and B). Metagenomic sequencing results confirmed that the majority of microbial strains present in the initial
15 inoculum persisted through both the initial and seed train bioreactors (Figure 23 A and B). This consistency suggests that the microbial strains were not only viable after the first fermentation but also retained the capacity to proliferate in subsequent fermentations. The ability to maintain a stable and diverse microbial community through the seed train process is critical for the scalability of the co-culture system, ensuring reproducible outcomes as bioreactor
20 volumes are increased. These findings support the potential for scaling this microbial co-culture system to larger commercial applications while preserving the desired microbial characteristics.

[00791] The innovative nature of this co-culture system lies in its ability to maintain microbial diversity and performance across various scales, offering a practical alternative to
25 traditional methods.

[00792] Although a single bioreactor is used herein and has advantages, multiple bioreactors may be used in some embodiments.

[00793] Although 143 isolates were used in this embodiment and example, in other embodiments, the consortium will comprise or consist essentially of any number of the core community microbial strains of Table 14 and any number of the keystone strains of Table 13
30 that, for example produces a therapeutic benefit (e.g., are therapeutically effective) by for example restoring a healthy gut ecology, reducing undesired symptoms of disease, reducing inflammation, reducing food intolerance, enhancing immunity and/or increasing nutrient absorption. In the Examples described herein, it is contemplated that a formulation will
35 comprise or consist essentially of (i) 85-90%, 90%-95%, or all of the core community strains in Table 14 and/or (ii) 85-90%, 90%-95% or all of the keystone strains selected from Table 13. In several embodiments, the formulation comprises or consists essentially of 20-26 core

community strains selected from Table 14, and keystone strains from Table 13 at a core:keystone strain ratio at 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1. In some embodiments, the formulation comprises or consists essentially of from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage of total number or mass microorganisms in the formulation. In several embodiments, the core and keystone strains have been co-cultured together. With respect to the numbers, amounts and ratios disclosed herein, the formulation may be the formulation administered to a subject or in the co-culture.

G EXAMPLE 6 – DEFINING A MINIMUM VIABLE COMMUNITY

G.1 STUDY AIM

[00794] The aim of this study was to estimate the minimum viable size of a microbial consortium designed to restore lost microbial functions in disease. By comparing the functional diversity, as represented by Clusters of Orthologous Genes (COGs), in the BB265 consortium against those present in healthy donor fecal metagenomes, the inventors sought to identify the degree of functional redundancy within the consortium. Through rarefaction analysis, the inventors aimed to estimate the minimum community necessary to achieve a functionally robust and efficient therapeutic consortium.

G.2 MATERIALS AND METHODS

[00795] *Genome assembly and annotation of BB265 isolates*

[00796] Candidate BB265 isolates were whole genome sequenced on an Illumina NextSeq platform with paired-end reads. Genomes for the BB265 isolates were assembled using an in-house pipeline using Shovill (<https://github.com/tseemann/shovill>), which utilizes Skesa (Souvorov, A., Agarwala, R. & Lipman, D. J. SKESA: strategic k-mer extension for scrupulous assemblies. *Genome Biol.* 19, 153 (2018). Following assembly, genome annotation was performed using Prokka (Seemann, T. Prokka: rapid prokaryotic genome annotation. *Bioinformatics* 30, 2068–2069 (2014). Prokka annotations focused on identifying Clusters of Orthologous Genes (COGs), and only COG categories were considered for further analysis, excluding hypothetical proteins and tRNAs unless necessary.

[00797] *Assembly and annotation of healthy donor fecal metagenomes*

[00798] Metagenome-assembled genomes (MAGs) were obtained from 6 fecal samples derived from fecal microbiota transplantation (FMT) donors (3 donors, 2 time points). These metagenomes were sequenced using various platforms, and MAGs were subsequently extracted and assembled. The resulting MAGs were annotated using the same Prokka pipeline applied to the BB265 genome assemblies.

[00799] *COG identification and analysis*

[00800] For both BB265 candidate genomes and FMT-donor-derived MAGs, counts of identified COG categories were used to assess functional diversity. Other annotations that

could not be assigned a COG ID, such as hypothetical proteins and tRNAs, were excluded from the analysis.

[00801] *Resampling and Rarefaction Analysis of COGs*

[00802] To estimate the functional redundancy within the BB265 consortium, a resampling procedure was conducted. The original 143 BB265 isolates were resampled with replacement for each subset of isolates ranging from 1 to 143. For each subset size (n), the total number of unique COG IDs annotated to the sampled isolates was counted. This resampling was repeated 50 times to account for variability. The resampled counts were plotted, resulting in a rarefaction curve (Figure 17). A model ($y \sim \log(x)$) was fitted using polynomial regression, represented by a blue trend line on the plot (Figure 17). A golden horizontal line was drawn at 1677 COGs, representing the estimated number of COGs expected to be shared among FMT donor samples (Figure 17). The objective was to design a consortium that approaches or exceeds the functional potential of the average FMT community.

G.3 RESULTS

15 [00803] *Estimation of the 'Healthy Core' Functional Potential in FMT Donor Samples*

[00804] Analysis of FMT donor samples revealed that, on average, these samples could be annotated with approximately 2000 COG categories (mean = 1874 ± 95). Within this set, the intersection of shared COG IDs across the samples comprised 1677 COG IDs, representing 82% of the total COGs identified. This intersection was used as an estimate of the 'minimum community' of functional genetic potential provided by an FMT.

20 [00805] *Rarefaction Curve Analysis of the BB265 Consortium*

[00806] To assess the functional redundancy and diversity within the BB265 consortium, a rarefaction analysis was conducted. The curve generated from resampling subsets of the 143 BB265 isolates demonstrated a logistic-shaped relationship between the number of strains and the number of unique COGs identified (Figure 17). As the number of isolates increased, the curve began to approach an asymptote, suggesting a diminishing return in the number of new COGs identified with the addition of more isolates (Figure 17).

[00807] Notably, the point where the rarefaction curve starts to appear asymptotic coincides with the intersection of the curve and the 'healthy core' line at 1677 COGs (Figure 17). This alignment suggests a potential relationship between the functional capacity of the consortium and the estimated 'healthy core'.

30 [00808] *Evaluating the Functional Potential of Subsets of the BB265 Consortium*

[00809] The logistic-shaped curve allows for the evaluation of the functional potential of subsets of the BB265 consortium. By examining the angle of the tangent to the curve at various points, the fraction of the potential functional diversity that a given subset of isolates represents can be inferred. For example, the 45-degree tangent at mid-curve is particularly informative, suggesting that this point might represent a balance between the number of strains included

and the functional potential they collectively represent (Figure 17). In some embodiments, the smaller subset could include anyone of the subsets selected from the group consisting of: 143 isolates; 142 isolates; 141 isolates; 140 isolates; 139 isolates; 138 isolates; 137 isolates; 136 isolates; 135 isolates; 134 isolates; 133 isolates; 132 isolates; 131 isolates; 130 isolates; 129 isolates; 128 isolates; 127 isolates; 126 isolates; 125 isolates; 124 isolates; 123 isolates; 122 isolates; 121 isolates; 120 isolates; 119 isolates; 118 isolates; 117 isolates; 116 isolates; 115 isolates; 114 isolates; 113 isolates; 112 isolates; 111 isolates; 110 isolates; 109 isolates; 108 isolates; 107 isolates; 106 isolates; 105 isolates; 104 isolates; 103 isolates; 102 isolates; 101 isolates; 100 isolates; 99 isolates; 98 isolates; 97 isolates; 96 isolates; 95 isolates; 94 isolates; 93 isolates; 92 isolates; 91 isolates; 90 isolates; 89 isolates; 88 isolates; 87 isolates; 86 isolates; 85 isolates; 84 isolates; 83 isolates; 82 isolates; 81 isolates; 80 isolates; 79 isolates; 78 isolates; 77 isolates; 76 isolates; 75 isolates; 74 isolates; 73 isolates; 72 isolates; 71 isolates; 70 isolates; 69 isolates; 68 isolates; 67 isolates; 66 isolates; 65 isolates; 64 isolates; 63 isolates; 62 isolates; 61 isolates; 60 isolates; 59 isolates; 58 isolates; 57 isolates; 56 isolates; 55 isolates; 54 isolates; 53 isolates; 52 isolates; 51 isolates; 50 isolates; 49 isolates; 48 isolates; 47 isolates; 46 isolates; 45 isolates; 44 isolates; 43 isolates; 42 isolates; 41 isolates; 40 isolates; 39 isolates; 38 isolates; 37 isolates; 36 isolates; 35 isolates; 34 isolates; 33 isolates; 32 isolates; 31 isolates; 30 isolates; 29 isolates; 28 isolates; 27 isolates; 26 isolates; 25 isolates; 24 isolates; 23 isolates; 22 isolates; 21 isolates; 20 isolates; 19 isolates; 18 isolates; 17 isolates; 16 isolates; 15 isolates; 14 isolates; 13 isolates; 12 isolates; 11 isolates; 10 isolates; 9 isolates; 8 isolates; 7 isolates; 6 isolates; 5 isolates; 4 isolates; 3 isolates; 2 isolates; and 1 isolate.

[00810] These analyses provide insights into the design of a minimal viable consortium that could effectively recapitulate the functional potential of a healthy gut microbiome.

25 **G.4 DISCUSSION**

[00811] The inventors identified, in this embodiment, a 'healthy core' of 1677 COGs shared among FMT donor samples, representing a foundational set of functions critical for gut health. This core serves as a benchmark for designing microbial consortia aimed at restoring lost functions in dysbiosis

30 [00812] Through rarefaction analysis of the BB265 consortium, the inventors observed a logistic relationship between the number of isolates and the number of unique COGs identified, indicating substantial functional redundancy (Figure 17). The alignment of the curve's asymptote with the 'healthy core' estimate suggests that a smaller subset of the original 143 isolates could provide the necessary functional diversity required

35 [00813] The key outcome of this study is the ability to estimate the minimum number of isolates required to achieve a desired level of functional potential in complex community therapeutics. This approach enables the design of streamlined, effective microbial consortia

tailored to replicate the functional capabilities of a healthy gut microbiome. These analyses provide insights into the design of a minimal viable consortium that could effectively recapitulate the functional potential of a healthy gut microbiome.

5 **EXAMPLE 8 – SUCCESSFUL ENGRAFTMENT OF CO-CULTURED BB265 COMPLEX CONSORTIUM IN A MURINE MODEL**

H.1 STUDY AIM

[00814] The aim of this study was to demonstrate successful engraftment of a co-culture bioreactor harvest of BB265 in an animal model.

10 **H.2 MATERIALS AND METHODS**

[00815] *BB265 co-culture gavage*

[00816] A harvest of BB265 co-culture derived from a single bioreactor was used as the inoculum for the engraftment study. Ten male germ-free mice were randomly allocated into two groups: five in the treatment group and five in the control group. The treatment group
15 received a pre-dose of the BB265 co-culture suspended in PBS at a concentration of 1.96×10^7 ($\pm 5.67 \times 10^6$ SD) CFU per dose by oral gavage at T-1, followed by a one-week acclimatization period (Figure 18). The control group received PBS only. Post-acclimatization (T0), the treatment group was administered a post-dose of the BB265 co-culture at a concentration of 1.19×10^7 ($\pm 1.29 \times 10^6$ SD) CFU per dose, while the control group received
20 PBS only (Figure 18). Mice were then housed for an additional week, after which fecal samples were collected for CFU determination and shotgun metagenomic sequencing to assess engraftment of the BB265 co-culture (Figure 18).

[00817] *Data analysis*

[00818] Fecal samples were collected from each mouse in both the treatment and control
25 groups at four time points: T-1 (before gavage and acclimatization), T0 (before the pre-dose gavage), T1 (before the post-dose gavage), and T2 (one week following the post-dose gavage) (Figure 18). To assess microbial viability, colony-forming units (CFU) per gram of feces were determined using the spread plate method.

[00819] To evaluate microbial diversity and strain-specific engraftment, shotgun
30 metagenomic sequencing was performed on the collected fecal samples. Relative abundance data derived from the sequencing were used for statistical analysis.

[00820] Relative abundance data from fecal samples were analyzed using an ANOVA with the model: *relative abundance* ~ *time (pre/post dose)* x *mouse*. This analysis assessed whether microbial abundance changed significantly over different time points, the variability in
35 abundance among individual mice, and whether time-related changes in abundance differed statistically between mice.

[00821] A Pearson correlation matrix of coefficients was performed to assess the consistency of strain-specific relative abundances between pre- and post-dose samples. Correlations were calculated between the vectors of relative abundances for each strain across the different samples to evaluate the stability and changes in microbial composition following treatment.

H.3 RESULTS

[00822] CFU plating indicated that there were no viable organisms in the feces of mice at T0. However, CFU plating from the T2 (post-dose) treatment group identified successful engraftment of the BB265 co-culture, with no viable counts for the control group and an average of 4.81×10^{10} (3.27×10^{10} SD) CFU/g feces for the treatment group (Figure 19).

[00823] Metagenomic sequencing revealed substantial engraftment success of the BB265 co-culture, with similar trends of relative abundances for engrafted isolates identified in the feces of mice in the treatment group (Figure 20A and 20B). ANOVA analysis revealed a significant effect of treatment with the BB265 co-culture on microbial relative abundance in feces when comparing T0 (pre-dose) and T2 (post-dose) datasets ($p < 0.00001$). In contrast, no significant differences were found between mice, or for the interaction of mouse with time ($p = 0.99$).

[00824] The matrix of correlation coefficients among T0 (pre-dose) and T2 (post-dose) samples revealed low to negative correlations, ranging from -0.03 to 0.03, indicating minimal to no correlation between microbial relative abundances before and after treatment with the BB265 co-culture (Figure 21). Correlation coefficients among T2 (post-dose) samples were strong, ranging from 0.91 to 1.00, indicating significant overlap of the engraftment profiles among mice after treatment with the BB265 co-culture.

H.4 DISCUSSION

[00825] The inventors successfully demonstrated, in this embodiment, that the BB265 co-culture can be effectively and reproducibly engrafted into a germ-free mouse model (Figure 20). The presence of high concentrations of viable microorganisms in the treatment group's feces at T2 (post-dose) demonstrates that the BB265 co-culture effectively colonized the gut (Figure 19).

[00826] The ANOVA results indicate that the BB265 co-culture had a significant and consistent effect on microbial abundance across all mice treated, with no significant differences among individual mice. This uniform effect across subjects supports reproducibility of the engraftment process.

[00827] Correlation analysis further validated engraftment success. The minimal correlations between T0 (pre-dose) samples and T2 (post-dose) samples show that the microbial community observed post-treatment was indeed due to the engrafted co-culture (Figure 21). Additionally, the high correlations among T2 (post-dose) samples illustrate that

the co-culture established a reproducible community structure within the gastrointestinal tract of the treated mice (Figure 21).

[00828] In summary, these results demonstrate that the BB265 co-culture was effectively and consistently engrafted, establishing a reliable microbial community in the host.

- 5 [00829] The Examples should not be used to limit the scope of embodiments described herein. In the Examples described herein, it is contemplated that formulations also comprise or consist essentially of the following amounts that produce a therapeutic benefit (e.g., are therapeutically effective) (i) 85-90%, 90%-95%, or all of the core community strains in Table 14 and/or (ii) 85-90%, 90%-95% or all of the keystone strains selected from Table 13. In
10 several embodiments, the formulation comprises or consists essentially of 20-26 core community strains selected from Table 6, and keystone strains from Table 13 at a core:keystone strain ratio at 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1. In some embodiments, the formulation comprises or consists essentially of from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage
15 of total number or mass microorganisms in the formulation. In several embodiments, the core and keystone strains have been co-cultured together. With respect to the numbers, amounts and ratios disclosed herein, the formulation may be the formulation administered to a subject or in the co-culture.

CLAIMS

1. A formulation comprising:
 - 5 a plurality of core community microbial species,

wherein said core community microbial species comprise members of at least the following genera: *Dysosmobacter*, *Enterocloster*, *Ruthenibacterium*, *Vescimonas*, *Phocaeicola*, *Pusillimonas*, *Solibaculum*, and *Christensenella*,
 a plurality of keystone microbial species,
 - 10 wherein said keystone microbial species comprise members of at least the genus *Phocaeicola*, and
 a non-naturally occurring pharmaceutically acceptable excipient, wherein the formulation is formulated as a capsule, tablet, or powder.
2. The formulation of claim 1, wherein the plurality of core community microbial species
 - 15 comprises at least the following species: *Dysosmobacter welbionis*, *Enterocloster bolteae*, *Ruthenibacterium lactatiformans*, *Vescimonas coprocola*, *Phocaeicola salanitronis*, *Pusillimonas faecalis*, *Solibaculum mannosilyticum*, *Chrstensenella minuta*, *Alistipes magaguti*, *Parabacteroides goldsteinii*, *Alistipes communis*, *Ruminococcus bicirculans*, *Bacteroides caecimuris*, *Alistipes dispar*, and *Bacteroides salversiae*; and
 wherein the plurality of keystone microbial species comprises at least the following
 - 20 species: *Phocaeicola coprocola*, *Bifidobacterium bifidum*, and *Coprococcus catus*.
 3. The formulation of claim 1, wherein the plurality of core community microbial species comprises at least the following species: *Alistipes dispar*, *Bacteroides salyersiae*, *Bifidobacterium bifidum*, *Christensenella minuta*, *Coprococcus catus*, *Coprococcus*
 - 25 *sp000154245*, *Dysosmobacter faecalis*, *Faecalibacterium duncaniae*, *Gemmiger formicilis*, *Parabacteroides goldsteinii*, *Ruminococcus bicirculans*, *Ruthenibacterium lactatiformans*, *Solibaculum mannosilyticum*, and *Vescimonas coprocola*.
 4. The formulation of claim 1, wherein the formulation is generated by co-culturing the core community microbial species and the keystone microbial species in a single bioreactor.
 5. The formulation of claim 1, wherein the formulation is configured to metabolize hydrogen
 - 30 sulphide in the gastrointestinal tract of a subject post administration of the formulation.
 6. The formulation of claim 1, wherein the formulation is formulated for oral delivery.
 7. The formulation of claim 1, wherein the formulation is lyophilized.
 8. The formulation of claim 1, wherein the pharmaceutically acceptable excipient
 - 35 comprises maltodextrin.
 9. The formulation of claim 1, further comprising a prebiotic.

10. The formulation of claim 1, wherein the formulation is encapsulated within an enteric coating.
11. The formulation of claim 1, wherein the plurality of core community microbial species comprises all of the species in Table 14.
- 5 12. The formulation of claim 1, wherein the plurality of keystone microbial species comprises all of the species in Table 13.
13. A formulation comprising a plurality of microbial species comprising all of the species of Tables 13 and 14.
14. The use of the formulation of any one of claims 1-13 for the treatment of dysbiosis.
- 10 15. The use of the formulation of any one of claims 1-13 for the treatment of ulcerative colitis.
16. The use of the formulation of any one of claims 1-13 for the treatment of Crohn's Disease.
17. The use of the formulation of any one of claims 1-13 for the treatment of one or more diseases or disorders selected from the group consisting of: inflammatory bowel disease, checkpoint inhibitor colitis, primary sclerosing cholangitis, primary biliary sclerosis, irritable bowel syndrome, non-alcoholic steatohepatitis or non-alcoholic fatty liver disease, alcoholic hepatitis, hepatic encephalopathy, obesity, insulin resistance, type 2 diabetes, melanoma, renal cell carcinoma, bowel cancer and precancerous polyps, lymphoma, leukemia, myeloma, pancreatic cancer, breast cancer, lung cancer, testicular cancer, sarcoma, dyslipidaemia, atherosclerotic heart disease, hypertension, type 1 diabetes, rheumatoid arthritis, psoriatic arthritis, psoriasis, systemic lupus erythematosus, Sjogren's disease, food allergy, anaphylaxis, atopic dermatitis, atopic rhinitis or sinusitis, clostridioides difficile infection, multidrug resistant infection or colonisation, renal tract or urinary tract infections, blood stream infections, respiratory infections, sepsis, autism, multiple sclerosis, Parkinson's disease, depression, anxiety, bipolar disorder, and schizophrenia.
- 15 18. The use of the formulation of claim 17 in combination with a therapy specific to the one or more diseases or disorders.
19. The formulation according to any one of claims 1-13, wherein the formulation comprises a ratio of core community microbial strains to keystone microbial strains of 10:1, 9:1, 8:1, 7:1, 6:1, 5:1, 4:1, 3:1, 2:1, or 1:1 with respect to number of bacteria.
- 20 20. The formulation according to any one of claims 1-13, wherein the formulation comprises from 50% to 80% core community microbial strains and from 20% to 50% keystone microbial strains as a percentage of total microorganisms in the formulation.
- 25 21. The formulation of claim 1, wherein the plurality of core community microbial species comprise strains selected from the strains identified in Table 14; and wherein the plurality
- 30
- 35

- of keystone microbial species comprise strains selected from the strains identified in Table 13.
22. A formulation for oral administration comprising: a plurality of core community microbial species; and a plurality of keystone microbial species, wherein the plurality of core community microbial species are species of at least the following genera: *Akkermansia*, *Alistipes*, *Bacteroides*, *Bifidobacterium*, *Butyricimonas*, *Christensenella*, *Clostridium*, *Collinsella*, *Coprococcus*, *Dysosmobacter*, *Enterocloster*, *Faecalibacterium*, *Parabacteroides*, *Phocaeicola*, *Pusillimonas*, *Ruminococcus*, *Ruthenibacterium*, *Solibaculum*, and *Vescimonas*; and wherein the plurality of keystone microbial species are species of at least the following genera: *Alistipes*, *Bacteroides*, *Bifidobacterium*, *Coprococcus*, *Faecalibacterium*, *Methanobrevibacter*, *Parabacteroides*, *Phocaeicola*, *Roseburia*, *Ruminococcus*, and *Subdoligranulum*.
23. A formulation comprising a plurality of core community microbial species and a plurality of keystone microbial species comprising 80-100% of the species identified on Tables 4 and 5.
24. A formulation comprising: a plurality of core community microbial strains in lyophilized form; a plurality keystone microbial strains in lyophilized form; at least one of a prebiotic, surfactant, a polyester, or a polyvinylalcohol; and where the formulation is produced by co-culturing the plurality of core community microbial strains with the plurality keystone microbial strains in a single vessel.
25. The formulation of any one of claims 1-13 or 19-24, where the formulation does not comprise any bacteria from the phylum Pseudomonadota or Campylobacterota.
26. A method of co-culturing one or more core community microbial strains with one or more keystone microbial strains, comprising selecting one or more core community microbial strains selected from Table 14 and one or more keystone microbial strains selected from Table 13, and co-culturing the strains under suitable culture conditions.
27. The method of claim 26, wherein the co-culture comprises 3, 5, 10, 15, 20, or all core community microbial strains selected from Table 14 and 1, 3, 5, 10, 15, 20, or all keystone microbial strains selected from Table 13.
28. The method of claim 26, wherein the co-culture comprises 20 or more core community microbial strains selected from Table 14 and 10 or more keystone microbial strains selected from Table 13.
29. A composition comprising a microbial consortium comprising at least one microbe, wherein the at least one microbe is selected from the group consisting of: bacteria and archaea; and wherein the at least one microbe is a member of a phylum, selected from the group consisting of: any one of the phyla listed in Table 1; any one of the phyla listed in Table 2; any one of the phyla listed in Table 3; and any combination, subgroup or

- multitude thereof, wherein the microbial consortium comprising a plurality of microbes, and wherein the microbe is a member of a species selected from the group consisting of: any one of the species listed in Table 9; any one of the species listed in Table 10; any one of the species listed in Table 11; any one of the species listed in Table 12; any one of the species listed in Table 13; any one of the species listed in Table 14; any one of the species listed in Table 15; and any one of the species listed in Table 16; and any combination, subgroup or multitude thereof; and wherein the composition comprises a plurality of core community microbial species, wherein said core community microbial species comprise members of at least the following genera: *Dysosmobacter*, *Enterocloster*, *Ruthenibacterium*, *Vescimonas*, *Phocaeicola*, *Pusillimonas*, *Solibaculum*, and *Christensenella*. a plurality of keystone microbial species, and wherein said keystone microbial species comprise members of at least the genus *Phocaeicola*.
30. A biotherapeutic composition comprising the composition of claim 29, together with an acceptable diluent or carrier.
31. A pharmaceutical composition comprising the composition of claim 29, together with a pharmaceutically acceptable diluent or carrier.
32. A dosage form comprising the composition of claim 29, wherein the dosage form is a unity dosage form.
33. An isolated non-inflammatory strain of bacteria comprising a 16S ribosomal RNA (rRNA) gene having a nucleotide sequence selected from the group consisting of: SEQ ID NO'S 1 to 286.
34. A novel species or strain of microbe, wherein the microbe is selected from the group consisting of: any one of the species selected from a table selected from: Table 9; Table 10; Table 11; Table 12; Table 13; Table 14; Table 15; Table 16.
35. A method of decreasing inflammation in a subject in need thereof, said method comprising administering to the subject an effective amount of the composition of claim 29.
36. A method of decreasing dysbiosis in a subject in need thereof, said method comprising administering to the subject an effective amount of the composition of claim 29.
37. A method of preventing or treating a medical disorder or disease associated with dysbiosis in a subject in need thereof, said method comprising administering to the subject an effective amount of a composition of claim 29.
38. A method of promoting the growth of a member of a genus selected from the group consisting of: *Acidaminococcaceae* (family), *Acidaminococcus*, *Adlercreutzia*, *Agathobaculum*, *Akkermansia*, *Alistipes*, *Alterileibacterium*, *Amedibacillus*, *Amedibacterium*, *Aminipila*, *Anaerobutyricum*, *Anaerococcus*, *Anaerocolumna*, *Anaerofustis*, *Anaerostipes*, *Anaerotignum*, *Anaerotruncus*, *Bacillus*, *Bacteroides*,

- Barnesiella*, *Bifidobacterium*, *Bilophila*, *Blautia*, *Butyricimonas*, *Butyrivibrio*,
Campylobacter, *Caproicibacter*, *Caproicibacterium*, *Caproiciproducens*, *Casaltella*,
Catenibacterium, *Christensenella*, *Clostridium*, *Collinsella*, *Coprobacillus*, *Coprobacter*,
Coprococcus, *Desulfovibrio*, *Dorea*, *Duodenibacillus*, *Dysosmobacter*, *Eggerthella*,
5 *Enorma*, *Enterocloster*, *Enterococcus*, *Escherichia*, *Ethanoligenens*, *Eubacterium*,
Faecalibacillus, *Faecalibacterium*, *Faecalibaculum*, *Finegoldia*, *Flavonifractor*,
Flintibacter, *Fusicatenibacter*, *Gemmiger*, *Gordonibacter*, *Granulicatella*, *Herbinix*,
Holdemanella, *Holdemania*, *Hoylesella*, *Hungatella*, *Intestinibacter*, *Intestinibaculum*,
Intestinimonas, *Lachnoanaerobaculum*, *Lachnoclostridium*, *Lachnospira*,
10 *Lachnospiraceae incertae sedis* (unclassified rank, *Lachnospiraceae* family),
Lacrimispora, *Lactococcus*, *Ligilactobacillus*, *Longibaculum*, *Longicatena*,
Mageeibacillus, *Maliibacterium*, *Marvinbryantia*, *Massilimicrobiota*, *Massiliprevotella*,
Massilistercora, *Mediterraneibacter*, *Megamonas*, *Megasphaera*, *Merdibacter*,
Mesosutterella, *Mitsuokella*, *Mogibacterium*, *Muribaculum*, *Negativibacillus*,
15 *Novisyntrophococcus*, *Odoribacter*, *Olsenella*, *Oscillibacter*, *Oscillospiraceae* (family),
Oscillospiraceae incertae sedis (unclassified rank, *Oscillospiraceae* family),
Parabacteroides, *Paraclostridium*, *Paraprevotella*, *Parolsenella*, *Peptacetobacter*,
Peptoniphilus, *Peptostreptococcus*, *Phascolarctobacterium*, *Phocaeicola*,
Porphyromonas, *Prevotella*, *Pseudobutyrvibrio*, *Pusillibacter*, *Romboutsia*, *Roseburia*,
20 *Ruminiclostridium*, *Ruminococcus*, *Ruthenibacterium*, *Schaalia*, *Segatella*,
Selenomonas, *Sellimonas*, *Senegalimassilia*, *Slackia*, *Sodaliphilus*, *Solibaculum*,
Streptococcus, *Subdoligranulum*, *Thomasclavelia*, *Tyzzereella*, *Veillonella*, *Vescimonas*
and any combination or multitude thereof, said method comprising the step of
administering to a patient in need thereof, the composition of claim 29.
25 39. A method of decreasing the growth of a member of a genus selected from the group
consisting of: *Achromobacter*, *Acidaminococcus*, *Aeromonas*, *Alicyclobacillus*,
Bacteroides, *Bifidobacterium*, *Blautia*, *Bosea*, *Burkholderiales*, *Clostridium*,
Cutibacterium, *Desulfovibrio*, *Eggerthella*, *Enterobacter*, *Enterococcus*, *Escherichia*,
Eubacterium, *Flavonifractor*, *Granulicatella*, *Hungatella*, *Klebsiella*, *Ligilactobacillus*,
30 *Mediterraneibacter*, *Minicystis*, *Oscillibacter*, *Parabacteroides*, *Pluralibacter*, *Prevotella*,
Prosthecochloris, *Pseudomonas*, *Rhodococcus*, *Salmonella*, *Schaalia*, *Serratia*,
Shewanella, *Staphylococcus*, *Streptomyces*, *Sutterella*, *Veillonella*, and any
combination or multitude thereof, said method comprising the step of administering to a
patient in need thereof, a composition of claim 29.
35 40. A method of preparing the composition of claim 29, the method comprising culturing the
composition of claim 29.

41. A method of preparing the biotherapeutic composition of any one of claim 30, the method comprising mixing the composition with a pharmaceutically acceptable carrier.
42. A method of preparing the pharmaceutical composition of any one of claim 31, the method comprising mixing the composition with a pharmaceutically acceptable carrier.
- 5 43. A method of preparing the dosage form of claim 32, the method comprising mixing the composition with a pharmaceutically acceptable carrier.
44. A method of co-culturing one or more core community microbial strains with one or more keystone microbial strains, comprising selecting one or more core community microbial strains selected from Table 14 and one or more keystone microbial strains selected from
- 10 Table 13, and co-culturing the strains under suitable culture conditions.
45. A method of estimating the minimum number of isolates required to achieve a desired level of functional potential or property in a microbial consortium or other complex community, said method comprising identifying the point on a rarefaction curve where the model's asymptote intersects with the benchmark functional potential or property.
- 15 46. Use of the composition of claim 29 in the manufacture of a medicament for a use selected from the group consisting of: reducing or preventing a medical disorder or disease associated with dysbiosis in a subject in need thereof; decreasing inflammation in a subject in need thereof; and decreasing dysbiosis in a subject.
47. A kit comprising the dosage form of claim 32 together with instructions for its use.
- 20 48. A formulation comprising: a plurality of core community microbial species, wherein said core community microbial species comprise members of at least one of the following genera: *Dysosmobacter*, *Enterocloster*, *Ruthenibacterium*, *Vescimonas*, *Phocaeicola*, *Pusillimonas*, *Solibaculum*, and *Christensenella*. a plurality of keystone microbial species, wherein said keystone microbial species comprise members of at least the
- 25 genus *Phocaeicola* and a non-naturally occurring pharmaceutically acceptable excipient, wherein the formulation is formulated as a capsule, tablet, or powder.
49. The formulation of claim 1, wherein the plurality of core community microbial species comprises at least one of the following species: *Dysosmobacter welbionis*, *Enterocloster bolteae*, *Ruthenibacterium lactatiformans*, *Vescimonas coprocola*,
- 30 *Phocaeicola salanitronis*, *Pusillimonas faecalis*, *Solibaculum mannosilyticum*, *Christensenella minuta*, *Alistipes magaguti*, *Parabacteroides goldsteinii*, *Alistipes communis*, *Ruminococcus bicirculans*, *Bacteroides caecimuris*, *Alistipes dispar*, and *Bacteroides salyersiae*; and wherein the plurality of keystone microbial species comprises at least one of the following species: *Phocaeicola coprocola*, *Bifidobacterium bifidum*, and *Coprococcus catus*.
- 35 50. The formulation of claim 1, wherein the plurality of core community microbial species comprises at least one of the following species: *Alistipes dispar*, *Bacteroides salyersiae*,

Bifidobacterium bifidum, *Christensenella minuta*, *Coprococcus catus*, *Coprococcus* sp000154245, *Dysosmobacter faecalis*, *Faecalibacterium duncaniae*, *Gemmiger formicilis*, *Parabacteroides goldsteinii*, *Ruminococcus bicirculans*, *Ruthenibacterium lactatiformans*, *Solibaculum mannosilyticum*, and *Vescimonas coprocola*.