

Table S2. Relative abundance of differential microbial genera across *LEPR* genotypes

Genera, %	<i>LEPR</i> genotype ¹		
	TT	CT	CC
<i>UCG-005</i>	4.8 ^b (4.0;5.7)	7.6 ^a (6.1;9.5)	8.5 ^a (6.6;10.8)
<i>Subdoligranulum</i>	3.0 ^a (2.3;3.9)	1.3 ^b (0.9;1.9)	1.4 ^b (0.9;2.1)
<i>Coprococcus</i>	2.0 ^a (1.6;2.4)	1.2 ^b (0.9;1.6)	1.2 ^b (0.9;1.6)
<i>NK4A214</i>	1.7 ^b (1.4;2.1)	3.2 ^a (2.4;4.2)	3.0 ^a (2.2;4.1)
<i>UCG-002</i>	1.2 ^a (0.9;1.5)	2.7 ^a (1.9;3.7)	2.2 ^a (1.5;3.1)
<i>Treponema</i>	0.3 ^b (0.2;0.6)	1.6 ^a (0.7;3.4)	1.2 ^a (0.5;2.8)
<i>Dialister (x10)</i>	0.6 ^a (0.1;3.0)	0.0 ^b (0.0;0.2)	0.0 ^b (0.0;0.0)
<i>Lachnospiraceae NK3A20 (x10)</i>	0.4 ^a (0.1;1.8)	0.0 ^b (0.0;0.1)	0.0 ^b (0.0;0.0)
<i>Megasphaera (x10)</i>	0.4 ^a (0.1;0.2)	0.0 ^{ab} (0.0;0.1)	0.0 ^b (0.0;0.0)
<i>Frisingicoccus (x100)</i>	0.2 ^b (0.0;0.8)	80 ^a (1; 600)	70 ^a (9; 580)
<i>dgA-11 gut group (x100)</i>	0.2 ^b (0.1;0.8)	4 ^a (0.7; 20)	70 ^a (1;40)
<i>Methanobrevibacter (x100)</i>	0.1 ^b (0.0;1.0)	90 ^a (1;60)	10 ^a (1;70)
<i>Lachnospiraceae XPB1014 (x1000)</i>	0.3 ^b (0.1;2.0)	30 ^a (3; 200)	90 ^a (7;1100)
<i>Lachnospiraceae UCG-009 (x1000)</i>	0.1 ^b (0.0;0.5)	2 ^{ab} (0.2;200)	40 ^a (4;400)

¹ Means (95% confidence interval)

^{a,b} Within each trait, means with different superscripts indicate significant differences between *LEPR* genotypes according to Tukey's test (p<0.05).