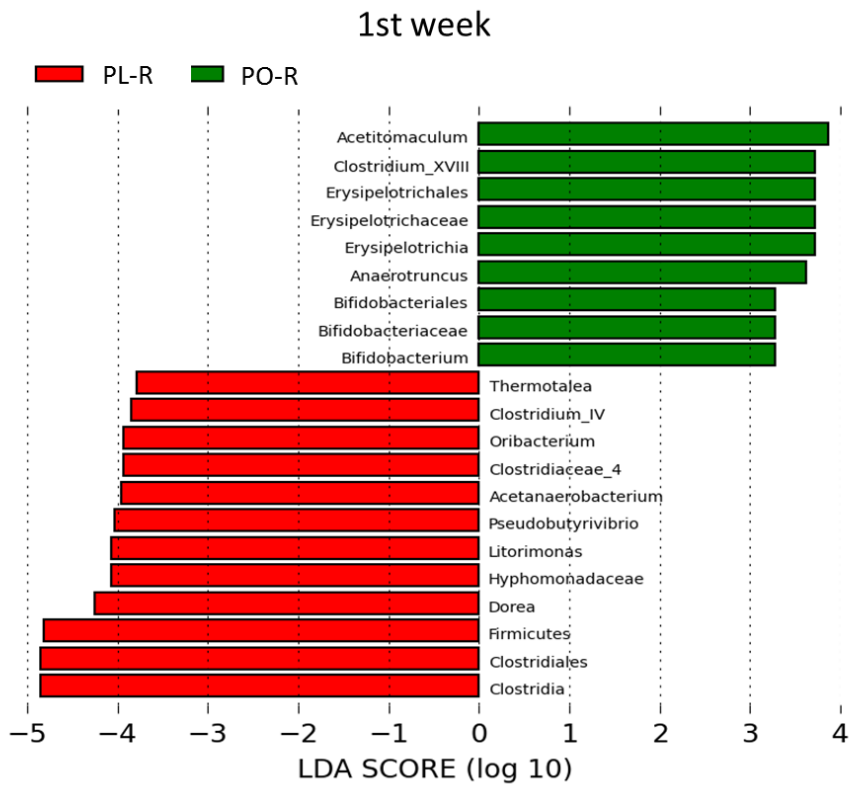


Supplementary information

High fat diet drives obesity regardless the composition of gut microbiota in mice

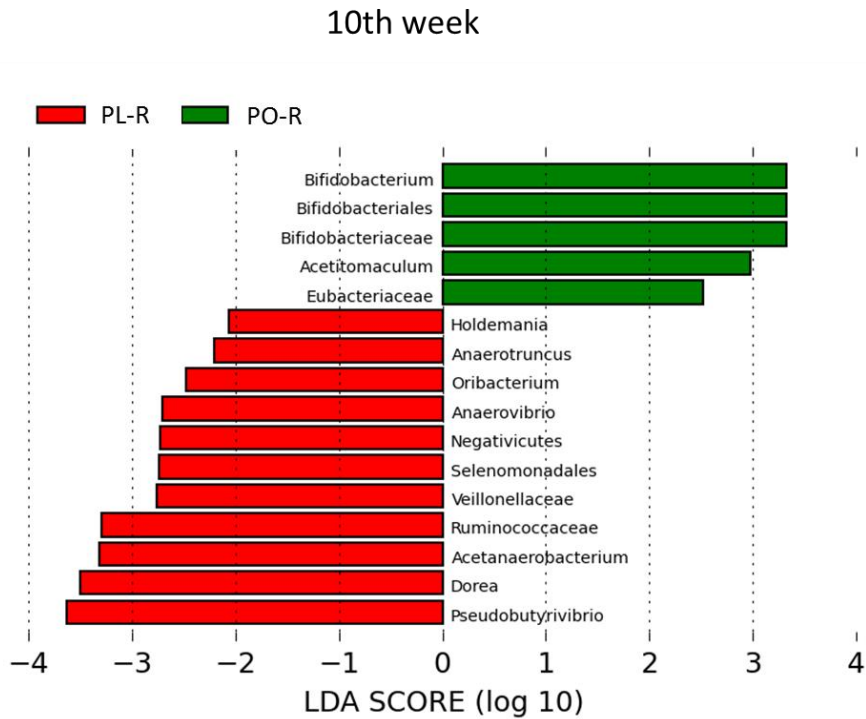
Sylvie Rabot¹, Mathieu Membrez², Florence Blancher², Bernard Berger², Déborah Moine^{2,3}, Lutz Krause^{2,4},
Rodrigo Bibiloni^{2,5}, Aurélia Bruneau¹, Philippe Gérard¹, Jay Siddharth³, Christian L. Lauber³ and Chieh
Jason Chou^{2,3*}

Supplementary figure S1: Fecal microbiota comparison of PL-R and PO-R mice after one week of HF feeding



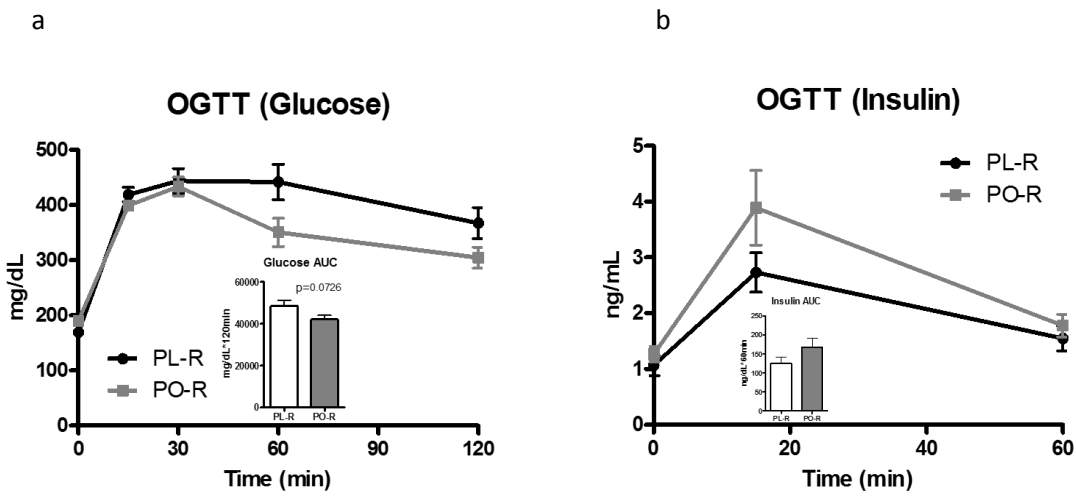
Germfree mice received the transplantation of the PL or PO microbiota and a high fat diet. Fecal samples of PL-R and PO-R mice were collected in 1 week after microbiota transplantation. Comparison of fecal microbiota was performed with LDA effect size (LEfSe). The red area indicates the over-abundance in PL-R microbiota where the green area indicated the over-abundance in PO-R microbiota.

Supplementary figure S2: Fecal microbiota comparison of PL-R and PO-R mice after 10 weeks of HF feeding



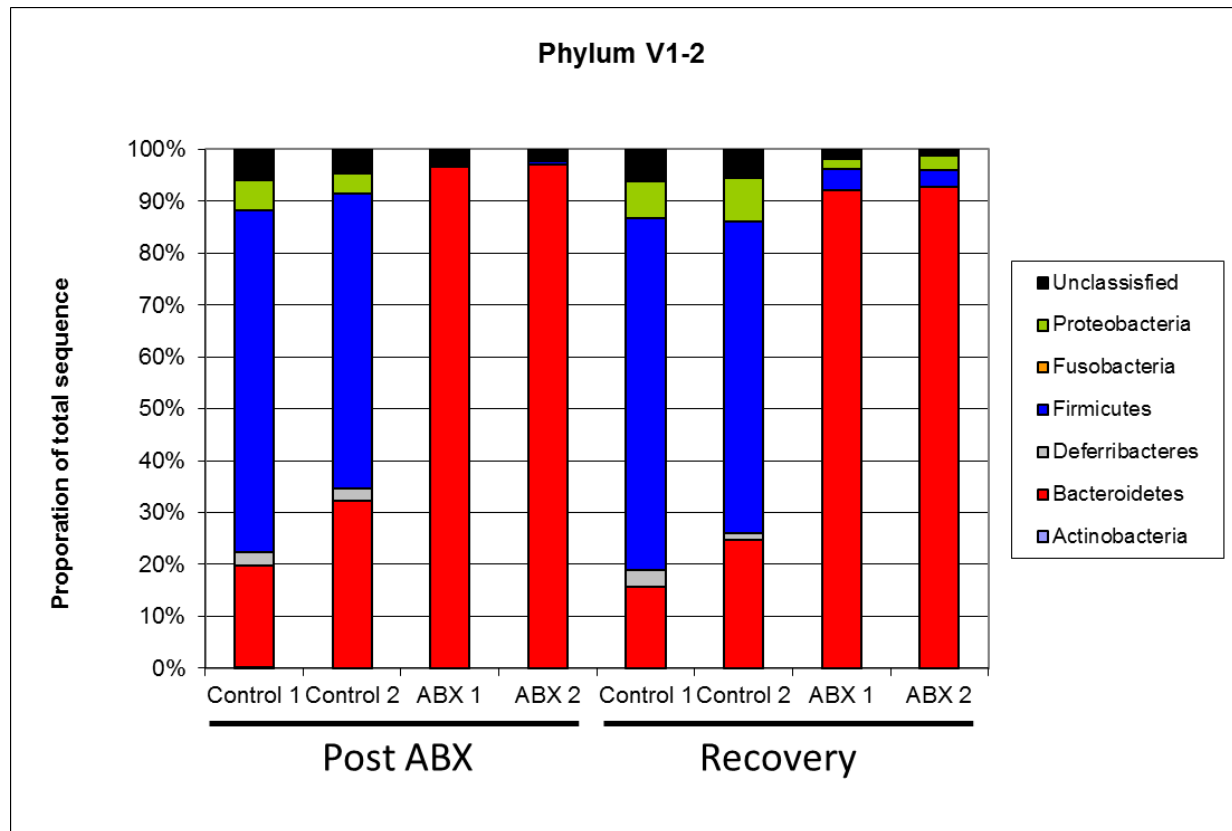
Microbiota composition of PL-R and PO-R mice after 10 weeks HF feeding. Comparison of fecal microbiota was performed with LDA effect size (LEfSe). The red area indicates the over-abundance in PL-R microbiota where the green area indicated the over-abundance in PO-R microbiota.

Supplementary figure S3: Oral glucose tolerance of PL-R and PO-R mice



Oral glucose tolerance test was performed after 10 weeks HF feeding. After 6 hours fasting, a bolus of glucose (2 g/kg) was gavaged to PL-R and PO-R mice and glucose (a) and insulin (b) concentrations are shown. The inserts are area under the glucose and insulin curves. Data are mean \pm s.e.m., n=12/group. P=0.0726 by unpaired t-test when comparing glucose area under the curve or PL-R and PO-R mice.

Supplementary figure S4: Microbiota composition of the antibiotic treated DIO mice



The V1-2 region of bacterial 16S rDNA genes were sequenced and the abundance of bacterial phyla is shown. DIO mice received either a combination of polymyxin B (0.5 g/L) and neomycin (1.0 g/L) in drinking water (ABX) or normal drinking water (Control) for two weeks. Caecal samples were taken from two mice in each group at the end of 2 weeks treatment period (post ABX) and at 4 weeks after the termination of the treatment (Recovery) for microbiota measurement.

Taxon	V4 NR10	V4 NR11	V4 NR12	V4 NR13	V4 NR14	V4 NR15	V4 NR1	V4 NR2	V4 NR3	V4 NR4	V4 NR5	V4 NR6	V4 NR7	V4 NR8	V4 RR10	V4 RR12	V4 RR13	V4 RR14	V4 RR15	V4 RR16	V4 RR2	V4 RR3	V4 RR4	V4 RR5	V4 RR6	V4 RR7	V4 RR8	V4 RR9
Actinobacteria	1	14	12	0	1	4	1	8	16	14	4	25	2	5	4	1	1	6	13	6	5	0	0	6	9	1	1	7
Bacteroidia	213	228	190	77	124	133	31	100	218	789	183	1814	48	170	132	120	143	257	171	486	350	63	76	467	386	143	142	171
Sphingobacteria	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Deferribacteres	36	52	58	35	76	26	18	36	87	177	41	431	9	34	37	42	63	76	84	150	68	77	15	78	188	28	26	54
Bacilli Bacilli	2	18	1	1	2	2	1	4	11	39	5	56	0	1	1	1	4	3	4	11	48	4	0	4	7	6	9	4
Clostridia	717	965	881	370	859	476	143	507	409	2113	582	5637	250	498	766	611	659	1193	660	2163	1685	596	311	1952	2993	502	562	678
Erysipelotrichi	12	127	250	22	105	67	5	162	481	408	98	600	38	73	129	97	85	122	297	399	271	9	59	221	210	87	25	247
Alphaproteobacteria	0	0	1	0	0	0	0	0	0	0	0	4	0	0	0	1	0	0	0	0	0	0	0	2	1	0	0	0
Betaproteobacteria	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Deltaproteobacteria	23	31	37	16	39	24	5	23	16	133	42	260	15	25	32	24	41	49	21	91	37	22	7	77	112	20	14	53
Gammaproteobacteria	1	1	0	7	0	0	0	1	1	1	19	4	10	0	0	0	1	2	0	0	4	1	0	0	1	0	3	0
Verrucomicrobiae	0	0	0	0	0	0	0	0	9	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
Unclassified	30	36	27	9	13	18	4	15	18	79	16	264	12	21	25	8	22	32	24	60	60	10	9	61	73	18	24	30

Supplementary table S2

Microbiota composition of antibiotics treated and untreated mice.

Diet-induced obesity mice were treated with a mixture of polymyxin B and neomycin in drinking water for 2 weeks. Mice were sacrificed at the end of treatment and caecal contents were used for DNA extraction (post ABX group). In parallel, another group of mice was kept for additional 4 weeks without antibiotics (Recovery group) and their caecal contents were harvest for the DNA preparation. PCR was performed using primers specific to the V1-2 region of bacterial 16S rDNA gene. The resulting amplicons were sequenced using the GS FLX System. After removing the low quality reads, remaining sequences were classified using the RDP-Classifer (80% confidence cut-off). Results are presented at phylum, family and genus levels.

RDP Classifications			V12	V12	V12	V12	V12	V12	V12	V12
Rank	Full	Taxon	Post ABX				Recovery			
			Control 1	Control 2	ABX 1	ABX 2	Control 1	Control 2	ABX 1	ABX 2
Phylum	Root Bacteria Actinobacteria	Actinobacteria	5	0	0	0	0	0	1	0
Phylum	Root Bacteria Bacteroidetes	Bacteroidetes	477	509	2065	1971	229	578	1970	1814
Phylum	Root Bacteria Deferribacteres	Deferribacteres	65	36	0	0	49	26	0	0
Phylum	Root Bacteria Firmicutes	Firmicutes	1606	896	6	13	996	1401	85	64
Phylum	Root Bacteria Fusobacteria	Fusobacteria	0	0	0	0	0	0	0	0
Phylum	Root Bacteria Proteobacteria	Proteobacteria	140	63	0	0	106	194	41	52
Phylum	Unclassified	Unclassified	146	72	64	45	89	129	41	25
		Total	2439	1576	2135	2029	1469	2328	2138	1955

RDP Classifications			V12	V12	V12	V12	V12	V12	V12	V12
Rank	Full	Taxon	Post ABX				Recovery			
			Control 1	Control 2	ABX 1	ABX 2	Control 1	Control 2	ABX 1	ABX 2
Genus	Root Bacteria Actinobacteria Actinobacteria Bifidobacteriales Bifidobacteriaceae Bifidobacterium	Actinobacteria Bifidobacterium	4	0	0	0	0	0	0	0
Genus	Root Bacteria Bacteroidetes Bacteroidetes Bacteroidales Bacteroidaceae Bacteroides	Bacteroidetes Bacteroides	104	275	1835	1724	55	189	1510	1557
Genus	Root Bacteria Bacteroidetes Bacteroidetes Bacteroidales Porphyromonadaceae Parabacteroides	Bacteroidetes Parabacteroides	8	15	103	165	5	14	225	163
Genus	Root Bacteria Bacteroidetes Bacteroidetes Bacteroidales Prevotellaceae Prevotella	Bacteroidetes Prevotella	0	0	0	0	0	0	1	0
Genus	Root Bacteria Bacteroidetes Bacteroidetes Bacteroidales Rikenellaceae Alistipes	Bacteroidetes Alistipes	199	124	103	61	112	260	211	84
Genus	Root Bacteria Deferribacteres Deferribacteres Deferribacterales Deferribacteraceae Mucispirillum	Deferribacteres Mucispirillum	65	36	0	0	49	26	0	0
Genus	Root Bacteria Firmicutes Bacilli Bacillales Staphylococcaceae Staphylococcus	Firmicutes Staphylococcus	0	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Bacilli Lactobacillales Enterococcaceae Enterococcus	Firmicutes Enterococcus	0	0	1	2	0	0	0	2
Genus	Root Bacteria Firmicutes Bacilli Lactobacillales Lactobacillaceae Lactobacillus	Firmicutes Lactobacillus	1	6	1	0	1	1	3	0
Genus	Root Bacteria Firmicutes Bacilli Lactobacillales Leuconostocaceae Weissella	Firmicutes Weissella	1	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Bacilli Lactobacillales Streptococcaceae Lactococcus	Firmicutes Lactococcus	1	0	0	6	3	1	4	19
Genus	Root Bacteria Firmicutes Bacilli Lactobacillales Streptococcaceae Streptococcus	Firmicutes Streptococcus	0	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales IncertaeSedisXIII Anaerovorax	Firmicutes Anaerovorax	4	0	0	0	3	1	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Anaerostipes	Firmicutes Anaerostipes	0	0	2	0	0	0	2	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Butyrivibrio	Firmicutes Butyrivibrio	1	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Dorea	Firmicutes Dorea	1	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Johnsonella	Firmicutes Johnsonella	0	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Lachnospiraceae Roseburia	Firmicutes Roseburia	1	1	0	0	34	0	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Anaerotruncus	Firmicutes Anaerotruncus	0	1	0	0	3	6	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Faecalibacterium	Firmicutes Faecalibacterium	3	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Sporobacter	Firmicutes Sporobacter	0	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Ruminococcaceae Subdoligranulum	Firmicutes Subdoligranulum	1	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Clostridia Clostridiales Veillonellaceae Megasphaera	Firmicutes Megasphaera	0	0	0	0	0	1	0	0
Genus	Root Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Allobaculum	Firmicutes Allobaculum	0	0	0	0	0	0	0	0
Genus	Root Bacteria Firmicutes Erysipelotrichi Erysipelotrichales Erysipelotrichaceae Catenibacterium	Firmicutes Catenibacterium	0	0	0	0	0	1	0	0
Genus	Root Bacteria Fusobacteria Fusobacteria Fusobacteriales Fusobacteriaceae Fusobacterium	Fusobacteria Fusobacterium	0	0	0	0	0	0	0	0
Genus	Root Bacteria Proteobacteria Deltaproteobacteria Desulfovibrionales Desulfovibrionaceae Bilophila	Proteobacteria Bilophila	132	57	0	0	101	183	0	0
Genus	Root Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae Citrobacter	Proteobacteria Citrobacter	0	0	0	0	0	0	0	1
Genus	Root Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae Enterobacter	Proteobacteria Enterobacter	0	0	0	0	0	0	4	2
Genus	Root Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae Klebsiella	Proteobacteria Klebsiella	0	0	0	0	0	0	0	0
Genus	Root Bacteria Proteobacteria Gammaproteobacteria Enterobacteriales Enterobacteriaceae Shigella	Proteobacteria Shigella	0	0	0	0	0	0	0	0
Genus	Unclassified	Unclassified	1913	1061	90	71	1103	1645	178	127
		Total	2439	1576	2135	2029	1469	2328	2138	1955