

Table S3 Bacterial strains used in the study and genome information (from <https://www.ncbi.nlm.nih.gov/genome/microbes/>).

Organism ¹	Reference	Genome size [Mb]	Assembly level	Number of scaffolds or contigs	Contig N50	Contig L50	Total assembly gap length [kb] ²
<i>Faecalibacterium prausnitzii</i> A2-165	1	3.09035	Scaffold	20	63,061	14	9.5
<i>Faecalibacterium prausnitzii</i> SL3/3	2	3.21442	Chromosome	1	67,073	14	48.5
<i>Subdoligranulum variabile</i> DSM 15176	3	3.24547	Scaffold	11	166,480	6	8.0
<i>Anaerobutyricum hallii</i> DSM 3353	4, 5	3.29	Contig	175	33,110	28	0
<i>Anaerostipes caccae</i> DSM 14662 (L1-92)	1, 6	3.60694	Scaffold	26	261,254	4	1.3
<i>Anaerostipes hadrus</i> SSC/2	2	3.11479	Chromosome	1	46,563	22	63.8
<i>Coprococcus catus</i> GD/7	7	3.5227	Chromosome	1	92,485	12	59.3
<i>Clostridium</i> sp. L2-50	1, 8	2.95462	Scaffold	20	197,148	6	0.5
<i>Coprococcus</i> sp. ART55/1	2, 8	3.12301	Chromosome	1	15,489	53	235.0
[<i>Eubacterium</i>] <i>rectale</i> DSM 17629 (A1-86)	1	3.34495	Chromosome	1	80,495	13	85.9
[<i>Eubacterium</i>] <i>rectale</i> M104/1	2	3.69842	Chromosome	1	62,843	18	131.8
<i>Roseburia faecis</i> M72/1	2	3.33469	Contig	101	143,514	7	0
<i>Roseburia intestinalis</i> L1-82	1, 9	4.49335	Complete genome				0
<i>Roseburia intestinalis</i> M50/1	2	4.14355	Chromosome	1	57,879	22	82.9
<i>Roseburia inulinivorans</i> DSM 16841 (A2-194)	1	4.04846	Contig	179	57,343	23	0
<i>Bifidobacterium bifidum</i> CNCM I-3650	This study						
<i>Lactobacillus paracasei</i> CNCM I-1518	10						
<i>Streptococcus thermophilus</i> CNCM I-3862	This study						

¹The names of the organisms are given as they are recorded on the NCBI Taxonomy website (<https://www.ncbi.nlm.nih.gov/Taxonomy/taxonomyhome.html/>).

²Based on subtraction of 'total ungapped length' from 'total sequence length' provided at <https://www.ncbi.nlm.nih.gov/genome/microbes/>.

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