

Supplementary data file 1. Microbial profiling using quantitative PCR.

In order to validate results obtained during Illumina sequencing, the abundance of Bacteroidetes (B) and Firmicutes (F) phyla were checked by qPCR technique.

Material and method

Total bacterial DNA was extracted from ~200 mg of faecal sample using QIAamp® DNA Stool Mini Kit (kit QA) as previously described. The relative amount of bacterial phyla of interest was checked by measuring DNA abundance of the 16S rRNA gene sequences of each group of bacteria using quantitative PCR with Bio-Rad iCycler (Bio-Rad Inc, Mississauga, ON, Canada) and group-specific primers following previously described protocols¹⁻². The group-specific primers are shown in Table S1. Primers were verified with Multalin software³, and Primer3⁴ and finally *in silico* checked with the Probe Match tool in RDP (Ribosomal Database Project)⁵. Primer specificity, amplification efficiency and the limit of detection were determined using serial dilutions of a standard DNA. qPCR assays were run in triplicate and standard curves constructed for each experiment using 10-fold serial dilutions of standard bacterial genomic DNA (Institute Charles Viollette culture collection, Lille, France). The amplification program consisted of one cycle at 95°C for 10 min and 40 cycles of initial denaturation at 95°C for 15 s and an annealing temperature for 1 min at 60°C. Each reaction was carried out in a final volume of 20 µL containing 10 µL of 2X iQ SYBR Green Supermix (Bio-Rad), 1.5 µL of 4 µM of forward and reverse primers and 1 ng of DNA. The efficiency and threshold cycle (Ct) were calculated with the CFX Manager software (Bio-Rad). The size and purity of the targeted PCR products were confirmed by agarose gel electrophoresis. *Total Bacteria* is a broad-range primer that identifies the conserved region of the 16S rRNA encoding gene for a wide range of bacteria. Data obtained by this qPCR reaction gives the amount of total bacteria present in the sample. Then the relative quantification of each target bacteria or group was normalized with the total bacteria content in the sample, following the mathematical model defined by Pfaffl⁶. Data were calculated as means ± SD and comparisons were performed using one-way ANOVA with Tukey's test. Log2 ratio $\Delta\text{Ct Firmicutes}/\Delta\text{Ct Bacteroidetes}$ were presented in the graphs as relative abundance.

Table S1. Sequence of primers used for microbial profiling in mice faeces.

Target group	Primer	Sequence (5'-3')	Tm (°C)	Amplicon length (bp)	Reference
<i>Total bacteria</i>	Tot1	ACTCCTACGGGAGGCAG	55	194	Chaplin et al. ²
	Tot2	GTATTACCGCGGCTGCTG	59		
<i>Firmicutes</i>	Fir1	TGAAACTYAAAGGAATTGACG	53	135	Luu et al. ⁷
	Fir2	ACCATGCACCACTGTGTC	53		
<i>Bacteroidetes</i>	Bac1	ATACGCGAGGAACCTTACC	57	187	Luu et al. ⁷
	Bac2	AGCTGACGACAACCATGCAG	57		

Results

qPCR results confirmed the most important modification of the ratio F/B for the G35 treatment, as presented in the next figure S1.

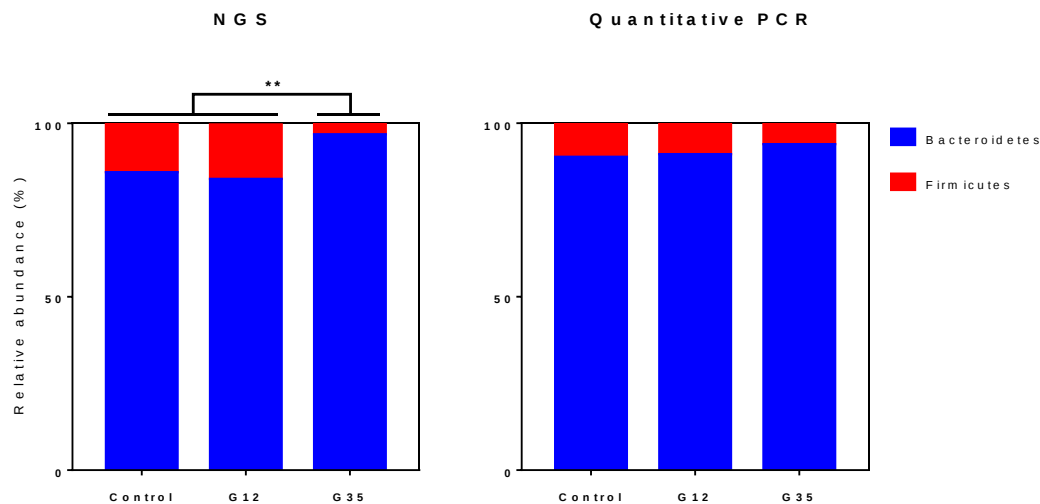


Figure S1. Relative abundance (%) of *Firmicutes* and *Bacteroidetes* in mice microbiota after chicory treatments. A. Relative abundance of phyla *Firmicutes* and *Bacteroidetes* detected by NGS was expressed as a mean $\pm$ SD (Tukey's test, $n=5/\text{group}$), ** for $p<0.01$. B. qPCR results expressed as $\log_2$ ratio $\Delta\text{Ct } \textit{Firmicutes}/\Delta\text{Ct } \textit{Bacteroidetes}$, mean $\pm$ SD (Tukey's test, $n=3/\text{group}$).

References

- ¹ Parnell, J.A.; Reimer, R.A. Prebiotic fiber modulation of the gut microbiota improves risk factors for obesity and the metabolic syndrome. *Gut Microbes* **2012**, *3*(1), 29-34.
- ² Chaplin, A.; Parra, P.; Laraichi, S.; Serra, F. and Palou, A. Calcium supplementation modulates gut microbiota in a prebiotic manner in dietary obese mice. *Mol. Nutr. Food Res.* **2016**, *60*, 468–480.
- ³ Corpet, F. Multiple sequence alignment with hierarchical clustering. *Nucl. Acids Res.* **1988**, *16*(22), 10881-10890.
- ⁴ Untergasser, A.; Cutcutache, I.; Koressaar, T.; Ye, J.; Faircloth, B.C.; Remm, M.; Rozen, S.G. Primer3 - new capabilities and interfaces. *Nucl. Acids Res.* **2012**, *40*(15), e115.
- ⁵ Cole, J.R.; Wang, Q.; Fish, J.A.; Chai, B.; McGarrell, D.M.; Sun, Y.; Brown, C.T.; Porras-Alfaro, A.; Kuske, C.R. Tiedje JM. Ribosomal Database Project: data and tools for high throughput rRNA analysis. *Nucl. Acids Res.* **2014**, *42* (Database issue), D633-D642.

⁶ Pfaffl, M.W. A new mathematical model for relative quantification in real-time RT-PCR., *Nucl. Acids Res.* **2001**, 29(9), e45.

⁷ Luu, T.H.; Michel, C.; Bard, J-M.; Dravet, F.; Nazih, H. and Bobin-Dubigeon, C. Intestinal Proportion of *Blautia* sp. is Associated with Clinical Stage and Histoprognostic Grade in Patients with Early-Stage Breast Cancer. *Nutr. Cancer* **2017**, 69(2), 267-275.

Supplementary data file 2. Body weight of mice during chicory feeding.

During mice feeding period, the body weight was weekly registered (Figure S2). Roasted chicory roots intake does not significantly alter body weight, however, a small sensitive decrease was observed for G35 feed mice.

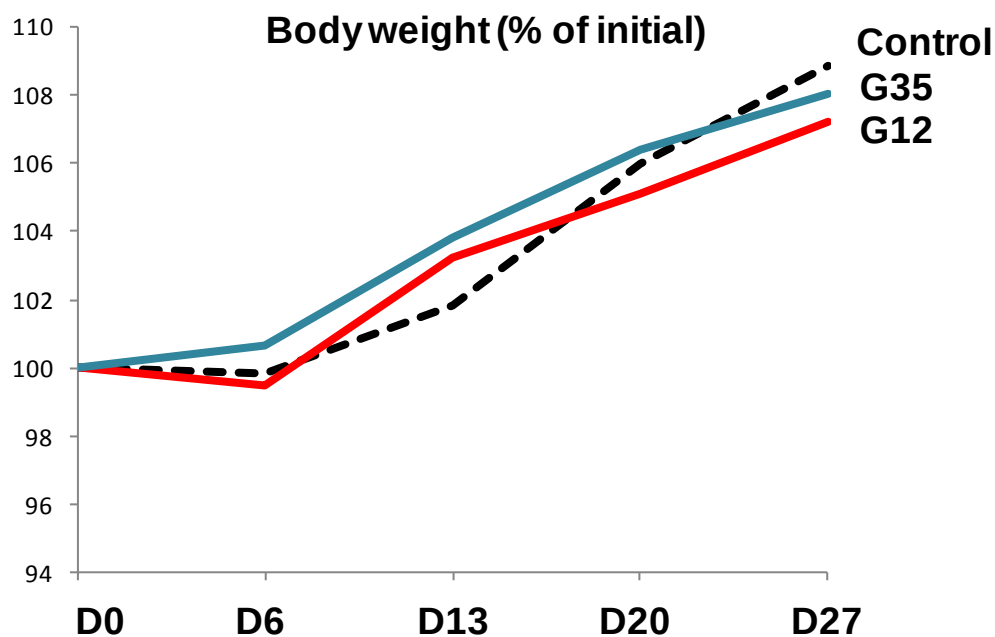


Figure S2. Body weight of chicory feed mice.

Supplementary data file 3.

Changes in the relative abundance of bacterial genera after daily feeding with roasted chicory roots.

G12 and G35 are the two analyzed chicory genotypes.

Genera	DAY 0			DAY 30		
	Control	G12	G35	Control	G12	G35
S24-7_unclassified	59.96%	58.72%	54.07%	70.51%	64.21%	79.41%
Bacteroidales_unclassified	5.31%	5.98%	4.11%	5.60%	7.82%	9.31%
Bacteroides	1.79%	2.29%	2.46%	3.11%	3.95%	3.54%
Blautia	7.31%	6.18%	12.20%	8.07%	8.83%	1.03%
Alistipes	5.07%	4.45%	7.48%	3.07%	4.22%	1.45%
Bacteria_unclassified	2.47%	2.41%	2.04%	2.58%	2.30%	1.33%
Lachnospiraceae_unclassified	1.22%	3.01%	2.44%	2.29%	2.48%	1.19%
Alloprevotella	0.58%	0.51%	0.25%	0.79%	0.91%	1.26%
Ruminococcaceae_unclassified	8.91%	7.51%	5.65%	1.82%	2.24%	0.37%
Clostridiales_unclassified	1.47%	1.19%	1.16%	0.99%	1.10%	0.20%
Akkermansia	0.24%	1.39%	0.02%	0.02%	0.06%	0.03%
Parabacteroides	0.45%	0.32%	0.54%	0.01%	0.07%	0.14%
Oscillibacter	0.17%	0.18%	0.22%	0.12%	0.14%	0.05%
Odoribacter	0.71%	0.01%	0.68%	0.30%	0.51%	0.02%
vadinBB60_unclassified	0.78%	0.39%	0.98%	0.22%	0.22%	0.13%
RF9_unclassified	0.12%	0.17%	0.16%	0.03%	0.05%	0.02%
Parasutterella	0.04%	0.09%	0.05%	0.03%	0.01%	0.14%
Coprococcus	0.06%	0.13%	0.16%	0.04%	0.08%	0.00%
Ruminococcus	0.09%	0.39%	0.05%	0.02%	0.02%	0.00%
Anaerotruncus	0.07%	0.12%	0.22%	0.04%	0.05%	0.00%
Candidatus_Saccharimonas	0.01%	0.02%	0.05%	0.01%	0.04%	0.00%
Erysipelotrichaceae_unclassified	0.04%	0.03%	0.08%	0.01%	0.00%	0.05%
Gastranaerophilales_unclassified	0.23%	0.46%	0.20%	0.15%	0.45%	0.14%
Defluviitaleaceae_unclassified	0.02%	0.01%	0.01%	0.00%	0.01%	0.00%
Lactobacillus	0.52%	0.62%	1.65%	0.05%	0.04%	0.02%
Porphyromonadaceae_unclassified	0.02%	0.04%	0.02%	0.00%	0.00%	0.01%
Firmicutes_unclassified	0.01%	0.06%	0.04%	0.04%	0.02%	0.02%
Bilophila	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%
Roseburia	0.01%	0.10%	0.08%	0.01%	0.00%	0.00%
Anaeroplasma	0.13%	0.05%	0.19%	0.01%	0.04%	0.00%
Coprobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Fusobacterium	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%
Bacteroidetes_unclassified	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%
Intestinimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Candidatus_Arthromitus	0.02%	0.00%	0.02%	0.01%	0.02%	0.00%
Christensenella	0.01%	0.01%	0.02%	0.00%	0.01%	0.00%
Marvinbryantia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Christensenellaceae_unclassified	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%
Family_XIII_unclassified	0.01%	0.03%	0.04%	0.01%	0.01%	0.01%
Parvibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
RC9_gut_group	0.59%	0.50%	0.09%	0.00%	0.04%	0.04%
Sutterella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Acetatifactor	0.01%	0.01%	0.02%	0.00%	0.00%	0.00%
Allobaculum	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Alphaproteobacteria_unclassified	1.47%	2.46%	1.89%	0.00%	0.01%	0.02%
Anaerostipes	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%
Anaerovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Bradyrhizobiaceae_unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Buttiauxella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Clostridia_unclassified	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Coriobacteriaceae_unclassified	0.01%	0.02%	0.06%	0.01%	0.00%	0.00%
Enterorhabdus	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Escherichia-Shigella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Klebsiella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Lactobacillales_unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Leuconostoc	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Lysinibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Marinilabiaceae_unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Mitsuokella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Mollicutes_unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Mucispirillum	0.02%	0.02%	0.51%	0.00%	0.00%	0.00%
Oscillospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Paenibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Pantoea	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
Parasporobacterium	0.00%	0.00%	0.00%	0.01%	0.00%	0.00%
possible_genus_Sk018	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%
Prevotella	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%

Prevotellaceae_unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Proteobacteria_unclassified	0.00%	0.02%	0.01%	0.00%	0.00%	0.00%
Pseudoflavonifractor	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
ratAN060301C_unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Solobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Sphingobacterium	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
Stenotrophomonas	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%
Streptococcus	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%
Turicibacter	0.00%	0.01%	0.00%	0.00%	0.01%	0.00%
Veillonella	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%

Supplementary data file 4.

Changes in the relative abundance of significant and genotype-specific bacterial genera after daily feeding with roasted chicory roots.

Means were calculated (n=5) for D0 and D30 for each treatment.

G12 and G35 are the two analyzed chicory genotypes.

Taxon	Condition	Mean D0	Mean D30	P-value
Alistipes	Control	5.07 ± 1.47	3.07 ± 1.07	0.0805
	G12	4.46 ± 1.52	2.64 ± 0.33	0.1615
	G35	7.48 ± 3.76	1.45 ± 0.55	0.0152
Alloprevotella	Control	0.58 ± 0.43	0.79 ± 0.91	0.6855
	G12	0.43 ± 0.40	0.91 ± 1.3	0.5113
	G35	0.25 ± 0.31	1.26 ± 0.57	0.0102
Bacteroidales_unclassified	Control	5.31 ± 1.51	5.60 ± 3.37	0.8427
	G12	5.66 ± 1.73	7.82 ± 3.00	0.3411
	G35	4.11 ± 2.21	9.31 ± 0.69	0.0020
Blautia	Control	9.08 ± 8.21	8.07 ± 5.04	0.7662
	G12	6.86 ± 4.72	8.83 ± 2.72	0.2473
	G35	8.59 ± 6.64	1.03 ± 0.47	0.0104
Clostridiales_unclassified	Control	1.47 ± 1.40	0.99 ± 0.45	0.4977
	G12	1.09 ± 0.79	1.10 ± 0.38	0.9691
	G35	1.41 ± 0.53	0.21 ± 0.11	0.0286
Lachnospiraceae_unclassified	Control	1.22 ± 1.02	1.80 ± 1.21	0.5001
	G12	1.04 ± 0.55	2.48 ± 0.99	0.1037
	G35	1.47 ± 0.70	1.19 ± 0.65	0.1111
Ocillibacter	Control	0.16 ± 0.22	0.12 ± 0.08	0.5993
	G12	0.19 ± 0.09	0.14 ± 0.19	0.5628
	G35	0.22 ± 0.13	0.05 ± 0.03	0.0368
Ruminococcaceae_unclassified	Control	10.97 ± 4.35	1.81 ± 1.16	0.0318
	G12	7.14 ± 5.27	2.24 ± 0.52	0.1167
	G35	5.65 ± 3.00	0.37 ± 0.18	0.0183