

Table S3. List of the most abundant genera in fecal samples of older mice before and after 10-day broad-spectrum antibiotic treatment

Genus	Average relative abundance	
	Before Abx	After Abx
<i>A2</i>	2.70%	0.40%
<i>Acetatifactor</i>	0.49%	0.16%
<i>Alistipes</i>	10.65%	
<i>Anaeroplasma</i>	16.85%	0.07%
<i>ASF356</i>	0.75%	0.56%
<i>Bifidobacterium</i>	7.10%	28.37%
<i>Bilophila</i>	0.19%	0.09%
<i>Clostridium_sensu_stricto_1</i>	3.72%	
<i>Coriobacteriaceae_UCG-002</i>	0.32%	
<i>Desulfovibrio</i>	1.12%	0.29%
<i>Enterorhabdus</i>	0.08%	0.06%
<i>Erysipelatoclostridium</i>	0.13%	0.72%
<i>Faecalibaculum</i>	10.26%	
<i>GCA-900066575</i>	0.14%	0.06%
<i>Intestinimonas</i>	0.45%	1.09%
<i>Lachnoclostridium</i>	0.56%	0.44%
<i>Lachnospiraceae_FCS020_group</i>	0.09%	0.55%
<i>Lachnospiraceae_NK4A136_group</i>	27.39%	9.43%
<i>Lachnospiraceae_UCG-001</i>	0.94%	4.14%
<i>Lactobacillus</i>	4.15%	39.71%
<i>Muribaculum</i>	0.74%	0.24%
<i>Oscillibacter</i>	1.53%	1.47%
<i>Parabacteroides</i>	1.28%	8.65%
<i>Romboutsia</i>	0.45%	
<i>Roseburia</i>	0.64%	0.72%
<i>Ruminiclostridium</i>	1.09%	0.24%
<i>Ruminiclostridium_5</i>	0.39%	0.39%
<i>Ruminiclostridium_6</i>	0.48%	0.23%
<i>Ruminiclostridium_9</i>	1.05%	0.74%
<i>Ruminococcaceae_UCG-005</i>	0.25%	
<i>Ruminococcaceae_UCG-009</i>	0.38%	
<i>Ruminococcaceae_UCG-010</i>	0.79%	
<i>Ruminococcaceae_UCG-014</i>	0.30%	0.85%
<i>Ruminococcus_1</i>	0.30%	
<i>Turicibacter</i>	1.72%	
<i>Tyzzerella</i>	0.09%	0.06%