

Fig. S1. Indices of bacterial diversity obtained from cecum contents samples (n=4). (A) Rarefaction curve; (B) Rank-Abundance; (C) Chao1 index; (D) Shannon index.

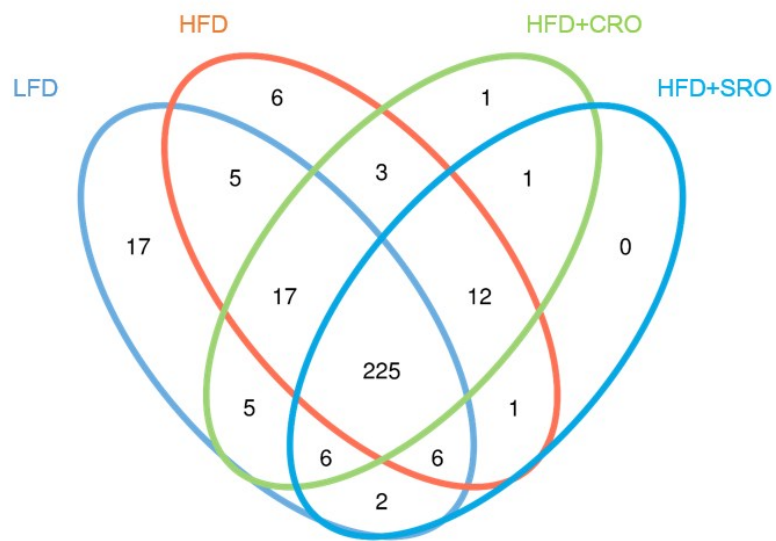


Fig. S2. Overlap and differences of gut microbiota in four groups. The plot was based on operational taxonomic unit (OTUs) detected in all samples.

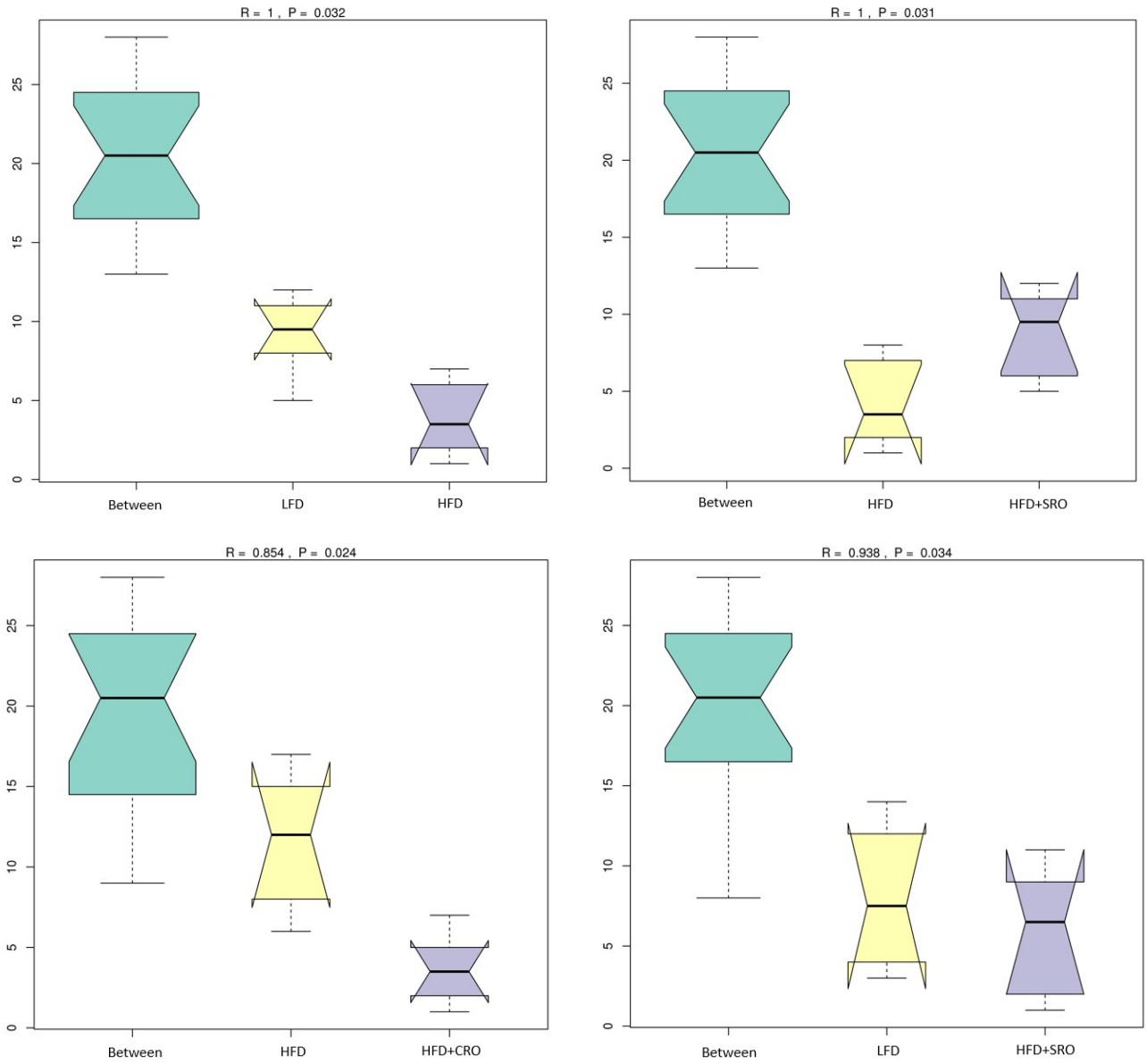
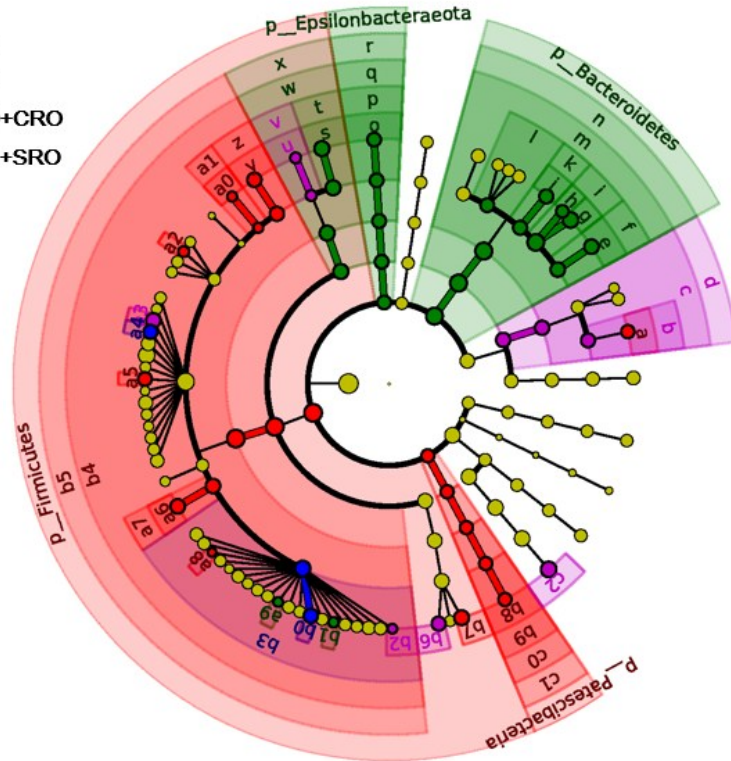


Fig. S3. Inter-group difference analysis by ANOSIM. A value of R close to 1 indicates that the difference between the groups is larger than the difference within the group, and $P < 0.05$ indicates that the statistics are significant.

A

Cladogram

- HFD
- LFD
- HFD+CRO
- HFD+SRO



- a: g_Coriobacteriaceae_UCG_002
- b: f_Atopobiaceae
- c: o_Coriobacteriales
- d: c_Coriobacteria
- e: g_Bacteroides
- f: f_Bacteroidaceae
- g: g_Ambiguous_taxa
- h: g_Muribaculum
- i: f_Muribaculaceae
- j: g_Alloprevotella
- k: f_Prevotellaceae
- l: f_Rikenellaceae
- m: o_Bacteroidales
- n: c_Bacteroidia
- o: g_Helicobacter
- p: f_Helicobacteraceae
- q: o_Campylobacterales
- r: c_Campylobacteria
- s: g_Lactobacillus
- t: f_Lactobacillaceae
- u: g_Streptococcus
- v: f_Streptococcaceae
- w: o_Lactobacillales
- x: c_Bacilli
- y: g_Clostridium_sensu_stricto_1
- z: f_Clostridiaceae_1
- a0: g_Defluviitaleaceae_UCG_011
- a1: f_Defluviitaleaceae
- a2: g_Family_XIII_UCG_001
- a3: g_Blautia
- a4: g_GCA_900066575
- a5: g_Lachnospiraceae_UCG_006
- a6: g_Romboutsia
- a7: f_Peptostreptococcaceae
- a8: g_Candidatus_Soleaferrea
- a9: g_Ruminiclostridium_1
- b0: g_Ruminiclostridium_9
- b1: g_Ruminococcaceae_UCG_009
- b2: g_UBA1819
- b3: f_Ruminococcaceae
- b4: o_Clostridiales
- b5: c_Clostridia
- b6: g_Dubosiella
- b7: g_Faecalibaculum
- b8: g_Candidatus_Saccharimonas
- b9: f_Saccharimonadaceae
- c0: o_Saccharimonadales
- c1: c_Saccharimonadia
- c2: g_Desulfovibrio

B

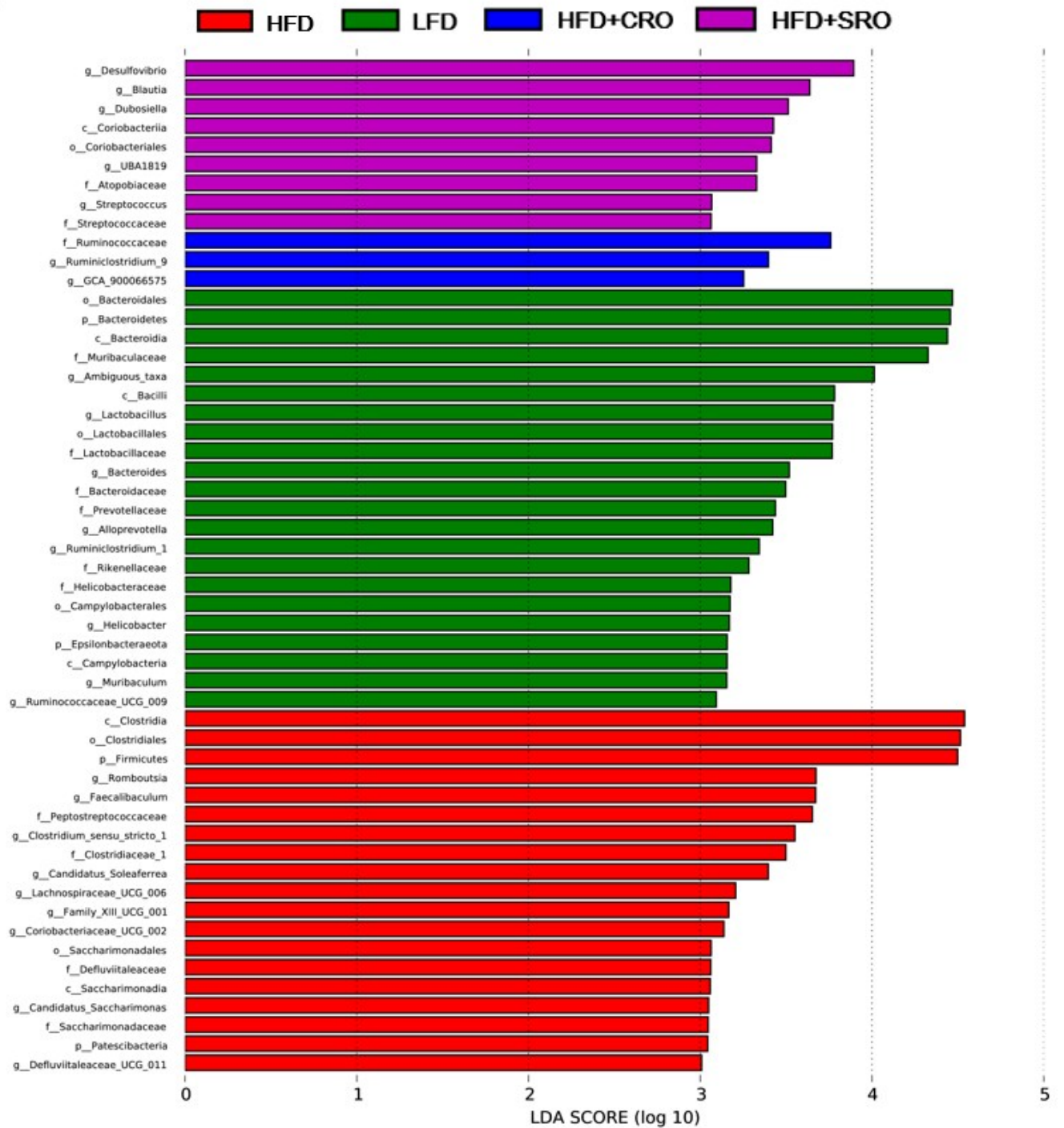


Fig. S4. LefSe analysis of key genera of gut microbiota in mice. (A) Taxonomic cladogram derived from LefSe analysis of 16S rRNA sequences. (B) LDA score plot of bacterial taxa with LDA scores higher than 3.

Table S1

The sequencing reads for the fecal microbiota.

Sample	Reads	Nochimera	AvgLen (bp)	GC (%)
LFD_1	70982	47982	450.06	54.25
LFD_2	80287	56755	452.82	54.57
LFD_3	70229	48031	452.47	54.53
LFD_4	62304	43991	449.78	54.46
HFD_1	52509	45708	443.57	54.59
HFD_2	63263	53635	444.34	54.43
HFD_3	64538	52016	449.23	54.77
HFD_4	62985	53958	445.35	54.92
HFD+CRO_1	72244	46699	446.27	54.99
HFD+CRO_2	70926	46487	446.75	54.55
HFD+CRO_3	72419	51289	443.46	54.52
HFD+CRO_4	68514	44962	446.06	54.3
HFD+SRO_1	61599	41754	448.89	54.94
HFD+SRO_2	63630	41201	447.95	55.04
HFD+SRO_3	62204	41603	449.33	55.52
HFD+SRO_4	62595	45894	444.74	55.28
Total	1061228			

Table S2

Statistics of OTU sequence numbers of each sample.

OTU_ID	LFD_1	LFD_2	LFD_3	LFD_4	HFD_1	HFD_2	HFD_3	HFD_4	HFD+C	HFD+C	HFD+C	HFD+C	HFD+S	HFD+S	HFD+S	HFD+S
									RO_1	RO_2	RO_3	RO_4	RO_1	RO_2	RO_3	RO_4
OTU1	6026	2231	3771	5427	5339	1955	198	3245	195	155	104	75	5276	1455	3043	9312
OTU2	917	1684	1566	1387	1359	904	1350	1400	3819	2958	2173	2584	4288	3239	6303	1799
OTU3	1085	829	871	815	469	1110	1993	935	2148	2047	1085	1635	1504	2876	1897	1008
OTU4	0	3	6	3	1	3363	304	2333	4147	2485	2973	3787	2	1341	928	2
OTU5	500	3646	1285	842	1326	1224	3460	2171	811	299	158	221	817	245	951	392
OTU9	0	4	25	1	32	2262	0	174	1817	3148	3625	2992	47	829	495	0
OTU12	322	485	626	605	494	1227	2547	1751	716	840	261	428	891	856	1014	491
OTU7	688	2851	4120	1338	315	74	57	197	129	44	7	225	2009	189	161	1149
OTU18	483	857	503	306	1481	517	671	820	1010	735	786	606	1073	602	598	1459
OTU6	1	1	1	0	1894	1072	1656	1540	1090	519	734	678	1295	437	266	935
OTU11	67	88	47	89	495	1836	383	447	211	780	1867	382	154	3340	597	1298
OTU15	0	2	25	42	1	1081	139	1178	1493	1786	2251	958	0	37	45	2
OTU16	829	1038	1257	1155	0	0	0	1	711	2186	702	1417	0	0	0	0
OTU27	1466	1762	2206	2133	24	195	215	48	0	2	3	0	203	294	254	41
OTU17	413	194	210	1150	15	196	16	28	1642	600	771	1318	981	116	927	5
OTU52	1667	1112	1546	1025	0	30	3	0	1	2	1	0	570	884	931	522
OTU41	114	67	80	89	134	699	1700	368	755	1060	750	1222	263	276	230	84
OTU14	3	0	0	0	1229	851	1893	412	1321	343	638	468	105	16	63	5
OTU29	457	544	190	387	1801	455	216	805	243	231	319	442	336	193	344	420
OTU13	193	1412	746	447	190	166	483	427	866	168	95	194	816	126	409	391
OTU22	145	242	245	557	1926	783	327	531	66	292	240	141	144	386	154	825
OTU10	4	4	2	10	192	1387	24	251	696	830	1417	314	270	430	64	713
OTU91	1036	700	1032	725	0	0	0	0	355	315	85	328	406	658	561	466
OTU56	1092	605	1072	678	0	1	0	1	351	316	109	362	384	693	576	440
OTU50	169	129	178	238	133	321	502	188	630	956	1349	1079	167	145	146	58
OTU48	696	504	746	544	94	224	633	223	161	322	149	184	220	329	340	164

