SUPPLEMENTARY INFORMATION

Dietary fiber mitigates the differential impact of beef and chicken meat consumption on rat intestinal health

Núria Elias Masiques [1], Jo De Vrieze [2, 3], Lieselot Y. Hemeryck [4], Lynn Vanhaecke [4, 5], Stefaan De Smet [1], Thomas Van Hecke [1*]

[1] Laboratory for Animal Nutrition and Animal Product Quality, Department of Animal Sciences and Aquatic Ecology, Ghent University, Coupure Links 653, B-9000, Ghent, Belgium

[2] Center for Microbial Ecology and Technology, Ghent University, Frieda Saeysstraat 1, B-9052 Gent, Belgium

[3] Centre for Advanced Process Technology for Urban Resource recovery (CAPTURE), Frieda Saeysstraat 1, B-9052 Gent, Belgium

[4] Laboratory of Integrative Metabolomics, Faculty of Veterinary Medicine, Ghent University, Salisburylaan 133, B-9820, Merelbeke, Belgium

[5] Institute for Global Food Security, School of Biological Sciences, Queen's University, University Road, Belfast, United Kingdom

[*] Corresponding author: thomas.vanhecke@ugent.be, phone: +32 9 264 90 03

Supplementary Table 1. Oxidative stress parameters in the rats

Organ		Units	Beef		Chicken		SEM	P_m	P_f	P_{m*f}
			- FOS	+ FOS	- FOS	+ FOS				
Blood	TBARS	nmol/g plasma	13.3	13.4	10.8	11.8	0.60	*.070*	.603	.748
	GSH-Px	U/g plasma	0.96	0.98	0.88	0.86	0.02	**.028**	.981	.644
	GSH	nmol / ml RBC	**302** ^{b}	**385** ^{ab}	**427** ^{a}	**353** ^{ab}	14.6	*.097*	.890	**.006**
	GSSG	nmol / ml RBC	47.7	58.4	61.8	51.6	2.60	.511	.980	*.058*
Stomach content	TBARS	nmol/g	**138** ^{a}	**133** ^{a}	**76.4** ^{b}	**88.4** ^{b}	6.04	**.001**	.563	.353
	PCC	nmol/mg protein	6.89	7.44	6.27	7.34	0.32	.775	.340	.885
Duodenal mucosa	TBARS	nmol/g	26.8	29.8	25.6	28.6	0.76	.417	**.046**	.964
	GSH-Px	U/g	0.66	0.69	0.64	0.72	0.01	.944	.102	.523
Colon mucosa	TBARS	nmol/g	57.3	68.9	59.0	64.7	2.28	.780	*.062*	.509
	GSH-Px	U/g	**2.47**	**1.12**	**2.21**	**1.26**	0.16	.818	**.001**	.431
Liver	TBARS	nmol/g	310	267	304	286	7.04	.599	**.021**	.316
	GSH-Px	U/g	18.0	17.5	17.6	15.3	0.61	.286	.242	.453
Kidney	TBARS	nmol/g	90.9	92.7	82.8	87.2	1.92	*.074*	.410	.718
	GSH-Px	U/g	6.07 ^{ab}	**6.51** ^{a}	6.04 ^{ab}	**5.88** ^{b}	0.08	**.028**	.356	**.049**
Heart	TBARS	nmol/g	67.5 ^{b}	77.7 ^{a}	72.4 ^{ab}	72.0 ^{ab}	1.19	.598	**.017**	*.051*
	GSH-Px	U/g	4.37	4.25	4.51	4.29	0.07	.509	.240	.747
Feces	Hexanal	10^6 x AUC / g feces	73.3 ^{a}	7.78 ^{bc}	49.6 ^{ac}	7.93 ^{b}	5.62	.256	**.001**	**.001**

P values of the fixed factors meat source (Pm), FOS (Pf) and their interaction term (Pm*f) in the mixed model procedure. SEM = standard error of the mean. Superscripts letters indicate significant differences between treatments.

Supplementary Table 2: Concentration of DNA and target analysis of DNA adduct levels in the colon mucosa of rats.

Rat ID	Diet	**DNA** (µg)	**N^7-MeG** (corrected AUC)	**N^6-MeA** (corrected AUC)
1	Chicken	42.12	ND	ND
2	Chicken	47.30	ND	ND
3	Chicken & FOS	42.78	ND	ND
4	Chicken & FOS	53.56	ND	ND
5	Beef	57.16	ND	ND
6	Beef	61.92	ND	ND
7	Beef & FOS	44.46	ND	ND
8	Beef & FOS	77.44	9794	5550
9	Chicken	24.76	ND	ND
10	Chicken	38.72	3941	ND
11	Chicken & FOS	48.16	ND	ND
12	Chicken & FOS	40.50	ND	ND
13	Beef	29.44	4090	ND
14	Beef	8.04	ND	ND
15	Beef & FOS	41.22	ND	5779
16	Beef & FOS	47.40	ND	ND
17	Chicken	42.88	ND	ND
18	Chicken	70.98	ND	ND
19	Chicken & FOS	43.88	ND	ND
20	Chicken & FOS	37.06	ND	ND
21	Beef	31.66	ND	ND
22	Beef	57.66	ND	ND
23	Beef & FOS	41.98	ND	ND
24	Beef & FOS	79.08	4892	ND
25	Chicken	73.24	4821	ND
26	Chicken	84.78	ND	ND
27	Chicken & FOS	78.62	ND	ND
28	Chicken & FOS	95.32	ND	ND
29	Beef	99.60	ND	ND
30	Beef	63.66	953	ND
31	Beef & FOS	70.02	ND	ND
32	Beef & FOS	39.64	ND	ND
33	Chicken	10.60	ND	ND
34	Chicken	18.76	ND	ND
35	Chicken & FOS	79.84	ND	ND
36	Chicken & FOS	37.70	ND	ND
37	Beef	59.16	ND	ND
38	Beef	37.60	ND	ND
39	Beef & FOS	36.78	ND	ND
40	Beef & FOS	73.72	15476	ND

Corrected AUC = area under the curve corrected for the DNA concentration per sample; ND = not detected

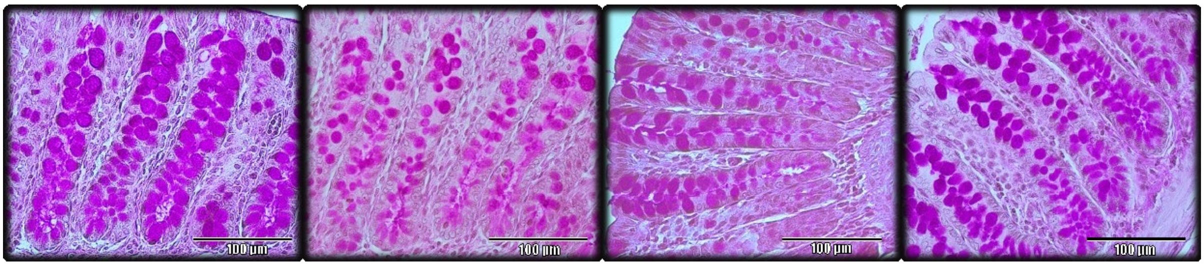
Supplementary Table 3: Spearman correlation values with Benjamini-Hochberg procedure.

		Correlation coefficient (r)	p-value
Bifidobacterium	Rothia	-0.269	0.179
Bifidobacterium	Bacteroides	-0.767	<0.001
Rothia	Bacteroides	0.351	0.077
Bifidobacterium	F_Muribaculaceae	-0.413	0.040
Rothia	F_Muribaculaceae	0.265	0.186
Bacteroides	F_Muribaculaceae	0.421	0.037
Bifidobacterium	Alloprevotella	-0.696	<0.001
Rothia	Alloprevotella	0.255	0.197
Bacteroides	Alloprevotella	0.666	<0.001
F_Muribaculaceae	Alloprevotella	0.466	0.019
Bifidobacterium	Prevotellaceae Ga6A1 group	-0.634	0.001
Rothia	Prevotellaceae Ga6A1 group	0.324	0.103
Bacteroides	Prevotellaceae Ga6A1 group	0.657	<0.001
F_Muribaculaceae	Prevotellaceae Ga6A1 group	0.374	0.062
Alloprevotella	Prevotellaceae Ga6A1 group	0.363	0.067
Bifidobacterium	F_Desulfovibrionaceae	-0.844	<0.001
Rothia	F_Desulfovibrionaceae	0.333	0.095
Bacteroides	F_Desulfovibrionaceae	0.708	<0.001
F_Muribaculaceae	F_Desulfovibrionaceae	0.570	0.003
Alloprevotella	F_Desulfovibrionaceae	0.794	<0.001
Prevotellaceae Ga6A1 group	F_Desulfovibrionaceae	0.504	0.010
Bifidobacterium	Lactobacillus	0.279	0.165
Rothia	Lactobacillus	0.039	0.842
Bacteroides	Lactobacillus	-0.413	0.040
F_Muribaculaceae	Lactobacillus	-0.551	0.004
Alloprevotella	Lactobacillus	-0.374	0.062
Prevotellaceae Ga6A1 group	Lactobacillus	-0.374	0.062
F_Desulfovibrionaceae	Lactobacillus	-0.259	0.192
Bifidobacterium	Ruminococcus torques group	0.518	0.008
Rothia	Ruminococcus torques group	-0.491	0.012
Bacteroides	Ruminococcus torques group	-0.504	0.010
F_Muribaculaceae	Ruminococcus torques group	-0.538	0.005
Alloprevotella	Ruminococcus torques group	-0.536	0.005
Prevotellaceae Ga6A1 group	Ruminococcus torques group	-0.453	0.022
F_Desulfovibrionaceae	Ruminococcus torques group	-0.664	<0.001
Lactobacillus	Ruminococcus torques group	0.225	0.259
Bifidobacterium	Anaerostipes	0.613	0.001
Rothia	Anaerostipes	-0.372	0.062
Bacteroides	Anaerostipes	-0.462	0.020
F_Muribaculaceae	Anaerostipes	-0.399	0.048
Alloprevotella	Anaerostipes	-0.558	0.004
Prevotellaceae Ga6A1 group	Anaerostipes	-0.259	0.192
F_Desulfovibrionaceae	Anaerostipes	-0.643	0.001

Lactobacillus	Anaerostipes	0.032	0.864
Ruminococcus torques group	Anaerostipes	0.491	0.012
Bifidobacterium	F_Lachnospiraceae	-0.669	<0.001
Rothia	F_Lachnospiraceae	0.137	0.502
Bacteroides	F_Lachnospiraceae	0.625	0.001
F_Muribaculaceae	F_Lachnospiraceae	0.608	0.001
Alloprevotella	F_Lachnospiraceae	0.454	0.022
Prevotellaceae Ga6A1 group	F_Lachnospiraceae	0.703	<0.001
F_Desulfovibrionaceae	F_Lachnospiraceae	0.612	0.001
Lactobacillus	F_Lachnospiraceae	-0.578	0.002
Ruminococcus torques group	F_Lachnospiraceae	-0.380	0.060
Anaerostipes	F_Lachnospiraceae	-0.260	0.192
Bifidobacterium	Roseburia	-0.615	0.001
Rothia	Roseburia	0.128	0.528
Bacteroides	Roseburia	0.443	0.026
F_Muribaculaceae	Roseburia	0.635	0.001
Alloprevotella	Roseburia	0.588	0.002
Prevotellaceae Ga6A1 group	Roseburia	0.377	0.062
F_Desulfovibrionaceae	Roseburia	0.734	<0.001
Lactobacillus	Roseburia	-0.392	0.053
Ruminococcus torques group	Roseburia	-0.470	0.018
Anaerostipes	Roseburia	-0.501	0.010
F_Lachnospiraceae	Roseburia	0.594	0.002
Bifidobacterium	F_Oscillospiraceae	-0.733	<0.001
Rothia	F_Oscillospiraceae	0.456	0.022
Bacteroides	F_Oscillospiraceae	0.627	0.001
F_Muribaculaceae	F_Oscillospiraceae	0.712	<0.001
Alloprevotella	F_Oscillospiraceae	0.678	<0.001
Prevotellaceae Ga6A1 group	F_Oscillospiraceae	0.567	0.003
F_Desulfovibrionaceae	F_Oscillospiraceae	0.870	<0.001
Lactobacillus	F_Oscillospiraceae	-0.373	0.062
Ruminococcus torques group	F_Oscillospiraceae	-0.644	0.001
Anaerostipes	F_Oscillospiraceae	-0.626	0.001
F_Lachnospiraceae	F_Oscillospiraceae	0.726	<0.001
Roseburia	F_Oscillospiraceae	0.790	<0.001
Bifidobacterium	Anaerofilum	-0.288	0.149
Rothia	Anaerofilum	0.163	0.422
Bacteroides	Anaerofilum	0.382	0.060
F_Muribaculaceae	Anaerofilum	0.531	0.006
Alloprevotella	Anaerofilum	0.228	0.253
Prevotellaceae Ga6A1 group	Anaerofilum	0.179	0.384
F_Desulfovibrionaceae	Anaerofilum	0.379	0.061
Lactobacillus	Anaerofilum	-0.327	0.102
Ruminococcus torques group	Anaerofilum	-0.162	0.422
Anaerostipes	Anaerofilum	-0.306	0.127
F_Lachnospiraceae	Anaerofilum	0.653	<0.001

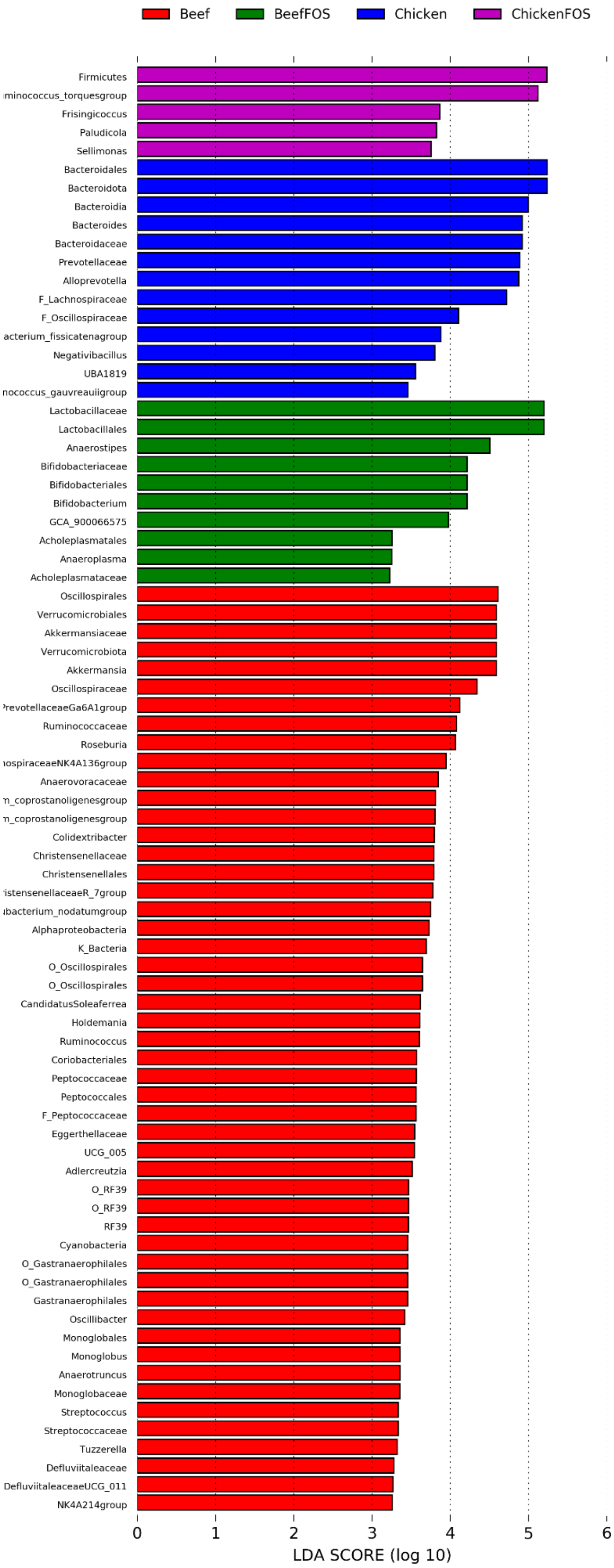
Roseburia	Anaerofilum	0.487	0.013
F_Oscillospiraceae	Anaerofilum	0.583	0.002
Bifidobacterium	Paludicola	0.416	0.039
Rothia	Paludicola	-0.136	0.502
Bacteroides	Paludicola	-0.365	0.066
F_Muribaculaceae	Paludicola	0.088	0.658
Alloprevotella	Paludicola	-0.293	0.145
Prevotellaceae Ga6A1 group	Paludicola	-0.170	0.407
F_Desulfovibrionaceae	Paludicola	-0.271	0.178
Lactobacillus	Paludicola	0.105	0.611
Ruminococcus torques group	Paludicola	0.365	0.066
Anaerostipes	Paludicola	0.289	0.149
F_Lachnospiraceae	Paludicola	-0.252	0.202
Roseburia	Paludicola	0.090	0.658
F_Oscillospiraceae	Paludicola	-0.165	0.422
Anaerofilum	Paludicola	-0.101	0.621
Bifidobacterium	Akkermansia	-0.367	0.066
Rothia	Akkermansia	0.295	0.142
Bacteroides	Akkermansia	0.384	0.059
F_Muribaculaceae	Akkermansia	0.540	0.005
Alloprevotella	Akkermansia	0.338	0.090
Prevotellaceae Ga6A1 group	Akkermansia	0.409	0.042
F_Desulfovibrionaceae	Akkermansia	0.333	0.095
Lactobacillus	Akkermansia	-0.504	0.010
Ruminococcus torques group	Akkermansia	-0.355	0.074
Anaerostipes	Akkermansia	-0.040	0.842
F_Lachnospiraceae	Akkermansia	0.657	<0.001
Roseburia	Akkermansia	0.321	0.107
F_Oscillospiraceae	Akkermansia	0.435	0.030
Anaerofilum	Akkermansia	0.457	0.022
Paludicola	Akkermansia	-0.074	0.711

Supplementary Figure 1. Histological snapshots of the colon mucosa stained with periodic acid Schiff (PAS) in rats following the beef, beef with FOS, chicken and chicken and FOS diets, respectively.

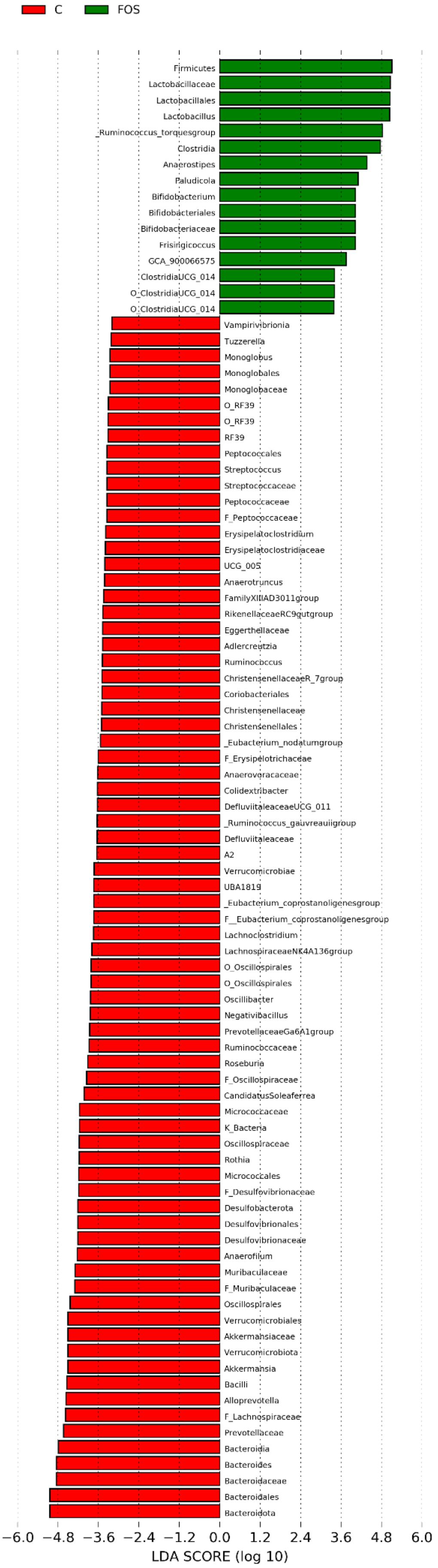


Supplementary Figure 2. LEfSe results LDA 2.

(A) Diets



(B) FOS (Meat)



🟥 C
🟩 FOS
Firmicutes
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Lactobacillales
Lactobacillus
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Clostridia
Anaerostipes
Paludicola
Bifidobacterium
Bifidobacteriales
Bifidobacteriaceae
Frisingicoccus
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ClostridiaUCG_014
O_ClostridiaUCG_014
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Vampirivibrionia
Tuzzerella
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RF39
Peptococcales
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Streptococcaceae
Peptococcaceae
F_Peptococcaceae
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Erysipelatoclostridiaceae
UCG_005
Anaerotruncus
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Eggerthellaceae
Adlercreutzia
Ruminococcus
ChristensenellaceaeR_7group
Coriobacteriales
Christensenellaceae
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Anaerovoracaceae
Colidextribacter
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Roseburia
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Micrococcaceae
K_Bacteria
Oscillospiraceae
Rothia
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Anaerofilum
Muribaculaceae
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Oscillospirales
Verrucomicrobiales
Akkermansiaceae
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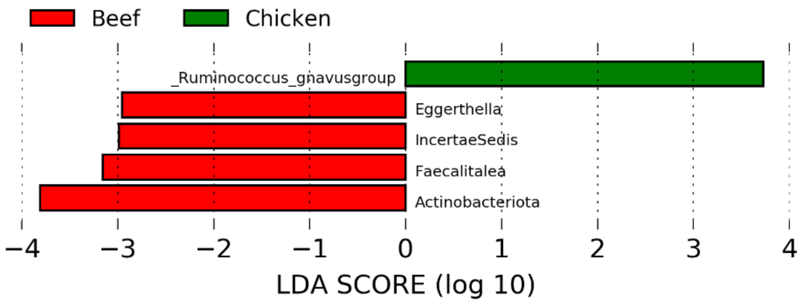
Akkermansia
Bacilli
Alloprevotella
F_Lachnospiraceae
Prevotellaceae
Bacteroidia
Bacteroides
Bacteroidaceae
Bacteroidales
Bacteroidota
−6.0
−4.8
−3.6
−2.4
−1.2
0.0
1.2
2.4
3.6
4.8
6.0
LDA SCORE (log 10)

(C) Meat(FOS)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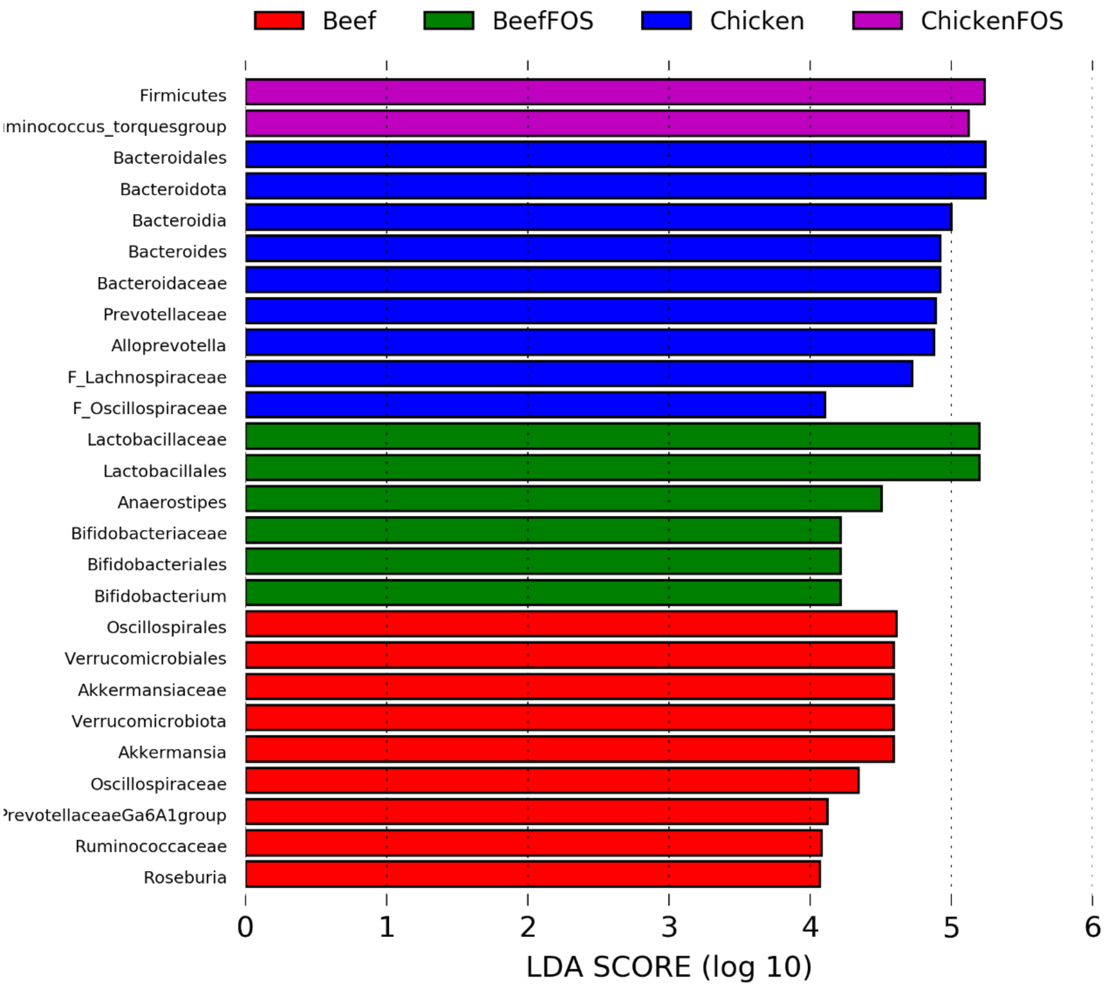
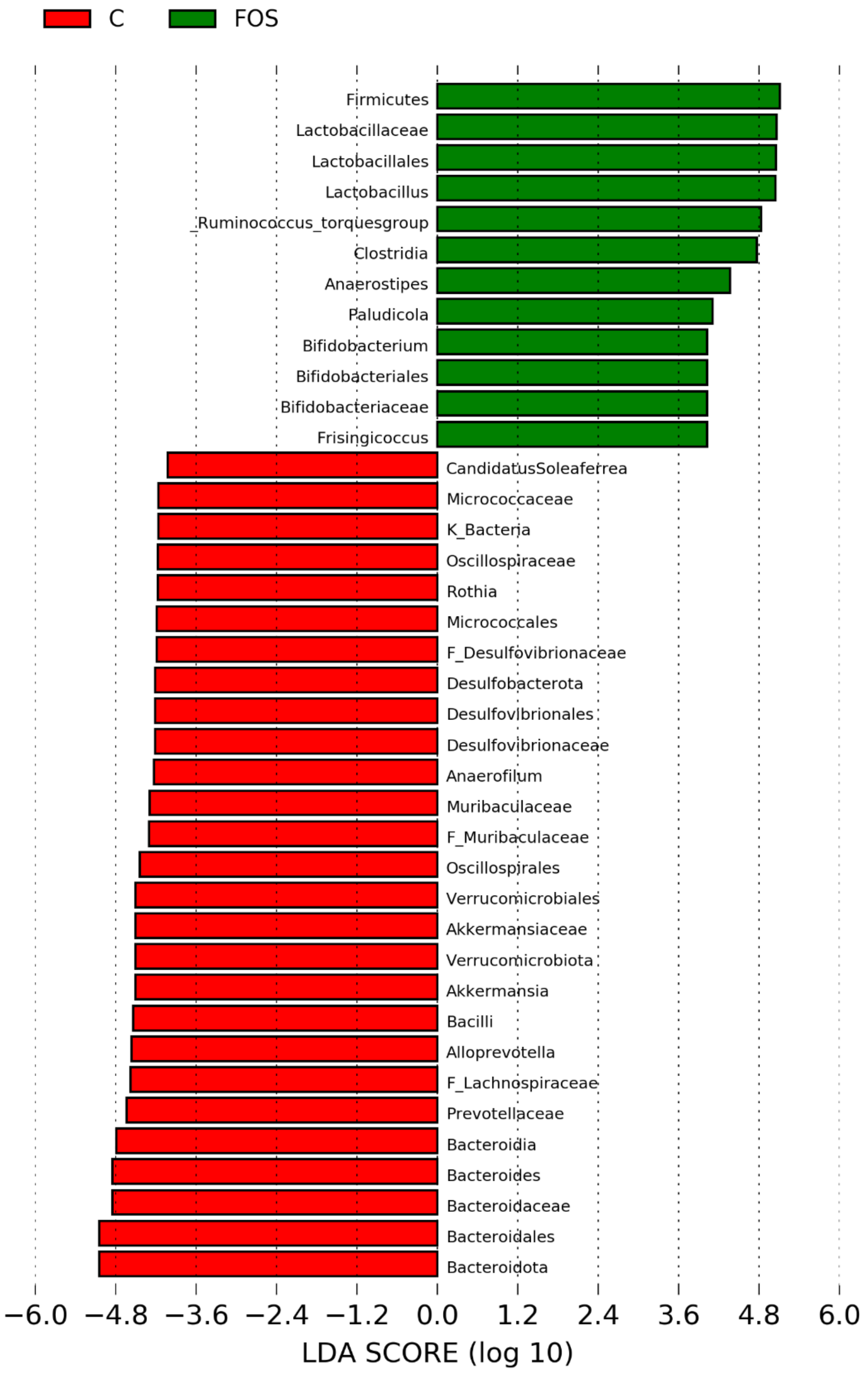
4
LDA SCORE (log 10)

Supplementary Figure 3. LEfSe results LDA 4

(A) Diet



(B) FOS(MEAT)


C
FOS
Firmicutes
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Clostridia
Anaerostipes
Paludicola
Bifidobacterium
Bifidobacteriales
Bifidobacteriaceae
Frisingicoccus
CandidatusSoleaferrea
Micrococcaceae
K_Bacteria
Oscillospiraceae
Rothia
Micrococcales
F_Desulfovibrionaceae
Desulfobacterota
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Desulfovibrionaceae
Anaerofilum
Muribaculaceae
F_Muribaculaceae
Oscillospirales
Verrucomicrobiales
Akkermansiaceae
Verrucomicrobiota
Akkermansia
Bacilli
Alloprevotella
F_Lachnospiraceae
Prevotellaceae
Bacteroidia
Bacteroides
Bacteroidaceae
Bacteroidales
Bacteroidota
−6.0
−4.8
−3.6
−2.4
−1.2
0.0
1.2
2.4
3.6
4.8
6.0
LDA SCORE (log 10)

Supplementary Figure 4. Non-significant fecal metabolites and LDL levels in the plasma of the rats.