

S2 Table. Bacterial genera detected^a in cecum content of mice administered saline (control) or *Lactobacillus casei* 32G once per day by oral gavage sorted based on dose.

Taxon	Percentage (mean ± SE) ^{bc}							
	Control				Low			
	0.5h	3.5h	12h	24h	0.5h	3.5h	12h	24h
<i>S24-7 IS</i>	66.2 ± 15.2	75.0 ± 15.8	84.6 ± 10.3	53.6 ± 22.0	61.4 ± 27.7	81.3 ± 17.5	86.2 ± 5.9	70.8 ± 20.7
<i>Lachnospiraceae IS</i>	15.9 ± 9.9	8.9 ± 7.2	7.1 ± 6.0	28.8 ± 19.7	26.1 ± 25.0	8.0 ± 10.2	3.3 ± 2.5	12.3 ± 11.3
<i>Oscillospira</i>	10.0 ± 4.7	3.3 ± 3.0	2.4 ± 2.8	7.2 ± 3.3	3.8 ± 1.6	2.7 ± 3.6	1.0 ± 0.6	7.1 ± 6.2
<i>Ruminococcaceae Other</i>	2.1 ± 1.2	0.6 ± 0.3	2.0 ± 1.4	2.3 ± 1.4	3.2 ± 2.3	1.4 ± 0.6	3.3 ± 1.9	3.2 ± 1.9
<i>Ruminococcus</i>	1.3 ± 0.6	0.7 ± 0.4	1.0 ± 0.5	0.8 ± 0.3	1.1 ± 0.7	0.5 ± 0.4	1.9 ± 1.4	1.0 ± 0.3
<i>Clostridia Other</i>	1.2 ± 0.8	0.3 ± 0.1	0.5 ± 0.5	0.9 ± 0.3	1.0 ± 0.6	0.6 ± 0.6	0.6 ± 0.3	0.8 ± 1.2
<i>Lactobacillus</i>	0.9 ± 1.6	6.8 ± 7.7	0.4 ± 0.5	3.7 ± 4.3	0.5 ± 0.9	3.6 ± 6.9	0.6 ± 0.9	1.1 ± 1.0
<i>Lachnospiraceae Other</i>	0.9 ± 0.4	0.3 ± 0.2	0.4 ± 0.5	0.8 ± 0.4	0.9 ± 0.5	0.3 ± 0.4	0.7 ± 0.8	1.1 ± 1.5
<i>Clostridiales Other</i>	0.6 ± 0.3	0.1 ± 0.1	0.3 ± 0.3	0.6 ± 0.3	0.6 ± 0.4	0.3 ± 0.3	0.2 ± 0.1	0.5 ± 0.3
<i>Ruminococcaceae IS</i>	0.2 ± 0.1	0.3 ± 0.2	0.2 ± 0.1	0.2 ± 0.1	0.3 ± 0.4	0.2 ± 0.3	0.6 ± 0.7	0.4 ± 0.2
<i>Firmicutes Other</i>	0.2 ± 0.1	0.2 ± 0.1	0.2 ± 0.2	0.2 ± 0.1	0.1 ± 0.2	0.2 ± 0.2	0.2 ± 0.1	0.4 ± 0.3
<i>Bacteria Other</i>	0.2 ± 0.0	0.2 ± 0.1	0.2 ± 0.1	0.2 ± 0.1	0.1 ± 0.1	0.2 ± 0.1	0.1 ± 0.0	0.2 ± 0.1
<i>Erysipelotrichaceae IS</i>	0.1 ± 0.1	0.0 ± 0.0	0.1 ± 0.1	0.0 ± 0.0	0.2 ± 0.2	0.1 ± 0.0	0.1 ± 0.1	0.1 ± 0.1
<i>Turicibacter</i>	0.0 ± 0.1	2.7 ± 2.6	0.4 ± 0.5	0.1 ± 0.1	0.1 ± 0.2	0.2 ± 0.2	0.8 ± 0.9	0.3 ± 0.3
<i>Coprobacillaceae IS</i>	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.0 ± 0.0	0.1 ± 0.1	0.0 ± 0.0	0.2 ± 0.2
<i>Adlercreutzia</i>	BQL	0.2 ± 0.5	0.1 ± 0.2	0.1 ± 0.0	0.1 ± 0.1	0.1 ± 0.2	0.1 ± 0.2	0.2 ± 0.3
<i>Coriobacteriales IS</i>	BQL	0.0 ± 0.0	BQL	0.0 ± 0.0	BQL	BQL	BQL	0.0 ± 0.0

^aOnly genera that were present at ≥1% in a sample are included in this table.

^bThe detection limit was 0.00003 and this value was used to calculate the p-value.

^cGenera that differ from 0.5 h time point within each group are shown in bold (p≤0.05).

IS: Incertae Sedis.

BQL: Below quantifiable limit.

Table S1. (Continued)

Taxon	Percentage (mean \pm SE) ^{bc}							
	Medium				High			
	0.5h	3.5h	12h	24h	0.5h	3.5h	12h	24h
<i>S24-7 IS</i>	70.4 \pm 13.0	65.9 \pm 5.9	78.8 \pm 20.3	52.9 \pm 31.2	64.3 \pm 25.3	69.7 \pm 15.6	74.1 \pm 14.0	60.9 \pm 18.1
<i>Lachnospiraceae IS</i>	13.8 \pm 9.6	13.9 \pm 8.3	12.2 \pm 14.6	10.7 \pm 12.2	13.2 \pm 8.5	2.7 \pm 1.6	8.8 \pm 8.4	10.2 \pm 6.7
<i>Oscillospira</i>	5.9 \pm 3.9	2.0 \pm 1.3	2.1 \pm 2.7	4.9 \pm 4.9	4.3 \pm 4.1	0.8 \pm 0.6	1.9 \pm 1.6	4.2 \pm 3.1
<i>Ruminococcaceae Other</i>	1.2 \pm 0.8	0.5 \pm 0.2	2.0 \pm 2.1	2.6 \pm 2.5	2.4 \pm 1.9	1.5 \pm 1.0	8.3 \pm 4.1	2.2 \pm 0.9
<i>Ruminococcus</i>	0.4 \pm 0.2	0.2 \pm 0.1	0.7 \pm 0.8	0.6 \pm 0.5	1.2 \pm 1.4	0.7 \pm 0.8	1.2 \pm 0.7	1.4 \pm 1.2
<i>Clostridia Other</i>	0.4 \pm 0.4	0.2 \pm 0.1	0.3 \pm 0.2	0.7 \pm 0.7	0.7 \pm 0.7	0.2 \pm 0.1	0.6 \pm 0.5	0.8 \pm 0.6
<i>Lactobacillus</i>	5.0 \pm 4.6	15.0 \pm 9.6	0.6 \pm 0.4	24.8 \pm 17.3	11.0 \pm 16.4	22.2 \pm 14.6	1.9 \pm 2.7	16.9 \pm 19.5
<i>Lachnospiraceae Other</i>	0.4 \pm 0.2	0.2 \pm 0.1	0.3 \pm 0.2	0.5 \pm 0.5	0.7 \pm 0.6	0.2 \pm 0.1	0.6 \pm 0.5	0.8 \pm 0.4
<i>Clostridiales Other</i>	0.5 \pm 0.4	0.2 \pm 0.1	0.3 \pm 0.2	0.6 \pm 0.8	0.4 \pm 0.4	0.1 \pm 0.1	0.6 \pm 0.5	0.4 \pm 0.2
<i>Ruminococcaceae IS</i>	0.9 \pm 0.6	0.6 \pm 0.3	1.0 \pm 0.6	0.4 \pm 0.3	0.7 \pm 0.9	0.8 \pm 0.4	0.8 \pm 0.5	0.5 \pm 0.2
<i>Firmicutes Other</i>	0.2 \pm 0.1	0.2 \pm 0.1	0.2 \pm 0.1	0.4 \pm 0.2	0.2 \pm 0.2	0.2 \pm 0.1	0.1 \pm 0.1	0.4 \pm 0.2
<i>Bacteria Other</i>	0.3 \pm 0.1	0.4 \pm 0.2	0.2 \pm 0.1	0.3 \pm 0.1	0.2 \pm 0.1	0.3 \pm 0.1	0.4 \pm 0.2	0.5 \pm 0.1
<i>Erysipelotrichaceae IS</i>	0.1 \pm 0.1	0.1 \pm 0.1	0.2 \pm 0.2	0.1 \pm 0.0	0.0 \pm 0.0	0.0 \pm 0.0	0.0 \pm 0.0	0.1 \pm 0.0
<i>Turicibacter</i>	0.0 \pm 0.0	0.1 \pm 0.2	0.8 \pm 1.1	0.0 \pm 0.0	0.3 \pm 0.4	0.4 \pm 0.7	0.4 \pm 0.5	0.0 \pm 0.1
<i>Coprobacillaceae IS</i>	0.0 \pm 0.0	0.0 \pm 0.0	0.0 \pm 0.0	0.0 \pm 0.0	0.0 \pm 0.0	0.0 \pm 0.0	0.0 \pm 0.0	0.0 \pm 0.0
<i>Adlercreutzia</i>	0.2 \pm 0.1	0.3 \pm 0.2	0.2 \pm 0.1	0.2 \pm 0.2	0.0 \pm 0.0	0.1 \pm 0.0	0.0 \pm 0.0	0.1 \pm 0.1
<i>Coriobacteriales IS</i>	BQL	BQL	BQL	BQL	BQL	BQL	BQL	0.2 \pm 0.2

^aOnly genera that were present at $\geq 1\%$ in a sample are included in this table, the complete data set is presented in Table SX.

^bThe detection limit was 0.00003 and this value was used to calculate the p-value.

^cGenera that differ from 0.5 h time point within each group are shown in bold ($p \leq 0.05$).

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