CLAIMS

1. A method of determining healthy aging in an individual, the method comprising:

(a) determining the presence or an amount of at least one microorganism in a sample representing the individual's gut microbiome, wherein the at least one microorganism selected from *Alistipes senegalensis*, *Alistipes indistinctus*, *Alistipes* unclassified, and *Alistipes shahii*, wherein an enrichment of said microorganisms being any increase in the amounts of the relevant microorganism relative to an average individual,

is indicative of healthy aging.

2. Use of a probiotic composition or a pharmaceutical formulation in the manufacture of a medicament for the treatment or prevention of age-related gut microbiome dysbiosis characterised by a depletion of classical butyrate-producing species, wherein the medicament is to be administered to a subject, and wherein the medicament improves intestinal flora by enriching at least one of *Alistipes senegalensis*, *Alistipes indistinctus*, *Alistipes* unclassified, and *Alistipes shahii*, wherein enriching refers to any increase in the amounts of the relevant microorganism relative to an average individual.

3. Use of a pharmaceutical composition comprising an isolated microorganism in the manufacture of a medicament for the treatment or prevention of age-related gut microbiome dysbiosis characterised by a depletion of classical butyrate-producing species in a subject, wherein the isolated microorganism is selected from *Alistipes senegalensis*, *Alistipes indistinctus*, *Alistipes* unclassified, and *Alistipes shahii*.

4. A method of determining the likelihood of healthy aging in an individual, the method comprising:

(a) determining a gut microbiome signature of the individual by determining an amount of, or presence or absence of, each microorganism in a group of microorganisms comprising at least one of *Alistipes senegalensis*, *Alistipes indistinctus*, *Alistipes* unclassified, and *Alistipes shahii*, present in a sample obtained from the individual; and

(b) applying a prediction model to assess the gut microbiome signature with respect to a gut profile representative of an individual that is aging healthily,

wherein the prediction model is trained using a dataset of microbiome profiles of a plurality of individuals who are aging healthily and said gut profile comprises an enrichment of at least one microorganism selected from *Alistipes senegalensis*, *Alistipes indistinctus*, *Alistipes* unclassified, and *Alistipes shahii*, wherein enrichment refers to any increase in the amounts of the relevant microorganism relative to an average individual.

5. The method according to claim 4, wherein the prediction model comprises a machine learning probability model.

6 A computer readable storage medium comprising computer readable instructions operable when executed by a computer to predict the likelihood of healthy aging in an individual, the computer readable instructions configured to perform a method according to any one of claims 4 or 5.

7. An apparatus or system comprising:

(a) a receiving unit configured to receive a dataset of values representing a gut microbiome signature of an individual by determining an amount of, or presence or absence of, each microorganism in a group of microorganisms comprising at least one of *Alistipes senegalensis*, *Alistipes indistinctus*, *Alistipes* unclassified, and *Alistipes shahii*, present in a sample obtained from the individual; and

(b) a processor configured to process a prediction model to assess the gut microbiome signature with respect to a gut profile representative of good gut health to obtain a likelihood of healthy aging in the individual,

wherein the prediction model is trained using a dataset of microbiome profiles of a plurality of individuals who are aging healthily and said profile comprises an enrichment of at least one microorganism selected from *Alistipes senegalensis*, *Alistipes indistinctus*, *Alistipes* unclassified, and *Alistipes shahii*, wherein enrichment refers to any increase in the amounts of the relevant microorganism relative to an average individual.