Claims

1. Use of a pharmaceutical composition comprising a plurality of bacterial isolates in manufacture of a medicament for treating or preventing inflammatory bowel disease (IBD) in a subject in need thereof, wherein the plurality of bacterial isolates comprises *Bacteroides stercoris and Bacteroides cellulosilyticus*, and at least one of *Bacteroides uniformis*, *Suboligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*, wherein the *Bacteroides stercoris* comprises a 16S ribosomal ribonucleic acid (rRNA) sequence that has at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with the nucleotide sequence of SEQ ID NO: 13.

2. The use of claim 1, wherein at least two of the plurality of bacterial isolates are isolated from a stool of different human donors

3. The use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least two of *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

4. The use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least three of *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

5. The use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least four of *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

6. The use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least five of *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

7. The use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least six of *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

8. The use of claim 1 or 2, wherein the plurality of bacterial isolates comprises at least seven of *Bacteroides uniformis*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Anaerostipes hadrus*, *Faecalibacterium prausnitzii*, *Subdoligranulum variabile*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

9. The use of any one of claims 1-8, wherein the plurality of bacterial isolates comprises a 16S rRNA sequence that has at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequences selected from SEQ ID NOs: 1, 2, 3, 7, 8, 11, 14, 18, 19, 20, 22 and 23.

10. The use of any one of claims 1-9, wherein the plurality of bacterial isolates comprises:

(a) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NOs: 1 and/or 7,

(b) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 2,

(c) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 3.

(d) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 8,

(e) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 11

(f) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 14,

(g) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 18,

(h) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 19,

(i) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NO: 20, and/or

(j) a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequence of SEQ ID NOs: 22 and/or 23.

11. The use of any one of claims 1-10, wherein the plurality of bacterial isolates comprises at least two bacterial isolates comprising *Faecalibacterium prausnitzii*, wherein the at least two bacterial isolates comprise different 16S rRNA sequences.

12. The use of claim 11, wherein the at least two bacterial isolates comprising *Faecalibacterium prausnitzii* comprise 16S rRNA sequences that are at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% identity sequence identity with nucleotide sequences of SEQ ID NOs: 1 and/or 7.

13. The use of claim 11 or 12, wherein the at least two bacterial isolates comprising Faecalib*acterim prausnitzii* are isolated from a stool of different human donors.

14. The use of any one of claims 1-13, wherein the plurality of bacterial isolates comprises lyophilized bacteria.

15. The use of any one of claims 1-14, wherein the plurality of bacterial isolates does not include *Escherichia coli*.

16. A pharmaceutical composition comprising a plurality of bacterial isolates, wherein the plurality of bacterial isolates comprise *Bacteroides stercoris and Bacteroides cellulosilyticus*,, and at least one of *Bacteroides uniformis*, *Subodligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*, wherein the *Bacteroides stercoris* comprises a 16S ribosomal ribonucleic acid (rRNA) sequence that has at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with the nucleotide sequence of SEQ ID NO: 13, and optionally wherein at least two of the plurality of bacterial isolates are isolated from a stool of different human donors.

17. The pharmaceutical composition of claim 16, wherein the plurality of bacterial isolates comprises at least two of *Bacteroides uniformis*, *Subodligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

18. The pharmaceutical composition of claim 16 or 17, wherein the plurality of bacterial isolates comprises at least three of *Bacteroides uniformis*, *Subodligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

19. The pharmaceutical composition of any one of claims 16-18, wherein the plurality of bacterial isolates comprises at least four of *Bacteroides uniformis*, *Subdoligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

20. The pharmaceutical composition of any one of claims 16-19, wherein the plurality of bacterial isolates comprises at least five of *Bacteroides uniformis*, *Subdoligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter*

splanchnicus, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

21. The pharmaceutical composition of any one of claims 16-20, wherein the plurality of bacterial isolates comprises at least six of *Bacteroides uniformis*, *Subdoligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

22. The pharmaceutical composition of any one of claims 16-21, wherein the plurality of bacterial isolates comprises at least seven of *Bacteroides uniformis*, *Subdoligranulum variabile*, *Anaerostipes hadrus*, *Odoribacter splanchnicus*, *Roseburia faecis*, *Faecalibacterium prausnitzii*, *Akkermansia muciniphila*, *Alistipes shahii*, and *Eubacterium rectale*.

23. The pharmaceutical composition of any one of claims 16-22, wherein the composition comprises a 16S rRNA sequence that is at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% sequence identity with nucleotide sequences selected from SEQ ID NOs: 1, 2, 3, 7, 8, 11, 14, 18, 19, 20, 22 and 23.

24. The pharmaceutical composition of any one of claims 16-23, wherein the pharmaceutical composition comprises at least two bacterial isolates comprising *Faecalibacterium prausnitzii*, wherein the at least two bacterial isolates comprise different 16S rRNA sequences.

25. The pharmaceutical composition of claim 24, wherein the pharmaceutical composition comprises 16S rRNA sequences that are at least about 95%, or at least about 97%, or at least about 98%, or at least about 99% identity sequence identity with nucleotide sequences of SEQ ID NOs: 1 and 7.

26. The pharmaceutical composition of any one of claims 16-25, wherein the plurality of bacterial isolates comprises lyophilized bacteria.

27. The pharmaceutical composition of any one of claims 16-26, wherein the plurality of bacterial isolates does not include *Escherichia coli*.