

Table S1. Effects of nucleotides (NTs) on gut microbial composition in caecum content of the rats. (Mean values and standard deviations, n 6 per group)

Levels	Bacterium	Dextrose control		Alcohol control		0.04% NTs		0.16% NTs	
		Mean	SD	Mean	SD	Mean	SD	Mean	SD
Phylum	Bacteroidetes	42.4%	7.9%	50.6%*	5.5%	37.0%##	3.0%	36.7%##	7.0%
	Firmicutes	53.6%	9.2%	44.8%*	4.6%	57.5%##	3.7%	59.6%##	8.6%
	Proteobacteria	3.7%	2.0%	4.0%	1.9%	5.2%	3.5%	3.2%	1.8%
	Cyanobacteria	0.2%	0.3%	0.3%	0.2%	0.3%	0.1%	0.2%	0.1%
Order	Bacteroidales	42.3%	8.0%	50.0%*	4.8%	36.9%##	3.0%	36.7%##	7.0%
	Clostridiales	47.7%	11.6%	44.2%*	4.3%	56.9%##	3.7%	56.3%##	10.9%
	Lactobacillales	3.5%	4.3%	0.1%**	0.1%	0.2%	0.1%	0.3%##	0.1%
	Erysipelotrichales	2.9%	3.8%	0.9%*	1.0%	0.4%	0.4%	3.0%†	3.7%
	Desulfovibrionales	1.0%	1.2%	0.5%	0.3%	0.4%	0.2%	1.0%†	0.6%
	Campylobacterales	2.3%	1.4%	3.1%	1.6%	4.6%	3.5%	2.0%	0.5%
Genus	Bacteroides	10.8%	5.4%	11.6%	5.4%	7.5%	3.2%	2.0%##†	1.4%
	Blautia	9.3%	6.7%	17.6%*	3.8%	7.0%##	6.6%	12.0%	6.8%
	Helicobacteraceae_norank	2.3%	1.4%	3.1%	1.6%	4.6%	3.5%	0.2%##††	0.4%
	Lachnospiraceae_incertae_sedis	6.0%	13.7%	0.4%	0.1%	6.7%##	4.3%	0.5%	0.2%
	Lachnospiraceae_unclassified	3.2%	3.4%	2.5%	1.4%	8.8%##	5.8%	6.0%#	4.1%
	Lachnospiraceae_uncultured	1.6%	1.7%	1.5%	0.8%	1.5%	0.8%	1.7%	0.6%
	Lactobacillus	2.9%	4.1%	0.1%**	0.1%	0.1%	0.1%	0.3%	0.2%
	Oscillibacter	4.6%	3.9%	5.8%	2.4%	9.1%	1.2%	4.8%	2.3%
	Ruminococcaceae_incertae_sedis	1.6%	0.9%	1.6%	0.5%	1.4%	0.4%	3.3%	2.2%
	Ruminococcaceae_unclassified	5.3%	3.1%	3.1%*	0.8%	5.3%#	1.9%	4.7%	1.6%
	Ruminococcaceae_uncultured	9.3%	4.0%	5.2%	2.7%	9.6%	2.6%	9.5%	5.3%
	S24-7_norank	29.9%	6.4%	35.5%	7.0%	28.4%	2.9%	29.9%	9.1%

Mean values were significantly different from those of the dextrose control group: * $p < 0.05$, ** $p < 0.01$.

Mean values were significantly different from those of the alcohol control group: # $p < 0.05$, ## $p < 0.01$.

Mean values were significantly different from those of the 0.04% NTs group: † $p < 0.05$, †† $p < 0.01$.