

**Supplementary Table 1 The used primers for RT-qPCR in our study**

Target group	Sequence (5'-3')	Annealing temperature (°C)	Reference
<i>Faecalibacterium prausnitzii</i>	GATGGCCTCGCGTCCGATTA G CCGAAGACCTTCTTCCTCC	58	[1]
<i>Bifidobacterium spp.</i>	GGGTGGTAATGCCGGATG TAAGCCATGGACTTTCACAC C	59	[1]
<i>Bacteroides-Prevotella</i> group	GAAGGTCCCCCACAATTG CAATCGGAGTTCTTCGTG	56	[1]
Enterobacteriaceae	CATTGACGTTACCCGCAGAA GAAGC CTCTACGAGACTCAAGCTTG C	63	[1]
<i>Clostridium</i> clusters I	TACCHRAGGAGGAAGCCAC GTTCTTCCTAATCTCTACGCA T	63	[2]
<i>Clostridium</i> clusters XI	ACGCTACTTGAGGAGGA GAGCCGTAGCCTTTCACT	58	[2]
<i>Enterococcus faecalis</i>	AACCTACCCATCAGAGGG GACG TTCAGTTACTAACG	57	[1]
<i>Clostridium</i> cluster XIVab	GAWGAAGTATYTCGGTATGT CTACGCWCCCTTTACAC	54	[2]
<i>Lactobacillus</i>	AGCAGTAGGGAATCTTCCA ATTYCACCGCTACACATG	58	[1]

1. Bartosch S, Fite A, Macfarlane GT, McMurdo ME (2004) Characterization of bacterial communities in feces from healthy elderly volunteers and hospitalized elderly patients by using realtime PCR and effects of antibiotic treatment on the fecal microbiota. Appl Environ Microbiol 70:3575–3581.

2. Song Y, Liu C, Finegold SM (2004) Real-time PCR quantitation of clostridia in feces of autistic children. Appl Environ Microbiol 70:6459–6465.

**Supplementary Table 2 Identification of key bacteria of gut microbial alteration induced by FK506-M**

Band	Band class (%)	Closest BLAST match	Identity (%)	Accession no.	Phylum	In FK506-M
1	18.2	Helicobacter_sp.	100	HG737502.1	(-Proteobacteria	↓
2	19.9	Lachnospiraceae	100	JQ178126.1	Firmicutes	↓
9	61.0	Bacteroidetes	100	GU959253.1	Bacteroidetes	↓
15	72.9	Bacteroidales	99	AB702722.1	Bacteroidetes	↓
16	81.0	Uncultured bacterium	100	KC856782.1	Bacteroidetes	↓
26	82.0	Uncultured Bacteroidetes	99	GU959582.1	Bacteroidetes	↓
17	85.3	Uncultured Bacteroidetes	98	GU958550.1	Bacteroidetes	↓
18	86.5	Uncultured Bacteroidetes	100	GU957869.1	Bacteroidetes	↓
19	88.2	Uncultured bacterium	99	KC856454.1	Bacteroidetes	↓
20	33.7	Parasutterella excrementihominis	99	NR041667.1	(-Proteobacteria	↑
41.8	39	Pasteurella_sp.	99	KC866224.1	(-Proteobacteria	↑
56.8	41	Lactobacillus_sp. Bifidobacterium sp.	99	DQ857096.1 JF519689.1	Firmicutes	↑
47	82.7	Uncultured bacterium	98	KC856659.1	Bacteroidetes	↑