Retinitis pigmentosa is associated with shifts in the gut microbiome

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Supplementary Table S1. Number of reads variation previous to QIIME2 analysis.

Sample name	No. Raw Sequenced reads	No. Reads after QC	No. Joined reads
C57.25	F: 157704	F: 156314	133979
	R: 157704	R: 156314	
C57.26	F: 120828	F: 119283	94596
	R: 120828	R: 119283	
C57.27	F: 110848	F: 109902	93635
	R: 110848	R: 109902	
C57.32	F: 115625	F: 114685	98528
	R: 115625	R: 114685	
rd10.88	F: 125328	F: 124248	108651
	R: 125328	R: 124248	
rd10.89	F: 98154	F: 97336	84398
	R: 98154	R: 97336	
rd10.102	F: 101379	F: 100547	85878
	R: 101379	R: 100547	
rd10.109	F: 130339	F: 129309	114404
	R: 130339	R: 129309	

For the 8 samples tested (4 from C57BL/6J mice and 4 from rd10 mice): Number (No.) of reads decrease from sequenced raw reads (No. Raw Sequenced reads) to merged reads with FLASH (No. Joined reads) [1], including the passing reads of the quality filtering step performed with prinseq-lite (No. Reads after QC) [2]. F: Forward Read. R: Reverse Read.

Supplementary Table S2. Deblur denoising statistics.

Sample	Reads	Filtered reads	Percentage of input passed filter	Denoised	Chimeras	No. of final Reads	% of reads that passed the denoiser	No. ASV found
C57.25	133904	86027	64.25	50360	1408	48952	36.56	94
C57.26	94555	60103	63.56	33873	1720	32153	34.00	92
C57.27	93592	54585	58.32	34085	767	33318	35.60	96
C57.32	98477	55385	56.24	35569	320	35249	35.79	94
rd10.102	85821	53760	62.64	36889	1338	35551	41.42	84
rd10.109	114339	65513	57.30	42684	708	41976	36.71	88
rd10.88	108599	76453	70.40	48081	1771	46310	42.64	83
rd10.89	84350	51617	61.19	35118	2151	32967	39.08	88

Deblur [3] denoiser' s effect in different samples (C57BL/6J and rd10 mice). The input (Reads input) was filtered, removing singletons and artifacts (Filtered reads passed). Then, reads were denoised (Denoised), the chimeras were found and eliminated (Chimeras), to produce the final reads count (No. of final Reads), and the % of the final reads compared with the initial input (% of reads that passed the denoiser). Last column shows the number of ASV found in each sample (No. ASV found).

Supplementary Table S3. Unique ASV and relative abundance.

SILVA 138 Classification	**ASV ID**	**Relative abundance c57 (%)**	**Relative abundance rd10 (%)**
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	8fe55c3953a92b957f64876d03aed609	0	6,85323601
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	4b439e9677e560cbf2178aa2a0c1be47	0	2,36829362
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	f12afab62c73afc04a7671678ef9de96	0	1,68562908
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	a5d25160ed7029c3aaa6a1a68372f63f	0	0,83425545
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides; s__Bacteroides_caecimuris	4a178a9e45c6faf13bdadbd53a4f2028	0	0,70306996
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Marinifilaceae; g__Odoribacter	003eb23d0c6f66f14a53fdd762abe6e9	0	0,69504002
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	32e289e3b1914406c8f7fc140c216d61	0	0,50655507
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	dc9f79ac9e6f880da114f520a216e45e	0	0,4446846
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	515255b61da63b9e602b78270f3f4dad	0	0,39556033
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	5784fa5805f604f9472e5676e2f881c7	0	0,3314337
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	efe3ee8ed5ea37809f29b5943742dfed	0	0,29768771
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	302a42730df2ccd3c661841b6421f30a	0	0,28187409
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	c3a6d64ff6f5672832fa1393194ac562	0	0,26233929
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	d4847c37d6e999e9f1398b34d26e8b92	0	0,25075174
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group	0e370fd4ec92f50c541e5572b562a397	0	0,19086114

d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	d17d221a71fcfb3cf0e3d5a13438ee2f	0	0,17222883
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	0d293735d22331898a4413a8d43a8806	0	0,16187567
d__Bacteria; p__Firmicutes; c__Bacilli; o__Staphylococcales; f__Staphylococcaceae; g__Staphylococcus	f79a13aeeb02307eac37dae9c73fb26a	0	0,11256413
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Enterococcaceae; g__Enterococcus	1a5b347c9d6b40bff9b504d7126e5b19	0	0,08910462
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	2590da681572248f1046446ebb810538	0	0,08670496
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	e33516650520a532b7f62148db647207	0	0,08629969
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	5487a84271b262185804ed07cd015753	0	0,07758391
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotellaceae_UCG-001; s__uncultured_bacterium	c7a5584ad3e77067f7c1587fa16e2037	0	0,07588774
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	8708905fa4617d0071a59b7829baa4e2	0	0,07043285
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	a6e24cf4ebe57d3b2d30de7fd3182f7c	0	0,06440346
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	dfda03b9b3de00a1929a737fb4ebeafa	0	0,06316064
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Marinifilaceae; g__Odoribacter; s__uncultured_bacterium	dfa994441b74f436d590e3e612929930	0	0,060749
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	6651d3d542a93c649aa39448ca8ee015	0	0,05657995
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	b0c501d54eae1676b5820a1238051360	0	0,04861066
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	54ddc8458d991fce45d039ea11be41ec	0	0,04149265
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	34a77af51d3dbc2e93ef09af2805ce8c	0	0,03972629

d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group; s__uncultured_bacterium	73612fb29191406b37ff36b0db4d44ba	0	0,03156566
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	69494f3650ae0fd8a0319c72b9aca342	0	0,02348169
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	0e815c6449e618b4da0fce6a96c6aad7	0	0,0220364
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	fb89b85997d260628c126c5718b84635	0	0,02105411
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae	01f5b34acc5a84f0b40314f6416bcb76	0	0,01608062
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group	f97ebde97cd04fdc3a882088b76f0ca6	0	0,01310273
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	c862d7e33284897b9583e48965f02f51	0	0,01265787
d__Bacteria; p__Firmicutes; c__Bacilli; o__Staphylococcales; f__Staphylococcaceae; g__Jeotgalicoccus	61846f6550679f1eef066723da13f7c8	0	0,01223422
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	5ea89ed231e3db9b2f5d4b718660ae6d	0	0,01012483
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	4990c0d22cc0fde25bacb3429d9a3f52	0	0,00984501
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__Turicibacter; s__uncultured_bacterium	f8e53fb45dd0bf3f6e053cedc4c207ae	0	0,00984501
d__Bacteria; p__Firmicutes; c__Clostridia	b37e76a9cf11e9d60457135e84e5713e	0	0,00952421
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	9325c913e0755dd75ac1271ca5d7b7f6	0	0,00875308
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	ca913340b37d7733139efb464c47fb21	0	0,00774252
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae	8cb99e773f716c1342f9cfbc29479a0a	0	0,00665226
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae	584ef1f217e3bc89457c06a00d048107	0	0,00655136
d__Bacteria; p__Firmicutes; c__Bacilli; o__Erysipelotrichales; f__Erysipelotrichaceae; g__uncultured; s__unidentified	3188c1bdeddaeb3a625004b41b01ff4d	0	0,00627238
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae	74c52127c1bea3f1f94c58f21ca00558	0	0,00605388

d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	452433a28f3bbc3f70da063824cd6bbf	0,00777532	0
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptococcales; f__Peptococcaceae; g__uncultured; s__uncultured_bacterium	861c32723edae1ab3abb31f7e3469514	0,00801774	0
d__Bacteria; p__Firmicutes; c__Clostridia; o__Peptococcales; f__Peptococcaceae; g__uncultured; s__unidentified	0a8dc3b5bb8df0eb1834f3aed9744e95	0,00804827	0
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group	2bd246c6114e43805cd8c6c6320b8991	0,00817127	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	81a5a5e5b7fe8650536683ab8c439c2d	0,01059063	0
d__Bacteria; p__Firmicutes; c__Bacilli; o__RF39; f__RF39; g__RF39; s__uncultured_bacterium	df8a6e092c5a3d2f3993c34108287999	0,0106386	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	a0009e240781ae79fffd5f9e560b96b3	0,01260895	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	bf4c38add9b7b73e53d4a0ecfb85900a	0,01450331	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	da77008241881cd622c6e32564cf1293	0,01552346	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculum; s__uncultured_bacterium	76ba7d55c7fa461d33b29f315b266735	0,01684689	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	76339fd65b9741cc235e74469b7505b6	0,02029581	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	a384a57add3a050f64b65123e6b29e4c	0,02136339	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	83a1199ece86f770179563e69aefc4ff	0,02864535	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_organism	50f8c7d97bfbb7e7ab445a43ff7d5497	0,03049732	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	7cd293b474a6426e4d38d421c71df82e	0,03226484	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Rikenellaceae_RC9_gut_group; s__uncultured_bacterium	929d38142d421d776e3afd228d991b39	0,03504928	0

d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	076b08feb8624fffb494c56458b6fdca	0,04915723	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	81b15c3e47c2a9c6a8a8ddfb3b944ed0	0,04951662	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes	02666e3c9fa9366c506317bc991fb8e5	0,05801671	0
d__Bacteria; p__Firmicutes; c__Bacilli; o__RF39; f__RF39; g__RF39; s__uncultured_bacterium	e7b8dd4833a3dc4239ecc60f22f626c9	0,07305172	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	6ab2d861718ae223299224694dc3856b	0,07381994	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	da9466b3aa7756ca9863c9489b9c6e99	0,07671257	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	fb7fccd1e895b8aa572a0c4861ab7439	0,08634445	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Rikenellaceae_RC9_gut_group; s__uncultured_bacterium	4a1da5d3a694fe63856ba961f0a182ba	0,08720079	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Prevotellaceae; g__Prevotellaceae_UCG-001	1fa14fcc39b443db34eff353fe83b2eb	0,10360187	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	6f85c2ca4faded8df244da4248136875	0,1313626	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	f1408d3533904b2a644333acca09958b	0,13512363	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Rikenella; s__uncultured_bacterium	f4f26450a111ac933922fe1a9c957828	0,14214778	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	4ba388633b78983aa34359843ff8d1cf	0,15428123	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	3ab77c93cd92d2758958fc5ce7c3c304	0,17732632	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	0a9b8d560680dfd0a1bf6c3efb7dee9c	0,28469178	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Muribaculaceae	2257f0fb4e5d8fb95c6bda219b3a54aa	0,31885831	0
d__Bacteria; p__Firmicutes; c__Bacilli	e341c27da09ab0bc4406b23af9559799	0,43478408	0

d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	64632422c9c6f49984eff1a2958ac858	0,45959887	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	654076a2db1c205e3b1b1a21f38cad2d	0,52612402	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	48b788d41dd55b90e90393a5a9e04f7d	0,53584928	0
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group	fce2ee99b4cb5ecdcc288c72830bd9de	0,6197057	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Rikenellaceae; g__Alistipes; s__uncultured_bacterium	8084921b74f294415c19175a495cf1e5	0,65009482	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	4d5291d2b9492417101f2b90099cd2d5	0,76456554	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	fe0a96f04a2f988c362e909a22875e99	0,83830256	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	6cc7cfde091344267009e57804b96434	0,90672874	0
d__Bacteria; p__Firmicutes; c__Bacilli; o__Lactobacillales; f__Lactobacillaceae; g__Lactobacillus	5385725ae7329489f770fff4eb68c53c	1,44174035	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_Bacteroidales	02c5beb524a661ed23808ed136a98fc0	1,63564282	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	f998eb3e30406a3e36e3ec7bbaac0aa7	1,6985594	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae	be77e43e8197e57897bb796d1c06446f	2,17166811	0
d__Bacteria; p__Firmicutes; c__Clostridia; o__Lachnospirales; f__Lachnospiraceae; g__Lachnospiraceae_NK4A136_group	82d62f5551512bf9e6aadc2dcbaa6d4f	2,36896612	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Bacteroidaceae; g__Bacteroides	00db9171fb73c28da6eed2b0dd84ada2	2,65169135	0
d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Bacteroidales; f__Muribaculaceae; g__Muribaculaceae; s__uncultured_bacterium	32cf014be175782af90bbba43cc93bf0	6,71337177	0

Relative abundance (%) of unique ASVs that were found only in rd10 or C57BL/6J mice group. For each ASV ID, it is shown the SILVA 138 classification and the relative abundance (%) for the two studied mice groups.

Supplementary Table S4. Mice's gut microbiota alpha and beta diversity study.

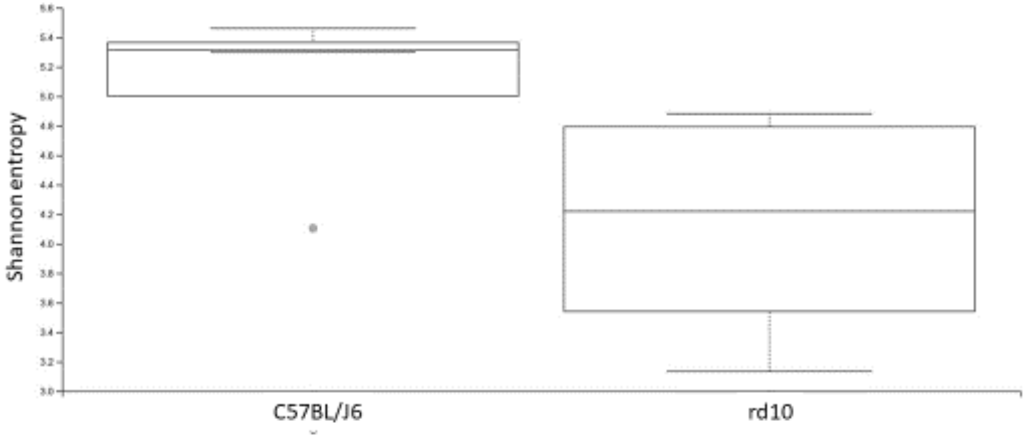
	β-diversity Distance (P)						**α-diversity Index (P)**
Samples	**Weigthed Unifrac Distance**	**Unweighted Unifrac Distance**	**Jaccard Distance**	**Bray-courtis Distance**	**Pielou's Eveness Index**	**Shannon's Diversity Index**	**Faith's Phylogenetic Diversity Index**
C57-rd10	0.25	0.03*	0.03*	0.03*	0.08	0.08	0.25
Sex	0.31	0.71	0.62	0.1	0.25	0.24	0.56

Statistical p-value results (P) from the comparison of mice gut microbiota. The contrast was performed between C57BL/6J and rd10 mice (C57-rd10) or between the male and female mice (Sex). For testing the β-diversity, a PERMANOVA test was employed, while for testing the α-diversity the no-parametric Kruskal-Wallis test was used; $*p < 0.05$.

Supplementary Table S5. Significantly represented species according to ANCOM.

	Deblur (W-value)	**More abundant**
***Rikenella* spp.**	22	C57
***Muribaculaceace* spp.**	27	C57
***Prevotellaceae* UCG-001 spp.**	23	C57
***Bacilli* spp.**	19	C57
Bacteroides caecimuris	25	rd10

ANCOM stat (W-value) [4] for species that were found to be statistically more abundant in control (C57) or rd10 mice (More abundant). ANCOM compares the relative abundance of each taxon with all the remaining features of the same category, showing which ones are significantly more abundant.



Supplementary Figure S1. Alpha diversity comparison between C57BL/J6 and rd10 mice gut microbiota measured with Shannon's Diversity Index and compared with no-parametric statistical Kruskal-Wallis test. No significant differences were found ($p > 0.05$).

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