

A

ND_IH+SH vs. ND_NM

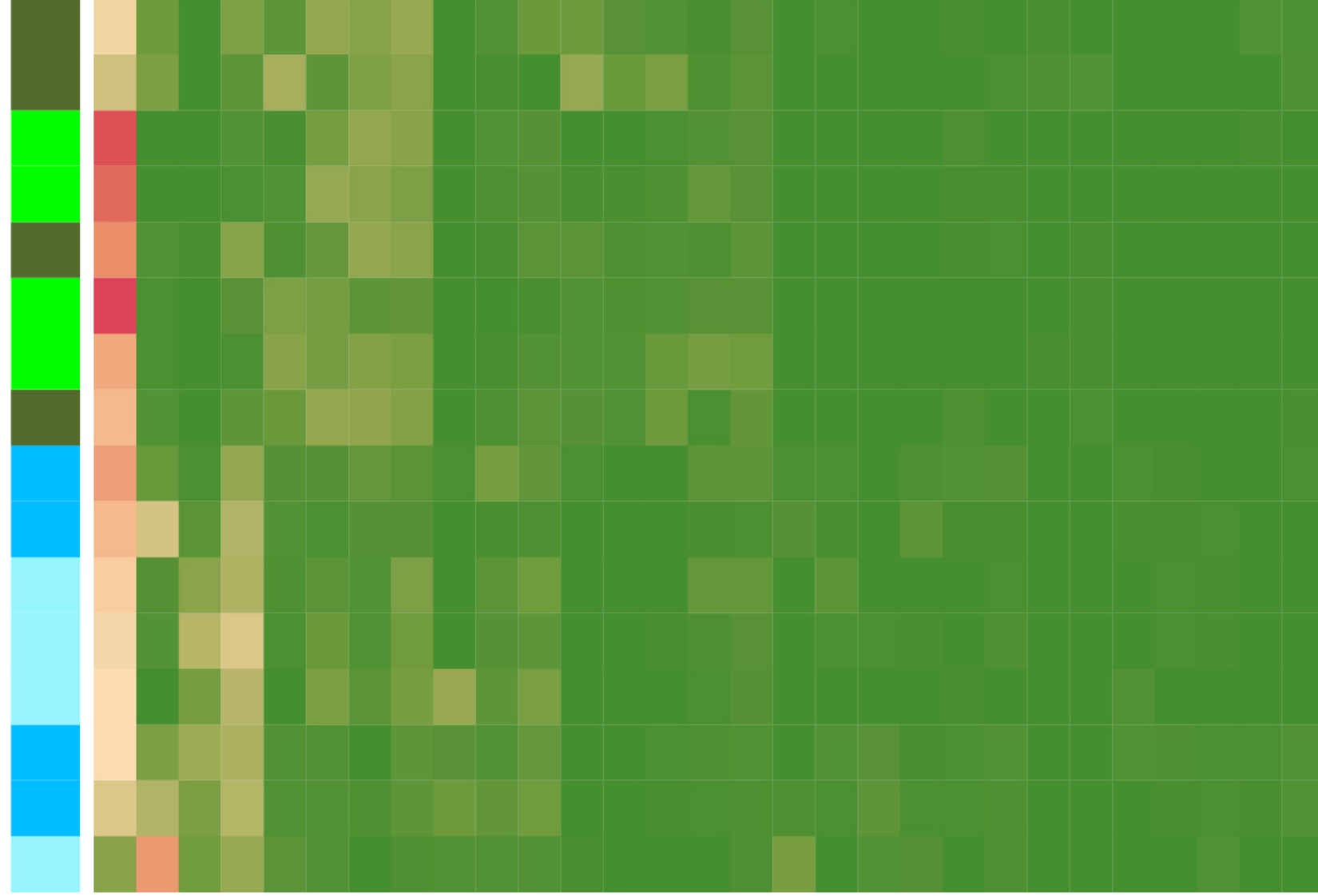
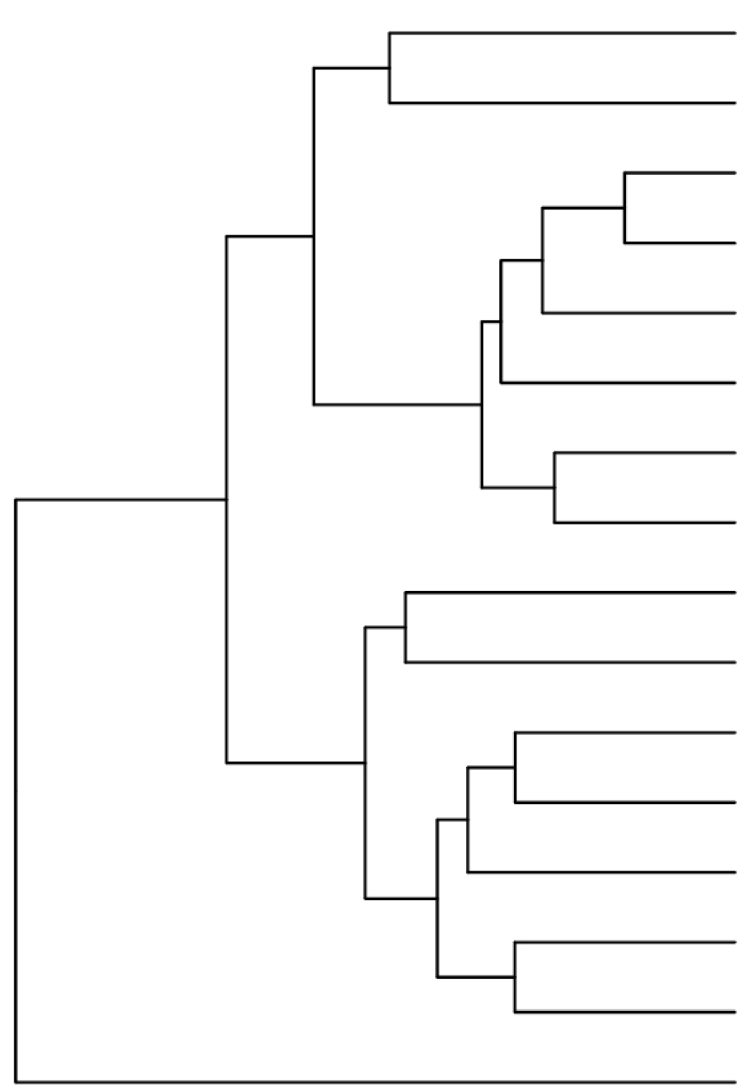
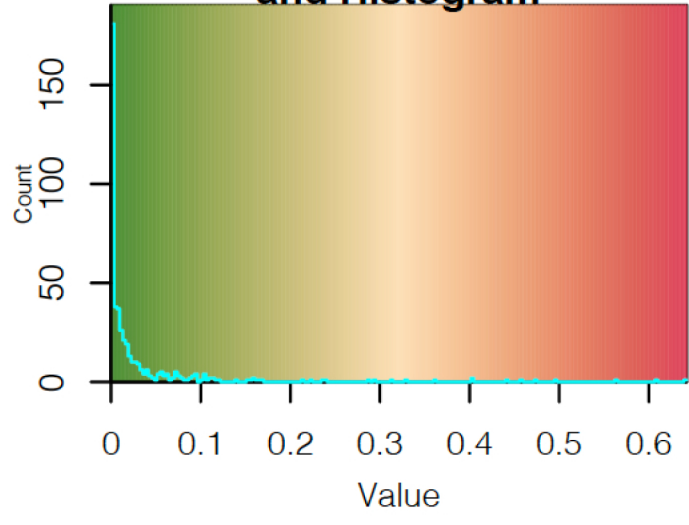
log2FoldChange



Family ● Muribaculaceae

B

Color Key
and Histogram



Lachnospiraceae_NK4A136_group
 Dubosiella
 Anaeroplasma
 Alistipes
 Lactobacillus
 Ruminiclostridium_9
 Acetatifactor
 Ruminiclostridium
 Lachnospiraceae_UCG-001
 Intestinimonas
 Oscillibacter
 Romboutsia
 Lactococcus
 GCA-900066575
 A2
 Lachnoclostridium
 Bifidobacterium
 Roseburia
 Ruminococcaceae_UCG-014
 Akkermansia
 ASF356
 Ruminiclostridium_5
 Lachnospiraceae_UCG-006
 Erysipelatoclostridium
 Eisenbergiella
 Ruminococcaceae_UCG-009
 Turicibacter
 Pseudoflavonifractor
 Clostridium_sensu_stricto_1

ejm.012 - HFD_NM
 ejm.011 - HFD_NM
 ejm.024 - HFD_IH+SH
 ejm.021 - HFD_IH+SH
 ejm.009 - HFD_NM
 ejm.022 - HFD_IH+SH
 ejm.023 - HFD_IH+SH
 ejm.010 - HFD_NM
 ejm.048 - ND_NM
 ejm.047 - ND_NM
 ejm.035 - ND_IH+SH
 ejm.033 - ND_IH+SH
 ejm.036 - ND_IH+SH
 ejm.046 - ND_NM
 ejm.045 - ND_NM
 ejm.034 - ND_IH+SH

C

Phylum_Class_Order_Family_Genus_Species	HFD_IH v:
	log2FoldChange
Firmicutes_Bacilli_Lactobacillales_Streptococcaceae_Lactococcus_NA	4.84
Firmicutes_Clostridia_Clostridiales_Clostridiales_vadinBB60_group_NA_NA	-6.69
Firmicutes_Clostridia_Clostridiales_Clostridiales_vadinBB60_group_NA_NA	-7.83
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group_NA	11.56
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group_NA	-6.21
Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Turcibacter_NA	-7.75
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group_NA	-7.70
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Eisenbergiella_NA	-7.63
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group_NA	-11.97
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group_NA	NA
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group_NA	NA
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group_NA	7.65
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnoclostridium_NA	NA
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Lachnospiraceae_NK4A136_group_NA	NA
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_A2_NA	5.87
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_A2_NA	-8.18
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA_NA	-6.67
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_A2_NA	NA
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA_NA	3.07
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_A2_NA	NA
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_GCA-900066575_NA	NA
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminococcaceae_UCG-009_NA	-4.98
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_9_NA	1.88
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_9_NA	-2.01
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA_NA	NA
Firmicutes_Bacilli_Lactobacillales_Lactobacillaceae_Lactobacillus_NA	5.64
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Intestinimonas_NA	NA
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA_NA	NA
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_NA_NA	NA
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Oscillibacter_NA	-5.74

Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Oscillibacter_NA	1.58
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_NA	-9.18
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_NA	4.84
Firmicutes_Clostridia_Clostridiales_Ruminococcaceae_Ruminiclostridium_NA	6.73
Firmicutes_Clostridia_Clostridiales_Clostridiales_vadinBB60_group_NA_NA	-9.03
Firmicutes_Erysipelotrichia_Erysipelotrichales_Erysipelotrichaceae_Dubosiella_newyorkensis	-4.80
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_NA_NA	NA
Tenericutes_Mollicutes_Anaeroplasmatales_Anaeroplasmataceae_Anaeroplasma_NA	-6.11
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Acetatifactor_NA	4.80
Firmicutes_Clostridia_Clostridiales_Lachnospiraceae_Acetatifactor_NA	NA
Tenericutes_Mollicutes_Mollicutes_RF39_NA_NA_NA	-3.23
Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA_NA	-12.29
Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA_NA	-9.83
Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA_NA	5.45
Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA_NA	NA
Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA_NA	5.32
Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA_NA	-8.98
Bacteroidetes_Bacteroidia_Bacteroidales_Muribaculaceae_NA_NA	-4.43
Firmicutes_Clostridia_Clostridiales_Clostridiales_vadinBB60_group_NA_NA	-6.68
Firmicutes_Clostridia_Clostridiales_Clostridiaceae_1_Clostridium_sensu_stricto_1_NA	-1.05
Bacteroidetes_Bacteroidia_Bacteroidales_Rikenellaceae_Alistipes_NA	-4.06
Verrucomicrobia_Verrucomicrobiae_Verrucomicrobiales_Akkermansiaceae_Akkermansia_muciniphila	-8.98

s ND_NM	HFD_NM vs ND_NM		ND_IH vs ND_NM		ND_NM vs
padj	log2FoldChange	padj	log2FoldChange	padj	log2FoldChange
0.00891556	6.38	0.00165718	NA	NA	-6.50
0.00891556	NA	NA	NA	NA	7.14
0.00446833	NA	NA	NA	NA	8.23
0.00004358	NA	NA	NA	NA	NA
0.00000133	-2.80	0.00898250	NA	NA	2.83
0.00076657	-8.15	0.00071812	NA	NA	8.04
0.00162964	-8.12	0.00161799	NA	NA	8.04
0.00199744	-8.05	0.00165718	NA	NA	7.96
0.00000773	-12.34	0.00000625	NA	NA	12.09
NA	NA	NA	NA	NA	NA
NA	6.41	0.01886644	NA	NA	NA
0.00546553	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
0.00891556	NA	NA	NA	NA	NA
0.00076657	-8.58	0.00071812	NA	NA	8.49
0.00144956	-7.09	0.00125956	NA	NA	7.00
NA	NA	NA	NA	NA	NA
0.00162964	2.54	0.00898250	NA	NA	-2.53
NA	-5.56	0.01742801	NA	NA	5.27
NA	NA	NA	NA	NA	NA
0.00127157	-6.30	0.00031515	NA	NA	6.27
0.00446833	NA	NA	NA	NA	NA
0.04460553	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
0.01210229	NA	NA	NA	NA	NA
NA	-2.42	0.03794028	NA	NA	2.45
NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
0.00006935	-10.60	0.00000028	NA	NA	10.24

0.02587644	4.33	0.03043592	NA	NA	-4.62
0.00000351	-9.55	0.00000227	NA	NA	9.39
0.00076657	4.50	0.00165718	NA	NA	-4.53
0.00002255	5.57	0.00064711	NA	NA	-5.73
0.00090323	-9.44	0.00091363	NA	NA	9.31
0.00106616	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA
0.00011283	-6.06	0.00021398	NA	NA	6.07
0.00446833	5.65	0.00165718	NA	NA	-5.75
NA	-2.31	0.04580906	NA	NA	2.32
0.00973894	NA	NA	NA	NA	NA
0.00000112	-5.23	0.00196375	NA	NA	5.35
0.00000000	-8.20	0.00000003	NA	NA	8.22
0.00919035	NA	NA	10.39	0.00018012	NA
NA	NA	NA	NA	NA	NA
0.00763808	NA	NA	9.79	0.00018012	NA
0.00026885	-3.60	0.01721137	NA	NA	3.76
0.00003618	NA	NA	NA	NA	NA
0.00891556	NA	NA	NA	NA	7.19
0.00407539	NA	NA	NA	NA	NA
0.00000051	-2.63	0.00091363	NA	NA	2.64
0.00016976	-9.37	0.00020499	NA	NA	9.23

HFD_NM	HFD_IH vs HFD_NM		ND_IH vs HFD_NM	
padj	log2FoldChange	padj	log2FoldChange	padj
0.00165713	NA	NA	-4.72	0.00599014
0.00898272	NA	NA	NA	NA
0.00431965	NA	NA	NA	NA
NA	6.50	0.00804640	NA	NA
0.00898272	NA	NA	3.08	0.00599014
0.00071810	NA	NA	8.23	0.00053193
0.00161793	NA	NA	6.26	0.01013989
0.00165713	NA	NA	7.05	0.00599014
0.00000625	NA	NA	12.15	0.00000470
NA	NA	NA	-8.75	0.00053193
NA	NA	NA	NA	NA
NA	NA	NA	NA	NA
NA	NA	NA	5.37	0.02655271
NA	7.36	0.03126161	NA	NA
NA	8.17	0.00426303	NA	NA
0.00071810	NA	NA	6.54	0.00599014
0.00125954	NA	NA	7.30	0.00080258
NA	5.93	0.04912345	NA	NA
0.00898272	NA	NA	-5.19	0.00002397
0.01742816	NA	NA	4.60	0.02863824
NA	NA	NA	-2.24	0.02289942
0.00031514	NA	NA	5.54	0.00107063
NA	NA	NA	NA	NA
NA	NA	NA	NA	NA
NA	NA	NA	-5.24	0.00784891
NA	NA	NA	NA	NA
0.03793957	NA	NA	NA	NA
NA	NA	NA	1.04	0.03892775
NA	NA	NA	-8.44	0.00055347
0.00000028	NA	NA	10.72	0.00000007

0.03043589	NA	NA	NA	NA
0.00000227	NA	NA	10.09	0.00000024
0.00165713	NA	NA	NA	NA
0.00064712	NA	NA	NA	NA
0.00091361	NA	NA	7.77	0.00492065
NA	NA	NA	2.51	0.03887604
NA	NA	NA	3.12	0.02655124
0.00021398	NA	NA	6.66	0.00003999
0.00165713	NA	NA	-4.17	0.00599014
0.04580753	NA	NA	NA	NA
NA	NA	NA	2.32	0.03892775
0.00196361	NA	NA	4.69	0.00599014
0.00000003	NA	NA	8.44	0.00000001
NA	7.77	0.00426303	12.31	0.00000028
NA	7.19	0.03227305	NA	NA
NA	7.58	0.00426303	11.72	0.00000011
0.01721045	NA	NA	NA	NA
NA	-2.60	0.02441552	NA	NA
0.00898272	NA	NA	NA	NA
NA	NA	NA	NA	NA
0.00091361	NA	NA	2.78	0.00053193
0.00020498	NA	NA	8.66	0.00041788

Row.names

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GCGAGCGTTATCCGGATTTATTGGGCGTAAAGCGTCCGCAGCCGGTTTATTAAGTATAGAATAAACTTCGGGGC
GCGAGCGTTATCCGGATTTATTGGGTTTAAAGGGTGCCTAGGCGGACTGTCAAGTCAGCGGTAAAATTGAGAGG

HFD_IH_vs_I	HFD_IH_vs_I	HFD_NM_vs_I	HFD_NM_vs_I	ND_IH_vs_I	NIND_IH_vs_I	NIND_NM_vs_I
4.8367052	0.00891556	6.38093592	0.00165718	NA	NA	-6.4968508
-6.6915638	0.00891556	NA	NA	NA	NA	7.14259467
-7.8306593	0.00446833	NA	NA	NA	NA	8.22734035
11.5632754	4.36E-05	NA	NA	NA	NA	NA
-6.2122222	1.33E-06	-2.8038391	0.0089825	NA	NA	2.8287503
-7.7458296	0.00076657	-8.1539879	0.00071812	NA	NA	8.03874409
-7.6996192	0.00162964	-8.1215331	0.00161799	NA	NA	8.03650865
-7.6282193	0.00199744	-8.0528393	0.00165718	NA	NA	7.95686279
-11.969931	7.73E-06	-12.337919	6.25E-06	NA	NA	12.0889534
NA	NA	NA	NA	NA	NA	NA
NA	NA	6.40865245	0.01886644	NA	NA	NA
7.65231457	0.00546553	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
5.87482541	0.00891556	NA	NA	NA	NA	NA
-8.1775355	0.00076657	-8.5829632	0.00071812	NA	NA	8.4897534
-6.6662763	0.00144956	-7.0882381	0.00125956	NA	NA	7.00392823
NA	NA	NA	NA	NA	NA	NA
3.07406302	0.00162964	2.54074119	0.0089825	NA	NA	-2.5256038
NA	NA	-5.5626944	0.01742801	NA	NA	5.27410205
NA	NA	NA	NA	NA	NA	NA
-4.9782938	0.00127157	-6.3045001	0.00031515	NA	NA	6.2726804
1.87967127	0.00446833	NA	NA	NA	NA	NA
-2.0075268	0.04460553	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
5.6424045	0.01210229	NA	NA	NA	NA	NA
NA	NA	-2.4213586	0.03794028	NA	NA	2.45108624
NA	NA	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
-5.735928	6.94E-05	-10.59919	2.78E-07	NA	NA	10.2441154
1.57953809	0.02587644	4.33174305	0.03043592	NA	NA	-4.6243184
-9.1771061	3.51E-06	-9.5547761	2.27E-06	NA	NA	9.39126396
4.83546766	0.00076657	4.49641485	0.00165718	NA	NA	-4.5331543
6.72713465	2.26E-05	5.56550557	0.00064711	NA	NA	-5.7277433
-9.0334953	0.00090323	-9.4380495	0.00091363	NA	NA	9.30734613
-4.7972235	0.00106616	NA	NA	NA	NA	NA
NA	NA	NA	NA	NA	NA	NA
-6.1067512	0.00011283	-6.0619215	0.00021398	NA	NA	6.06894912
4.79525473	0.00446833	5.65403021	0.00165718	NA	NA	-5.7519947
NA	NA	-2.3131606	0.04580906	NA	NA	2.31977695
-3.2270901	0.00973894	NA	NA	NA	NA	NA
-12.285624	1.12E-06	-5.2308722	0.00196375	NA	NA	5.34601982

-9.83394	8.88E-10	-8.1996191	3.02E-08	NA	NA	8.21788795
5.44652648	0.00919035	NA	NA	10.3921008	0.00018012	NA
NA	NA	NA	NA	NA	NA	NA
5.32456204	0.00763808	NA	NA	9.78670971	0.00018012	NA
-8.9760842	0.00026885	-3.5989725	0.01721137	NA	NA	3.75717801
-4.4310062	3.62E-05	NA	NA	NA	NA	NA
-6.6764367	0.00891556	NA	NA	NA	NA	7.18607637
-1.0460644	0.00407539	NA	NA	NA	NA	NA
-4.0624955	5.07E-07	-2.6321351	0.00091363	NA	NA	2.63988423
-8.9824467	0.00016976	-9.3728948	0.00020499	NA	NA	9.23431765

ND_NM_vs_I	HFD_IH_vs_F	HFD_IH_vs_F	ND_IH_vs_HI	ND_IH_vs_HI	Kingdom	Phylum
0.00165713	NA	NA	-4.7186277	0.00599014	Bacteria	Firmicutes
0.00898272	NA	NA	NA	NA	Bacteria	Firmicutes
0.00431965	NA	NA	NA	NA	Bacteria	Firmicutes
NA	6.50014625	0.0080464	NA	NA	Bacteria	Firmicutes
0.00898272	NA	NA	3.0802569	0.00599014	Bacteria	Firmicutes
0.0007181	NA	NA	8.22502124	0.00053193	Bacteria	Firmicutes
0.00161793	NA	NA	6.26289494	0.01013989	Bacteria	Firmicutes
0.00165713	NA	NA	7.04802426	0.00599014	Bacteria	Firmicutes
6.25E-06	NA	NA	12.1547773	4.70E-06	Bacteria	Firmicutes
NA	NA	NA	-8.7515595	0.00053193	Bacteria	Firmicutes
NA	NA	NA	NA	NA	Bacteria	Firmicutes
NA	NA	NA	NA	NA	Bacteria	Firmicutes
NA	NA	NA	5.36906532	0.02655271	Bacteria	Firmicutes
NA	7.36270882	0.03126161	NA	NA	Bacteria	Firmicutes
NA	8.17376681	0.00426303	NA	NA	Bacteria	Firmicutes
0.0007181	NA	NA	6.54049842	0.00599014	Bacteria	Firmicutes
0.00125954	NA	NA	7.3038088	0.00080258	Bacteria	Firmicutes
NA	5.92958643	0.04912345	NA	NA	Bacteria	Firmicutes
0.00898272	NA	NA	-5.1865246	2.40E-05	Bacteria	Firmicutes
0.01742816	NA	NA	4.59945997	0.02863824	Bacteria	Firmicutes
NA	NA	NA	-2.2409721	0.02289942	Bacteria	Firmicutes
0.00031514	NA	NA	5.53868344	0.00107063	Bacteria	Firmicutes
NA	NA	NA	NA	NA	Bacteria	Firmicutes
NA	NA	NA	NA	NA	Bacteria	Firmicutes
NA	NA	NA	-5.237536	0.00784891	Bacteria	Firmicutes
NA	NA	NA	NA	NA	Bacteria	Firmicutes
0.03793957	NA	NA	NA	NA	Bacteria	Firmicutes
NA	NA	NA	1.04437894	0.03892775	Bacteria	Firmicutes
NA	NA	NA	-8.4435837	0.00055347	Bacteria	Firmicutes
2.78E-07	NA	NA	10.7210738	7.02E-08	Bacteria	Firmicutes
0.03043589	NA	NA	NA	NA	Bacteria	Firmicutes
2.27E-06	NA	NA	10.0936283	2.44E-07	Bacteria	Firmicutes
0.00165713	NA	NA	NA	NA	Bacteria	Firmicutes
0.00064712	NA	NA	NA	NA	Bacteria	Firmicutes
0.00091361	NA	NA	7.76744988	0.00492065	Bacteria	Firmicutes
NA	NA	NA	2.50524144	0.03887604	Bacteria	Firmicutes
NA	NA	NA	3.12478065	0.02655124	Bacteria	Firmicutes
0.00021398	NA	NA	6.65940957	4.00E-05	Bacteria	Tenericutes
0.00165713	NA	NA	-4.166239	0.00599014	Bacteria	Firmicutes
0.04580753	NA	NA	NA	NA	Bacteria	Firmicutes
NA	NA	NA	2.32327489	0.03892775	Bacteria	Tenericutes
0.00196361	NA	NA	4.68574718	0.00599014	Bacteria	Bacteroidete:

3.02E-08	NA	NA	8.43797142	1.37E-08	Bacteria	Bacteroidete:
NA	7.77103377	0.00426303	12.3121124	2.77E-07	Bacteria	Bacteroidete:
NA	7.18576421	0.03227305	NA	NA	Bacteria	Bacteroidete:
NA	7.57626486	0.00426303	11.7189326	1.08E-07	Bacteria	Bacteroidete:
0.01721045	NA	NA	NA	NA	Bacteria	Bacteroidete:
NA	-2.5988459	0.02441552	NA	NA	Bacteria	Bacteroidete:
0.00898272	NA	NA	NA	NA	Bacteria	Firmicutes
NA	NA	NA	NA	NA	Bacteria	Firmicutes
0.00091361	NA	NA	2.77860877	0.00053193	Bacteria	Bacteroidete:
0.00020498	NA	NA	8.66256465	0.00041788	Bacteria	Verrucomicrobia

Class	Order	Family	Genus	Species
Bacilli	Lactobacillales	Streptococcae	Lactococcus	NA
Clostridia	Clostridiales	Clostridiales_NA		NA
Clostridia	Clostridiales	Clostridiales_NA		NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnospirac	NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnospirac	NA
Erysipelotrichi	Erysipelotrichi	Erysipelotrichi	Turicibacter	NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnospirac	NA
Clostridia	Clostridiales	Lachnospiraceae	Eisenbergiella	NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnospirac	NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnospirac	NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnospirac	NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnospirac	NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnoclostr	NA
Clostridia	Clostridiales	Lachnospiraceae	Lachnospirac	NA
Clostridia	Clostridiales	Lachnospiraceae	A2	NA
Clostridia	Clostridiales	Lachnospiraceae	A2	NA
Clostridia	Clostridiales	Lachnospiraceae	NA	NA
Clostridia	Clostridiales	Lachnospiraceae	A2	NA
Clostridia	Clostridiales	Lachnospiraceae	NA	NA
Clostridia	Clostridiales	Lachnospiraceae	A2	NA
Clostridia	Clostridiales	Lachnospiraceae	GCA-900066	NA
Clostridia	Clostridiales	Ruminococcae	Ruminococca	NA
Clostridia	Clostridiales	Ruminococcae	Ruminiclostr	NA
Clostridia	Clostridiales	Ruminococcae	Ruminiclostr	NA
Clostridia	Clostridiales	Lachnospiraceae	NA	NA
Bacilli	Lactobacillales	Lactobacillaceae	Lactobacillus	NA
Clostridia	Clostridiales	Ruminococcae	Intestinimon	NA
Clostridia	Clostridiales	Ruminococcae	NA	NA
Clostridia	Clostridiales	Ruminococcae	NA	NA
Clostridia	Clostridiales	Ruminococcae	Oscillibacter	NA
Clostridia	Clostridiales	Ruminococcae	Oscillibacter	NA
Clostridia	Clostridiales	Ruminococcae	Ruminiclostr	NA
Clostridia	Clostridiales	Ruminococcae	Ruminiclostr	NA
Clostridia	Clostridiales	Ruminococcae	Ruminiclostr	NA
Clostridia	Clostridiales	Clostridiales_NA		NA
Erysipelotrichi	Erysipelotrichi	Erysipelotrichi	Dubosiella	newyorkensis
Clostridia	Clostridiales	Lachnospiraceae	NA	NA
Mollicutes	Anaeroplasm	Anaeroplasm	Anaeroplasm	NA
Clostridia	Clostridiales	Lachnospiraceae	Acetatifactor	NA
Clostridia	Clostridiales	Lachnospiraceae	Acetatifactor	NA
Mollicutes	Mollicutes_R	NA	NA	NA
Bacteroidia	Bacteroidales	Muribaculaceae	NA	NA

Bacteroidia	Bacteroidales	Muribaculaceae	NA	NA
Bacteroidia	Bacteroidales	Muribaculaceae	NA	NA
Bacteroidia	Bacteroidales	Muribaculaceae	NA	NA
Bacteroidia	Bacteroidales	Muribaculaceae	NA	NA
Bacteroidia	Bacteroidales	Muribaculaceae	NA	NA
Bacteroidia	Bacteroidales	Muribaculaceae	NA	NA
Clostridia	Clostridiales	Clostridiales	_NA	NA
Clostridia	Clostridiales	Clostridiaceae	Clostridium	_NA
Bacteroidia	Bacteroidales	Rikenellaceae	Alistipes	NA
Verrucomicrobia	Verrucomicrobia	Akkermansia	Akkermansia	muciniphila

Supplementary data-A (p 1). Two unclassified genera from the Muribaculaceae family that passed DESeq2 analysis.

Supplementary data-B (p 2). Heatmap (Genus level analysis) confirming that diet was the most significant variable shaping mucosal colonic microbiota.

Supplementary data-C (p 3-16). A summary of the microbial community changes between the experimental groups.