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Next-generation sequencing characterization of the gut bacterial community of gilthead sea bream (*Sparus aurata*, L.) fed low fishmeal based diets with increasing soybean meal levels

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1 **Next-generation sequencing characterization of the gut**
2 **bacterial community of gilthead sea bream (*Sparus aurata*,**
3 **L.) fed low fishmeal based diets with increasing soybean**
4 **meal levels**

5

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24 Keywords: *Sparus aurata*, Soybean meal, Gut bacterial
25 community, Next-generation sequencing, Growth, Gut

26 histology.

27

28 **Abstract**

29 The present study was carried out to evaluate growth, gut
30 histology and gut bacterial community of gilthead sea bream
31 (*Sparus aurata*) fed with increasing dietary soybean meal
32 (SBM) levels in a low fishmeal (FM) based diet, in comparison
33 with a control diet. Five isoproteic and isolipidic experimental
34 diets were formulated to contain increasing levels of SBM (0,
35 100, 200, and 300 g kg⁻¹ named S0, S10, S20 and S30,
36 respectively) with 150 g kg⁻¹ of FM, and one control diet (C)
37 without SBM and containing 350 g kg⁻¹ of FM. Sixty sea bream
38 (initial body weight 75.9 ± 1.9 g, n = 900) per tank were reared
39 in a recirculation system at 23.0 ± 1.0 °C and fed to satiation.
40 The trial was run in triplicate and lasted 100 days. At the end of
41 the trial fish fed the S30 diet showed a higher ($P \leq 0.05$)
42 specific growth rate (SGR) compared to S0 (SGR, 1.17 ± 0.03,
43 1.20 ± 0.01, 1.22 ± 0.01, 1.25 ± 0.01 and 1.21 ± 0.04 for S0,
44 S10, S20, S30 and C, respectively), and a higher feed intake
45 (FI) compared to S0, S10 and S20. Sea bream fed the C diet
46 had a higher ($P \leq 0.05$) FI compared to S0 (FI, 1.40 ± 0.01,
47 1.45 ± 0.01, 1.44 ± 0.03, 1.51 ± 0.03 and 1.46 ± 0.02 for S0,
48 S10, S20, S30 and C, respectively). No significant differences
49 in feed conversion rate, protein efficiency ratio, gross protein
50 efficiency and gross lipid efficiency among the treatments were
51 detected. No specific histopathological changes indicative of
52 soy-induced enteritis were observed in the intestine of any fish

53 examined. Gut bacterial community of the distal intestine
54 content was analyzed by Next-Generation Sequencing. At the
55 phylum level, the gut bacterial community was dominated by
56 *Firmicutes* (relative abundance 71%), while the most
57 represented family was *Lactobacillaceae* (26%). Even if no
58 significant differences ($P \leq 0.05$) in the gut bacterial
59 community α and β -diversity according to the different diets
60 were detected, *Cyanobacteria* and *Lactobacillaceae*
61 progressively increased from diet C to diet S30. In conclusion
62 results of growth, nutrient utilization, gut histology and gut
63 bacterial community indicate that SBM can be successfully
64 incorporated up to a level of 300 g kg⁻¹ with the inclusion of
65 150 g kg⁻¹ of FM, without any deleterious effects on growth,
66 protein utilization and gut health during the on-growing of sea
67 bream.

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77 **1. Introduction**

78

79 Gilthead sea bream is one of the most important species for
80 European aquaculture, representing around 51% of the total
81 finfish marine production in the Mediterranean area (FAO,
82 2010). Due to the current economic downturn and the
83 fluctuation of the gilthead sea bream market, a reduction in
84 feed costs while ensuring optimal growth and fish health is
85 essential to maintain the profitability of its farming (Martinez-
86 Llorens et al., 2009; Mongile et al., 2014). In this context, the
87 importance of vegetable protein is well recognized by feed
88 industry operators due to the growing pressure for alternative
89 fishmeal (FM) substitutes in fish diets. Among the different
90 ingredients, soybean meal (SBM) is one of the most interesting
91 alternative FM because of the advantages of supply, price, and
92 protein and amino acid composition (Bonaldo et al., 2008).
93 However this ingredient may induce a variety of histological
94 and functional changes in the gastrointestinal tracts of fish,
95 especially in salmonids, including morphological alterations
96 and inflammation (Krogdahl et al., 2003, 2010). These changes
97 may be due to direct effects of anti-nutritional factors in plant
98 ingredients and/or the indirect result of diet-induced changes in
99 the structure and function of the intestinal bacterial community
100 (Olsen et al., 2001; Ringø et al., 2006).

101 Previous studies on gilthead sea bream have shown that the
102 optimum dietary SBM levels, using a dietary FM content
103 higher than 200 g kg⁻¹, were 205 g kg⁻¹ for maximum growth
104 (Martinez-Llorens et al., 2009). Further increasing the level of
105 SBM up to 300 g kg⁻¹ of the diet had no significant effects on
106 the specific growth rate (SGR), feed intake (FI) and feed
107 conversion rate (FCR) in juvenile specimens of the same
108 species, although high SBM level led to some changes in the
109 distal intestine, with the presence of cellular infiltration of the
110 submucosa and lamina propria (Bonaldo et al., 2008).

111 In this context the exploration of fish gut bacterial
112 community can represent an emerging tool to evaluate the
113 application of vegetal ingredients in fish feed formulations.
114 Increased knowledge of the human gut microbiota is driving
115 research into development, immunity, disease, lifestyle and
116 nutrition (Furusawa et al., 2013). Similarly, the knowledge and
117 manipulation of the gut microbiome in teleosts, especially in
118 aquaculture, could be potentially addressed through nutrient
119 digestion, synthesis, absorption, pathogen resistance, growth,
120 sexual maturation, morphogenesis and survivorship (Llewellyn
121 et al., 2014). To date, our understanding of the teleost gut
122 bacterial community and of its functional significance has
123 lagged well behind that of humans and other terrestrial
124 vertebrates (Ray et al., 2012). Most understanding of the
125 intestinal microbiota of fish is largely derived from culture-

126 based approaches and 16S rRNA gene fingerprinting methods
127 such as denaturing gradient gel electrophoresis (DGGE).
128 However, these methods usually reveal only a limited range of
129 microbial diversity (Desai et al., 2012; Carda-Diéguez et al.,
130 2014). Next-Generation Sequencing (NGS) has been used in
131 recent years to examine the gut microbiome of humans,
132 terrestrial and marine vertebrate including some fish species as
133 recently reviewed by Ghanbari et al. (2015). However, only for
134 a few species such as rainbow trout *Oncorhynchus mykiss*,
135 Siberian sturgeon *Acipenser baerii* and zebrafish *Danio rerio*,
136 was this technique applied to explore the impact of diet on the
137 gut bacterial community (Desai et al., 2012; Semova et al.,
138 2012; Geraylou et al., 2013). In sea bream, *Sparus aurata*, data
139 on gut bacterial community using NGS have been recently
140 published regarding fish fed exclusively fishmeal or vegetable
141 protein based diets (Estruch et al., 2015), while no data are
142 available for this species fed increasing SBM levels in practical
143 diet formulations.

144 Furthermore few studies have explored in this species the
145 effects of increasing levels of SBM on performance using low
146 FM based diets as the only animal protein source and most of
147 the data on literature were restricted to replace FM with SBM.
148 At this regards, we evaluated the effects of SBM by replacing a
149 mixture of vegetal ingredients, wheat meal (WM), wheat gluten
150 (WG), corn gluten (CG) and sunflower meal (SM) which are

151 currently used in practical formulation at industrial level to
152 determine the optimal inclusion rate in practical low fish meal
153 diet.

154 The aims of this study were: 1) to evaluate the effects of
155 dietary inclusion of SBM and a low FM content in practical
156 diet formulations on growth, nutrient utilization and gut
157 histology of gilthead sea bream; 2) to evaluate changes in the
158 gut bacterial community of gilthead sea bream fed practical
159 diets with increasing levels of SBM and a low FM content, in
160 comparison to a control diet.

161

162 **2. Materials and methods**

163

164 *2.1. Diets*

165

166 Ingredients and proximate composition of the experimental
167 diets are presented in Table 1. Four isoproteic and isolipidic
168 diets were formulated with practical ingredients to contain
169 increasing levels of SBM (0, 100, 200, and 300 g kg⁻¹, named
170 S0, S10, S20, and S30, respectively) with a low FM content
171 (150 g kg⁻¹), while a control diet (C) was formulated to contain
172 0 g kg⁻¹ SBM and 350 g kg⁻¹ FM content. SBM was replaced
173 by adding WM, WG, CG and SM. The diets were
174 manufactured by Skretting Aquaculture Research Centre
175 (Stavanger, Norway) using extrusion technology. According to

176 the feed manufacturer, the protein and lipid levels were within
177 the range of the commercial diets for sea bream as well as the
178 FM level in the C group which was chosen as optimal standard
179 level for commercial diet of this species. All feeds were
180 produced as extruded sinking pellets (specific gravity 1.15)
181 with a diameter of 4 mm.

182

183 *2.2. Fish, experimental set-up and sampling*

184

185 The experiment was carried out at the Laboratory of
186 Aquaculture, Department of Veterinary Medical Sciences of the
187 University of Bologna, Cesenatico, Italy. Sea bream with an
188 initial average weight of 75.9 ± 1.9 g were obtained from the
189 hatchery Panittica Italia, Fasano, Italy. Before the experiment,
190 fish were acclimated for 2 weeks to the experimental tanks and
191 fed a mix of the experimental diets. At the beginning of the
192 trial, 60 fish per tank were randomly distributed into 15, 1000 L
193 square conical bottom tanks to obtain five triplicate fish groups,
194 each per dietary treatment. Tanks were provided with natural
195 seawater and connected to a closed recirculation system
196 consisting of a mechanical sand filter (Astralpool, Spain), an
197 ultraviolet light (Philips, the Netherlands) and a biofilter
198 (Astralpool, Spain). The water exchange rate within each tank
199 was 100% every hour. The water renewal of the total system
200 was 5 % daily. Mean water temperature was maintained at 23.0

201 ± 1.0 °C throughout the experiment; photoperiod was held
202 constant at a 12 h day length through artificial light (300 lux at
203 the water surface — Delta Ohm luxmeter HD-9221; Delta-
204 Ohm, Padua, Italy). The oxygen level was kept constant ($8.0 \pm$
205 1.0 mg L⁻¹) by a liquid oxygen system connected to a software
206 controller (B&G Sinergia snc, Chioggia, Italy). Ammonia (total
207 ammonia nitrogen, TAN ≤ 0.1 mg L⁻¹), nitrite (NO₂ ≤ 0.2 mg
208 L⁻¹) and nitrate (NO₃ ≤ 50 mg L⁻¹) were determined
209 spectrophotometrically once a day (Spectroquant Nova 60,
210 Merk, Lab business) at 12.00 p.m. At the same time, pH (7.8–
211 8.2) and salinity (28-33 g L⁻¹) were determined. The feeding
212 trial lasted a total of 100 days. Fish were overfed by automatic
213 feeders twice a day with a 5-10 % overfeeding ration for six
214 days a week, while one meal was supplied on Sundays. Each
215 meal lasted 1 hour and after that the uneaten feed was trapped
216 by a feed collector at the water output of tanks, dried overnight
217 at 105°C and the weight deducted from the feed intake for
218 overall calculations.

219 At the beginning and at the end of the experiment, all the
220 fish of each tank were individually weighed. At the end of the
221 trial digesta samples from 3 fish per tank were collected
222 individually. The gastrointestinal tract was dissected under
223 sterile conditions and the distal gut content was squeezed out
224 into an Eppendorf tube (one per fish) and placed at -80 °C until
225 DNA extraction (Desai et al., 2012).

226 Carcass proximate composition was determined on a pooled
227 sample of ten fish collected at the beginning of the trial and on
228 pooled samples of five fish per tank collected at the end of the
229 trial. Furthermore, at the end of the trial, wet weight of viscera
230 and liver was individually recorded from five fish per tank to
231 determine visceral (VSI) and hepatosomatic (HSI) indices.

232 All experimental procedures were evaluated and approved
233 by the Ethical-scientific Committee for Animal
234 Experimentation of the University of Bologna, in accordance
235 with the European directive 2010/63/UE on the protection of
236 animals used for scientific purposes.

237

238 *2.3. Gut histology*

239

240 At the end of the trial 15 animals per treatment were
241 randomly sampled. After euthanasia with a lethal dose of 2-
242 phenoxyethanol, the gut was removed and the intestine was
243 divided into two segments, proximal and distal; from each
244 segment a 5 mm-long piece was sectioned and fixed in 10%
245 buffered formalin. Samples were then processed for routine
246 histology to obtain 3 µm thick transverse sections, which were
247 stained with haematoxylin-eosin (H&E). Sections were
248 evaluated under a light microscope (Nikon Eclipse 80i).

249

250 *2.4. Gut bacterial community 16S sequencing*

251

252 Total bacterial DNA was extracted from a pool of distal
253 intestine content obtained from 3 fish per tank (100 mg of distal
254 intestine content per fish) as reported by Schnorr et al. (2014).
255 PCR amplifications of the V3-V4 region of the 16S rRNA gene
256 were carried out in 25 µl volumes with 25 ng of microbial
257 DNA, 2x KAPA HiFi HotStart ReadyMix (KAPA Biosystems),
258 and 200 nM of the primers S-D-Bact-0341-b-S-17/S-D-Bact-
259 0785-a-A-21 (Klindworth et al., 2013) including Illumina
260 overhang adapters. Reaction conditions were as follows: initial
261 denaturation at 98°C for 3 min, followed by 30 cycles of
262 denaturation at 95°C for 30 sec, annealing at 55°C for 30 sec,
263 and extension at 72°C for 30 sec, with a final extension step at
264 72°C for 5 min. Amplicons were purified using Agencourt
265 AMPure XP magnetic beads. This magnetic bead-based system
266 is recommended in the Illumina protocol “16S Metagenomic
267 Sequencing Library Preparation” for the MiSeq system, and has
268 been used in several other publications (Soverini et al., 2016).
269 According to the Illumina protocol, 20% PhiX control was
270 used. Indexed libraries were prepared by using Nextera
271 technology and cleaned up with Agencourt® magnetic beads.
272 The final libraries were pooled at equimolar concentrations,
273 denatured and diluted to 6 pM before loading onto the MiSeq
274 flow cell. Sequencing was performed on Illumina MiSeq
275 platform using a 2 × 300 bp paired end protocol, according to

276 the manufacturer's instructions (Illumina, San Diego, CA).
277 Raw sequences were processed using the QIIME pipeline
278 (Caporaso et al., 2010). After length (minimum/maximum =
279 300/600 bp) and quality filtering with default parameters, reads
280 were binned into OTUs at a 0.97 similarity threshold using
281 UCLUST (Edgar, 2010). Assignment was carried out by using
282 the RDP classifier against Greengenes database (May 2013
283 version). Alpha-diversity rarefaction curves were performed
284 using the Faith's phylogenetic diversity, Chao1, observed
285 species, and Shannon index metrics. Beta-diversity was
286 estimated by weighted and unweighted UniFrac distances,
287 which were used as input for principal coordinates analysis
288 (PCoA).

289

290 *2.5. Analytical methods*

291

292 Diets and whole body samples were analyzed for proximate
293 composition. Moisture content was obtained by weight loss
294 after drying samples in a stove at 105 °C until a constant
295 weight was achieved. Crude protein was determined as total
296 nitrogen (N) by using the Kjeldahl method and multiplying N
297 by 6.25. Total lipids were determined according to Bligh and
298 Dyer's (1959) extraction method. Ash content was estimated by
299 incineration to a constant weight in a muffle oven at 450 °C.

300

301 2.6. Calculations

302

303 The formulae employed were as follows:

304 Specific growth rate (SGR) (day^{-1}) = $100 * (\ln \text{FBW} - \ln$
305 $\text{IBW})/\text{days}$ (where FBW and IBW represent the final and the
306 initial body weights).

307 Feed intake (FI) ($\% \text{ day}^{-1}$) = $100 * (\text{crude feed intake}/$
308 $\text{ABW}/\text{day})$ (where ABW (g) = average body weight = $(\text{FBW} +$
309 $\text{IBW})/2$).

310 Feed conversion ratio (FCR) = feed intake/weight gain.

311 Visceral somatic index (VSI) (%) = $100 * (\text{viscera}$
312 $\text{weight}/\text{body weight})$.

313 Hepatosomatic index (HSI) (%) = $100 * (\text{liver weight}/\text{body}$
314 $\text{weight})$.

315 Protein efficiency ratio (PER) = $(\text{FBW} - \text{IBW})/\text{protein}$
316 intake .

317 Gross protein efficiency (GPE) (%) = $100 * [(\% \text{ final body}$
318 $\text{protein} * \text{FBW}) - (\% \text{ initial body protein} * \text{IBW})]/\text{total protein}$
319 intake fish^{-1} .

320 Gross lipid efficiency (GLE) (%) = $100 * [(\% \text{ final body}$
321 $\text{lipid} * \text{FBW}) - (\% \text{ initial body lipid} * \text{IBW})]/\text{total lipid intake}$
322 fish^{-1} .

323

324 2.7. Statistics

325

326 Data of growth performance, VSI, HSI, and nutritional
327 indices are presented as mean \pm standard deviation (SD) of
328 three replicate groups and were analyzed by a one-way
329 ANOVA followed by a Tukey's multiple comparison test.
330 Statistical analysis of gut bacterial community was carried out
331 by using R packages Stats and Vegan. Significant differences in
332 the relative abundance of gut bacterial community components
333 were obtained by Kruskal-wallis test. Data separation in the
334 PCoA was tested using a permutation test with pseudo F-ratios
335 (function Adonis in the Vegan package).

336

337 **3. Results**

338

339 *3.1. Growth and histology*

340

341 Growth performance is summarized in Table 2. At the end
342 of the trial fish fed the S30 diet showed a higher ($P \leq 0.05$)
343 SGR compared to S0 and a higher FI compared to S0, S10 and
344 S20. Sea bream fed the C diet had a higher ($P \leq 0.05$) FI
345 compared to S0, while no significant differences in FCR among
346 the treatments were detected (Table 2). No significant
347 differences in VSI, HSI, whole body composition and the
348 nutritional indices PER, GPE, GLE, were observed among the
349 treatments (Table 3). No specific histopathological changes

350 indicative of soy-induced enteritis were observed in the
351 intestine of any fish examined (Fig. 1).

352

353 *3.2. Gut bacterial community characterization*

354

355 Fifteen pools of distal intestine content were analyzed by
356 NGS of the V3 and V4 regions of the 16S rDNA gene. A total
357 of 5,584,914 high quality reads were obtained from the starting
358 15,956,896 reads obtained, ranging from a minimum of 93,673
359 to a maximum of 687,596 reads per sample, with an average of
360 372,327 reads per sample. Further information about the
361 number of reads for each sample and the coverage are reported
362 in Supplementary Table 1. The number of reads across samples
363 was normalized basing on the sample with the lowest number
364 of reads and singletons were omitted from the analysis. Reads
365 were clustered into 13,099 operational taxonomic units (OTUs)
366 at 97% of identity, of which a total of 5,525 diet-specific OTUs
367 were found (1,082 for diet S30; 1,016 for diet S20; 1,038 for
368 diet S10; 833 for diet S0; 1,556 for control diet). Different
369 metrics have been utilized to calculate α -diversity, including
370 phylogenetic diversity, OTU species count, Chao 1 index for
371 microbial richness and Shannon index for biodiversity (Fig.
372 2a). Rarefaction curves of the phylogenetic diversity
373 approximated saturation, indicating a good coverage of the gut
374 bacterial community. No differences in the gut bacterial

375 community α -diversity according to the different diets were
376 detected (Fig. 2b).

377 At the phylum level, the average sea bream gut bacterial
378 community is dominated by *Firmicutes* (relative abundance
379 (rel. ab.) 71%), *Actinobacteria* (rel. ab. 9%), *Bacteroidetes* (rel.
380 ab. 7%) and *Proteobacteria* (rel. ab. 6%), while *Cyanobacteria*
381 (rel. ab. 3%) and *Verrucomicrobia* (rel. ab. 3%) were
382 subdominant (Fig. 3a). The most represented families are:
383 *Lactobacillaceae* (rel. ab. 26%), *Ruminococcaceae* (rel. ab.
384 12%), *Lachnospiraceae* (rel. ab. 10%) and *Clostridiales*
385 families (rel. ab. 7%) (Fig. 3b). Among the subdominant
386 families the most represented were, *Streptococcaceae* (rel. ab.
387 3%), *Cyanobacteria* (rel. ab. 3%), *Staphylococcaceae* (rel. ab.
388 3%), *Verrucomicrobia* (rel. ab. 3%) and *Enterobacteriaceae*
389 (rel. ab. 2 %).

390 In order to highlight the impact of the different diets (S0, S10,
391 S20, S30 and C) on the gut bacterial ecology of sea bream, we
392 performed the PCoA analysis of the UniFrac distances among
393 the gut bacterial community profiles (Fig. 4). Even though no
394 significant differences among dietary groups were detected,
395 both weighted and unweighted PCoA showed a tendency
396 toward a samples separation according to the different diets.
397 Fig. 5 shows the relative abundance of bacteria composition per
398 sample at phylum (a) and family (b) levels, while in Fig. 6 we
399 report the gut bacterial community components which showed

400 a different abundance in the different dietary groups. In
401 particular, the abundance of *Cyanobacteria* progressively
402 increased from diet C to diet S30 (Fig. 6a), while *Synergistetes*
403 tend to show an opposite trend (Fig. 6b). Differently,
404 *Actinobacteria* showed a higher abundance in diets S0 and S30
405 (Fig. 6c). Although there were no statistically significant
406 effects, the *Lactobacillaceae* family was highly represented in
407 fish fed S30 (Rel. ab. 43.3%) compared to those fed C diet
408 (Rel. ab. 11.2%) (Fig. 6d).

409

410 **4. Discussion**

411

412 The inclusion of SBM at 100, 200 and 300 g kg⁻¹ (S10-S30)
413 of the diet with a low FM content (150 g kg⁻¹) led to equal
414 growth and protein utilization in comparison to a control diet
415 without SBM and having 350 g kg⁻¹ of FM. The present results
416 are in agreement with previous studies which have
417 demonstrated the feasibility of including up to 300, 390 and
418 395 g kg⁻¹ SBM in diets for on-growing sea bream without
419 negative effects on growth and nutritive efficiency (Bonaldo et
420 al., 2008; Martinez-Llorens et al., 2009; Kokou et al., 2012),
421 although FM levels in these studies were higher than in the
422 present trial or amino acid supplements were used. In the
423 present study the lack of differences in the SGR, FCR, PER and
424 GPE between S10, S20, S30, the C diet suggests that the

425 inclusion of 150 g kg⁻¹ of FM in combination with SBM, WG
426 and CG will supply sufficient protein quality for this species.
427 Similarly, Dias. et al. (2009), showed that the growth
428 performance of sea bream towards the end of the grow-out
429 phase can be sustained by a practical dietary formulation
430 containing plant protein-derived and as little as 13% of marine-
431 derived proteins. However, in that study AA supplementation
432 and haemoglobin powder were also incorporated in the feed
433 while in the present study FM was the only animal protein
434 source. Focusing on the diets at low FM level (S0, S10, S20,
435 S30), fish fed S30 showed a higher SGR compared to those fed
436 S0. This seems mainly due to an increment of FI with
437 increasing dietary content of SBM. The reduced FI commonly
438 observed in fish given feeds containing plant protein may be
439 related to a reduced feed palatability and, in this regard, the use
440 of several mixtures of plant protein should reduce the potential
441 inhibition of feed consumption due to the specific effect of a
442 single ingredient (Fournier et al., 2004). Other studies reported
443 an increased feed consumption with increasing dietary levels of
444 SBM assuming that fish to meet their energy needs would have
445 increased the FI for a reduced available energy content as SBM
446 inclusion increased (Venou et al., 2006; Kokou et al., 2012).
447 SBM contains about 20% of non-starch polysaccharides (NSP)
448 and 10% oligosaccharides (Snyder and Kwon, 1987; Bach
449 Knudsen, 1997), which are considered indigestible by fish

450 compared to wheat and gltens. Therefore, despite the
451 isoenergetic content of the diets, a reduction of available energy
452 content would be expected at higher SBM inclusion level
453 (Kokou et al., 2012). However, possible action of the gut
454 bacterial community could allow part of SBM energy
455 originating from NSP to be available to the fish in the form of
456 low molecular weight fatty acids (Kihara and Sakata, 2002;
457 Mountfort et al., 2002; Refstie et al., 2005; Kokou et al., 2012).

458 Gut histology revealed no specific histopathological changes
459 indicative of soy-induced enteritis in the intestines of any fish
460 examined. In a previous study on sea bream the inclusion of
461 30% SBM seemed to cause moderate and diffused expansion of
462 lamina propria in the distal intestine due to an increase of
463 mononuclear cell infiltration when compared to other
464 treatments with 18 and 0% of SBM (Bonaldo et al., 2008). A
465 dilatation of the submucosa by eosinophilic cells infiltration
466 was also found in the distal intestine of sea bream fed diet
467 containing bioprocessed SBM at the 40 and 60% levels (Kokou
468 et al., 2012). However both studies were conducted at juveniles
469 stage (weight range, 17.4 - 96.0 g and 15.7 - 48.9 g,
470 respectively) compared to the on-growing stage of the present
471 study (weight range 75.1 - 259.5 g). The inclusion levels of
472 SBM seem to be better tolerated by fish at on-growing phase as
473 supported by Martinez-Llorens et al. (2007) which concluded
474 that dietary SBM might be included in the diets up to 30% in

475 juveniles and up to 50% in grow-out fish without affecting
476 animal performance. In addition sea bream in grow-out phase
477 showed high tolerance for soy saponins while in juvenile sea
478 bream fed diets containing phytosterols and soy saponins some
479 disturbances of the intestinal mucosa were observed (Couto et
480 al., 2014 a, b); however, the histomorphological changes
481 observed were very mild and, although statistically significant,
482 the differences were judged to be minor and to represent
483 normal adaptation to changes in diet composition (Couto et al.,
484 2014a).

485 In the present study the gut bacterial community was
486 characterized. According to our findings, the gut bacterial
487 community is widely dominated by *Firmicutes* (rel. ab. 71%),
488 showing *Actinobacteria* as the second dominant phyla (rel. ab.
489 9%). *Bacteroidetes*, *Proteobacteria* and *Cyanobacteria* were
490 subdominant components with a relative abundance ranging
491 from 3 to 7 % of the bacterial community. Our data are in
492 general agreement with the previous Next Generation
493 Sequencing-based survey of the gut bacterial community in sea
494 bream (Estruch et al., 2015). Further, by mean of
495 pyrosequencing of the V1-V3 region of the 16S rDNA, the
496 Authors showed a co-dominance of *Actinobacteria* (rel. ab.
497 35%), *Proteobacteria* (rel. ab. 32%) and *Firmicutes* (rel. ab.
498 24%) in the hindgut bacterial community. The dominance of
499 *Firmicutes* we observed in the sea bream analyzed in the

500 present study may be imputed to their specific dietary regimen
501 and rearing conditions, which represent environmental
502 variables known to mold the compositional structure of the gut
503 bacterial community. According to our findings, the gut
504 bacterial community of sea bream was enriched in several
505 fibrolytic *Firmicutes*, such as *Ruminococcaceae*,
506 *Lachnospiraceae* and *Clostridiales*. By producing butyrate
507 from indigestible complex polysaccharides, these
508 microorganisms may provide important beneficial functions for
509 the host (Nicholson et al., 2012). Indeed, butyrate plays
510 multiple roles in host physiology, being strategic for the
511 amelioration of energy extraction from diet, for the
512 reinforcement of the gut epithelium barrier as well as for
513 modulation of the host immune function (Petersson et al., 2011;
514 Arpaia et al., 2013; Russell et al., 2013). In addition, our
515 finding of *Cyanobacteria* in the sea bream gut bacterial
516 community is of particular interest in the context of the recent
517 findings by Di Rienzi et al. (2013). The Authors performed the
518 first whole genome reconstruction of *Cyanobacteria* detected in
519 the gut and proposed their specific designation as a new
520 candidate sibling phylum named *Melainabacteria*. Differently
521 from environmental *Cyanobacteria*, gut *Melainabacteria* are
522 non-photosynthetic and non-respiratory, while, according to the
523 authors, these microorganisms are obligate anaerobic
524 fermenters capable to relay on the different carbon sources

525 present in the gut. Analogous to certain *Firmicutes*,
526 *Melainabacteria* can ferment plant polysaccharides in the gut,
527 and being able to provide the host with B and K vitamins, these
528 microorganisms have been included among the mutualistic
529 components of the gut bacterial community (Di Rienzi et al.,
530 2013).

531 Our finding showed only a subtle impact for the different
532 diets on the overall gut bacterial composition of sea bream, as
533 shown by PCoA analysis. However, evidence suggesting the
534 impact of different levels of SBM on specific components of
535 the gut bacterial community was obtained. At phylum level,
536 increasing SBM dietary levels seem to favor the increase of
537 *Cyanobacteria* and a correspondent decrease in *Synergistetes*.
538 While the first is considered as a mutualistic gut bacterial
539 community component able to provide the host with essential
540 vitamins, *Synergistetes* act as opportunistic pathogens in the gut
541 (Marchandin et al., 2010). Moreover, within the phylum of
542 *Firmicutes* the fish fed a high level of SBM (S30) were
543 enriched with the family of *Lactobacillaceae*, compared to
544 those fed the control diet. The functional impact of lactic acid
545 bacteria on fish intestine is still unclear, but potentially they
546 may have beneficial effects on the immune system, could
547 protect the fish against pathogenic invasion through the
548 intestinal surface, are probiotic candidates and are generally
549 considered as organisms associated with a healthy intestinal

550 epithelium (Cai et al., 1998; Nayak, 2010; Salinas et al., 2008;
551 Dimitroglou et al., 2009; Ingerslev et al., 2014). Interestingly,
552 in rainbow trout, Wong et al. (2013) described a trend of taxa
553 within the phylum *Firmicutes* that were significantly
554 discriminatory for diet type in which the relative abundance of
555 *Lactobacillaceae* was enriched in fish fed a grain-based diet.
556 Also the cichlid, *Astatotilapia burtoni*, which mostly feeds on
557 plants and algae, exhibited most of the gut microbial
558 biodiversity seen in cichlids with several nearly exclusive
559 bacterial taxa such as *Lactobacillales* and gut *Melainabacteria*
560 (Baldo et al., 2015).

561 What favors the presence of *Lactobacillaceae* in fish fed a plant
562 diet is not well known, but some studies have shown that
563 polyunsaturated fatty acids depress the intestinal lactobacilli
564 population in fish (Ringø, 1993) in accordance with the more
565 recent finding of Ingerslev et al. (2014), where a significantly
566 lower amount of lactic acid bacteria was found in rainbow trout
567 fed a marine-based diet compared to the fish fed a plant-based
568 diet containing rape seed oil and pea meal. In contrast, in sea
569 bream total fishmeal replacement with plant protein had a
570 negative effect on the relative abundance of *Firmicutes*
571 throughout the gut, particularly on the lactic acid bacteria
572 *Lactobacillus* and *Streptococcus* (Estruch et al., 2015).
573 *Lactobacillus* species are well equipped to metabolize
574 oligosaccharides that occur in their habitats, such as sucrose,

575 stachyose and raffinose which are contained in soybeans at
576 approximately 10 % (Espinosa-Martosy and Rupérez, 2006;
577 NRC, 2011; Gänzle and Follador, 2012). Moreover,
578 *Lactobacillus* can benefit from simple sugars derived from
579 primary degraders in the gut, establishing syntrophic networks.
580 Thus, in the context of our research, it is reasonable to
581 hypothesize that the *Lactobacillaceae* growth could be
582 supported by these oligosaccharides.

583

584 **5. Conclusion**

585

586 In conclusion results of growth, nutrient utilization and gut
587 histology indicate that SBM can be successfully incorporated
588 up to a level of 300 g kg⁻¹ with the inclusion of 150 g kg⁻¹ of
589 FM as the only animal protein source, without any deleterious
590 effects on growth, protein utilization and gut health during the
591 on-growing phase.

592 A deep sequencing of the gut bacterial community of sea
593 bream during the on-growing phase was successfully obtained.
594 For the first time in this species, the gut bacterial community
595 was analyzed by NGS in fish fed increasing SBM levels using
596 practical current formulations. The overall gut bacterial
597 community was largely dominated by *Firmicutes*, including
598 several fibrolytic bacteria, supporting the hypothesis that this
599 species could be predisposed to digest plant-based ingredients.

600 A minimal impact of increasing dietary SBM levels on the
601 overall gut bacterial community was observed. However SBM
602 seems to favor positively specific components of the gut
603 bacterial community such as *Cyanobacteria* and
604 *Lactobacillaceae* which may provide important beneficial
605 functions for the host and be associated with a healthy intestinal
606 epithelium.

607

608 **Conflicts of interest**

609

610 The authors declare no conflicts of interest.

611

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613

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616

617 **References**

618

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862

863 **Figure captions**

864 Figure 1: histology of sea bream foregut (a,c,e,g,i) and hindgut
865 (b,d,f,h,l). Control diet, C (a,b); 0 g kg⁻¹ SBM diet, S0 (c,d);
866 100 g kg⁻¹ SBM diet, S10 (e,f); 200 g kg⁻¹ SBM diet, S20 (g,h)
867 and 300 g kg⁻¹ SBM diet, S30 (I,l). Intestine does not show any
868 differences in terms of inflammatory or degenerative changes
869 among diets (H&E, 20x objective).

870 Figure 2 a, b: OTUs rarefaction curves carried out with
871 different α -diversity metrics (Faith's phylogenetic diversity
872 (PD whole tree), observed OTUs, the Chao1 measure of
873 microbial richness, and the Shannon index of biodiversity).

874 Figure 3: sea bream gut bacterial community composition at
875 phylum (a) and family levels (b).

876 Figure 4: weighted and unweighted UniFrac distance PCoA of
877 the gut bacterial community of sea bream treated with different
878 diets, color code: S30 diet red, S20 diet green, S10 diet yellow,
879 S0 diet blue, C diet purple. MDS1 and MDS1 represent the
880 15.4 and 2.6 % of the total variability, respectively.
881 Permutation test with pseudo F-ratios: $P = 0.107$ and $P = 0.091$
882 for weighted and unweighted UniFrac, respectively.

883 Figure 5: relative abundance of bacteria composition per
884 sample at phylum (a) and family levels (b).

885 Figure 6: box plot showing the relative abundance of (a)
886 *Cyanobacteria*, (b) *Synergistetes*, (c) *Actinobacteria* and (d)

887 *Lactobacillaceae* in different diets. Significance of the
888 differences was obtained by Kruskal-Wallis test.

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Table 1. Formulation and proximate composition of the experimental diets

<i>Ingredients (g kg⁻¹)</i>	S0	S10	S20	S30	C
FM North Atlantic	150	150	150	150	350
Hi Pro SBM	0	100	200	300	0
Wheat meal	206.4	165.6	125.8	84.0	229.3
Wheat gluten	226	199.1	175.9	150	127.7
Corn gluten	200	185	165	150	130
Sunflower meal	80	60	40	20	40
Fish oil North Atlantic	132.5	135.3	138.3	141	118
Vit/Min premix*	5	5	5	5	5
<i>Proximate composition (g kg⁻¹)</i>					
Moisture	77	76	78	80	60
Crude protein	466	466	479	478	460
Crude fat	194	192	199	209	197
Ash	45	47	48	57	69

FM, fishmeal; SBM, soybean meal; S0, 0 g kg⁻¹ SBM diet; S10, 100 g kg⁻¹ SBM diet; S20, 200 g kg⁻¹ SBM diet; S30, 300 g kg⁻¹ SBM diet; C, control diet.

*Vitamin and mineral premix; Skretting, Stavanger, Norway (fulfilling recommendations for marine fish species given by NRC, 2011).

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Table 2. Growth performance of sea bream fed the experimental diets

	Experimental diet				
	S0	S10	S20	S30	C
<i>Growth</i>					
IBW (g)	76.0 ± 1.6	75.1 ± 0.6	77.1 ± 3.1	76.7 ± 1.9	74.4 ± 0.9
FBW (g)	249.1 ± 6.1	249.2 ± 3.9	257.6 ± 6.2	259.5 ± 5.9	256.2 ± 5.8
SGR (day ⁻¹)	1.17 ± 0.03 ^a	1.20 ± 0.01 ^{ab}	1.22 ± 0.01 ^{ab}	1.25 ± 0.01 ^b	1.21 ± 0.04 ^{ab}
FI (% day ⁻¹)	1.40 ± 0.01 ^a	1.45 ± 0.01 ^{ab}	1.44 ± 0.03 ^{ab}	1.51 ± 0.03 ^c	1.46 ± 0.02 ^{bc}
FCR	1.33 ± 0.03	1.35 ± 0.01	1.33 ± 0.01	1.36 ± 0.04	1.36 ± 0.05

S0, 0 g kg⁻¹ soybean meal SBM diet; S10, 100 g kg⁻¹ SBM diet; S20, 200 g kg⁻¹ SBM diet; S30, 300 g kg⁻¹ SBM diet; C, control diet. IBW, initial body weight; FBW, final body weight; SGR, specific growth rate, 100 * (ln FBW - ln IBW) / days; FI, feed intake, 100 * (crude feed intake / ((FBW + IBW) / 2) / days; FCR, feed conversion rate, (feed intake / weight gain).

Data are given as the mean (n=3; n=60 for IBW and FBW) ± SD. In each line, different superscript letters indicate significant differences among treatments ($P \leq 0.05$).

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Table 3. Viscerosomatic index, hepatosomatic index, body composition and nutritional indices of sea bream fed the experimental diets.

<i>Experimental diet</i>					
	S0	S10	S20	S30	C
VSI	5.62 ± 0.83	5.98 ± 0.95	5.99 ± 0.93	5.72 ± 0.70	5.78 ± 1.03
HSI	1.70 ± 0.34	1.60 ± 0.31	1.64 ± 0.33	1.59 ± 0.32	1.59 ± 0.35
<i>Whole body composition (g kg⁻¹)</i>					
Moisture	619 ± 4.7	626 ± 6.2	628 ± 4.6	632 ± 1.3	615 ± 5.1
Crude protein	174 ± 2.4	174 ± 2.6	175 ± 2.6	179 ± 0.9	173 ± 0.7
Total lipids	173 ± 9.3	175 ± 7.1	175 ± 9.2	180 ± 5.6	174 ± 6.0
Ash	33 ± 2.1	33 ± 1.3	32 ± 2.5	30 ± 0.7	33 ± 2.0
<i>Nutritional indices</i>					
PER	1.62 ± 0.04	1.59 ± 0.01	1.58 ± 0.03	1.54 ± 0.04	1.60 ± 0.06
GPE	28.8 ± 0.92	28.2 ± 0.50	28.4 ± 1.07	28.3 ± 0.86	28.2 ± 1.21
GLE	69.6 ± 4.14	70.1 ± 3.98	69.8 ± 5.26	67.2 ± 4.10	70.3 ± 4.92

S0, 0 g kg⁻¹ soybean meal SBM diet; S10, 100 g kg⁻¹ SBM diet; S20, 200 g kg⁻¹ SBM diet; S30, 300 g kg⁻¹ SBM diet; C, control diet. VSI, viscerosomatic index; HSI, hepatosomatic index; PER, protein efficiency ratio; GPE, gross protein efficiency; GLE, gross lipid efficiency.

Data are given as the mean (n=3; n=15 for VSI and HSI) ± SD. In each line, different superscript letters indicate significant differences among treatments ($P \leq 0.05$). PER, ((final body weight - initial body weight) / protein intake); GPE, (100*[(% final body protein * final body weight) - (% initial body protein * initial body weight)] / total protein intake fish⁻¹); GLE, (100*[(% final body lipid * final body weight) - (% initial body lipid * initial body weight)] / total lipid intake fish⁻¹).

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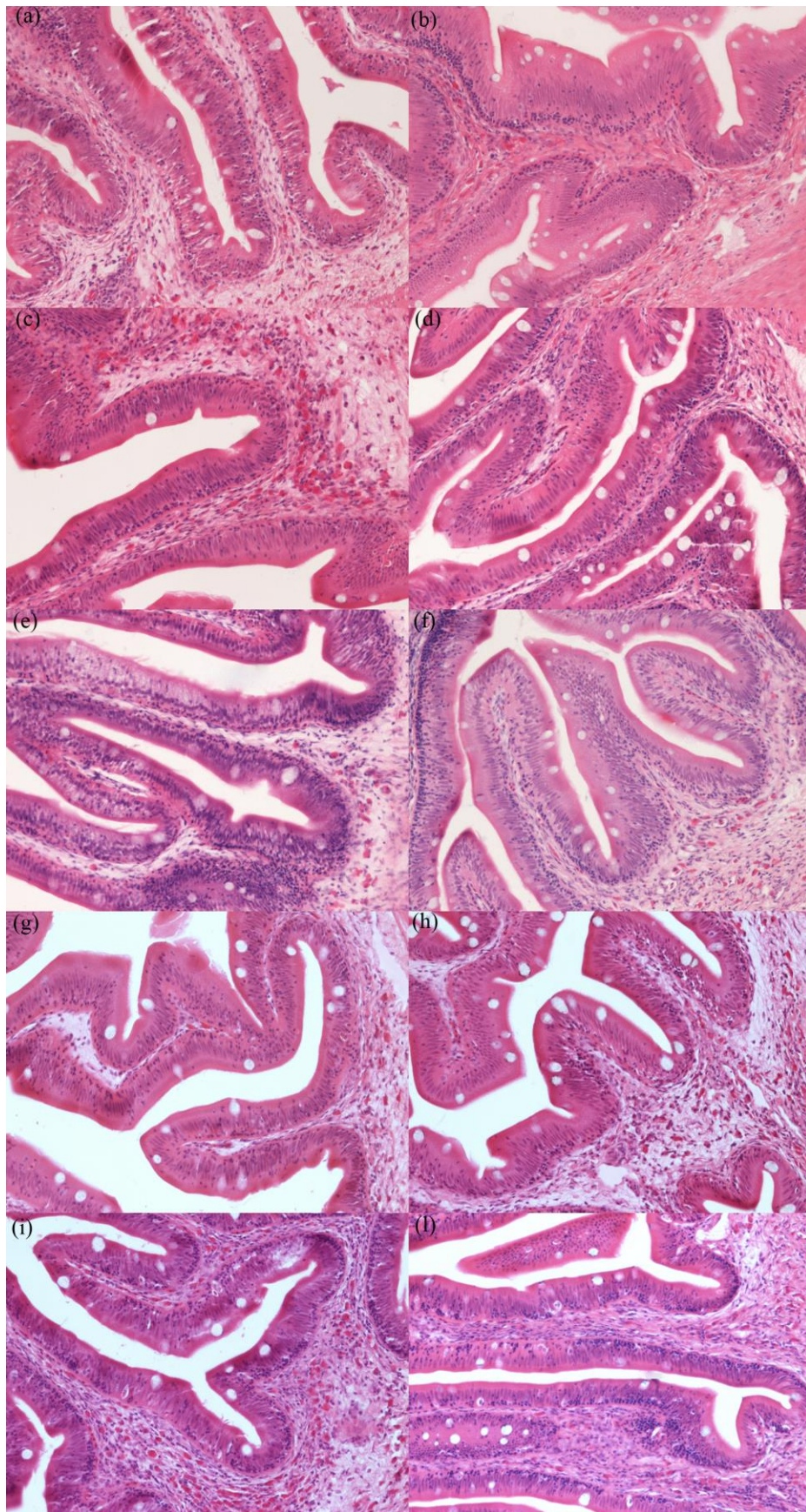
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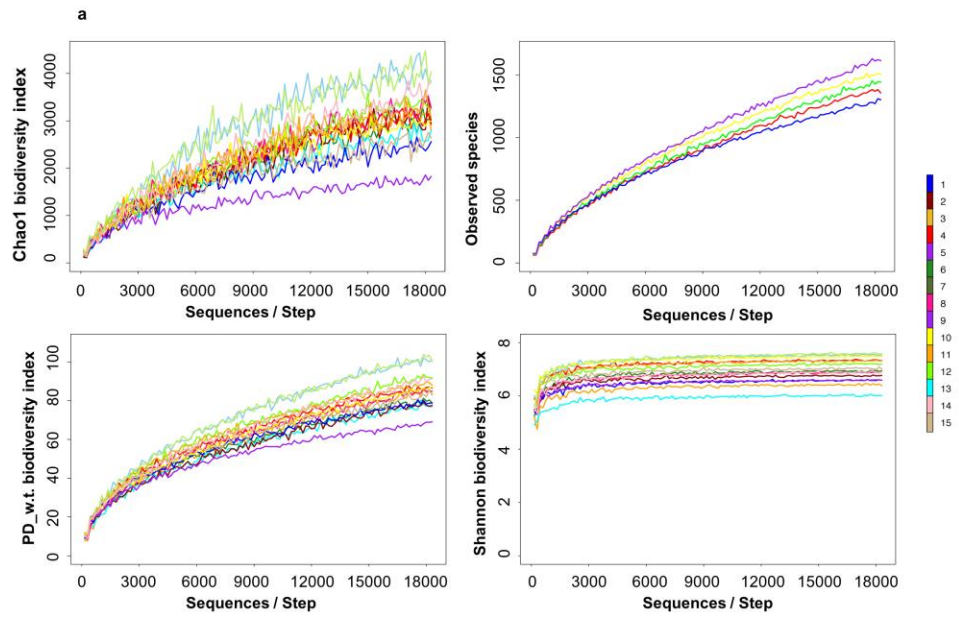
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941 Figure 1



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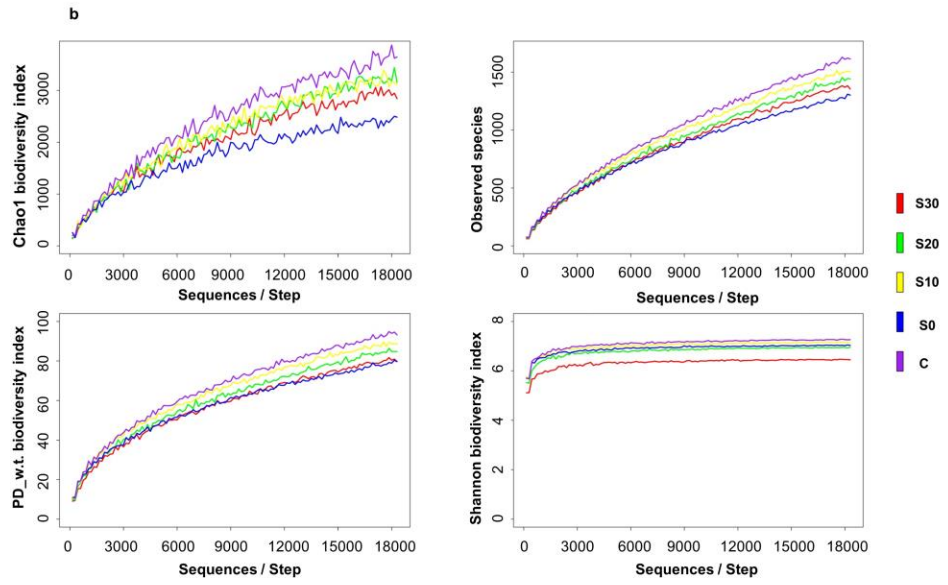
943 Figure 2a



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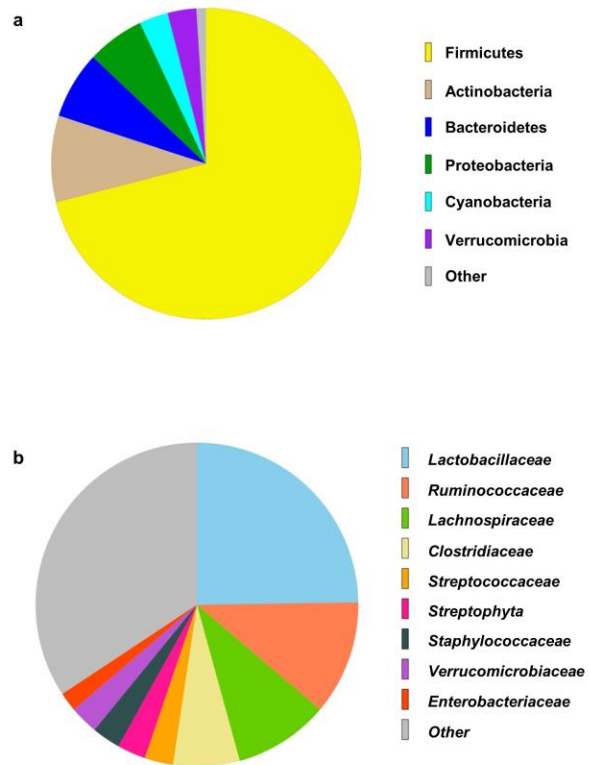


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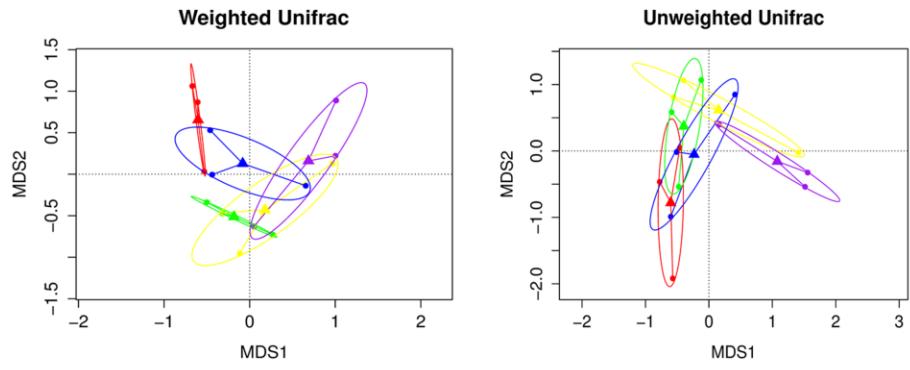
951 Figure 3



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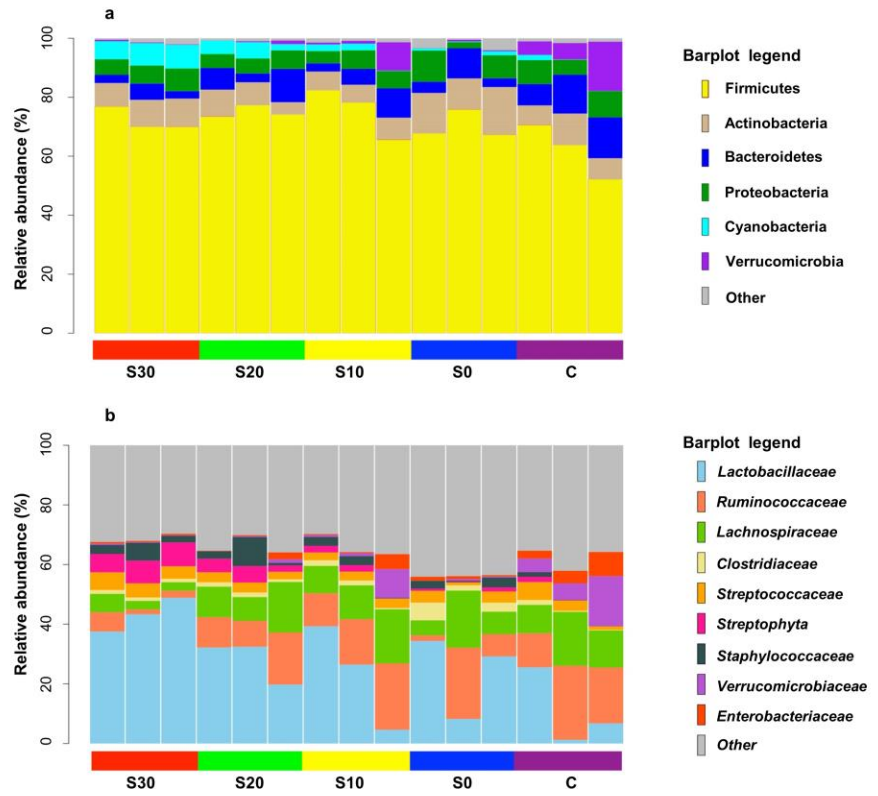
954 Figure 4



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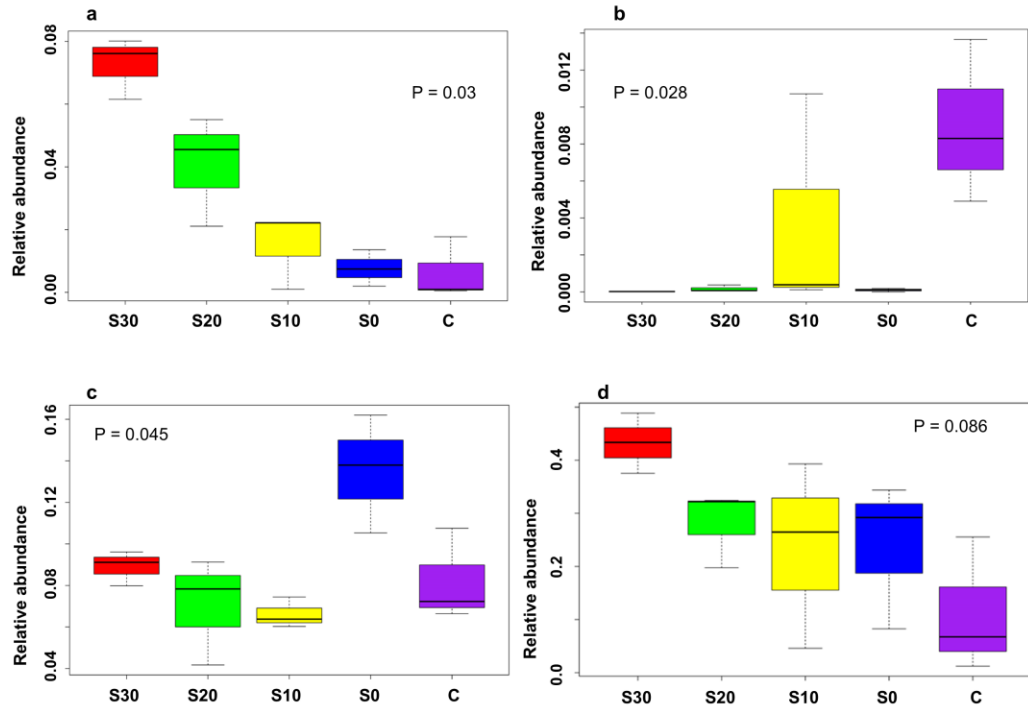
957 Figure 5



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960 Figure 6



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