

# **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 |
|-----------------|-------------------------|--------------------|------------------|
| <b>C57.25</b>   | F: 157704               | F: 156314          | 133979           |
|                 | R: 157704               | R: 156314          |                  |
| <b>C57.26</b>   | F: 120828               | F: 119283          | 94596            |
|                 | R: 120828               | R: 119283          |                  |
| <b>C57.27</b>   | F: 110848               | F: 109902          | 93635            |
|                 | R: 110848               | R: 109902          |                  |
| <b>C57.32</b>   | F: 115625               | F: 114685          | 98528            |
|                 | R: 115625               | R: 114685          |                  |
| <b>rd10.88</b>  | F: 125328               | F: 124248          | 108651           |
|                 | R: 125328               | R: 124248          |                  |
| <b>rd10.89</b>  | F: 98154                | F: 97336           | 84398            |
|                 | R: 98154                | R: 97336           |                  |
| <b>rd10.102</b> | F: 101379               | F: 100547          | 85878            |
|                 | R: 101379               | R: 100547          |                  |
| <b>rd10.109</b> | 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) <sup>1</sup>, including the passing reads of the quality filtering step performed with prinseq-lite (No. Reads after QC) <sup>2</sup>. 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 |
|-----------------|--------|----------------|-----------------------------------|----------|----------|--------------------|-------------------------------------|---------------|
| <b>C57.25</b>   | 133904 | 86027          | 64.25                             | 50360    | 1408     | 48952              | 36.56                               | 94            |
| <b>C57.26</b>   | 94555  | 60103          | 63.56                             | 33873    | 1720     | 32153              | 34.00                               | 92            |
| <b>C57.27</b>   | 93592  | 54585          | 58.32                             | 34085    | 767      | 33318              | 35.60                               | 96            |
| <b>C57.32</b>   | 98477  | 55385          | 56.24                             | 35569    | 320      | 35249              | 35.79                               | 94            |
| <b>rd10.102</b> | 85821  | 53760          | 62.64                             | 36889    | 1338     | 35551              | 41.42                               | 84            |
| <b>rd10.109</b> | 114339 | 65513          | 57.30                             | 42684    | 708      | 41976              | 36.71                               | 88            |
| <b>rd10.88</b>  | 108599 | 76453          | 70.40                             | 48081    | 1771     | 46310              | 42.64                               | 83            |
| <b>rd10.89</b>  | 84350  | 51617          | 61.19                             | 35118    | 2151     | 32967              | 39.08                               | 88            |

Deblur <sup>3</sup> 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      | 4a178a9e45c6faf13bdadb53a4f2028  | 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 |

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|---------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------|---|------------|
| 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                | 82d62f5551512bf9e6aad2dcbaa6d4f  | 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 group or C57 mice group. For each ASV ID, it is shown the SILVA 138 classification and the relative abundance (%) for the two studied mice group.

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

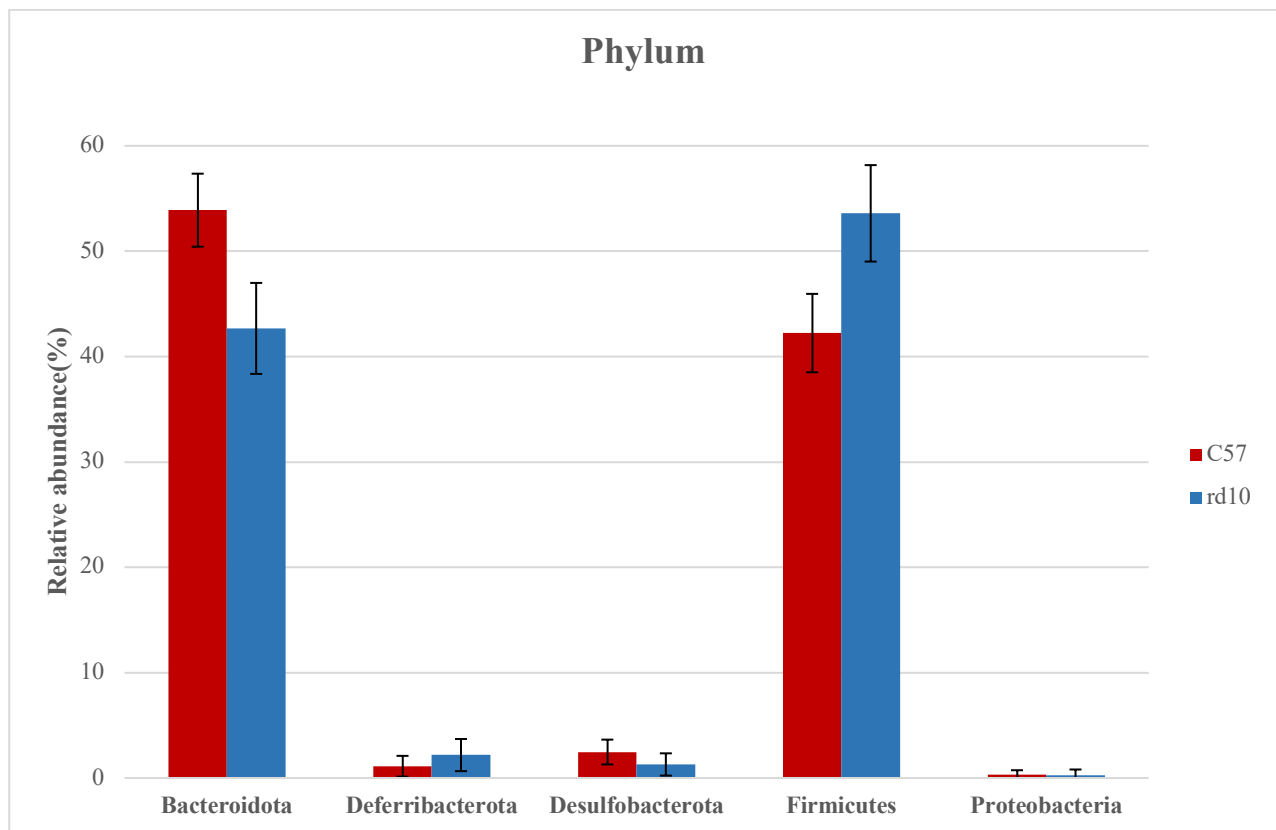
|              | $\beta$ -diversity Distance      |                                   |                     |                              |                              | $\alpha$ -diversity Index    |                                         |
|--------------|----------------------------------|-----------------------------------|---------------------|------------------------------|------------------------------|------------------------------|-----------------------------------------|
|              | (P)                              |                                   |                     |                              |                              | (P)                          |                                         |
| Samples      | Weighthed<br>Unifrac<br>Distance | Unweighted<br>Unifrac<br>Distance | Jaccard<br>Distance | Bray-<br>courtis<br>Distance | Pielou’s<br>Eveness<br>Index | Shannon’s<br>Diversity Index | Faith’s Phylogenetic<br>Diversity Index |
| C57-<br>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 mice and rd10 mice (C57-rd10) or between the male and female mice (Sex). For testing the  $\beta$ -diversity, a PERMANOVA test was employed, while for testing the  $\alpha$ -diversity the no-parametric Kruskal-Wallis test was used; \*p < 0.05.

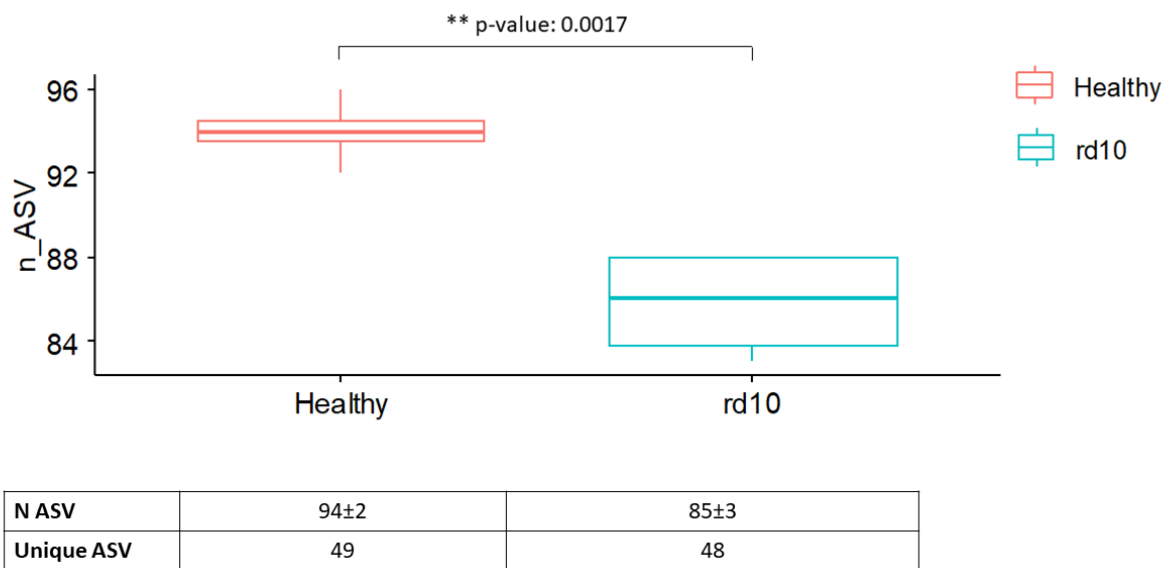
**Supplementary Table S5.** Significantly represented species according to ANCOM.

|                                    | Deblur (W-value) | More abundant |
|------------------------------------|------------------|---------------|
| <i>Rikenella</i> spp.              | 22               | C57           |
| <i>Muribaculaceae</i> spp.         | 27               | C57           |
| <i>Prevotellaceae</i> UCG-001 spp. | 23               | C57           |
| <i>Bacilli</i> spp.                | 19               | C57           |
| <i>Bacteroides caecimuris</i>      | 25               | rd10          |

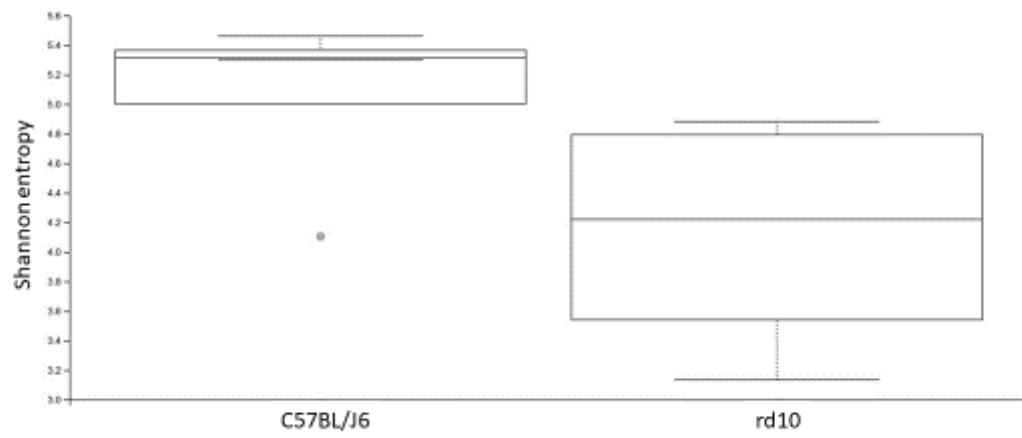
ANCOM stat (W-value) <sup>4</sup> for species that were found to be statistically more abundant in control mice (C57) or rd10 mice (More abundant). ANCOM compares the relative abundance of each taxon with all the remaining features of the same category, showing which ones are significantly more abundant.



**Supplementary Figure S1.** Relative abundance (%) at Phylum level for C57BL/J6 mice and rd10 mice gut microbiota. Dominant phyla were Bacteroidota and Firmicutes in both samples. Each bar shows the mean $\pm$  SE per type of mice. All Phyla found were represented. No statistically significant differences were found when one-way ANOVA was performed ( $p > 0.05$ ).



**Supplementary Figure S2.** Amplicon Single Variant study. Top panel: boxplot comparing the number of Amplicon Single Variants (n\_ASV). One-way ANOVA test showed statistically significant differences between the number of ASV in healthy <sup>5</sup> and rd10 (blue) mice. First row of the table contains mean  $\pm$  SD of ASV, the second one contains the number of unique ASV (not shared with the other group) for Healthy (left) and rd10 mice (right). Graphic performed with the library ggboxplot available in R <sup>6</sup>.



**Supplementary Figure S3.** Alpha diversity comparison between C57BL/J6 mice 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 ( $p > 0.05$ ).

## References

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