

**Supplementary Table S1: List of primary antibodies used for Western blot technique.**

Primary antibodies were purchased from Abnova Corporation (Walnut, CA), Cosmo Bio (Carlsbad, CA), Santa Cruz Biotechnology, Inc. (Dallas,TX) , GeneTex, Inc. (Irvine, CA) Cell Signaling Technology, Inc. (Denver, MA), Adipogen Corporation(San Diego, CA).

<b>Code</b>	<b>Antibody</b>
PAB1293	anti-CML
KAL-KH025	anti-CEL
sc-365154	anti-RAGE
sc-13032	anti-Nrf2
Gtx15747	anti-Glo-1
8242S	anti-NF $\kappa$ B p65
AG-20B-0014-C100	anti-NLRP3
93709	anti-Gasdermin
5174S	anti-GAPDH
4499S	anti-Histone H3

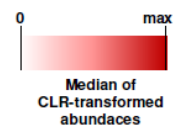
**Supplementary Figure S1:** Bacterial taxa that resulted differently represented among experimental groups in feces. ASV, Amplicon Sequence Variants. P, statistical significance according to Mann-Whitney test performed on centered log-ratio (CLR)-transformed abundances.

[SD] vs [HFHS]				
ASV	Taxonomy	P	SD	HFHS
	<i>p_Acidobacteria</i>	0.0432	0.00	0.32
	<i>p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium;s_</i>	0.0395	0.34	0.00
	<i>p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus</i>	0.0393	0.00	0.74
	<i>p_Firmicutes;c_Bacilli;o_Bacillales;f_Staphylococcaceae;g_Staphylococcus;s_sciuri</i>	0.0432	0.00	0.68
	<i>p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae</i>	0.0395	0.00	0.18
	<i>p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;_</i>	0.0395	0.00	0.18
	<i>p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Enterococcaceae;_;</i>	0.0395	0.00	0.18
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Ruminococcus;s_</i>	0.0395	0.00	0.64
	<i>p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_</i>	0.0110	1.32	0.00
	<i>p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_s</i>	0.0110	1.32	0.00

[SD] vs [HFHS+Zn-SP]				
ASV	Taxonomy	P	SD	HFHS+ Zn-SP
	<i>p_Actinobacteria</i>	0.0070	6.24	4.77
_0011	<i>p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium</i>	0.0236	2.42	0.00
_0028	<i>p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium</i>	0.0307	0.73	0.00
_0053	<i>p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium</i>	0.0307	0.63	0.00
	<i>p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium;s_</i>	0.0307	0.34	0.00
	<i>p_Actinobacteria;c_Coriobacteriales;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia</i>	0.0262	2.33	4.35
	<i>p_Actinobacteria;c_Coriobacteriales;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia;s_</i>	0.0262	2.33	4.35
_0090	<i>p_Actinobacteria;c_Coriobacteriales;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia;s_</i>	0.0307	0.00	1.22
_0135	<i>p_Actinobacteria;c_Coriobacteriales;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia;s_</i>	0.0307	0.00	0.64
	<i>p_Actinobacteria;c_Coriobacteriales;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella</i>	0.0291	0.57	1.23
	<i>p_Actinobacteria;c_Coriobacteriales;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_aerofaciens</i>	0.0114	0.00	0.79
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteriaceae]</i>	0.0338	0.00	0.78
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteriaceae];g_Odoribacter</i>	0.0338	0.00	0.78
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteriaceae];g_Odoribacter;s_</i>	0.0338	0.00	0.78
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae</i>	0.0111	3.23	2.66
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides</i>	0.0111	3.23	2.66
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Bacteroidaceae;g_Bacteroides;s_</i>	0.0379	2.71	2.17
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella;s_melaninogenica</i>	0.0209	0.98	1.42
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae</i>	0.0070	3.17	2.60
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_</i>	0.0070	3.07	2.51
	<i>p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;g_s_</i>	0.0070	3.07	2.51
	<i>p_Firmicutes</i>	0.0070	6.15	7.13
	<i>p_Firmicutes;c_Bacilli</i>	0.0070	3.73	4.20
	<i>p_Firmicutes;c_Bacilli;o_Lactobacillales</i>	0.0070	3.72	4.01
_0139	<i>p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus;s_</i>	0.0307	0.96	0.00
	<i>p_Firmicutes;c_Clostridia</i>	0.0262	5.78	5.02
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales</i>	0.0262	5.78	5.02
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_</i>	0.0111	4.84	4.30
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_g_</i>	0.0111	4.84	4.30
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_g_s_</i>	0.0111	4.84	4.30
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Mogibacteriaceae;g_Anaerovorax</i>	0.0307	0.23	0.00
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Mogibacteriaceae;g_Anaerovorax;s_</i>	0.0307	0.23	0.00
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae</i>	0.0187	1.26	0.00
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae;g_Dehalobacterium</i>	0.0187	1.26	0.00
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Dehalobacteriaceae;g_Dehalobacterium;s_</i>	0.0187	1.26	0.00
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae</i>	0.0175	3.87	2.95
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_</i>	0.0175	3.00	1.52
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_s_</i>	0.0175	3.00	1.52
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coproccoccus</i>	0.0476	1.11	0.00
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coproccoccus;s_</i>	0.0476	1.11	0.00
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae</i>	0.0070	4.84	3.62
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_</i>	0.0041	4.02	2.88
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_s_</i>	0.0041	4.02	2.88
	<i>p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus</i>	0.0452	2.39	0.81
	<i>p_Firmicutes;c_Erysipelotrichi</i>	0.0041	4.30	6.95
	<i>p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales</i>	0.0041	4.30	6.95
	<i>p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae</i>	0.0041	4.30	6.95
	<i>p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum</i>	0.0041	4.24	6.95
	<i>p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum;s_</i>	0.0041	4.24	6.95
	<i>p_Proteobacteria;c_Alphaproteobacteria;o_RF32</i>	0.0175	1.02	1.30
	<i>p_Proteobacteria;c_Alphaproteobacteria;o_RF32;f_</i>	0.0175	1.02	1.30
	<i>p_Proteobacteria;c_Alphaproteobacteria;o_RF32;f_g_</i>	0.0175	1.02	1.30
	<i>p_Proteobacteria;c_Alphaproteobacteria;o_RF32;f_g_s_</i>	0.0175	1.02	1.30
	<i>p_Proteobacteria;c_Betaproteobacteria</i>	0.0379	2.98	3.41
	<i>p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales</i>	0.0070	2.18	2.74
	<i>p_Tenericutes</i>	0.0204	0.67	0.00
	<i>p_Tenericutes;c_Mollicutes</i>	0.0204	0.67	0.00
	<i>p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales</i>	0.0307	0.67	0.00
	<i>p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales;f_Anaeroplasmataceae</i>	0.0307	0.67	0.00
	<i>p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales;f_Anaeroplasmataceae;g_Anaeroplasma</i>	0.0307	0.67	0.00
	<i>p_Tenericutes;c_Mollicutes;o_Anaeroplasmatales;f_Anaeroplasmataceae;g_Anaeroplasma;s_</i>	0.0307	0.67	0.00

[HFHS] vs [HFHS+Zn-SP]				
ASV	Taxonomy	P	HFHS	HFHS+Zn-SP
_0031	p_Actinobacteria;c_Actinobacteria;o_Bifidobacteriales;f_Bifidobacteriaceae;g_Bifidobacterium	0.0432	1.86	0.00
	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia	0.0001	2.38	4.35
	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia;s_	0.0001	2.38	4.35
_0090	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia;s_	0.0293	0.00	1.22
	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Collinsella;s_aerofaciens	0.0192	0.00	0.79
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteraceae]	0.0140	0.00	0.78
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteraceae];g_Odoribacter	0.0140	0.00	0.78
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Odoribacteraceae];g_Odoribacter;s_	0.0140	0.00	0.78
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae]	0.0072	0.99	1.70
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae];g_[Prevotella]	0.0072	0.99	1.70
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_[Paraprevotellaceae];g_[Prevotella];s_	0.0072	0.99	1.70
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Parabacteroides	0.0336	1.78	0.56
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Porphyromonadaceae;g_Parabacteroides;s_	0.0262	1.78	0.56
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae	0.0185	1.33	1.83
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella	0.0185	1.33	1.83
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;	0.0106	0.00	0.66
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Rikenellaceae;_;	0.0106	0.00	0.66
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7	0.0185	4.16	4.95
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_	0.0185	4.16	4.95
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_	0.0185	4.16	4.95
_0100	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_	0.0106	0.00	1.24
_0151	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_	0.0334	0.00	0.00
0234	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_S24-7;g_;s_	0.0334	0.00	0.00
	p_Firmicutes	0.0020	6.10	7.13
	p_Firmicutes;c_Bacilli	0.0431	3.87	4.20
	p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae	0.0330	3.17	3.52
	p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus	0.0330	3.17	3.52
	p_Firmicutes;c_Clostridia	0.0431	5.69	5.02
	p_Firmicutes;c_Clostridia;o_Clostridiales	0.0431	5.69	5.02
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae	0.0146	2.02	0.85
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_	0.0250	2.76	1.52
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_;s_	0.0250	2.76	1.52
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coproccoccus	0.0432	2.05	0.00
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Coproccoccus;s_	0.0432	2.05	0.00
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus	0.0071	2.37	0.81
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus;s_	0.0320	2.30	0.00
	p_Firmicutes;c_Erysipelotrichi	0.0012	4.28	6.95
	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales	0.0012	4.28	6.95
	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae	0.0012	4.28	6.95
	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum	0.0012	4.10	6.95
	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum;s_	0.0012	4.10	6.95
	p_Proteobacteria;c_Betaproteobacteria	0.0431	3.03	3.41
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales	0.0031	2.15	2.74
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae	0.0063	0.00	0.82
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Sutterella	0.0063	0.00	0.82
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Alcaligenaceae;g_Sutterella;s_	0.0063	0.00	0.82
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae	0.0330	1.00	1.29
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_	0.0280	0.98	1.27
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Comamonadaceae;g_;s_	0.0280	0.98	1.27
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae	0.0453	1.80	2.27
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Ralstonia	0.0449	1.80	2.27
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Ralstonia;s_	0.0449	1.80	2.27
	p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_	0.0132	0.00	1.31
	p_Proteobacteria;c_Deltaproteobacteria;o_Desulfovibrionales;f_Desulfovibrionaceae;g_;s_	0.0132	0.00	1.31



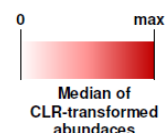
**Supplementary Figure S2:** Bacterial taxa that resulted differently represented among experimental groups in ileum. ASV, Amplicon Sequence Variants. P, statistical significance according to Mann-Whitney test performed on centered log-ratio (CLR)-transformed abundances.

[SD] vs [HFHS]				
ASV	Taxonomy	P	SD	HFHS
0020	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_s	0.0292	1.60	0.00
0058	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_s	0.0292	1.01	0.00
0072	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia;s	0.0048	1.43	0.00
0098	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia;s	0.0105	1.76	0.00
0135	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_Adlercreutzia;s	0.0358	0.62	0.00
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella;s_copri	0.0398	0.00	0.48
	p_Firmicutes;c_Bacilli;o_Gemellales	0.0106	0.00	1.79
	p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae	0.0106	0.00	1.79
	p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae;g	0.0106	0.00	1.79
	p_Firmicutes;c_Bacilli;o_Gemellales;f_Gemellaceae;g_s	0.0106	0.00	1.79
0110	p_Firmicutes;c_Bacilli;o_Lactobacillales;f_Lactobacillaceae;g_Lactobacillus;s	0.0458	1.37	0.00
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Ruminococcus;s_gnavus	0.0304	0.00	2.74
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae	0.0283	2.25	3.61
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Dialister	0.0216	0.00	1.37
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Dialister;s	0.0216	0.00	1.37
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megamonas	0.0252	0.00	2.33
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megamonas;s	0.0252	0.00	2.33
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megasphaera	0.0028	0.00	1.79
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megasphaera;s	0.0028	0.00	1.79
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Phacolarctobacterium	0.0351	0.00	1.91
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Phacolarctobacterium;s	0.0351	0.00	1.91
0001	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum;s	0.0140	3.68	0.00
0004	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum;s	0.0179	3.56	0.00
0008	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum;s	0.0109	3.39	0.00
0009	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum;s	0.0109	3.42	0.00
0024	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum;s	0.0227	2.84	0.00
0030	p_Firmicutes;c_Erysipelotrichi;o_Erysipelotrichales;f_Erysipelotrichaceae;g_Allobaculum;s	0.0084	2.83	0.00
	p_Proteobacteria;c_Deltaproteobacteria;o_Desulfobibrionales;f_Desulfobibrionaceae;g	0.0358	1.11	0.00
	p_Proteobacteria;c_Deltaproteobacteria;o_Desulfobibrionales;f_Desulfobibrionaceae;g_s	0.0358	1.11	0.00
	p_Proteobacteria;c_Gammaproteobacteria	0.0052	2.37	2.88
	p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales	0.0437	0.00	2.06
	p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae	0.0437	0.00	2.06
	p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g	0.0437	0.00	2.06
	p_Proteobacteria;c_Gammaproteobacteria;o_Enterobacteriales;f_Enterobacteriaceae;g_s	0.0437	0.00	2.06
	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Moraxella	0.0357	0.00	0.33
	p_Proteobacteria;c_Gammaproteobacteria;o_Pseudomonadales;f_Moraxellaceae;g_Moraxella;s	0.0357	0.00	0.33

[SD] vs [HFHS+Zn-SP]				
ASV	Taxonomy	P	SD	HFHS+Zn-SP
	p_Actinobacteria	0.0262	6.99	3.57
	p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae	0.0407	0.00	0.95
	p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces	0.0407	0.00	0.95
	p_Actinobacteria;c_Actinobacteria;o_Actinomycetales;f_Actinomycetaceae;g_Actinomyces;s	0.0407	0.00	0.95
	p_Actinobacteria;c_Coriobacteriia	0.0379	3.74	2.91
	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales	0.0379	3.74	2.91
	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae	0.0379	3.74	2.91
	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g	0.0474	3.04	1.71
	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales;f_Coriobacteriaceae;g_s	0.0474	3.04	1.71
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f	0.0238	0.00	0.40
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_g	0.0238	0.00	0.40
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_g_s	0.0238	0.00	0.40
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales;f_Prevotellaceae;g_Prevotella;s	0.0338	0.63	0.00
	p_Firmicutes;c_Clostridia	0.0379	5.01	5.81
	p_Firmicutes;c_Clostridia;o_Clostridiales	0.0379	5.01	5.81
	p_Firmicutes;c_Clostridia;o_Clostridiales;f	0.0262	4.10	4.73
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_g	0.0262	4.10	4.73
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_g_s	0.0262	4.10	4.73
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Clostridiaceae	0.0282	0.00	0.83
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea	0.0199	0.00	1.56
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Lachnospiraceae;g_Dorea;s	0.0199	0.00	1.56
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae	0.0379	3.61	4.82
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira	0.0387	0.00	3.96
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Oscillospira;s	0.0387	0.00	3.96
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus	0.0330	0.93	2.45
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Ruminococcaceae;g_Ruminococcus;s	0.0263	0.00	2.45
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megasphaera	0.0407	0.00	0.66
	p_Firmicutes;c_Clostridia;o_Clostridiales;f_Veillonellaceae;g_Megasphaera;s	0.0407	0.00	0.66
0105	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales;f_Oxalobacteraceae;g_Ralstonia;s	0.0407	0.00	1.99



[HFHS] vs [HFHS+Zn-SP]			
ASV	Taxonomy	P	HFHS HFHS+Zn-SP
0072	p_Actinobacteria	0.0072	6.36 3.57
	p_Actinobacteria;c_Coriobacteriia;o_Coriobacteriales,f_Coriobacteriaceae,g_Adlercreutzia;s	0.0292	0.00 0.81
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_	0.0135	0.00 0.40
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_;g_	0.0135	0.00 0.40
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_;g_;s_	0.0135	0.00 0.40
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_Bacteroidaceae,g_Bacteroides;s_fragilis	0.0375	1.53 0.06
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_Prevotellaceae	0.0037	2.03 1.34
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_Prevotellaceae,g_Prevotella	0.0026	2.03 1.31
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_Prevotellaceae,g_Prevotella;s_melaninogenica	0.0221	1.40 1.10
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_Rikenellaceae	0.0358	2.02 3.48
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_Rikenellaceae,g_	0.0358	2.02 3.48
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_Rikenellaceae,g_;s_	0.0358	2.02 3.48
	p_Bacteroidetes;c_Bacteroidia;o_Bacteroidales,f_S24;7;g_;s_	0.0497	0.00 0.58
	p_Firmicutes;c_Bacilli;o_Bacillales	0.0449	1.62 1.17
	p_Firmicutes;c_Bacilli;o_Bacillales,f_Bacillaceae	0.0283	1.53 1.17
0100	p_Firmicutes;c_Bacilli;o_Bacillales,f_Bacillaceae,g_Bacillus	0.0283	1.53 1.17
	p_Firmicutes;c_Bacilli;o_Bacillales,f_Bacillaceae,g_Bacillus;s_	0.0311	1.53 1.17
	p_Firmicutes;c_Bacilli;o_Gemellales	0.0381	1.79 0.62
	p_Firmicutes;c_Bacilli;o_Gemellales,f_Gemellaceae	0.0381	1.79 0.62
	p_Firmicutes;c_Bacilli;o_Gemellales,f_Gemellaceae,g_	0.0381	1.79 0.62
	p_Firmicutes;c_Bacilli;o_Gemellales,f_Gemellaceae,g_;s_	0.0381	1.79 0.62
	p_Firmicutes;c_Clostridia;o_Clostridiales,f_Peptococcaceae,g_Desulfosporosinus	0.0497	0.00 0.51
	p_Firmicutes;c_Clostridia;o_Clostridiales,f_Peptococcaceae,g_Desulfosporosinus;s_meridiei	0.0497	0.00 0.51
	p_Firmicutes;c_Clostridia;o_Clostridiales,f_Veillonellaceae	0.0449	3.61 2.29
	p_Firmicutes;c_Clostridia;o_Clostridiales,f_Veillonellaceae,g_Dialister	0.0351	1.37 0.00
	p_Firmicutes;c_Clostridia;o_Clostridiales,f_Veillonellaceae,g_Dialister;s_	0.0351	1.37 0.00
	p_Fusobacteria	0.0283	2.07 1.49
	p_Fusobacteria;c_Fusobacteriia	0.0283	2.07 1.49
	p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales	0.0283	2.07 1.49
	p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales,f_Fusobacteriaceae	0.0221	2.07 1.49
0105	p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales,f_Fusobacteriaceae,g_Fusobacterium	0.0221	2.07 1.49
	p_Fusobacteria;c_Fusobacteriia;o_Fusobacteriales,f_Fusobacteriaceae,g_Fusobacterium;s	0.0221	2.07 1.49
	p_Proteobacteria;c_Alphaproteobacteria	0.0451	0.96 1.31
	p_Proteobacteria;c_Alphaproteobacteria;o_RF32	0.0351	0.00 0.89
	p_Proteobacteria;c_Alphaproteobacteria;o_RF32,f_	0.0351	0.00 0.89
	p_Proteobacteria;c_Alphaproteobacteria;o_RF32,f_;g_	0.0351	0.00 0.89
	p_Proteobacteria;c_Alphaproteobacteria;o_RF32,f_;g_;s_	0.0351	0.00 0.89
	p_Proteobacteria;c_Betaproteobacteria;o_Burkholderiales,f_Oxalobacteraceae,g_Ralstonia;s_	0.0072	0.00 1.99
	p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales,f_Pasteurellaceae,g_Haemophilus	0.0358	1.87 1.32
	p_Proteobacteria;c_Gammaproteobacteria;o_Pasteurellales,f_Pasteurellaceae,g_Haemophilus;s_parainfluenzae	0.0358	1.87 1.32



**Supplementary Figure S3:** The abundances of Rikenellaceae and Veilonellaceae in the ileum of HFHS and HFHS+Zn-SP mice are illustrated. The centered log-ratio (CLR)-transformed abundances are presented for each family, along with their respective ratios. In one ileum sample both Rikenellaceae and Veilonellaceae were not detected (indicated in red); therefore, this sample was not considered in ratio calculations. Statistics is according to Mann-Whitney test; \*\*,  $P<0.01$ ; \*\*\*,  $P<0.001$ ; \*\*\*\*,  $P<0.0001$ .

