

Additional file 4 The sequence analysis of DGGE bands from the feces

Band	Closest relative	Strain	GenBank accession	Identity (%)
1	<i>Citrobacter rodentium</i>	ICC168	NC_013716.1	97
2	<i>Bacteroides vulgatus</i>	ATCC 8482	NC_009614.1	99
3	<i>Bacteroides helcogenes</i>	P 36-108	NC_014933.1	96
4	<i>Bacteroides salanitronis</i>	DSM 18170	NC_015164.1	97
5	<i>Lactobacillus plantarum</i>	WCFS1	NC_004567.2	99
6	<i>Bacteroides thetaiotaomicron</i>	VPI-5482	NC_004663.1	97
7	<i>Bacteroides coprosuis</i>	DSM 18011	NZ_CM001167.1	98
8	<i>Acinetobacter baumannii</i>	MDR-TJ	NC_017847.1	97
9	<i>Veillonella sp.</i>	F0412	NZ_AENU01000007.1	99
10	<i>Lactobacillus salivarius</i>	UCC118	NC_007929.1	96
11	<i>Eubacterium eligens</i>	ATCC 27750	NC_012778.1	100
12	<i>Streptococcus gallolyticus</i>	UCN34	NC_013798.1	99
13	<i>Enterococcus faecalis</i>	OG1RF	NC_017316.1	99
14	<i>Eubacterium rectale</i>	ATCC 33656	NC_012781.1	99
15	<i>Streptococcus oralis</i>	Uo5	NC_015291.1	98
16	<i>Roseburia intestinalis</i>	XB6B4	NC_021012.1	97
17	<i>Streptococcus infantarius</i>	CJ18	NC_016826.1	99
18	<i>Streptococcus pasteurianus</i>	ATCC 43144	NC_015600.1	99
19	<i>Klebsiella pneumoniae</i>	MGH 78578	NC_009648.1	99
20	<i>Clostridium ljungdahlii</i>	DSM 13528	NC_014328.1	98
21	<i>Erwinia billingiae</i>	Eb661	NC_014306.1	97
22	<i>Clostridium saccharolyticum</i>	WM1	NC_014376.1	97
23	<i>Raoultella ornithinolytica</i>	B6	NC_021066.1	99
24	<i>Ruminococcus champanellensis</i>	18P13	NC_021039.1	96
25	<i>Streptococcus thermophilus</i>	CNRZ1066	NC_006449.1	99
26	<i>Yersinia enterocolitica</i>	subsp. palearctica 105.5R(r)	NC_015224.1	97
27	<i>Escherichia coli</i>	UMN026	NC_011751.1	100
28	<i>Shigella boydii</i>	CDC 3083-94	NC_011740.1	100
29	<i>Enterobacter cloacae</i>	SCF1	NC_014618.1	99
30	<i>Lactobacillus reuteri</i>	DSM 20016	NC_009513.1	97
31	<i>Enterobacter sp.</i>	638	NC_009436.1	96
32	<i>Veillonella dispar</i>	ATCC 17748	NZ_ACIK02000004.1	99