Supplementary data file 1. Microbial profiling using quantitative PCR.

In order to validate results obtained during Illumina sequencing, the abundance of Bacterioidetes (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 \pm SD and comparisons were performed using one-way ANOVA with Tukey's test. Log2 ratio ΔCt Firmicutes/ ΔCt Bacteroidetes were presented in the graphs as relative abundance.

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

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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/group), ** for p<0.01. B. qPCR results expressed as log2 ratio Δ Ct *Firmicutes*/ Δ Ct *Bacteroidetes*, mean \pm SD (Tukey's test, n=3/group).

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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 Control G12 G35 Control G12 G35 S24-7. unprissibled 59.90% 58.27% 54.07% 70.51% 74.21% 9.31% Baterondes_unclassibled 5.37% 5.99% 4.11% 5.90% 72.2% 9.31% Batalisipas 5.07% 4.42% 1.72% 8.07% 8.83% 1.03% Batalisipas 5.07% 4.43% 7.44% 2.04% 2.28% 2.43% 1.03% Alloprovolla 0.58% 0.51% 0.24% 2.29% 2.44% 1.93% Alloprovolla 0.58% 0.51% 0.22% 0.99% 1.00% 0.20% Alkermania 0.24% 1.19% 1.16% 0.99% 0.14% 0.29% Costilibactor 0.17% 0.89% 0.39% 0.42% 0.14% 0.29% 0.14% 0.29% 0.14% 0.29% 0.14% 0.29% 0.14% 0.29% 0.14% 0.29% 0.14% 0.29% 0.14% 0.29% 0.14		DAY 0			DAY 30			
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Erysipalotifichaceae_unclassified 0.04% 0.03% 0.08% 0.01% 0.00% 0.09% Gastranaerophilales_unclassified 0.23% 0.46% 0.20% 0.11% 0.00% 0.14% Defluvitielaceae_unclassified 0.22% 0.64% 0.02% 0.01% 0.00% 0.01% Porphyromonadaceae_unclassified 0.02% 0.04% 0.02% 0.00% 0.00% 0.00% Bilophila 0.01% 0.06% 0.04% 0.04% 0.02% 0.00% 0.00% 0.00% Coprobacillus 0.01% 0.06% 0.01% 0.00%	Candidatus Saccharimonas	0.01%	0.02%	0.05%	0.04%	0.00%	0.00%	
Dyspectivitie 0.23% 0.24% 0.20% 0.15% 0.45% 0.14% Defluvitie 0.25% 0.04% 0.02% 0.01% 0.00% 0.01% Defluvitie 0.65% 0.04% 0.02% 0.01% 0.00% 0.01% Porphyromonadaceae_unclassified 0.02% 0.04% 0.02% 0.00% 0.00% 0.00% Fininciutes_unclassified 0.01% 0.06% 0.01% 0.02% 0.00% 0.00% 0.00% Anaeroplasma 0.13% 0.10% 0.00%	Ervsipelotrichaceae unclassified	0.01%	0.02%	0.00%	0.01%	0.04%	0.00%	
Clashinaterophinaterophicacoae_unclassified 0.22% 0.01% 0.01% 0.01% 0.01% 0.01% Porphyromonadaceae_unclassified 0.22% 0.62% 1.65% 0.03% 0.04% 0.02% Porphyromonadaceae_unclassified 0.01% 0.06% 0.04% 0.04% 0.02% 0.02% Bilophila 0.01% 0.06% 0.04% 0.04% 0.02% 0.02% Coprobacillus 0.01% 0.16% 0.04% 0.04% 0.00% 0.00% Coprobacillus 0.01% 0.05% 0.19% 0.01% 0.00% 0.00% 0.00% Eacteroidetes unclassified 0.00% 0.01% 0.00% </td <td>Gastranaerophilales unclassified</td> <td>0.04%</td> <td>0.00%</td> <td>0.00%</td> <td>0.01%</td> <td>0.00%</td> <td>0.00%</td>	Gastranaerophilales unclassified	0.04%	0.00%	0.00%	0.01%	0.00%	0.00%	
Denumatical Laciobacillus 0.02% 0.01% 0.01% 0.01% 0.02% Porphyromonadaceae_unclassified 0.02% 0.04% 0.02% 0.00% 0.01% Pirmicutes_unclassified 0.02% 0.04% 0.02% 0.00% 0.01% Bilophila 0.00% 0.01% 0.02% 0.00% 0.00% 0.00% Anaeroplasma 0.11% 0.10% 0.08% 0.01% 0.00% 0.00% Coprobacillus 0.00%	Dofluviitaloacoao unclassified	0.23%	0.40%	0.20%	0.13%	0.43%	0.14 /0	
Lab.Doculatility 0.12% 0.02% 1.03% 0.09% 0.04% 0.01% Firmicutes_unclassified 0.11% 0.06% 0.04% 0.09% 0.02% 0.02% Bilophila 0.01% 0.06% 0.04% 0.09% 0.00% 0.00% Coprobactinus 0.01% 0.19% 0.01% 0.00% 0.00% Coprobacterium 0.00% 0.01% 0.00% 0.00% 0.00% 0.00% Eacteroidete_unclassified 0.00% 0.01% 0.00%		0.02 /0	0.01%	1 6 5 9/	0.00%	0.01%	0.00 %	
Profinitional addiede_initial 0.02% 0.04% 0.02% 0.00% 0.01% Bilophila 0.00% 0.01% 0.02% 0.00% 0.00% Bilophila 0.00% 0.01% 0.02% 0.00% 0.00% Anaeroplasma 0.13% 0.05% 0.19% 0.01% 0.00% Coprobacillus 0.00% 0.01% 0.00% 0.00% 0.00% Coprobacillus 0.00% 0.01% 0.00% 0.00% 0.01% Busbacterium 0.00% 0.01% 0.00% </td <td>Barphyromonodooooo unoloooifiod</td> <td>0.02%</td> <td>0.02%</td> <td>1.00%</td> <td>0.05%</td> <td>0.04%</td> <td>0.02%</td>	Barphyromonodooooo unoloooifiod	0.02%	0.02%	1.00%	0.05%	0.04%	0.02%	
Finitedies_Unclassified 0.01% 0.06% 0.04% 0.02% 0.02% Biophila 0.01% 0.01% 0.08% 0.01% 0.00% Roseburia 0.11% 0.10% 0.01% 0.00% 0.00% Anaeroplasma 0.13% 0.05% 0.19% 0.00% 0.00% Coprobactilus 0.00% 0.01% 0.00% 0.00% 0.00% Eacteroidetes unclassified 0.00% 0.01% 0.00% 0.00% 0.00% 0.00% Candidatus_Arthromitus 0.02% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Christensenella 0.01% 0.02% 0.00% 0.00% 0.00% 0.00% 0.00% Christensenellaceae_unclassified 0.01% 0.01% 0.00% <td>Forphyromonadaceae_unclassified</td> <td>0.02%</td> <td>0.04%</td> <td>0.02%</td> <td>0.00%</td> <td>0.00%</td> <td>0.01%</td>	Forphyromonadaceae_unclassified	0.02%	0.04%	0.02%	0.00%	0.00%	0.01%	
Bidopinia 0.00% 0.01% 0.00% 0.00% 0.00% Anaeroplasma 0.13% 0.05% 0.19% 0.01% 0.00% Fusobacterium 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Fusobacterium 0.00% 0.01% 0.00% 0.00% 0.00% 0.00% 0.00% 0.01% 0.00% 0.01% 0.00% 0.01% 0.00% 0.01% 0.00% 0.01% 0.00% 0.01% 0.00% </td <td>Firmicules_unclassified</td> <td>0.01%</td> <td>0.06%</td> <td>0.04%</td> <td>0.04%</td> <td>0.02%</td> <td>0.02%</td>	Firmicules_unclassified	0.01%	0.06%	0.04%	0.04%	0.02%	0.02%	
RoseDurial 0.01% 0.10% 0.01% 0.01% 0.01% 0.00% Anaeroplasma 0.13% 0.05% 0.19% 0.01% 0.00% 0.00% Fusobacterium 0.00% 0.01% 0.00% 0.00% 0.00% 0.00% 0.01% 0.00% 0.01% 0.00% 0.01% 0.00% 0.01% 0.00% 0.01% 0.00% 0.00% 0.01% 0.00%	Dioprilia	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	
Anaeroplasma 0.13% 0.05% 0.19% 0.01% 0.00% 0.00% Fusobacterium 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Bacteroidetes_unclassified 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Intestinimonas 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Candidatus_Arthromitus 0.02% 0.00% 0.00% 0.00% 0.00% 0.00% Christensenella 0.01% 0.01% 0.00% 0.00% 0.00% 0.00% Christensenellaceae_unclassified 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Parvibacter 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Sutterella 0.00%		0.01%	0.10%	0.08%	0.01%	0.00%	0.00%	
Coprobacillus 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Bacteroidetes_unclassified 0.00% 0.01% 0.00% 0.00% 0.01% Bacteroidetes_unclassified 0.00% 0.01% 0.00% 0.00% 0.00% Candidatus_Arthromitus 0.02% 0.00% 0.00% 0.00% 0.00% Christensenella 0.01% 0.00% 0.00% 0.00% 0.00% Christensenellaceae_unclassified 0.00% 0.01% 0.01% 0.01% 0.01% 0.01% Christensenellaceae_unclassified 0.01% 0.03% 0.04% 0.01% 0.01% Parvibacter 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Sutterella 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Allobaculum 0.00% 0.01% 0.00% 0.00% 0.00% 0.00% Allobaculum 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Anae	Anaeroplasma	0.13%	0.05%	0.19%	0.01%	0.04%	0.00%	
Fusobacterium 0.00% 0.01% 0.00% 0.01% 0.00% 0.01% Bacteroidetes_unclassified 0.00% <	Coprobacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Bacteroidetes_unclassified 0.00% 0.01% 0.00% 0.00% Intestinimonas 0.02% 0.00% 0.00% 0.00% 0.00% Candidatus_Arthromitus 0.02% 0.00% 0.00% 0.00% 0.00% Christensenella 0.01% 0.00% 0.00% 0.00% 0.00% 0.00% Christensenellaceae_unclassified 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Parvibacter 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Sutterella 0.00% <	Fusobacterium	0.00%	0.01%	0.00%	0.00%	0.00%	0.01%	
Intestimmonas 0.00%	Bacteroidetes_unclassified	0.00%	0.01%	0.01%	0.00%	0.00%	0.01%	
Candidatus_Arthromitus 0.02% 0.00% 0.02% 0.01% 0.02% 0.01% 0.02% 0.00% 0.01% 0.00% 0.01% 0.00%	Intestinimonas	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Christensenella 0.01% 0.01% 0.00%	Candidatus_Arthromitus	0.02%	0.00%	0.02%	0.01%	0.02%	0.00%	
Marvinbryantia 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Christensenellaceae_unclassified 0.01% 0.01% 0.01% 0.00%	Christensenella	0.01%	0.01%	0.02%	0.00%	0.01%	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% 0.01% 0.01% 0.01% 0.01% 0.01% 0.00% 0.0	Marvinbryantia	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Family_XII_unclassified 0.01% 0.03% 0.04% 0.01% 0.01% 0.01% Parvibacter 0.00% 0.	Christensenellaceae_unclassified	0.00%	0.01%	0.01%	0.00%	0.00%	0.00%	
Parvibacter 0.00%	Family_XIII_unclassified	0.01%	0.03%	0.04%	0.01%	0.01%	0.01%	
RC9_gut_group 0.59% 0.50% 0.09% 0.00%	Parvibacter	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
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%	RC9_gut_group	0.59%	0.50%	0.09%	0.00%	0.04%	0.04%	
Acetatifactor 0.01% 0.01% 0.02% 0.00% 0.00% 0.00% Allobaculum 0.00% 0.01% 0.00%	Sutterella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Allobaculum 0.00% 0.01% 0.00%	Acetatifactor	0.01%	0.01%	0.02%	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% 0.00% 0.00% 0.00% 0.00% Anaerovorax 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% 0.00% Bradyrhizobiaceae_unclassified 0.00% 0.0	Allobaculum	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	
Anaerostipes 0.00% 0.01% 0.00% 0.01% 0.00% 0.00% Anaerovarax 0.00%	Alphaproteobacteria_unclassified	1.47%	2.46%	1.89%	0.00%	0.01%	0.02%	
Anaerovorax 0.00%	Anaerostipes	0.00%	0.01%	0.00%	0.01%	0.00%	0.00%	
Bradyrhizobiaceae_unclassified 0.00% <	Anaerovorax	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Buttiauxella 0.00%	Bradyrhizobiaceae_unclassified	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% 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% Mitsuokella 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% Mucispirillum 0.02% 0.02% 0.51% 0.00% 0.00% 0.00% Scillospira 0.00% 0.00% 0.00% <td< td=""><td>Buttiauxella</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td></td<>	Buttiauxella	0.00%	0.00%	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%	Clostridia_unclassified	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	
Enterorhabdus0.00%0.00%0.01%0.00%0.00%0.00%Escherichia-Shigella0.00%0.00%0.00%0.00%0.00%0.00%0.00%Klebsiella0.00%0.00%0.00%0.00%0.00%0.00%0.00%Lactobacillales_unclassified0.00%0.00%0.00%0.00%0.00%0.00%Leuconostoc0.00%0.00%0.00%0.00%0.00%0.00%0.00%Lysinibacillus0.00%0.00%0.00%0.00%0.00%0.00%0.00%Marinilabiaceae_unclassified0.00%0.00%0.00%0.00%0.00%0.00%Mitsuokella0.00%0.00%0.00%0.00%0.00%0.00%0.00%Mucispirillum0.02%0.02%0.51%0.00%0.00%0.00%Oscillospira0.00%0.00%0.00%0.00%0.00%0.00%0.00%Paenibacillus0.00%0.00%0.00%0.00%0.00%0.00%0.00%Paratoea0.00%0.00%0.00%0.00%0.00%0.00%0.00%Parasporobacterium0.00%0.00%0.00%0.00%0.00%0.00%0.00%Prevotella0.00%0.00%0.00%0.00%0.00%0.00%0.00%	Coriobacteriaceae_unclassified	0.01%	0.02%	0.06%	0.01%	0.00%	0.00%	
Escherichia-Shigella 0.00% </td <td>Enterorhabdus</td> <td>0.00%</td> <td>0.00%</td> <td>0.01%</td> <td>0.00%</td> <td>0.00%</td> <td>0.00%</td>	Enterorhabdus	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	
Klebsiella 0.00%	Escherichia-Shigella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Lactobacillales_unclassified 0.00% <th< td=""><td>Klebsiella</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td></th<>	Klebsiella	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Leuconostoc 0.00%	Lactobacillales unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Lysinibacillus 0.00%	Leuconostoc	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Marinilabiaceae_unclassified 0.00% <th< td=""><td>Lvsinibacillus</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td><td>0.00%</td></th<>	Lvsinibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Mitsuokella 0.00%	Marinilabiaceae unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Mollicutes_unclassified 0.00% 0.00	Mitsuokella	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%	Mollicutes unclassified	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Oscillospira 0.00%	Mucispirillum	0.02%	0.02%	0.51%	0.00%	0.00%	0.00%	
Paenibacillus 0.00%	Oscillospira	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Pantoea 0.00% <	Paenibacillus	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	
Parasporobacterium 0.00% <td>Pantoea</td> <td>0.00 /8</td> <td>0.0078 0.007</td> <td>0.0078</td> <td>0.00%</td> <td>0.0078 0.007</td> <td>0.00 /8 0 010/</td>	Pantoea	0.00 /8	0.0078 0.007	0.0078	0.00%	0.0078 0.007	0.00 /8 0 010/	
possible_genus_Sk018 0.00% 0.00% 0.01% 0.00% 0.00% Prevotella 0.00% 0.00% 0.01% 0.00%<	Parasporobacterium	0.00 /8 0 00%	0.00 /o 0 00%	0.00 /o 0 00%	0.00 % 0.01%	0.00%	0.01%	
Prevotella 0.00% 0.00% 0.01% 0.00% 0.00%	nossible denus Sk018	0.00 /8	0.0078 0.007	0.0078 0.019/	0.01/0	0.0078 0.007	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	d chicory genot	ypes.		
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
Ruminoccocaceae_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