CLAIMS:

1. A host modifying (HM) CRISPR/Cas system for modifying a target nucleotide sequence of a bacterial host cell, the system comprising components according to (i) to (iv):-

   (i) at least one nucleic acid sequence encoding a Cas nuclease that is endogenous to the host cell;

   (ii) a host cell target sequence and an engineered host modifying (HM) CRISPR array comprising a spacer sequence (HM-spacer) and repeats encoding a HM-crRNA, the HM-crRNA comprising a sequence that is capable of hybridising to the host target sequence to guide said Cas to the target in the host cell to modify the target sequence;

   (iii) an optional tracrRNA sequence or a DNA sequence for expressing a tracrRNA sequence;

   (iv) wherein said components of the system are split between the host cell and at least one nucleic acid vector that can transform the host cell, whereby the HM-crRNA guides Cas to the target to modify the the target sequence in the host cell;

   wherein each vector lacks a Cas nuclease-encoding sequence; and

   wherein each vector is a phage vector.

2. The system of claim 1, wherein the system is for medical use.

3. Use of a host modifying (HM) CRISPR/Cas system for altering the relative ratio of sub-populations of first and second bacteria in a mixed population of bacteria *ex vivo* in an environment, the second bacteria comprising host cells,

   for each host cell the system comprising components according to (i) to (iv):-

   (i) at least one nucleic acid sequence encoding a Cas nuclease that is endogenous to the host cell;

   (ii) a host cell target sequence and an engineered host modifying (HM) CRISPR array comprising a spacer sequence (HM-spacer) and repeats encoding a HM-crRNA, the HM-crRNA comprising a sequence that hybridises to the host cell target sequence to guide said Cas to the target in the host cell to modify the target sequence;

   (iii) an optional tracrRNA sequence or a DNA sequence expressing a tracrRNA sequence;

   (iv) wherein said components of the system are split between the host cell and at least one nucleic acid vector that transforms the host cell, whereby the HM-crRNA guides Cas to the target to modify the the target sequence in the host cell;

   wherein the target sequence is modified by the Cas whereby the host cell is killed or host cell growth is reduced;

   wherein each vector lacks a Cas nuclease-encoding sequence and

   wherein each vector is a phage.

4. The use of claim 3 for treating an industrial or an *ex vivo* medical fluid, surface, apparatus or container; or for treating a waterway, water, a beverage, a foodstuff or a cosmetic, wherein the host cell(s) are comprised by or on the fluid, surface, apparatus, container, waterway, water, beverage, foodstuff or cosmetic.
5. The use of claim 3, wherein the use produces bacterial cultures for administration to humans or animals for favouring *Bacteroidetes* that are commensal or symbiotic in humans or animals.
6. The use of claim 3 or 5, wherein the mixed population is a gut microbiota population *ex vivo*; optionally wherein the host cells are *Firmicutes* or *Clostridium dificle* cells.
7. The use or system of any preceding claim, wherein
   (a) each host cell is of a strain or species found in human microbiota;
   (b) each host cell is a *Staphylococcus, Streptococcus, Pseudomonas, Salmonella, Listeria, E coli, Desulfovibrio,* or *Clostridium* host cell;
   (c) the first bacteria are probiotic, commensal or symbiotic with humans (eg, in the human gut);
   (d) the first and second bacteria are both *Firmicutes* and are bacteria of different species or strains;
   (e) the first bacteria are *Enterobacteriaceae* and the second bacteria are *Firmicutes*; and
   (f) the host cells are archaeal cells instead of bacterial cells or each population is an archaeal population instead of a bacterial population.
8. The use of any one of claims 3-7 for (a) the alteration of the proportion of *Bacteroidetes* bacteria in a mixed bacterial population; (b) reducing the proportion of a *Firmicutes* sub-population (host cells) in a mixed bacterial population; (c) reducing the proportion of a first *Firmicutes* species (host cells) in a mixed population, wherein the mixed population comprises a second *Firmicutes* species whose growth is not inhibited by said cRNA; (d) reducing the proportion of a first gram positive bacterial species (host cells) in a mixed bacterial population, wherein the mixed population comprises a second gram positive bacterial species whose growth is not inhibited by said cRNA; (e) reducing the proportion of a bacterial species (host cells) in a mixed bacterial population, wherein the mixed population comprises a different bacterial species whose growth is not inhibited by said cRNA, wherein the first species has 16s ribosomal RNA-encoding DNA sequence that is at least 80% identical to an 16s ribosomal RNA-encoding DNA sequence of the other species;(f) reducing the proportion of a first bacterial human gut microbiota species (host cells, eg, a *Firmicutes)* in a mixed bacterial population, wherein the mixed population comprises a different bacterial species, wherein the different species is a human gut probiotic species whose growth is not inhibited by said cRNA; or (g) reducing the proportion of a bacterial human gut microbiota species ((host cells, eg, a Firmicutes)

in a mixed bacterial population, wherein the mixed population comprises a different bacterial species , wherein the different species is a human gut commensal species whose growth is not inhibited by said cRNA.

9. The system of any one of claims 1,2 and 7 for (a) the alteration of the proportion of *Bacteroidetes* bacteria in a mixed bacterial population; (b) reducing the proportion of a *Firmicutes* sub-population (host cells) in a mixed bacterial population; (c) reducing the proportion of a first *Firmicutes* species (host cells) in a mixed population, wherein the mixed population comprises a second *Firmicutes* species whose growth is not inhibited by said cRNA; (d) reducing the proportion of a first gram positive bacterial species (host cells) in a mixed bacterial population, wherein the mixed population comprises a second gram positive bacterial species whose growth is not inhibited by said cRNA; (e) reducing the proportion of a bacterial species (host cells) in a mixed bacterial population, wherein the mixed population comprises a different bacterial species whose growth is not inhibited by said cRNA, wherein the first species has 16s ribosomal RNA-encoding DNA sequence that is at least 80% identical to an 16s ribosomal RNA-encoding DNA sequence of the other species;(f) reducing the proportion of a first bacterial human gut microbiota species (host cells, eg, a *Firmicutes*) in a mixed bacterial population, wherein the mixed population comprises a different bacterial species, wherein the different species is a human gut probiotic species whose growth is not inhibited by said cRNA; or (g) reducing the proportion of a bacterial human gut microbiota species ((host cells, eg, a Firmicutes) in a mixed bacterial population, wherein the mixed population comprises a different bacterial species , wherein the different species is a human gut commensal species whose growth is not inhibited by said cRNA; wherein (a) to (g) are for treating or preventing in a human or animal subject (i) a microbiota infection by said bacterial species whose proportion is reduced; or (ii) a disease or condition mediated by said bacterial species whose proportion is reduced.
10. The use or system of any preceding claim for
    (a) altering the relative ratio of the first and second sub-populations in the mixed population of bacteria, wherein the second bacteria are *Firmicutes*;
    (b) increasing the relative ratio of *Bacteroidetes* versus *Firmicutes;* or
    (c) altering the proportion of *Bacteroidetes* bacteria in the mixed bacterial population.
11. The use or system of any preceding claim, wherein alternatively HM-crRNA and tracrRNA are comprised by a single guide RNA (gRNA), eg provided by the vector.

12. An engineered nucleic acid vector for the use in the system of any one of claims 1, 2, 7 and 9-11 for modifying a bacterial host cell comprising an endogenous CRISPR/Cas system, the vector being a phage vector

    (a) comprising nucleic acid sequences for expressing a plurality of different crRNAs (eg, comprised by gRNAs) for use in a CRISPR/Cas system or use according to any preceding claim; and

    (b) lacking a nucleic acid sequence encoding a Cas nuclease,

    wherein a first of said crRNAs is capable of hybridising to a first nucleic acid sequence in said host cell; and a second of said crRNAs is capable of hybridising to a second nucleic acid sequence in said host cell, wherein said second sequence is different from said first sequence; and

    (c) the first sequence is comprised by an antibiotic resistance gene (or RNA thereof) and the second sequence is comprised by an antibiotic resistance gene (or RNA thereof); optionally wherein the genes are different;

    (d) the first sequence is comprised by an antibiotic resistance gene (or RNA thereof) and the second sequence is comprised by an essential or virulence gene (or RNA thereof);

    (e) the first sequence is comprised by an essential gene (or RNA thereof) and the second sequence is comprised by an essential or virulence gene (or RNA thereof); or

    (f) the first sequence is comprised by a virulence gene (or RNA thereof) and the second sequence is comprised by an essential or virulence gene (or RNA thereof).

13. The use, system or vector of any preceding claim wherein host cell population growth is reduced by of at least 5-fold compared to the growth of a population of said host cells not transformed with said HM-array or a nucleotide sequence encoding said gRNA.

14. The use, system or vector of any preceding claim wherein host cell population growth on a surface is inhibited.

15. A nucleic acid vector according to the vector of any one of claims 12-14, or for use in the use or system of any one of claims 1-11, 13 and 14, the vector comprising more than 1.4kb of exogenous DNA sequence, wherein the exogenous DNA encodes one or more components of a CRISPR/Cas system and comprises an engineered array for expressing HM-crRNAs or gRNAs in host cells, wherein the exogenous sequence is devoid of a nucleotide sequence encoding a Cas nuclease that is cognate to the cRNA(s) or gRNA(s); wherein at least 2 different cRNAs or gRNAs are encoded by the exogenous DNA (eg, by at least 2 HM-CRISPR arrays).