

Supplementary Table 6. Differential taxa in the gut microbiome between HFD fed rats and controls^a

Taxa ^b	Control (%) ^c	HFD (%) ^d	SD (control) ^e	SD (HFD) ^f	P value ^g	FDR ^h
p_Actinobacteria	4.029778902	0.3484431	2.412013301	0.18069445	0.00216	0.008
p_Actinobacteria;c_Actinobacteria	3.665722584	0.1226354	2.222434776	0.08057401	0.00216	0.015
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales	3.30E-03	0.1039172	3.22E-03	0.08145077	0.00433	0.019
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Corynebacteriaceae	0	2.90E-03	0	1.66E-03	0.00278	0.02
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Corynebacteriaceae;g_Corynebacterium	0	2.90E-03	0	1.66E-03	0.00278	0.022
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae	3.30E-03	0.1010146	3.22E-03	0.08042155	0.00433	0.02
p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Micrococcaceae;g_Rothia	3.30E-03	0.1010146	3.22E-03	0.08042155	0.00433	0.022
p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales	3.662426587	0.0187181	2.223961236	0.04305751	0.005	0.019
p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae	3.662426587	0.0187181	2.223961236	0.04305751	0.005	0.02
p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium	3.662426587	0.0187181	2.223961236	0.04305751	0.005	0.023
p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_	0.079428326	2.09E-03	0.073136173	1.45E-03	0.00216	0.022
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteraceae];g_Odoribacter	0	0.0724992	0	0.0573085	0.00278	0.022
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae	1.124305572	6.4851276	0.43558414	4.75443102	0.00866	0.03
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides	1.124305572	6.4851276	0.43558414	4.75443102	0.00866	0.033
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_AF12	0	0.0407839	0	0.03582782	0.00962	0.033
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_Alistipes	0.02800352	0.0573831	7.15E-03	0.0381522	0.01515	0.044
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7	7.821278606	1.8445615	1.607441647	0.98151079	0.00216	0.02
p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_	7.821278606	1.8445615	1.607441647	0.98151079	0.00216	0.022
p_Defribacteres	0	0.1401949	0	0.10336137	0.00278	0.008
p_Defribacteres;c_Defribacteres	0	0.1401949	0	0.10336137	0.00278	0.015
p_Defribacteres;c_Defribacteres;o_Defribacterales	0	0.1401949	0	0.10336137	0.00278	0.019
p_Defribacteres;c_Defribacteres;o_Defribacterales;f_Defribacteraceae	0	0.1401949	0	0.10336137	0.00278	0.02
p_Defribacteres;c_Defribacteres;o_Defribacterales;f_Defribacteraceae;g_Mucispirillum	0	0.1401949	0	0.10336137	0.00278	0.022
p_Firmicutes;c_Bacilli	17.47981426	3.5316271	6.501191468	6.83021191	0.01515	0.048
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae	2.29E-03	0	1.42E-03	0	0.00962	0.03
p_Firmicutes;c_Bacilli;o_Bacillales;f_Bacillaceae;Other	2.29E-03	0	1.42E-03	0	0.00962	0.033
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae	6.66E-04	0.0115024	1.04E-03	7.39E-03	0.00434	0.02
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Aerococcaceae;g_Facklamia	6.66E-04	0.0115024	1.04E-03	7.39E-03	0.00434	0.022
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae	1.13E-03	6.97E-03	1.37E-03	4.25E-03	0.01291	0.039
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;g_Enterococcus	1.13E-03	6.97E-03	1.37E-03	4.25E-03	0.01291	0.042
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;Other	0.323285979	0.0184738	0.116648939	0.03227513	0.005	0.023
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae	0.044953138	0.1935069	0.064213032	0.11350143	0.01515	0.043
p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Streptococcaceae;g_Streptococcus	0.023636544	0.158998	0.026170316	0.10667991	0.01515	0.044
p_Firmicutes;c_Bacilli;o_Lactobacillales;Other	0.154968687	7.65E-03	0.072441346	0.01499157	0.00433	0.02
p_Firmicutes;c_Bacilli;o_Lactobacillales;Other;Other	0.154968687	7.65E-03	0.072441346	0.01499157	0.00433	0.022
p_Firmicutes;c_Bacilli;o_Turicibacterales	4.994804053	0.1178966	2.798551225	0.06647922	0.00216	0.019
p_Firmicutes;c_Bacilli;o_Turicibacterales;f_Turicibacteraceae	4.994804053	0.1178966	2.798551225	0.06647922	0.00216	0.02
p_Firmicutes;c_Bacilli;o_Turicibacterales;f_Turicibacteraceae;g_Turicibacter	4.994804053	0.1178966	2.798551225	0.06647922	0.00216	0.022

p_Firmicutes;c_Bacilli;Other	0.324073188	9.15E-03	0.157308671	0.01960309	0.00477	0.019
p_Firmicutes;c_Bacilli;Other;Other	0.324073188	9.15E-03	0.157308671	0.01960309	0.00477	0.02
p_Firmicutes;c_Bacilli;Other;Other;Other	0.324073188	9.15E-03	0.157308671	0.01960309	0.00477	0.023
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Christensenellaceae	0.018218227	0.3909521	0.011258285	0.39967209	0.00216	0.02
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Christensenellaceae;g_	0.018218227	0.389203	0.011258285	0.39940752	0.00216	0.022
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae;g_Clostridium	0.630691462	0.2369333	0.204960357	0.14035892	0.00433	0.022
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae	0.056302768	0.1722881	0.034714207	0.08276419	0.00866	0.03
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae;g_Dehalobacterium	0.056302768	0.1722881	0.034714207	0.08276419	0.00866	0.033
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Anaerostipes	0.020361012	1.07E-03	0.014501235	1.68E-03	0.00434	0.022
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Blautia	0.021973444	0.7060149	0.047345874	0.63162652	0.01152	0.038
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Clostridium	0.04538691	0	0.048416056	0	0.00962	0.033
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae	0.282804404	2.5338338	0.145573425	2.0048704	0.00433	0.02
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Peptococcaceae;g_rc4-4	0.241020183	1.23565	0.160168574	1.40019644	0.01515	0.044
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Anaerotruncus	5.98E-03	0.0347436	2.87E-03	0.01798264	0.00216	0.022
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Butyricoccus	0.164552074	5.54E-04	0.0796705	9.02E-04	0.00434	0.022
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Clostridium	0	2.19E-03	0	1.59E-03	0.00962	0.033
p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira	4.524759919	9.9619908	2.478863413	3.82110116	0.01515	0.044
p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Clostridium	0	0.0830312	0	0.04904153	0.00278	0.022
p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Coprobacillus	0	0.0252972	0	0.03144246	0.00962	0.033
p_Firmicutes;Other	0.815320052	0.1435231	0.266351889	0.21627993	0.00433	0.019
p_Firmicutes;Other;Other	0.815320052	0.1435231	0.266351889	0.21627993	0.00433	0.019
p_Firmicutes;Other;Other;Other	0.815320052	0.1435231	0.266351889	0.21627993	0.00433	0.02
p_Proteobacteria	0.815320052	0.1435231	0.266351889	0.21627993	0.00433	0.022
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales	0.336951146	1.6402371	0.166955946	0.76254071	0.00216	0.008
p_Proteobacteria;c_Alphaproteobacteria;o_Caulobacterales;f_Caulobacteraceae	0	2.09E-03	0	1.25E-03	0.00278	0.019
p_Proteobacteria;c_Deltaproteobacteria	0	2.09E-03	0	1.25E-03	0.00278	0.02
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales	0.084824713	1.1225817	0.035997123	0.5392137	0.00216	0.015
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae	0.084824713	1.1213819	0.035997123	0.53819368	0.00216	0.019
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_	0.078739657	1.0632701	0.034198833	0.5153079	0.00216	0.02
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Bilophila	0.066107278	0.5151498	0.027528972	0.28295205	0.00216	0.022
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio	0	0.3608243	0	0.23864018	0.00278	0.022
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio	0.01263238	0.1611189	0.010611456	0.06009563	0.00216	0.022
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_Desulfovibrio;Other	0	0.0261771	0	0.02164655	0.00278	0.022
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;Other	6.09E-03	0.0581118	2.89E-03	0.02710348	0.00216	0.02
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;Other	6.09E-03	0.0581118	2.89E-03	0.02710348	0.00216	0.022
p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;Other;Other	0	3.28E-03	0	2.06E-03	0.00962	0.035
p_Proteobacteria;Other	0	3.28E-03	0	2.06E-03	0.00962	0.033
p_Proteobacteria;Other;Other	0	3.28E-03	0	2.06E-03	0.00962	0.03
p_Proteobacteria;Other;Other;Other	0	3.28E-03	0	2.06E-03	0.00962	0.033
p_Proteobacteria;Other;Other;Other;Other	0	3.28E-03	0	2.06E-03	0.00962	0.033
p_Tenericutes	0.11308136	0.8627701	0.057036266	0.43285286	0.00216	0.008
p_Tenericutes;c_Mollicutes	0.11308136	0.8614017	0.057036266	0.43127912	0.00216	0.015
p_Tenericutes;c_Mollicutes;o_Anæroplasmatales	0.028497408	0.5637793	0.035707217	0.3622443	0.00433	0.019

p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales;f_Anaeroplasmataceae	0.028497408	0.5637793	0.035707217	0.3622443	0.00433	0.02
p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales;f_Anaeroplasmataceae;g_Anaeroplasma	0.028497408	0.562291	0.035707217	0.3608432	0.00433	0.022
p_TM7	3.37E-03	0.0159886	3.81E-03	0.0122354	0.02002	0.044

FDR, False discovery rate; SD, standard deviation.

^a Rats were fed with HFD or standard chow for 16 weeks.

^b Taxa that are differentially represented between HFD fed rats and controls.

^c Average abundance in control rats .

^d Average abundance in HFD fed rats.

^e Standard Deviation of the taxa in control rats .

^f Standard Deviation of taxa in HFD fed rats.

^g Wilcox test.

^h FDR adjusted P values. FDR less than 0.05 were considered significantly different.