

CLAIMS

We claim:

1. A system for characterizing a panel of gut-related conditions associated with a set of taxa related to microorganisms, the system comprising:
 - a taxonomic database comprising reference features of the set of taxa associated with the panel of gut -related conditions;
 - a handling system operable to collect a container comprising biological sample from stool of a user, the handling system comprising a sequencer system operable to determine a microorganism sequence dataset for the user from the biological sample;
 - a panel characterization system operable to:
 - o extracting a set of panel-associated features for the user from the microorganism sequence dataset by applying feature-selection rules;
 - o comparing between the reference features and the set of panel-associated features for the user; and
 - o determine a panel characterization for the panel of gut-related conditions for the user based on the comparison; and
 - a treatment system operable to promote a therapy for a gut-related condition of the panel of gut -related conditions based on the panel characterization, wherein the set of panel-associated features comprises microbiome composition diversity features, microbiome functional diversity features and microbiome pharmacogenomics features of the set of panel-associated features based on the microorganism sequence dataset,

and wherein determining the comparison comprises determining the comparison of the reference features with the microbiome composition diversity features and the microbiome functional diversity features.

2. The system of Claim 1, wherein the reference features comprise the set of reference relative abundance ranges derived from:

- determining a target set of taxa associated with the panel of gut-related conditions,
- determining a set of reference markers; and
- determining the set of reference relative abundance ranges for the set of taxa selected based on a comparison between the set of reference markers and the target set of taxa.

3. The system of Claim 2, wherein determining the set of reference markers comprises determining the set of reference markers based on predicted reads derived from a set of primers selected based on a marker characteristic shared across a plurality of taxonomic groups.

4. The system of Claim 3, wherein the comparison between the set of reference markers and the target set of taxa comprises a sequence similarity between the predicted reads and reference microorganism sequences associated with the target set of taxa.

5. The system of Claim 3, wherein the handling system is operable to determine the microorganism sequence dataset based on amplification of nucleic acids from the biological sample using a primer of the set of primers, wherein the

primer targets a microorganism sequence corresponding to a taxonomic group associated with the gut-related condition, and wherein the set of taxa comprises the taxonomic group.

6. The system of Claim 1, wherein the treatment system is operable to facilitate provision of a consumable therapy based on the panel characterization, wherein the consumable therapy is operable to affect the user for at least one of a microbiome composition and a microbiome function associated with the gut-related condition, in promoting improvement of a state of the gut-related condition.

7. The system of Claim 1, wherein the set of taxa comprises at least one of: *Alistipes* (genus), *Barnesiella* (genus), *Bifidobacterium* (genus), *Campylobacter* (genus), *Peptoclostridium* (genus), *Escherichia-Shigella* (genus), *Fusobacterium* (genus), *Lactobacillus* (genus), *Odoribacter* (genus), *Prevotella* (genus), *Pseudoflavonifractor* (genus), *Roseburia* (genus), *Ruminococcus* (genus), *Salmonella* (genus), *Veillonella* (genus), *Akkermansia muciniphila* (species), *Anaerotruncus colihominis* (species), *Bacteroides fragilis* (species), *Bacteroides vulgatus* (species), *Bifidobacterium longum* (species), *Butyrivibrio crossotus* (species), *Campylobacter jejuni* (species), *Campylobacter coli* (species), *Campylobacter lari* (species), *Peptoclostridium difficile* (species), *Collinsella aerofaciens* (species), *Coprococcus eutactus* (species), *Desulfovibrio piger* (species), *Dialister invisus* (species), *Escherichia coli* (species), *Escherichia coli* O157 (species), *Faecalibacterium prausnitzii* (species), *Methanobrevibacter smithii* (species), *Oxalobacter formigenes* (species), *Ruminococcus albus* (species),

Ruminococcus bromii (species), Ruminococcus gnavus (species), Salmonella enterica (species), Salmonella bongori (species), Shigella boydii (species), Shigella sonnei (species), Shigella flexneri (species), Shigella dysenteriae (species), Streptococcus sanguinis (species), Streptococcus thermophilus (species), Vibrio cholerae (species), and Yersinia enterocolitica (species), Alloprevotella (genus), Anaerofilum (genus), Bacteroides (genus), Blautia (genus), Butyrivibrio (genus), Catenibacterium (genus), Christensenella (genus), Collinsella (genus), Coprococcus (genus), Dialister (genus), Eggerthella (genus), Faecalibacterium (genus), Flavonifractor (genus), Gelria (genus), Haemophilus (genus), Holdemania (genus), Oscillibacter (genus), Oscillospira (genus), Parabacteroides (genus), Paraprevotella (genus), Phascolarctobacterium (genus), Streptococcus (genus), Turicibacter (genus), Tyzzerella (genus), Acetobacter nitrogenifigens (species), Acinetobacter baumannii (species), Azospirillum brasilense (species), Bacillus cereus (species), Bacillus coagulans (species), Bacillus licheniformis (species), Bifidobacterium animalis (species), Bifidobacterium bifidum (species), Brevibacillus laterosporus (species), Christensenella minuta (species), Clavibacter michiganensis (species), Clostridium butyricum (species), Enterococcus italicus (species), Fibrobacter succinogenes (species), Kocuria rhizophila (species), Lactobacillus brevis (species), Lactobacillus coryniformis (species), Lactobacillus delbrueckii (species), Lactobacillus fermentum (species), Lactobacillus helveticus (species), Lactobacillus kefir anofaciens (species), Lactobacillus kunkeei (species), Lactobacillus rhamnosus (species), Lactobacillus salivarius (species), Lactococcus fujiensis (species), Lactococcus garvieae (species), Lactococcus lactis (species), Leptotrichia hofstadii (species), Leuconostoc fallax (species), Leuconostoc kimchii

(species), *Oenococcus oeni* (species), *Paenibacillus apiarius* (species), *Pediococcus pentosaceus* (species), *Propionibacterium freudenreichii* (species), *Pseudoclavibacter helvolus* (species), *Renibacterium salmoninarum* (species), *Ruminococcus flavefaciens* (species), *Staphylococcus sciuri* (species), *Weissella koreensis* (species), *Clostridium* (genus), and *Clostridium difficile* (species), and

wherein the therapy comprises a probiotics-related therapy for the gut-related condition, wherein the probiotics-related therapy is associated with the set of taxa, and wherein the treatment system comprises an interface for promoting the probiotics-related therapy in association with a taxonomic group from the set of taxa.

8. A method for characterizing a panel of microorganism-related conditions associated with a set of taxa, the method comprising:

- generating a taxonomic database comprising reference features associated with the set of taxa;
- generating a microorganism sequence dataset for a user based on a biological sample collected from the user;
- extracting a set of panel-associated features for the user based on the microorganism sequence dataset;
- determining a comparison between the reference features and the set of panel-associated features for the user;
- determining a panel characterization for the user for the panel of microorganism-related conditions based on the comparison; and
- promoting a therapy for a microorganism-related condition of the panel of microorganism-related conditions, based on the panel characterization.

9. The method of Claim 8, wherein promoting the therapy comprises promoting a probiotic consumable to the user based on the panel characterization, wherein the probiotic consumable is operable to improve a plurality of the microorganism- related conditions of the panel of microorganism-related conditions.

10. The method of Claim 9, further comprising: collecting a diet-associated supplementary dataset associated with a dietary behavior of the user, wherein promoting the probiotic consumable comprises promoting the probiotic consumable to the user based on the diet-associated supplementary dataset and the panel characterization.

11. The method of Claim 8, wherein extracting the set of panel-associated features comprises extracting microbiome composition diversity features and microbiome functional diversity features of the set of panel-associated features based on the microorganism sequence dataset, and wherein determining the comparison comprises determining the comparison of the reference features with the microbiome composition diversity features and the microbiome functional diversity features.

12. The method of Claim 8, wherein the panel of microorganism-related conditions comprises a set of gut-related conditions associated with antibiotics, wherein extracting the set of panel-associated features comprises extracting microbiome pharmacogenomics features of the set of panel-associated features based on the microorganism sequence dataset, and wherein promoting the

therapy comprises promoting an antibiotics-associated therapy for the set of gut-related conditions based on the microbiome pharmacogenomics features.

13. The method of Claim 8, wherein determining the comparison between the reference features and the set of panel-associated features comprises determining the set of panel-associated features as associated with at least one of: presence of microbiome composition features, absence of the microbiome composition features, relative abundance for taxonomic groups of the set of taxa, diversity of microbiome composition including taxonomic and functional features, a ratio between at least two features associated with the set of taxa, interactions between the taxonomic groups, and phylogenetic distance between the taxonomic groups.

14. The method of Claim 13,

- wherein generating the taxonomic database comprises determining a set of reference relative abundance ranges for the set of taxa, wherein the set of reference relative abundance ranges is associated with the panel of microorganism-related conditions,
- wherein extracting the set of panel-associated features comprises extracting a set of user relative abundance ranges for the set of taxa based on the microorganism sequence dataset, and
- wherein determining the comparison between the reference features and the set of panel-associated feature comprises determining the comparison between the set of reference relative abundance ranges and the set of user relative abundance ranges.

15. The method of Claim 14, wherein determining the set of reference relative abundance ranges for the set of taxa comprises:

- collecting a set of supplementary biological samples and a set of supplementary datasets for a population of users;
- processing the set of supplementary biological samples to generate a supplementary microorganism sequence dataset using a set of primers associated with the panel of microorganism-related conditions; and
- determining the set of reference relative abundance ranges based on the supplementary microorganism sequence dataset and the set of supplementary datasets.

16. The method of Claim 13, wherein determining the comparison between the reference features and the set of panel-associated features comprises performing at least one of: a prediction analysis, multi hypothesis testing, a random forest test, principal component analysis, significance index analysis, risk score analysis, and metaanalysis.

17. The method of Claim 8, wherein promoting the therapy comprises promoting a probiotics-related therapy for the microorganism-related condition, wherein the probiotics-related therapy is associated with the set of taxa, and wherein the set of taxa comprises at least one of: *Bacillus coagulans* (species), *Bifidobacterium animalis* (species), *Clostridium butyricum* (species), *Lactobacillus brevis* (species), *Lactobacillus coryniformis* (species), *Lactobacillus fermentum* (species), *Lactobacillus helveticus* (species), *Lactobacillus rhamnosus* (species), and *Streptococcus salivarius* (species).

18. The method of Claim 17, wherein the set of taxa further comprises at least one of: *Acetobacter nitrogenifigens* (species), *Azospirillum brasilense* (species), *Bacillus licheniformis* (species), *Bifidobacterium bifidum* (species), *Brevibacillus laterosporus* (species), *Clavibacter michiganensis* (species), *Enterococcus italicus* (species), *Kocuria rhizophila* (species), *Lactobacillus delbrueckii* (species), *Lactobacillus kefir anofaciens* (species), *Lactobacillus kunkeei* (species), *Lactobacillus salivarius* (species), *Lactococcus garvieae* (species), *Lactococcus lactis* (species), *Leptotrichia hofstadii* (species), *Leuconostoc fallax* (species), *Leuconostoc kimchii* (species), *Oenococcus oeni* (species), *Paenibacillus apiarius* (species), *Pediococcus pentosaceus* (species), *Propionibacterium freudenreichii* (species), *Pseudoclavibacter helvolus* (species), *Renibacterium salmoninarum* (species), *Ruminococcus flavefaciens* (species), *Staphylococcus sciuri* (species), *Streptococcus dysgalactiae* (species), *Streptococcus parauberis* (species), and *Weissella koreensis* (species).

19. The method of Claim 8, wherein the panel of microorganism-related conditions comprises at least one of: Diarrhea, Irritable Bowel Syndrome (IBS), Inflammatory Bowel Disease (IBD), Crohn's Disease, Ulcerative Colitis, Constipation, Abdominal Tenderness, Bloating, Flatulence, Obesity, Type II Diabetes, Prediabetes, Kidney Stones, Cardiovascular health, and Anxiety.

20. The method of Claim 8, wherein characterizing the panel of microorganism-related characterization comprises at least one of diagnosing and treating a gut-related panel of conditions.