

Table S1

bacterial species	non-treated		<i>L. casei</i>		placebo (<i>L. casei</i>)		<i>B. breve</i>		placebo (<i>B. breve</i>)	
	number		number		number		number		number	
Total bacteria	10.1 ± 0.2	(5/5)	10.2 ± 0.3	(5/5)	10.1 ± 0.3	(5/5)	10.1 ± 0.2	(5/5)	10.2 ± 0.3	(5/5)
Obligate anaerobic bacteria										
<i>Clostridium coccoides</i> group	9.7 ± 0.3	(5/5)	9.8 ± 0.5	(5/5)	9.7 ± 0.6	(5/5)	9.8 ± 0.4	(5/5)	9.6 ± 0.4	(5/5)
<i>C. leptum</i> subgroup	8.6 ± 0.5	(5/5)	8.7 ± 0.1	(5/5)	8.7 ± 0.2	(5/5)	8.5 ± 0.5	(5/5)	8.7 ± 0.3	(5/5)
<i>Bacteroides fragilis</i> group	8.7 ± 0.4	(5/5)	8.8 ± 0.2	(5/5)	8.7 ± 0.1	(5/5)	8.6 ± 0.2	(5/5)	8.8 ± 0.2	(5/5)
Total <i>Bifidobacterium</i>	7.5 ± 0.5	(5/5)	7.5 ± 0.7	(5/5)	7.6 ± 0.4	(5/5)	7.6 ± 0.3	(5/5)	7.6 ± 0.4	(5/5)
<i>Atopobium</i> cluster	7.6 ± 0.5	(5/5)	7.6 ± 0.6	(5/5)	7.9 ± 0.5	(5/5)	7.7 ± 0.5	(5/5)	7.6 ± 0.5	(5/5)
<i>Prevotella</i>	8.5 ± 0.3	(5/5)	8.5 ± 0.6	(5/5)	8.6 ± 0.4	(5/5)	8.5 ± 0.7	(5/5)	8.6 ± 0.5	(5/5)
<i>Eubacterium cylindroides</i> group	7.7 ± 0.6	(5/5)	7.5 ± 0.3	(5/5)	7.7 ± 0.3	(5/5)	7.6 ± 0.3	(5/5)	7.6 ± 0.4	(5/5)
<i>C. ramosum</i> subgroup	6.8 ± 0.3	(5/5)	6.8 ± 0.1	(5/5)	6.8 ± 0.5	(5/5)	6.9 ± 0.4	(5/5)	6.7 ± 0.3	(5/5)
<i>C. difficile</i>	<2.1	(0/5)	<2.1	(0/5)	<2.1	(0/5)	5.0	(1/5)	<2.1	(0/5)
<i>C. perfringens</i>	<3.0	(0/5)	<3.0	(0/5)	<3.0	(0/5)	<3.0	(0/5)	<3.0	(0/5)
Facultative anaerobic bacteria										
Total <i>Lactobacillus</i>	9.7 ± 0.2	(5/5)	9.7 ± 0.1	(5/5)	9.6 ± 0.1	(5/5)	9.3 ± 0.1	(5/5)	9.8 ± 0.5	(5/5)
<i>L. gasseri</i> subgroup	8.7 ± 0.2	(5/5)	8.7 ± 1.2	(5/5)	8.7 ± 0.2	(5/5)	8.6 ± 0.1	(5/5)	8.9 ± 0.2	(5/5)
<i>L. brevis</i>	3.8 ± 0.1	(4/5)	3.9 ± 0.3	(4/5)	3.8 ± 0.1	(5/5)	3.8 ± 0.1	(4/5)	4.0 ± 0.3	(5/5)
<i>L. casei</i> subgroup	<3.0	(0/5)	6.0 ± 0.5	(5/5)	<3.0	(0/5)	<3.0	(0/5)	<3.0	(0/5)
<i>L. fermentum</i>	<3.9	(0/5)	<3.9	(0/5)	<3.9	(0/5)	<3.9	(0/5)	<3.9	(0/5)
<i>L. fructivorans</i>	<2.0	(0/5)	<2.0	(0/5)	<2.0	(0/5)	<2.0	(0/5)	<2.0	(0/5)
<i>L. plantarum</i> subgroup	3.1 ± 0.1	(4/5)	3.2 ± 0.8	(4/5)	3.0 ± 0.1	(4/5)	3.1 ± 0.6	(4/5)	3.0 ± 0.2	(5/5)
<i>L. reuteri</i> subgroup	8.5 ± 0.3	(5/5)	6.6 ± 0.7	(5/5)	6.6 ± 0.5	(5/5)	8.6 ± 0.3	(5/5)	8.5 ± 0.4	(5/5)
<i>L. ruminis</i> subgroup	9.6 ± 0.2	(5/5)	9.5 ± 0.1	(5/5)	9.5 ± 0.2	(5/5)	9.5 ± 0.1	(5/5)	9.6 ± 0.6	(5/5)
<i>L. sakei</i> subgroup	5.4 ± 0.3	(5/5)	5.1 ± 0.2	(5/5)	5.3 ± 0.3	(5/5)	5.5 ± 0.4	(5/5)	5.3 ± 0.6	(5/5)
<i>Enterobacteriaceae</i>	6.5 ± 0.4	(5/5)	6.3 ± 0.6	(5/5)	6.4 ± 0.3	(5/5)	6.2 ± 0.2	(5/5)	6.3 ± 0.8	(5/5)
<i>Enterococcus</i>	8.6 ± 0.2	(5/5)	8.4 ± 0.1	(5/5)	8.4 ± 0.2	(5/5)	8.4 ± 0.2	(5/5)	8.5 ± 0.5	(5/5)
<i>Staphylococcus</i>	5.1 ± 0.6	(5/5)	5.1 ± 0.5	(5/5)	4.9 ± 0.4	(5/5)	5.0 ± 0.1	(5/5)	4.9 ± 0.5	(5/5)
Aerobic bacteria										
<i>Pseudomonas</i>	<3.7	(0/5)	<3.7	(0/5)	<3.7	(0/5)	<3.7	(0/5)	<3.7	(0/5)
Administered probiotic bacteria										
<i>L. casei</i> strain Shirota	<6.0	(0/5)	6.3 ± 0.4	(3/5)	<6.0	(0/5)	<3.7	(0/5)	<6.0	(0/5)
<i>B. breve</i> Yakult strain	<6.0	(0/5)	<6.0	(0/5)	<6.0	(0/5)	6.3 ± 0.3	(5/5)	<6.0	(0/5)

Table S1. Composition of fecal commensal microflora in probiotics-fed mice.

6-week-old C57BL/6 mice were fed with *L. casei*, *B. breve* or placebo daily (1×10^9) by oral gavage for 3 months (n=5, respectively). Fecal samples were collected, weighed and suspended in 9 volumes of sterilized anaerobic transfer medium. Total RNA and DNA fractions extracted from each sample were assessed by RT-qPCR or qPCR with the specific primers. “Number” indicates CFU of each bacteria calculated using control cultured bacteria. (x/5) indicated the right side of “number” show detection rate of mice analyzed.