CLAIMS

1. A method of monitoring the health of a mammal, comprising:
   a) obtaining a fecal sample from the mammal;
   b) determining the amount of one or more metabolites in the sample; and
   c) determining whether the mammal is dysmetabolic based on the amount of the one or more metabolites in the sample.
2. The method of claim 1, wherein the mammal is determined to be dysmetabolic, further comprising treating the dysmetabolic mammal by:
   i) administering a bacterial composition comprising bacteria capable of colonization of the intestine;
   ii) administering selective oligosaccharide (OS); or
   iii) both (i) and (ii);
   wherein the bacteria and/or the OS are administered in respective amounts sufficient to change the amount of the one or more metabolites as compared to the amount determined prior to administration of the bacterial composition and/or the OS.
3. A method of establishing and maintaining the health of the mammal, said method comprising the step of treating a mammal by:
   i. administering a bacterial composition comprising bacteria capable of colonization of the intestine;
   ii. administering OS; or
   iii. both (i) and (ii).
4. A method of claim 3, further comprising monitoring the health of the mammal treated in Claim 3 by:
   a) obtaining a fecal sample from the mammal;
   b) determining the amount and/or concentration, of one or more metabolites in the sample;
   c) identifying a dysmetabolic state in the mammal based on the amount and/or concentration of the one or more metabolites in the sample.
5. A method of claim 4, where health is maintained by administering or re-administering the bacterial composition and/or the OS in response to the identified dysmetabolic state.

6. A method of establishing or altering a mammalian intestinal metabolome, said method comprising the steps of:
   a) treating a mammal by:
      i. administering a bacterial composition comprising bacteria capable of colonization of the intestine;
      ii. administering OS; or
      iii. both (i) and (ii), and

   further comprising the steps of:
   b) monitoring the mammal by:
      i. obtaining a fecal sample from the mammal;
      ii. determining the amount and/or concentration, of one or more metabolites in the sample;
      iii. identifying a dysmetabolic state in the mammal based on the amount and/or concentration of the one or more metabolites in the sample; and
   c) administering the bacterial composition and/or the OS in response to the identified dysmetabolic state.

7. The method of any one of claims 4–6, wherein the amount, periodicity, and/or duration of the administration of the bacterial composition and/or the OS is adjusted in response to an identified dysmetabolic state.
8. The method of claim 6, wherein the amount and/or type of the bacterial composition and/or the OS administered in step (a) is different than the amount and/or type of the bacterial composition and/or the OS administered in step (c).
9. A method of increasing the amount of one or more metabolites in the intestine of a mammal, comprising:
   a) administering a bacterial composition comprising bacteria capable of colonization of the intestine; and
   b) administering OS;

   wherein the bacteria and the OS are administered in respective amounts sufficient to increase the amount of the one or more metabolites in the intestine of said mammal.

10. A method of decreasing the amount one or more metabolites in the intestine of a mammal, comprising:
    a) administering a bacterial composition comprising bacteria capable of colonization of the intestine; and
    b) administering OS;
    wherein the bacteria and the OS are administered in respective amounts sufficient to decrease the amount of one or more metabolites in the intestine of said mammal.
11. The method of any one of claims 1–10, wherein the one or more metabolites is selected from the compounds listed in column 2 of Table 1.
12. The method of claim 11, wherein the one or more metabolites comprises a metabolite selected from the group consisting of γ-glutamyl-containing di- or tri-peptides, γ-glutamyl-cysteine, pipecolic acid, hippurate, 3-hydroxyhippurate, 4-hydroxyhippurate, benzoic acid, cholate, cholate sulfate, chenodeoxycholate, choline, creatine, palmitic acid-9-hydroxy-stearic acid (PAHSA 16:0/OH-18:0), and Oleic Acid-Hydroxy Stearic Acid (OAHSA 18:1/OH-18:0), nonadeconate, arachinate, eiocosenoate, stearate, 15-methylplamitate, 17-methylpalmitate, behenate, margarate, palmitate, myristate, citrate, succinate, serotonin, tryptophan, lactate conjugates, 3-4 hydroxyphenyl lactate, indole lactate, and phenyllactate.
13. The method of claim 12, wherein the concentration of γ-glutamyl-containing di- or tri-peptides is at least 10-fold greater than the level in the colon of a mammal which is not colonized by the bacteria.
14. The method of claim 12, wherein the concentration of γ-glutamyl-cysteine is at least 20-fold greater than the γ -glutamyl-cysteine abundance in the colon of a mammal which is not colonized by the administered bacteria.
15. The method of any one of 12-14 where creatine is greater than the creatine abundance in the colon of a mammal which is not colonized by the administered bacteria.
16. The method of any one of claims 12-15, wherein the concentration of pipecolic acid or salt thereof is at least 10-fold greater than the pipecolic acid level in the colon of a mammal which is not colonized by the bacteria.
17. The method of any one of claims 12–16, wherein hippurate level is determined, said level of hippurate indicating detoxification of the intestine of said mammal.

18. The method of any one of claims 12–17, wherein the amount of bacterial hippurate degraders are reduced in the microbiome.
19. The method of claim 18, wherein the bacterial hippurate degrader comprises Group B Streptococci, *Camplyobacter jejuni*, or *Listeria monocytogenes*.
20. The method of any one of claims 17-19 wherein the level of hippurate is further compared to level of benzoic acid or other polyphenols
21. The method of any one of claims 12-20, further wherein supplemental glycine is added to the diet of an individual in need of benzoic acid or polyphenol detoxification
22. The method of any one of claims 12-21, wherein the concentration of cholate, chenodeoxycholate, cholate sulphate is greater than cholate, chenodeoxycholate, cholate sulphate abundance in the colon of a mammal which is not colonized by the administered bacteria.
23. The method of any one of claims 12-22, wherein long chain fatty acid metabolites are increased compared to levels in a mammal which is not colonized by the bacteria, said fatty acid metabolites preferably including palmitic acid-9-hydroxy-stearic acid (PAHSA 16:0/OH-18:0), Oleic Acid-Hydroxy Stearic Acid (OAHSA 18:1/OH-18:0), nonadeconate, arachinate, eiocosenoate, stearate, 15-methylplamitate, 17-methylpalmitate, behenate, margarate, palmitate, myristate, or a combination thereof.
24. The method of any one of claims 12-23, wherein the one or more metabolites comprise a TCA cycle metabolite, said TCA cycle metbolite preferably comprising citrate or succinate.
25. The method of any one of claims 12-24 wherein tryptophan metabolites are increased compared to levels in a mammal which is not colonized by the bacteria, said tryptophan metabolites preferably including serotonin, tryptophan, lactate conjugates, 3-4 hydroxyphenyl lactate, indole lactate, and/or phenyllactate.
26. The method of any one of claims 2–25 wherein jaundice is prevented or ameliorated.
27. The method of any one of claims 2–26 wherein oxidative stress in the mammal is reduced.
28. The method of any one of claims 2–27 wherein said method reduces the risk of said mammal developing a metabolic disorder, said metabolic disorder being preferably selected from metabolic disorders consisting of Obesity and Type 2 Diabetes and combinations thereof, said risk being reduced as compared to a dysmetabolic mammal.;
29. The method of claim 28 wherein the metabolic disorder is Obesity.

30. The method of claim 28, wherein the metabolic disorder is Type 2 Diabetes.
31. The method of any one of claims 2–30, wherein said method reduces the risk of said mammal developing an autoimmune disease, said autoimmune disease preferably selected from the following auto-immune diseases: Juvenile Diabetes (Type I), asthma, atopy, Celiac's Disease, food allergies and combinations thereof, said risk being reduced as compared to a dysmetabolic mammal.
32. The method of claim 31, wherein the autoimmune disease is Juvenile Diabetes (Type I).
33. The method of claim 31, wherein the autoimmune disease is asthma.
34. The method of claim 31, wherein the autoimmune disease is atopy.
35. The method of claim 31, wherein the autoimmune disease is Celiac's disease.
36. The method of claim 31, wherein the autoimmue disease is one or more food allergies.
37. The method of any one of claims 2–36 wherein said method reduces the risk of said mammal developing a cognitive disorder, said cognitive disorder being preferably selected from the following cognitive disorders: autism, depression, or learning disability, and combinations thereof, said risk being reduced as compared to a dysmetabolic mammal.
38. The method of claim 37, wherein the cognitive disorder is autism.
39. The method of claim 37, wherein the cognitive disorder is depression.
40. The method of claim 37, wherein the cognitive disorder is a learning disability.
41. The method of any one of claims 28-40, wherein the risk is reduced by 20, 30, 40, 50, 60, 70, 80, or 90%.
42. The method of any one of claims 2–41, wherein the OS comprises mammalian milk oligosaccharide (MMO), and wherein the MMO comprises N-acetyl lactosamine, lacto N-tetrose, lacto-N-biose, N-acetyllactosamine, lacto-N-triose, lacto-N-neotriose, , lacto-N-neotetrose, fucosyllactose, lacto-N-fucopentose, lactodifucotetrose, sialyllactose, disialyllactone-N-tetrose, 2'-fucosyllactose, 3'-sialyllactoseamin, 3'-fucosyllactose, 3'-sialyl-3-fucosyllactose, 3'-sialyllactose, 6'-sialyllactosamine, 6'-sialyllactose, difucosyllactose, lacto-N-fucosylpentose I, lacto-N-fucosylpentose II, lacto-N-fucosylpentose III, lacto-N-fucosylpentose V, sialyllacto-N-tetraose, their derivatives, or combinations thereof.
43. The method of any one of claims 2–41, wherein the OS comprises MMO, and wherein the MMO consists of carbohydrate polymers found in mammalian milk which are not metabolized by any combination of digestive enzymes expressed by mammalian genes.

44. The method of any one of claims 2–41, wherein the OS comprises:
    a) a Type II oligosaccharide core where representative species include LNnT or LNFPIII;
    b) Type II core OS and GOS in ratio 1:5 to 5:1
    c) Type II core OS and FL in ratio 1:5 to 5:1;
    d) Type II core and SL in ratio of 1:5 to 5:1; or
    e) a combination of (a)-(d).
45. The method of any one of claims 2–41, wherein the OS comprises:
    a) a Type I oligosaccharide core where representative species include LNT or LNFPI;
    b) Type I core OS and GOS in ratio 1:5 to 5:1
    c) Type I core OS and FL in ratio 1:5 to 5:1;
    d) Type I core OS and SL in ratio 1:5 to 5:1; or
    e) a combination of (a)-(d).
46. The method of any one claim 2-41, wherein the OS comprises:
    a) LNT and LNnT in ratio 1:5 to 5:1;
    b) GOS
    c) FOS
    d) FL;
    e) SL or
    f) a combination of (a)-(e).
47. The method of any one of claims 2–46, wherein the OS comprises pre-digested plant polysaccharides.
48. The method of claim 47, wherein the plant polysaccharides are from carrots, peas, broccoli, onions, tomato, pepper, rice, wheat, oats, bran, orange peel, cocao hulls, olive pomace, applecake, cabbage or tomato skins, grape pomace, sugar beet, corn silage, or a combination thereof.
49. The method of any one of claims 2–48, wherein the mammal is receiving OS at a dose representing over 25% of the total dietary fiber.
50. The method of any one of claims 2–48, wherein the mammal is receiving OS at a dose representing over 40% of the total dietary fiber.
51. The method of any one of claims 2–48, wherein the mammal is receiving OS at a dose representing over 50% of the total dietary fiber.

52. The method of any one claims 2–51, wherein the mammal is receiving OS that has over 10%, 25%, 40%, 50%, 60%, or over 75% of the total oligosaccharide represented by one or more units of N- acetyllactosamine.
53. The method of any one claims 2–52, wherein the OS comprises 2'FL and/or GOS.
54. The method of any one of claims 2–53, wherein the OS is administered to said mammal prior to the administration of the bacterial composition.
55. The method of any one of claims 2–53, wherein the OS is administered to said mammal after the administration of the bacterial composition.
56. The method of any one of claims 2–53, wherein the OS is administered to said mammal contemporaneously with the administration of the bacterial composition.
57. The method of any one of claims 2–53, wherein the bacterial composition is provided to the mammal contemporaneously or within 2 hours of the addition of the OS composition.
58. The method of any one of claims 2-57, wherein the bacterial composition and/or the OS are administered daily for a period of from at least 1, 3, 10, at least 20, at least 30, at least 60, at least 90, at least 120, at least 150, or at least 180 days.
59. The method of any one of claims 2–58, wherein the bacterial composition and/or the OS is administered in a food composition.
60. The method of claim 59, wherein the food composition comprises mammalian milk, mammalian milk derived product, and/or mammalian donor milk.
61. The method of claim 60 where the mammalian milk is human milk.
62. The method of claim 59 or 60, wherein the food composition comprises infant formula, a milk replacer, an enteral nutrition product, and/or a meal replacer for a mammal, preferably for a human.
63. The method of any one of claims 59–62, wherein the food composition food is sufficient to sustain growth of the mammal.
64. The method of any one of claims 2–63, wherein the bacterial composition comprises bacteria that are capable of consuming MMO by the internalization of that MMO within the bacterial cell.
65. The method of any one of claims 2–64, wherein the bacterial composition comprises bacteria that can grow in an anaerobic culture whose sole carbon source is OS.

66. The method of any one of claims 2–65, wherein at least one species of the bacterial composition comprises bacteria capable of and/or activated for colonization of the intestine.
67. The method of any one of claims 2–66, wherein the bacterial composition comprises bacteria capable of and/or activated for colonization of the intestine, and wherein the bacteria expresses genes for a transporter that internalizes one or more OSs intact.
68. The method of any one of claims 2–67, wherein the bacterial composition comprises bacteria of a genus selected from the group consisting of *Bifidobacteria*, *Lactobacillus*, and *Pediococcus*.
69. The method of claim 68, wherein the bacteria are *B. adolescentis, B. animalis*, *B. animalis* subsp. *animalis, B. animalis* subsp. *lactis, B. bifidum, B. breve, B. catenulatum, B. longum*, *B. longum* subsp. *infantis, B. longum* subsp. *longum, B. pseudocatanulatum, B. pseudolongum, L. acidophilus, L. antri, L. brevis, L. casei, L. coleohominis, L. crispatus, L. curvatus, L. equi, L. fermentum, L. gasseri, L. johnsonii, L. mucosae, L. pentosus, L. plantarum, L. reuteri, L. rhamnosus, L. sakei, L. salivarius, P. acidilactici, P. argentinicus, P. claussenii, P. pentosaceus, P. stilesii L. paracasei, L. kisonensis., L. paralimentarius, L. perolens, L. apis, L. ghanensis, L. dextrinicus*, *L. shenzenensis, L. harbinensis, P. parvulus,* or *P. lolii*.
70. The method of claim 68 or 69, wherein the bacteria are *B. longum.*
71. The method of claim 68, wherein the bacteria are *B. longum* subsp. *infantis or B. breve*.
72. The method of of any one of claims 2–71, wherein the bacterial composition comprises *Bifidobacterium longum* subsp. *infantis* comprising a functional H5 gene cluster.
73. The method of of any one of claims 2–71, wherein the bacterial composition comprises *Bifidobacterium longum* subsp. *infantis* is *Bifidobacterium longum* subsp. *infantis* EVC001 deposited under ATCC Accession No. PTA-125180 .
74. The method of claims 72 or 73, wherein the H5 cluster comprises Blon_2175, Blon_2176, and Blon_2177.
75. The method of any one of claims 72-74, wherein the functional H5 cluster comprises Blon_2171, Blon_2173, Blon_2174, Blon_2175, Blon_2176, Blon_2177, and galT.
76. The method of any one of claims 52-58, wherein the *Bifidobacterium longum* subsp. *infantis* is activated.
77. The method of any one of claims 2-76, wherein the *Bifidobacterium* contains a LNB transport system capable of internalizing one or more oligosaccharide before the

oligosaccharide is hydrolyzed and is capable of hydrolyzing the internalized oligosaccharide, wherein the oligosaccharide has the structure of an oligosaccharide found in a mammalian milk.

78. The method of any one of the above claims, wherein the mammal is a human.
79. The method of any one of the claims 1–77, wherein the mammal is a non-human mammal.
80. The method of any one of the above claims, wherein the mammal is a non-infant.
81. The method of any one of claims 1–79, wherein the mammal is an infant.
82. The method of claim 81, wherein the infant is a pre-term infant or a term infant.
83. The method of claim 81, wherein the infant is a pre-term infant.
84. The method of any one of claims 81-83, wherein the infant is an infant born by C-section.
85. The method of any one of claims 81-84, wherein the infant is a dysbiotic infant.
86. A method of altering the stool composition in a mammal comprising: administering a bacterial composition comprising at least one species capable of consuming MMO by the internalization of that MMO within the bacterial cell to the mammal, wherein the mammal is receiving MMO at a dose representing over 10% of the total dietary fiber, wherein the MMO comprises:
    a) a Type II oligosaccharide core where representative species include LnNT or LNFPIII;
    b) Type II oligosaccharide and GOS in ratio 1:5 to 5:1
    c) Type II oligosaccharide and FL in ratio 1:5 to 5:1;
    d) Type II oligosaccharide and SL; or
    e) a combination of (a)-(d).
87. A method of altering the stool composition in a mammal comprising: administering a bacterial composition comprising at least one species capable of consuming MMO by the internalization of that MMO within the bacterial cell to the mammal, wherein the mammal is receiving MMO at a dose representing over 10% of the total dietary fiber, wherein the MMO comprises:
    a) A Type I oligosaccharide core where representative species include LNT or LNFPI;
    b) Type I oligosaccharide and GOS in ratio 1:5 to 5:1
    c) Type I oligosaccharide and FL in ratio 1:5 to 5:1;
    d) Type I oligosaccharide and SL; or
    e) a combination of (a)-(d).

88. A method of reducing the risk of Juvenile Diabetes (Type I), comprising:
    a) administering a bacterial composition comprising at least one species capable of consuming MMO by the internalization of that MMO within the bacterial cell, and;
    b) administering OS at a dose sufficient to maintain colonization of the colon of the mammal by bacteria in the bacterial composition of step (a), wherein the risk is reduced as compared to a dysbiotic infant.
89. The method of claim 88, wherein the bacterial composition comprises *Bifidobacterium longum* subsp. *infantis* EVC001 deposited under ATCC Accession No. PTA-125180 .
90. The method of any one of claims 88-89, wherein the OS comprises carbohydrate polymers found in mammalian milk which are not metabolized by any combination of digestive enzymes expressed by mammalian genes.
91. The method of claim 90, wherein the OS comprises mammalian milk, mammalian milk derived product, and/or mammalian donor milk.
92. The method of claim 91, where the mammalian milk is human milk
93. The method of any one of claims 88-92, wherein the OS comprises one or more of N-acetyl lactosamine, lacto N-tetrose, lacto-N-biose, lacto-N-triose, lacto-N-neotriose, lacto-N-neotetrose, fucosyllactose, lacto-N-fucopentose, lactodifucotetrose, sialyllactose, disialyllactone-N-tetrose, 2'-fucosyllactose, 3'-sialyllactoseamin, 3'-fucosyllactose, 3'-sialyl-3-fucosyllactose, 3'-sialyllactose, 6'-sialyllactosamine, 6'-sialyllactose, difucosyllactose, lacto-N-fucosylpentose I, lacto-N-fucosylpentose II, lacto-N-fucosylpentose III, lacto-N-fucosylpentose V, sialyllacto-N-tetraose, their derivatives, or combinations thereof.
94. The method of any one of claims 88-93, wherein the OS comprises:
    a) a Type II oligosaccharide core where representative species include LNnT or LNFPIII;
    b) Type II core OS and GOS in ratio 1:5 to 5:1
    c) Type II core OS and FL in ratio 1:5 to 5:1;
    d) Type II core and SL in ratio of 1:5 to 5:1; or
    e) a combination of (a)-(d)
95. The method of any one of claims 88-93, wherein the OS comprises:
    a) a Type I oligosaccharide core where representative species include LNT or LNFPI;
    b) Type I core OS and GOS in ratio 1:5 to 5:1
    c) Type I core OS and FL in ratio 1:5 to 5:1;

d) Type I core OS and SL in ratio 1:5 to 5:1; or

e) a combination of (a)-(d).

96. The method of any one claim 88-93, wherein the OS comprises:

a) LNT and LNnT in ratio 1:5 to 5:1;

b) GOS

c) FOS

d) FL;

e) SL or

f) a combination of (a)-(e).