Supplementary Materials

Table S1. Oligonucleotide primer.

Primer Name	Sequence (5′–3′)	Reference
Eub338F	ACTCCTACGGGAGGCAGCAG	[33]
Eub518R	ATTACCGCGGCTGCTGG	
HDA1-GC-F	CGCCCGGGGCGCGCCCCGGGCGGGGCGGGGGCACGGGGGG ACTCCTACGGGAGGCAGCAGT	[34]
HDA2-R	GTATTACCGCGGCTGCTGGCAC	
Bact934F	GGARCATGTGGTTTAATTCGATGAT	[35]
Bact1060R	AGCTGACGACAACCATGCAG	
Firm934F	GGAGYATGTGGTTTAATTCGAAGCA	[35]
Firm1060R	AGCTGACGACAACCATGCAC	
Lactobacillus-F	AGCAGTAGGGAATCTTCCA	[36]
Lactobacillus-R	CACCGCTACACATGGAG	
Clostridia.IV-F	GCACAAGCAGTGGAGT	[37]
Clostridia.IV-R	CTTCCTCCGTTTTGTCAA	
ClostridiaXIVa-F	AAATGACGGTACCTGACTAA	[38]
Clostridia.XIVa-R	CTTTGAGTTTCATTCTTGCGAA	
Bacteroides-F	GAGAGGAAGGTCCCCCAC	[39]
Bacteroides-R	CGCTACTTGGCTGGTTCAG	
mouse CYP8b1-F	ACAAGCAGCAAGACCTGGAT	NM_010012.3
mouse CYP8b1-R	ATGGAAGAGACGCTGCAACT	
mouse CYP7a1-F	AAGTTTCGACATGCTCTCGC	NM_007824.2
mouse CYP7a1-R	CCTCATGGGAGCTGGAATTA	
mouse 18s-F	AAACGGCTACCACATCCAAG	NR_003278.3
mouse 18s-R	GGCCTCGAAAGAGTCCTGTA	

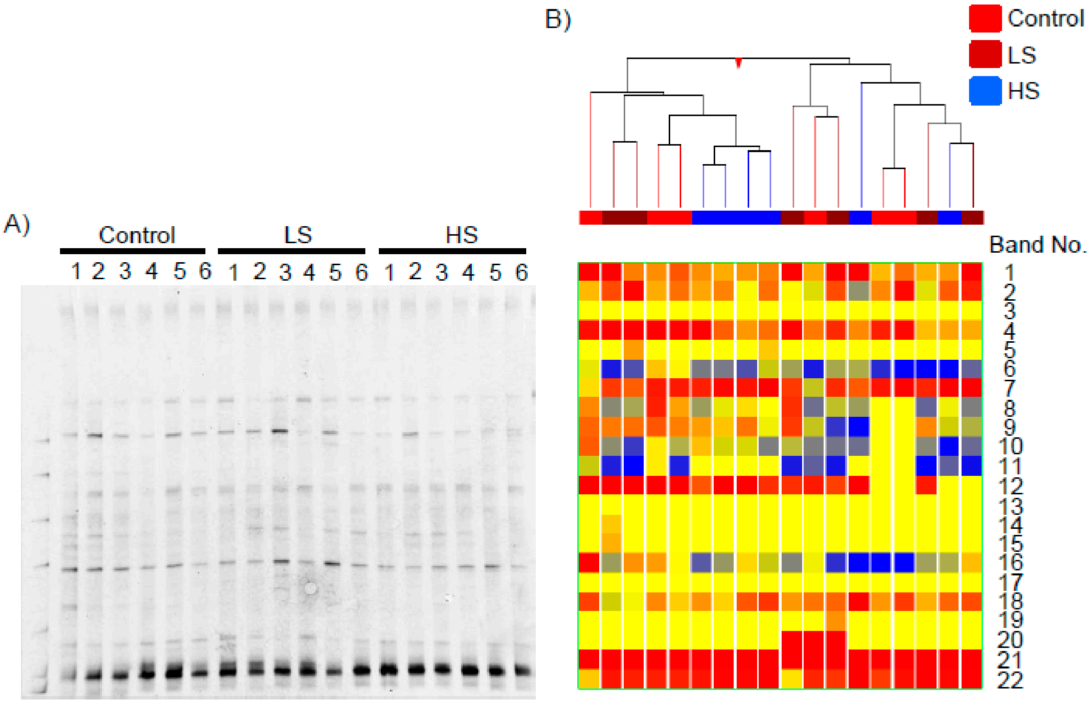

Figure S1. DGGE analysis of 16S V2-V3 rRNA in feces from mice fed sucralose. Band patterns (**A**) and hierarchical clustering of band patterns (**B**) for 16S V2-V3 rRNA in feces from mice fed sucralose for 8 weeks. LS: low sucralose (1.5 mg/kg BW/day), HS: high sucralose (15 mg/kg BW/day).

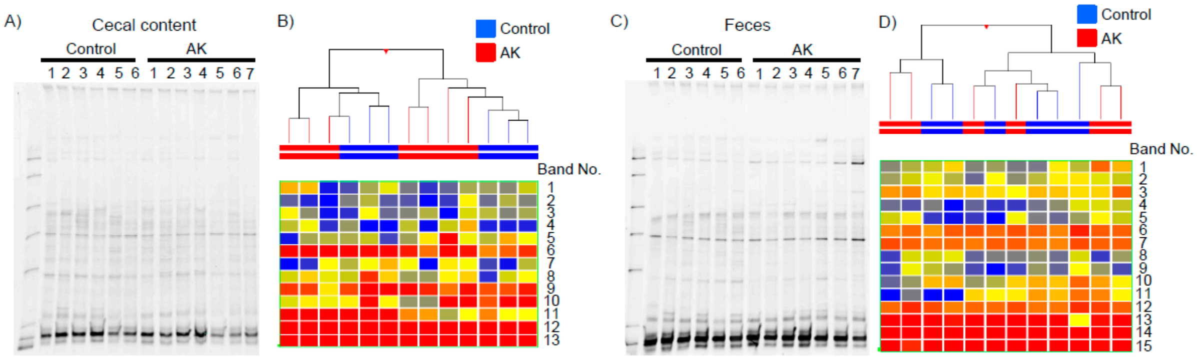

Figure S2. DGGE analysis of 16S V2-V3 rRNA in feces from mice fed acesulfame-K. Band patterns and hierarchical clustering of band patterns of 16S V2-V3 rRNA composition in cecal content (**A**) and feces (**B**) from mice fed acesulfame-K (AK) for 8 weeks.

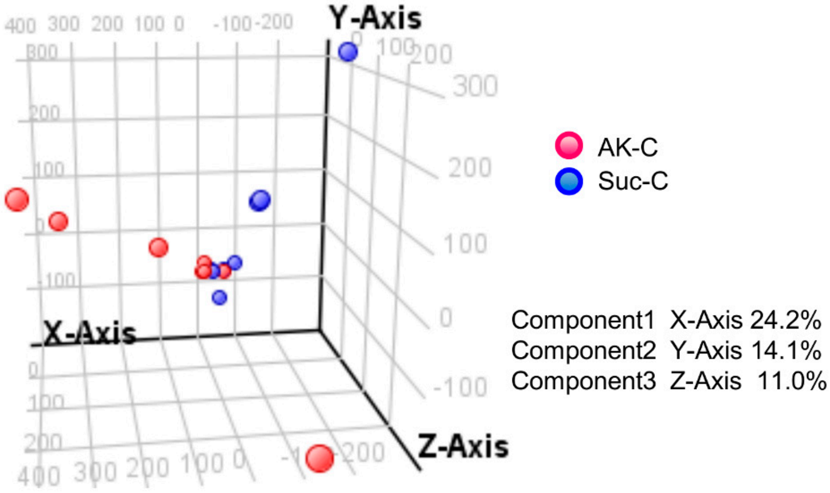

Figure S3. Lumial metabolome analysis in feces from both the control mice in Experiment 1 and 2. Principle component analysis of luminal metabolome data of the control groups from the sucralose experiment (Suc-C) and the acesulfam-K experiment (AK-C).