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(Article begins on next page)

1 **Metataxonomic signature of beef burger perishability depends on the meat origin prior grinding**

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3 Cristian Botta, Irene Franciosa, Valentina Alessandria, Vladimiro Cardenia, Luca Cocolin, Ilario
4 Ferrocino*.

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6 Department of Forestry, Agriculture and Food Sciences, University of Torino, Italy.

7

8 **Running title:** Potentiality of metataxonomic analysis to detect batch variability

9

10 **Key words:** ground beef, metataxonomic, metabolomic, spoilage profiles

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12 * Corresponding author:

13 Department of Agricultural, Forest, and Food Science, University of Turin, Largo Paolo Braccini 2,
14 10095, Grugliasco, Torino, Italy. E-mail address: ilario.ferrocino@unito.it (IF)

15

16 **Abstract**

17 Spoilage dynamics of two hamburger batches from different beef origins were followed from their shared
18 processing run until the use-by date and beyond. Amplicon based sequencing of bacterial and fungal
19 communities were compared with microbial counts and volatilome profile in order to determine whether
20 and at which extent their perishability was related to the batch origin.

21 Microbiological counts did not differ between batch A and B, whereas Volatile Organic Compounds
22 (VOCs) profiles were only distinguishable after the use-by date. Metataxonomic analysis showed that
23 both batches shared the same initial fungal and bacterial community, which however represented a
24 transient signature of the processing run. Indeed, it was rapidly replaced by batch-autochthonous species

25 of fungi and bacteria. Different temporal succession patterns of psychotropic lactic acid bacteria (LAB)
26 were observed between the batches from the fourth day of vacuum storage. In particular, the sequential
27 dominance of *Carnobacterium divergens* and *Leuconostoc piscium* in batch B was correlated with a more
28 heterogeneous volatilome and greater production of VOCs linked to off-odours, such as the acetoin.
29 The metataxonomic survey was able to discriminate between the two batches of hamburgers in relation
30 to their origin and regardless of the initially shared processing-derived contamination.

31

32 **1.INTRODUCTION**

33 Meat consumption has increased worldwide in the last decades in relation to the greater demand from
34 developing countries, in which the growing economic prosperity shifted the dietary habits towards a
35 larger consumption of animal derived proteins (Bonnet, Bouamra-Mechemache, Réquillart, & Treich,
36 2020). It is therefore a concern that every year great percentages of meat products are wasted due to
37 premature spoilage caused by bacteria, molds and yeasts development (Luong, Coroller, Zagorec,
38 Membre, & Guillou, 2020). Indeed, shelf life depends to the tight relationship between physical-chemical
39 composition of a given product and its microbiota. Food organoleptic traits are associated with the
40 metabolic activities of beneficial or unwanted microbial communities, which alternatively determine
41 shelf-life prolongation or reduction (De Filippis, Parente, & Ercolini, 2018).

42 High physical-chemical heterogeneity between different batches characterises meat and influences its
43 initial microbial diversity (Pieszczyk, Czarnik-Matusiewicz, & Daszykowski, 2018). The initial
44 composition of this animal-derived microbiota is subsequently modified by environmental sources of
45 contamination, such as the operator's handling, water, air and the contact with equipment surfaces (Botta,
46 Ferrocino, Pessione, Cocolin, & Rantsiou, 2020; Chaillou et al., 2015; Stellato et al., 2016). Impact of
47 process-derived contamination on the final shelf life are particularly high when hygienic parameters
48 suggested by the Good Manufacturing Practices (GMPs) are not fully accomplished (de Filippis, La

49 Storia, Villani, & Ercolini, 2013; Redondo-Solano et al., 2021). After packaging, the gaseous atmosphere
50 and the maintenance of the cold-supply chain are the only means available to contrast a premature
51 spoilage by slowing down microbial growth.

52 Among fresh meat products, beef burger is more prone to pigment degradation, proteins denaturation
53 and lipid oxidation than intact muscle cuts. The increased surface area leads to high nutrients availability
54 for the microbes growth and favors their catabolic activities (Bao, Puolanne, & Ertbjerg, 2016; Limbo,
55 Torri, Sinelli, Franzetti, & Casiraghi, 2010). In relation to the ISO standards for the enumeration of
56 spoilage population in meat its shelf-life under vacuum packages (VP) spans from ten to fourteen days
57 (Pothakos, Snauwaert, De Vos, Huys, & Devlieghere, 2014). However, the number of biochemical
58 reactions rises considerably in parallel to the microbial growth and compounds related to undesirable
59 sensory changes are produced even before the use-by date (Hultman, Johansson, & Björkroth, 2020;
60 Pothakos, Devlieghere, Villani, Björkroth, & Ercolini, 2015; Valerio et al., 2020).

61 One of the major causes of off-flavours and off-odours in ground beef is the lipid oxidation with the
62 following formation of Volatile Organic Compounds (VOCs) like aldehydes and ketones (Valerio et al.,
63 2020). Overall, VOCs accumulation over certain thresholds can lead to products rejection due to rancidity
64 odours and meat colour change (Casaburi, Piombino, Nychas, Villani, & Ercolini, 2015). These
65 compounds come from the enzymatic degradation of amino acids, of which psychotropic LAB,
66 *Brochothrix thermosphacta* and *Pseudomonas* spp. are known to be the main responsible (Casaburi et
67 al., 2015; Pennacchia, Ercolini, & Villani, 2011). Conversely, little is known on yeasts and molds
68 involvement in the spoilage of chilled packaged meat during shelf-life (Yang, Che, Qi, Liang, & Song,
69 2017), while in dry cold-aged beef the mycobiota is known to alternatively play a spoilage and pro-
70 technological role in relation to the species developed on the crust (Mikami et al., 2021; Oh, Lee, Lee,
71 Jo, & Yoon, 2019; Ryu et al., 2018).

72 In this context, meat industries are constantly seeking for preventative techniques able to maximize the
73 shelf-life of ground beef products by reducing or limiting their initial contamination levels. Different
74 possible strategies have been proposed to accomplish this request: boosting the in-house sanitizing
75 methods with environmental ozone treatments (Botta et al., 2020), prior-grinding decontamination of
76 meat cuts with electrolyzed water (Botta et al., 2021, 2018), and the use of biopreservatives during shelf-
77 life (Ferrocino, Greppi, Lastoria, Rantsiou, & Ercolini, 2016; Grispoli, Karama, Sechi, Iulieto, & Cenci-
78 Goga, 2020). It was however noticed that any preventative technique can be more or less effective in
79 relation to the initial microbiota composition of the treated product, which varies between production
80 runs (Botta et al., 2021; Ferrocino et al., 2016). Characterization of beef microbiota from the early
81 productive phases is therefore important to define its shelf-life the most suitable preventative strategy .
82 To understand at which level of accuracy the metataxonomic analyses can characterise and distinguish
83 ground beef microbiota in relation to their origin prior grinding, two batches of beef burgers
84 manufactured in the same production run were followed along their shelf-life and beyond. Bacterial and
85 fungal community were investigated and comprehensively compared with culture-dependent
86 microbiology and volatilomic profiles.

87

88 **2. MATERIALS AND METHODS**

89

90 **2.1 Beef burger preparation and sampling**

91 Beef burgers were manufactured in a local meat factory (Piedmont, Italy) with beef of *Fassona*
92 *Piedmontese* cattle breed. Two batches (A and B) were prepared (trimming, grinding, packaging)
93 consecutively the same day and in the same processing plant in February 2020: batches were provided
94 from two different breeders, undergone independent slaughtering/maturation processes and no
95 sanitization prior grinding. From each batch a total of 15 beef burgers (100 g each in a square shape)

96 were vacuum packed in a transparent linear low-density polyethylene bags (LLDPE; oxygen
97 transmission, $0.83 \text{ cm}^3 \cdot \text{m}^{-2} \cdot \text{h}^{-1}$ at $23 \text{ }^\circ\text{C}$, $30 \text{ cm} \times 30 \text{ cm}$) and stored at $4.0 \pm 0.5 \text{ }^\circ\text{C}$ without light
98 exposure.

99 The expiration date was fixed by the producer the 14th day of vacuum storage at $4 \text{ }^\circ\text{C}$ in relation to
100 previous shelf-life test performed following standard ISO indications for microbial analysis
101 (ISO13721:1995, ISO 15214:1998, ISO 4833:2003). Three samples for each batch were analysed along
102 five sampling points: the day 0, immediately after grinding-packaging; days 4 and 8, during regular shelf-
103 life; days 15 and 30, after the expiration date.

104

105 **2.2 Microbial counts**

106 Serial dilutions were set up from ground beef samples (10 g of meat in 90 mL Ringer's solution; Oxoid)
107 for each sampling point, with the exception of the the 30th day, due to the suspension of non-essential
108 activities occurred during the pandemic emergency of March 2020.

109 Microbial counts were performed following standard ISO indications for the enumeration of spoilage
110 population in meat products, without varying incubation parameters (temperature, oxygen) to favour the
111 psychotrophic detection. This choice has been operated to resemble the common output obtained from
112 analytical laboratories and metataxonomic analysis.

113 As far as viable population detected: Total Viable Count of mesophilic bacteria (TVC) on Plate Count
114 Agar (PCA) incubated for 48 h at $30 \text{ }^\circ\text{C}$; lactic acid bacteria (LAB) on De Man, Rogosa and Sharpe
115 (MRS) agar incubated for 48 h at $30 \text{ }^\circ\text{C}$ in microaerophilic condition; coagulase-negative cocci (CNC)
116 on Mannitol Salt Agar (MSA) incubated at $30 \text{ }^\circ\text{C}$ for 24 h; *Enterobacteriaceae* on Violet Red Bile
117 Glucose Agar (VRBGA) incubated for 24 h at $37 \text{ }^\circ\text{C}$; yeasts and moulds on Malt Extract agar (MEA)
118 supplemented with tetracycline (0.05 g/L ; Sigma-Aldrich, St. Louis, USA) and incubated at $25 \text{ }^\circ\text{C}$ for

119 five days. All media and supplements were provided by Biolife s.p.a. (Milan, Italy) unless differently
120 stated. The pH of each sample was measured by using a digital pH-meter (Crison, Modena, Italy).

121

122 **2.3 Analysis of volatile organic compounds (VOCs)**

123 The volatile organic compounds (VOCs) in both batches of beef burger samples were determined in
124 triplicate following the protocol suggested by Mentana and colleagues (2019) slightly modified. The
125 VOCs were extracted using headspace-solid phase microextraction (HS-SPME) and analysed by GC/MS
126 (QP-2010 Plus, Shimadzu, Japan), interfaced with a computerized system for data acquisition (Software
127 GC–MS Solution V. 2.5, Shimadzu, Japan). Briefly, 3.0 g of ground meat were accurately weighted in a
128 20 ml glass headspace vial with 20 μ l of internal standard solution (1-octanol, 1.05 μ g/mL) and sealed
129 with a PTFE silicone septum. The VOCs were isolated by a fused-silica fibre (10 mm length) coated with
130 a 50/30 mm thickness of DVB/CAR/PDMS and a Combi Pal system (CTC Analytics AG, Zwingen,
131 Switzerland). The samples were conditioned at 40 °C for 15 min in order to reach the equilibrium; then,
132 the fiber was exposed to headspace for 30 min. Next, the fiber was desorbed in split mode (split ratio
133 1:25) into the GC/MS injector at 248 °C for 5 min. The separation of VOCs was achieved using a
134 Stabilwax column (20 m, 0.18 mm i.d., 0.18 μ m film thickness, Restek, USA). Helium was used as
135 carrier gas at constant linear velocity of 36.2 cm/sec, the oven temperature was from 40 °C (maintained
136 for 4 min) to 210 °C by 5 °C/min, then increased up to 250 °C by 20 °C/min, the final temperature was
137 held for 5 min. The ion source and interface temperature were set at 200 and 230 °C, respectively. The
138 filament emission current was 70 eV and a mass range from 33 – 350 amu was scanned at 0.30 scan/s in
139 scan mode. VOCs were recognized by comparing their mass spectra with those reported in the NIST08s
140 (National Institute of Standards and Technology, Gaithersburg) library and pure commercial standards.
141 In addition, the blank injection of fiber and vials were also carried out to prevent environmental

142 contamination. For quantitative purposes the response factor between the total ion current of each analyte
143 and internal standard was used to determine VOCs concentrations as $\mu\text{g/g}$.

144

145 **2.4 Amplicon-based sequencing**

146 At each sampling point, 1 ml of the first 10-fold serial dilution was collected, centrifuged at 13,000 rpm
147 for 30 s, the pellet was collected and stored at $-80\text{ }^{\circ}\text{C}$ until DNA-extraction. Total DNA was extracted
148 from each sample collected as previously described (Ferrocino et al., 2016), standardized at 100 ng/L
149 (NanoDrop 1000 spectrophotometer; Thermo Scientific, Milan, Italy) and used to study the
150 metataxonomic profiles of bacterial and fungal microbiota in parallel. Amplicon library of V3-V4 region
151 was constructed from 16S rRNA gene of bacterial DNA using primers and conditions previously reported
152 (Klindworth et al., 2013), while amplicon library of the D1 domain from 26S rRNA gene of fungal Large
153 Ribosomal Subunit (LSU) was prepared with primers and conditions described by (Mota-Gutierrez,
154 Ferrocino, Rantsiou, & Cocolin, 2019).

155 The PCR products of both libraries were purified with Agencourt AMPure kit (Beckman Coulter, Milan,
156 Italy) and the resulting products were tagged with sequencing adapters using the Nextera XT library
157 preparation kit (Illumina Inc, San Diego, CA), according to the manufacturer's instructions. Sequencing
158 was performed using a MiSeq Illumina instrument (Illumina) with V3 chemistry, which generated 2 X
159 250 bp paired-end reads. MiSeq Control Software, V2.3.0.3, RTA, v1.18.42.0, and CASAVA, v1.8.2,
160 were used for the base-calling and Illumina barcode demultiplexing processes.

161

162 **2.5 Bioinformatic analysis**

163 A total of 570,943 and 1,673,760 raw-reads were respectively produced by 16S and 26S amplicon-based
164 sequencing of the thirty samples collected. To obtain Amplicon Sequence Variants (ASVs) the raw-reads

165 were analysed with *DADA2* package in R environment (Callahan et al., 2016), using R program for
166 Statistical Computing 4.1.1 (<http://www.r-project.org>).

167 For 16S amplicon-based sequencing, 325,271 reads passed the quality filtering parameters applied
168 [*truncLen=c(250,222); trimLeft = c(35,35); maxEE=c(2,2); minLen = c(50,50)*] with an average value
169 of 10,842 reads/sample. After merging (minimum overlap of 5 bp) and *de-novo* chimera removal (*per-*
170 *sample* method) all paired-end sequences shorter than 365 bp were discharged: 89.1 % of the initial
171 filtered sequences were used to construct bacterial ASVs frequency table. For 26S fungal gene, filtering
172 parameters [*truncLen=c(245,240); trimLeft = c(35,35); maxEE=c(2,2); minLen = c(50,50)*] reduced the
173 reads to 1,185,674 (40,781 reads/sample in average). After merging (minimum overlap of 12 bp) and *de-*
174 *novo* chimera removal (*per-sample* method) no trimming was performed in relation to the length
175 variability of this amplified region; one sample of production B collected from the fifteenth day was
176 removed due to low sequences number (< 1000). Finally, 54.2 % of the initially filtered sequences were
177 used to construct fungal ASVs frequency table. All parameters not reported for filtering/merging steps
178 are intended as default *DADA2* setting.

179 Taxonomy was assigned with a 99 % sequence similarity through Bayesian classifier method (Wang,
180 Garrity, Tiedje, & Cole, 2007) by matching bacterial ASVs to the 2021 release (version 138.1) of Silva
181 prokaryotic SSU reference database (<https://zenodo.org/record/4587955#.YObFvhMzZRE>), with a
182 further check at 100 % of similarity for ASVs assigned to the species level with the *addSpecies* script.
183 Fungal ASVs taxonomy was assigned at 99 % against an internal database of 26S rRNA (Mota-Gutierrez
184 et al., 2019), then confirmed against NCBI LSU-reference database by using BLASTn suite
185 (<https://www.ncbi.nlm.nih.gov/nucore?term=PRJNA51803>). When the taxonomic assignment was not
186 able to reach the species, the highest taxonomic level available was displayed. ASVs with uncertain
187 taxonomic assignment (to the Order rank or lower resolution) were aligned against NCBI nucleotide
188 collection (<https://www.ncbi.nlm.nih.gov/>) and all sequences matching (> 99 % similarity) vegetable

189 genomes (mainly pepper), animal genomes (meat), mitochondria and chloroplasts were removed from
190 the frequency tables.

191 ASVs were aligned with PyNAST (Caporaso et al., 2010) and unrooted phylogenetic trees were
192 constructed with FastTree (Price, Dehal, & Arkin, 2009) to allow further phylogenetic based analysis.

193 Alpha diversity metrics (Observed Species, ACE, Shannon, Simpson, Fisher, PD whole tree) and
194 weighted UniFrac beta-diversity distance were calculated with *phyloseq* and *picante* packages (Kembel
195 et al., 2010; McMurdie & Holmes, 2013): rarefaction limit was set to the lowest number of
196 sequences/sample.

197 Metagenome inference was performed from bacterial ASVs frequency table with MetGEMs toolbox
198 (Patumcharoenpol et al., 2021) using default parameters (<https://github.com/yumyai/MetGEMs>) and
199 AGORA collection as reference database of genome-scale models (Magnúsdóttir et al., 2017). Gene
200 family abundances were predicted and identified as KEGG orthologs (KO) and collapsed at level 3 of
201 the KEGG annotations.

202 Sequencing data were deposited at the Sequence Read Archive of the National Center for Biotechnology
203 Information under the bioproject accession number PRJNA777553.

204

205 **2.6 Statistics**

206 Statistical analyses and data plotting were performed in R environment unless otherwise stated. Normality
207 and homogeneity of the data (Log-Transformed abundances, alpha-diversity metrics, viable counts,
208 VOCs concentrations) were checked by means of Shapiro-Wilk's W and Levene's tests, respectively.

209 Variation and differences between multiple groups were assessed with one-way ANOVA (coupled with
210 Tukey's post-hoc test) and Kruskal–Wallis's test (coupled with pairwise Wilcoxon's test) for parametric
211 and not parametric data, respectively. Pairwise comparisons were alternatively performed with Wilcoxon
212 and T-tests according to data normality.

213 Principal Component Analysis (PCA) was performed on VOCs concentrations with *factominer* package.
214 Adonis and ANOSIM statistical tests were used to detect significant differences among VOCs (PCA
215 scores) and microbial communities (PCoA based on β -diversity weighted UniFrac distance). Non-metric
216 Multi-Dimensional Scaling (NMDS) analyses were based on Bray-Curtis dissimilarities and were
217 performed by using original ASVs frequency tables as input. The significance influence of time and batch
218 (individually or interactively) on clusters produced by NMDS was tested by Permutation Analysis of
219 Variance (PERMANOVA), using the *Adonis* function based on Bray-Curtis dissimilarity distance. Best
220 set of taxa and VOCs that were significantly fitting (Pearson's moment correlation; Bray-Curtis distance)
221 with the NMDS-based distribution of the samples were calculated by *bioenv* function and plotted in the
222 NMDS bi-plot as vectors (Torondel et al., 2016).

223 To construct the ASVs co-occurrence/exclusion network, the SparCC algorithm was run with default
224 parameters and 100 bootstraps using the package *SpiecEasi* (Friedman & Alm, 2012). Pseudo *P*-values
225 were calculated as the proportion of simulated bootstraps and only highly significant (pseudo *P*-values <
226 0.001) positive ($R > 0.5$) and negative ($R < -0.5$) correlations were used to infer the network with the
227 program Gephi 0.9.2-beta (<https://gephi.org>). Presence of recurrent sub-networks modules (group of
228 ASVs that are co-varying) were detected considering only co-occurrences through the modularity
229 algorithm implemented in Gephi suite with default parameters (Blondel, Guillaume, Lambiotte, &
230 Lefebvre, 2008). Correlation between taxa (ASVs merged at highest taxonomic level achieved) and
231 VOCs concentration was performed by means of Spearman's rank correlation.

232 Enrichment analysis was performed with *GAGE* package on the predicted KO abundance table to identify
233 biological pathways significantly overrepresented and underrepresented between batches (Luo,
234 Friedman, Shedden, Hankenson, & Woolf, 2009).

235

236 **3. RESULTS**

237

238 **3.1 Microbiological dynamics**

239 No differences were observed in microbiological dynamics between batches A and B by comparing each
240 single sampling point at 0, 4, 8 and 15 days, although in batch B we observed the tendency to reach
241 higher counts the fifteenth day (**Fig. 1**). As far as the time-dependent growth, in both batches TVC and
242 LAB counts increased significantly (Kruskal-Wallis; $P < 0.05$) from day 0 to the eighth day with a
243 progressive growth of 3 logarithms. On the other hand, yeast counts increased significantly from the
244 fourth to the eighth day (~ 1.5 Log CFU/g increase), whereas the *Enterobacteriaceae* population showed
245 a marked growth from eighth to the fifteenth day ($P < 0.05$). The pH value remained stable along the first
246 fifteen days of storage, with an average value of pH 5.52 ± 0.12 (**data not shown**).

247

248 **3.2 Metabolomic biomarkers of spoilage**

249 A total of fifty-two VOCs were quantified in the headspace of beef burger packages along the 30 days
250 of storage monitored (**Supplementary Table 1**). Alcohols represented the more abundant compounds
251 (10.3 ± 5.2 $\mu\text{g/g}$ in average), followed by aldehydes (7.0 ± 5.0 $\mu\text{g/g}$), ketones (2.0 ± 1.1 $\mu\text{g/g}$), organic
252 acids (1.5 ± 1.2 $\mu\text{g/g}$) and alkanes (1.1 ± 0.7 $\mu\text{g/g}$). Less abundant VOCs were represented by esters
253 (mainly ethyl acetate), aromatic compounds (indole) and one lactam (caprolactam). Changes in the
254 volatilomic profile were mainly related to storage time, with some VOCs that showed different dynamics
255 between batches. In particular, along the shelf-life of batch A the amounts of hexanal, isopropyl alcohol
256 and the acetic/formic acids decreased significantly (ANOVA and Tukey's post hoc; $P < 0.05$) after the
257 fourth day, while butanoic and propanoic acids concentrations increased after the eighth day. Less time-
258 dependent variability was observed in batch B, were only three VOCs (1-pentanol, 2-heptenal, ethyl-
259 cyclopentane) decreased progressively and significantly along the 30 day of vacuum storage. In both
260 batches, ethanol, 3-methyl-1-butanol, ethyl acetate and caprolactam showed the highest concentrations

261 the thirteenth day, whereas 1-octel-3-ol significantly decreased at the end of storage. Moreover,
262 comparing the volatilomes profile of the batches in each single day we observed that several VOCs
263 (pentanal, 2-butanone, acetoin, acetone, ethyl-cyclopentane, 3-methyl- heptane, ethyl acetate) were
264 significantly (T-test; $P < 0.01$) more abundant in batch B the eighth and fifteenth day.

265 Principal Component Analysis (PCA) confirmed that time had a greater impact on data variance in
266 comparison to the effect exerted by the batches. Indeed, scores plots show a significant (Anosim and
267 ADONIS tests; $P < 0.001$) separation of the thirtieth day samples from all the others (**Fig 2 A**).
268 Considering that the two first PCA dimensions explained 47.8 % of the variance, the discrimination of
269 the samples along time is mainly led by the first dimension (Dim1), with the second dimension (Dim2)
270 related to the minimal and not significant segregation of the samples between batches (**Fig 2 B**). The
271 corresponding loading plot of the variables shows that alkanes and aldehydes/alcohols are the main
272 VOCs that contribute to the variance explained by the first and second dimensions, respectively (**Fig 2**
273 **C and D**).

274

275 **3.3 Compositional changes in bacterial and fungal communities during shelf-life**

276 Bacterial community of beef burgers was mainly formed by members of Firmicutes phylum, namely
277 *Leuconostoc gelidum*, *Dellaglioia sp.*, *Carnobacterium divergens*, *Latilactobacillus sp.*, *Streptococcus*
278 *salivarius*, *Lactococcus piscium*, *Kocuria rhizophila* and different species belonging to *Staphylococcus*
279 (**Fig 3 A**). Gram negative bacteria were less abundant and primarily represented by *Bacteroides sp.* and
280 the psychrophiles *Pseudomonas fragi/psychrophila*, in the early and late stages of storage respectively.
281 Through the Permutational Analysis of Variance (PERMANOVA; **Supplementary Table 2**) we
282 observed that the greatest portion of variability in the microbiota composition was determined by the
283 batch ($R^2=0.122$; $P < 0.01$), while the time explained a lower portion of variability and not significantly
284 ($R^2=0.104$; $P>0.05$). Independently from time, batch B was characterized by greater ($P[FDR] < 0.05$)

285 richness, diversity and an overall higher ($P[\text{FDR}] < 0.001$) presence of *Lactococcus piscium*,
286 *Carnobacterium divergens*, *Pseudomonas psychrophila* and *Pseudomonas fragi* abundances, in
287 comparison to batch A (**Supplementary Figure 1**). Moreover, we observed during vacuum storage of
288 the batches different succession patterns of the main species, more easily appreciated by dividing the
289 period in three storage phases (**Fig 3 B**): hamburgers at day 0, shortly after production and packaging
290 (named “Production”); within the use-by date (day 4 and 8 collectively named “Shelf-life”); and after
291 the use-by date (day 15 and 30 collectively named “Expired”). In particular, ASVs assigned to
292 *Leuconostoc gelidum*, *Carnobacterium divergens* and *Dellagliola* sp. were not detected the first day. On
293 the contrary, *Streptococcus*, *Staphylococcus* and *Kokuria* were highly abundant the first day and not
294 anymore present after the fourth day of storage. Interestingly, the disappearance of initially dominating
295 taxa, like *Staphylococcus* and *Kokuria*, was less significant and more gradual in batch B, in which we
296 observed after the use-by date a greater increase of *Lactococcus piscium* and an undefined *Lactobacillus*
297 species included in the new *Latilactobacillus* genus. However, β -diversity analysis (**Fig 3 C**) showed
298 that beef burgers immediately after production (day 0) represented in both batches a phylogenetically
299 distinct community (weighted UniFrac distance; ADONIS and Anosim: $P[\text{FDR}] < 0.001$) compared to
300 all the following sampling points (days 4, 8, 15 and 30).

301 As far as fungi are concerned, we observed a core mycobiota composed by nine yeasts and three molds,
302 which represented together more than 50 % of total abundance in 70 % of the samples (**Figure 4**). In
303 particular, *Kurtzmaniella zeylanoides* and *Debaryomyces hansenii* were the most abundant yeasts and
304 were present in all samples, followed by less ubiquitous ASVs assigned to the *Trichosporonaceae* family
305 (*Trichosporon*, *Apiotrichum*) and to the genera *Starmerella*, *Cutaneotrichosporon* and *Malassezia*.
306 Filamentous fungi were mainly represented by *Cladosporium cladosporioides*, *Penicillium* sp. and, to a
307 lesser extent, *Phanerochaete australosanguinea*. As far as compositional variability of the mycobiota,
308 PERMANOVA did not highlight any significant effect of time and batch (**Supplementary Table 2**).

309 Accordingly, no significant differences in the distribution of the main taxa and alpha-diversity measures
310 were observed between batches, along the time course and in relation to the three phases aforementioned.
311

312 **3.4 Correlation patterns of bacterial and fungal communities**

313 In order to display and better understand the ecological associations determined by the succession
314 patterns observed, a co-occurrence/exclusion network was inferred using the significant SparCC
315 correlations (P -value < 0.001) existing among the core bacteria and fungi, at the level of each unique
316 ASV (**Fig. 5 A**).

317 The correlation network shows 45 nodes composed by 27 bacterial- and 18 fungal-ASVs, respectively;
318 these nodes are connected by 161 edges, of which 120 represent positive correlation. The majority of the
319 remaining 41 negative correlations were observed between ASVs of the same kingdom. Bacteria related
320 to the initial meat contamination, such as *Staphylococcus*, *Kokuria* and *Streptococcus*, were negatively
321 correlated to ASVs that were predominant from the fourth day of vacuum storage, namely *Dellaglioia*,
322 *Leuconostoc*, *Carnobacterium* and *Latilactobacillus*. Within fungi, ASVs assigned to *Kurtzmaniella*
323 *zeylanoides* and *Kurtzmaniella santamariae* showed the higher number of negative correlations with the
324 other yeasts and moulds and several positive correlations with the bacterial ASVs of *Dellaglioia*,
325 *Leuconostoc* and *Latilactobacillus* (**Supplementary Table 3**).

326 Taking into account only the co-occurrences (**Fig. 5 B**), five modules of highly co-occurring ASVs were
327 identified. The modules coded as 2 and 3 encompass the initial mycobiota and microbiota of hamburgers,
328 respectively, whereas the closely related modules 0 and 1 comprise all ASVs that dominated the
329 microbiota and mycobiota of hamburgers from the fourth to the thirteenth day. Notably, the bacterial
330 ASVs grouped in the module 0 are distinctive of the batch B (**Fig. 5 C**).

331

332 **3.5 Links between volatilomic profiles and microbiota composition**

333 To depict the significant batch-to-batch variation of the bacterial community, non-metric
334 multidimensional scaling (NMDS) based on core species (> 0.5 % average abundance) was performed
335 (**Fig. 6**). NMDS ordination was not plotted for the fungal community in relation to the not significant
336 influence of batches and time on its distribution.

337 In addition to the NMDS ordination of the samples, VOCs and bacterial taxa significantly correlated
338 (Pearson's correlation; $P < 0.001$) with the bacterial community variance were plotted as arrows, of
339 which vertexes represent the direction of change of each VOC and taxa (**Fig. 6 and Supplementary**
340 **Table 4**). The presence of *Kokuria rhizophila* and formic acid was markedly related to the moment of
341 packaging (day 0) in both batches. Acetoin, indole and hexanal were correlated to batch B, and in
342 particular to its shelf-life period (days 4 and 8), while benzenacetaldheyde was mostly correlated with
343 the expired samples of this batch (from 15 to 30 days). As far as the bacterial species are concerned, the
344 separation between samples of the two batches was highly correlated to the presence of *Carnobacterium*
345 *divergens* and the duo *Dellagliola sp./Leuconostoc gelidum* in batch A and B, respectively. Moreover,
346 NMDS plot highlighted the gradual change of microbiota composition in batch B during early stages
347 (from 0 to 4 days), in comparison to A in which it is graphically more marked.

348 Concerning the direct pairwise correlations between bacteria/fungi abundances and VOCs concentration,
349 we observed that the pattern of positive and negative correlations ($P[\text{FDR}] < 0.001$) were highly
350 dependent of the time course (**Supplementary Figure 2**). Indeed, all dominant taxa in the early stages
351 of storage (Bacteria: *Kokuria*, *Staphylococcus*, *Streptococcus*; Fungi: *Cladosporium*, *Apiotrichum*) were
352 positively correlated with the VOCs mostly present at day 0, such as hexanal, 1-pentanol, acetic and
353 formic acid. On the contrary, the most abundant taxa *Leuconostoc gelidum* and *Kurtzmaniella*
354 *zeylanoides*, which have developed after the fourth day, were negatively correlated with these VOCs.

355

356 **3.6 Functional differences in the inferred microbiome**

357 The majority of the metabolic pathways differentially represented (*GAGE* enrichment statistic: $P <$
358 0.001) between the two batches belonged to the carbohydrate metabolism (**Supplementary Figure 3**).
359 In particular, five pathways related to the monosaccharides/polysaccharide metabolisms (ko00052,
360 ko00500, ko00051, ko00040) and the central pathway of glycolysis/gluconeogenesis (ko00010) were
361 presumptively overrepresented in A and underrepresented in B. In parallel, the TCA cycle (ko00020),
362 the pathways of glyoxylate/dicarboxylate metabolism (ko00630), and two pathways responsible of
363 butyric and propionic acids production (ko00640, ko00650) were likely overrepresented in B.
364 Abundance differences of metabolic pathways related to amino acid metabolisms were observed as well,
365 with valine/leucine/isoleucine degradation (ko00280) and β -alanine metabolism presumptively enriched
366 in B, and an overall higher biosynthesis of amino acids (ko01230) histidine-glutathione metabolisms
367 (ko00340, ko00480) predicted in the batch A. Finally, lipopolysaccharide biosynthesis (ko00540) was
368 enriched in B, while conversely the glycerophospholipid metabolism (ko00564) was presumptively more
369 abundant in A.

370

371 **4. DISCUSSION**

372 Metataxonomic has already proved capable to characterize and clearly distinguish ground beef
373 microbiota among different production runs (Botta et al., 2021; Sade, Penttinen, Björkroth, & Hultman,
374 2017). Deeping the potentiality of this culture-independent analysis, here the possibility to
375 microbiologically discriminate between beef burger batches manufactured in the same processing run
376 but from different pre-grinding origin has been explored.

377 The two batches studied have shown the same microbial counts along time course, likely in reason of the
378 same initial contamination level and storage conditions. As expected in a vacuum packaged meat, LAB
379 population constituted the majority of the culturable fraction from the early storage stages (Ercolini,
380 Russo, Torrieri, Masi, & Villani, 2006; Pothakos et al., 2015), and reached a microbial spoilage threshold

381 capable to cause sensory deterioration already the eighth day (Stoops et al., 2015). On the basis of
382 stationary phase reached , we could assume that both batches were already in the early spoilage condition
383 at the end of the first week (Hultman et al., 2020).

384 On the other hand, metataxonomic analysis highlighted from the fourth day a marked discrepancy
385 between batches of most abundant taxa, mainly represented by psychrotrophic LAB species, which are
386 generally recognized as meat spoilers and usually underestimated by mesophilic enumeration protocols
387 (Jääskeläinen et al., 2015; Pennacchia et al., 2011; Pothakos et al., 2014; Stoops et al., 2015). Despite we
388 are aware that different incubation conditions would have potentially provide different LAB dynamics,
389 a distinction between the microbial composition of batches would have not be effective if not coupled
390 with a massive isolation and identification of the colonies (Pothakos et al., 2014). Moreover, due to the
391 advancement of new technologies, the current time to execute metataxonomic analysis are comparable
392 to those of a complete culture-based characterization of microbiota (Jagadeesan et al., 2019; Rhoads &
393 Au, 2015; van Dijk, Jaszczyszyn, Naquin, & Thermes, 2018). Therefore, metataxonomic analysis
394 demonstrated in the present study to provide a better discriminatory capability than culture-dependent
395 approaches.

396 Aside the comparison between culture-dependent and -independent outputs, we observed through
397 metataxonomic analysis a temporal succession of species in both bacterial and fungal ecologies. While
398 time course succession of spoilage bacteria has been widely observed during cold storage of packaged
399 meat , no information is available on mycobiota development in ground beef during its cold-vacuum
400 storage (Jääskeläinen, Hultman, Parshintsev, Riekkola, & Björkroth, 2016; Sade et al., 2017). Indeed,
401 the numerous culture-independent surveys carried out on cured meats are not directly comparable in
402 reason to significantly higher temperatures (Alapont, Martínez-Culebras, & López-Mendoza, 2015; Alía
403 et al., 2016; Belleggia et al., 2020; Franciosa et al., 2021). Our observation and the mycobiota dynamics
404 described in dry cold-aged beef indicate that a longitudinal succession of yeast species can occur also

405 during meat cold storage, and it is generally characterised by an increasing presence of *Kurtzmaniella*
406 *zeylanoides* along time course (Oh et al., 2019; Ryu et al., 2018). However, the weak increase of yeast
407 and mold counts showed their inability to actively affect beef burgers spoilage, confirming previous
408 observations in tray-packaged pork during cold storage (Yang et al., 2017).

409 Immediately after packaging, bacterial and fungal communities were composed in both batches by genera
410 and species that commonly inhabit the processing plant environment and can colonise meat during each
411 processing run (Botta et al., 2020; Chaillou et al., 2015; Kang, Ravensdale, Coorey, Dykes, & Barlow,
412 2019). In particular, several species of *Staphylococcus* and *Streptococcus*, as well as fungi like
413 *Malassezia*, *Trichosporon* and *Cutaneotrichosporon*, are well known members of human/animal skin,
414 nostrils and mouth (Cundell, 2018; Zhang et al., 2020). On the other hand, *Kocuria* spp. and filamentous
415 fungi (*Cladosporium*, *Penicillium*) were more probably transported on meat contact surfaces by dust and
416 air (Chaillou et al., 2015). A distinguishing composition of bacterial community at the moment of
417 production-packaging have already been observed during packaged beef shelf-life and associated to
418 different production days (Sade et al., 2017).

419 Noteworthy, this initial autochthonous community has here represented a transitory signature of the
420 production run shared by the two batches. Indeed, it has been soon replaced by other batch-
421 autochthonous species likely collected on the carcasses and cuts during the previous slaughtering-boning
422 phases carried out in the supplier's facilities (Kang et al., 2019). This second community was mainly
423 composed by psychotrophic LAB suited to develop during shelf-life and to cause the product spoilage
424 (Pothakos et al., 2015). The parallel logarithmic increase of LAB counts confirms the predominance of
425 this population over the rest of spoilage microbiota, in spite of the aforementioned culture-dependent
426 underestimation of psychrotrophs.

427 Not only bacteria distribution and abundances differed between batches, but also their temporal
428 succession patterns did. *Leuconostoc gelidum* and *Dellagliola* sp. took simultaneously and sharply over

429 the dominance after packaging in batch A, and remained predominant until the thirtieth day. On the
430 contrary, *Carnobacterium divergens* become the predominant species in batch B until the eighth day,
431 from which onwards a remarkable presence of *Lactococcus piscium* and *Pseudomonas spp* was observed.
432 The occurrence of *Pseudomonas spp.* in the late vacuum storage phases and a more heterogeneous
433 production of VOCs, with some concentrations over the threshold of sensory perception, indicates a
434 faster spoilage dynamic for the batch B in comparison to A (Casaburi et al., 2015; Ercolini et al., 2011).
435 This worst-case scenario in batch B is likely connected to the dynamic and rapid succession of spoilage
436 bacteria occurred during its vacuum storage.

437 Focusing on VOCs production, high concentrations of acetoin were observed in the second week of B
438 storage. The accumulation of this buttery-odour compound in vacuum packaged meat can be the result
439 of *Carnobacterium divergens* homofermentative metabolism or the catabolism of aspartate and alanine
440 by *Lactococcus piscium*: both predominant in this batch (Andreevskaya et al., 2018; Höll, Hilgarth,
441 Geissler, Behr, & Vogel, 2020). In particular, acetoin production by *Lactococcus piscium* take place in
442 the late stages of vacuum meat storage when glucose has been consumed by other fast-growing LAB
443 able to upregulate carbohydrate pathways, such as the *Leuconostoc gelidum* that was dominant in batch
444 A (Andreevskaya et al., 2018; Hultman et al., 2020). Noteworthy, metabolic pathways related to
445 monosaccharides and amino acids catabolisms were presumptively more abundant in batch A and B,
446 respectively.

447 Moreover, *Lactococcus piscium* is the main meat spoilage LAB in low oxygen conditions in which
448 represents an endpoint indicator of shelf-life, while in presence of oxygen the *Leuconostoc gelidum* is
449 favoured by its heme-dependent respiration capability (Botta et al., 2021; Jääskeläinen et al., 2016;
450 Rahkila, Nieminen, Johansson, Säde, & Björkroth, 2012). Different factors from the gaseous composition
451 have therefore alternatively boosted the development of these two species two vacuum packaged batches;
452 for instance the presence of more or less mutualistic species in the original batch-autochthonous

453 microbiota. Co-occurrence analysis has indeed suggested a limited ecological coexistence in these
454 batches between *Lactococcus piscium* and *Leuconostoc gelidum*. On the contrary, a better level of
455 coexistence seems to exist between *Leuconostoc gelidum* and *Dellagliola*, another predominant spoilage
456 species in low oxygen conditions (Jääskeläinen et al., 2016). Bearing in mind that inferred correlations
457 among abundances may not directly reflect the real ecological interactions, further physiological
458 confirmation of the co-occurrences observed are undoubtedly needed (Faust & Raes, 2012; Hirano &
459 Takemoto, 2019).

460 To conclude, this study showcases that metataxonomic-based profiling of meat microbiota represents an
461 effective approach to recognize in each production run the batches of different origin. In parallel we
462 showed that final production phases like trimming and grinding seems to produce transitory modification
463 of the autochthonous microbiota previously collected on carcasses and cuts. Although this is still a proof
464 of concept, the discriminatory potentiality of metataxonomic analysis has been here proved. In this light,
465 the characterisation of each beef batch microbiota in the early productive stages and its association with
466 the derived products spoilage fate will allow to create in future studies a benchmark database of those
467 profiles that can alternatively reduce or extend the final product shelf-life. This further advancement
468 would finally make the metataxonomic analysis an usable and practical tool for food industries.

469

470

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472

473 **AUTHOR CONTRIBUTIONS**

474 Ilario Ferrocino and Luca Cocolin designed and conceptualized the experiment. Irene Franciosa,
475 Vladimiro Cardenia and Valentina Alessandria performed microbiological and chemical analysis. Ilario
476 Ferrocino performed amplicon-based sequencing. Cristian Botta carried out the bioinformatic analysis,

477 statistics, data interpretation, generated the manuscript figures and wrote the original draft. Irene Franciosa
478 Ilario Ferrocino and Luca Cocolin supervised the data analysis and contributed to manuscript preparation.
479 All authors revised and approved the final version of the manuscript.

480

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693 **Tables and figures legends**

694

695 **Fig. 1. Microbiological dynamics during hamburgers vacuum storage at 4 °C.** Charts showing the
696 viable counts (mean \pm SD) of: Coagulase Negative Cocci (CNC); *Enterobacteriaceae*; Lactic Acid
697 Bacteria (LAB); Total Mesophilic Bacterial counts (TVC) and yeasts. Dashed line indicates the shelf-
698 life end (14th day).

699

700 **Fig. 2. Principal Component Analysis (PCA) of the fifty-two VOCs detected in the hamburgers.**
701 Score plots highlighting distribution of the samples in relation to the time (A) and batch (B); significant
702 separation between samples is reported (Anosim and ADONIS tests). Loading plot (C) and contribution
703 (D) of each variable (VOCs) on the variance explained by the first two components (Dim1, Dim2) of the
704 PCA.

705

706 **Fig. 3. Composition of bacterial community during hamburgers vacuum storage.** Stacked bar plots
707 (A) showing microbiota composition (relative abundance) at the highest taxonomic level assigned
708 (asterisks highlight 100 % of ASVs similarity to reference taxa) and relative colour coding key. Samples
709 are grouped by batch and sequentially displayed according to the time; taxa are sorted in the legend from
710 the most to the least abundant (> 0.5 %). Box plots (B) displaying Log-transformed abundances of the
711 core species/genera in the two batches along three distinct storage phases: production, shelf-life and
712 expired. Points display each single observation and are coloured according to belonging batch. Asterisks
713 are highlighting significant differences (Wilcoxon's test) between batches at each phase (*P*-value [FDR
714 adjusted]: *= <0.05; **= <0.01, ***= <0.001); differences among phases within each batch are shown
715 by connectors and *P*-value (Kruskal-Wallis and Pairwise Wilcoxon tests [FDR adjusted]). PCoA charts
716 (C) displaying for each batch the weighted UniFrac distance matrix (β -diversity). Days and phases of

717 storage are defined by different colours and shapes (legend); dashed ellipses are indicating significant
718 different communities ($P < 0.001$ [FDR adjusted], ANOSIM and Adonis tests).

719

720 **Figure 3. Composition of fungal community during hamburgers vacuum storage.** Stacked bar plots
721 showing mycobiota composition (relative abundance) at the highest taxonomic level assigned and
722 relative colour coding key. Samples are grouped by batch and sequentially displayed according to the
723 time; taxa are sorted in the legend from the most to the least abundant ($> 1\%$).

724

725 **Fig. 5. Co-occurrence/exclusion network of the hamburger microbiota and mycobiota.** Network is
726 constructed with bacterial and fungal ASVs (nodes), which are pairwise connected by lines (edges) in
727 relation to significant SparCC correlation (100 bootstraps; pseudo P -value < 0.001). Nodes are made
728 proportional to ASVs occurrences and coloured in relation to the belonging kingdom in **A** and co-
729 occurring modules in **B**, respectively, as reported in the relative colour coding keys. Network modularity
730 was calculated considering only co-occurrences by means of the community detection algorithm
731 implemented in Gephi 0.9.2-beta (<https://gephi.org>). Edges thicknesses are made proportional to SparCC
732 correlation value and colours indicate negative (red; SparCC correlation < -0.5) or positive (green;
733 SparCC correlation > 0.5) correlations; lengths have no specific meaning. In the graph **B**, only positive
734 correlations are shown. In the stacked-area plots (**C**) the cumulative relative abundances of each module
735 is displayed along the time (average of the three replicates) for each batch and considering separately
736 fungal and bacterial ASVs. Detailed information on correlation types are reported in **Supplementary**
737 **Table 3.**

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743 **Fig. 6. Biplot of the Non-Multidimensional Scaling (NMDS) analysis with best fitting VOCs and**

744 **taxa.** NMDS of the samples based on bacterial species composition with the set of VOCs (grey arrows)

745 and taxa (blue arrows) that are significantly correlated (Pearson; $P < 0.001$) with the NDMS distribution.

746 Arrows indicate the direction of change of each variable (VOCs and taxa). Only the main species were

747 considered for NMDS (> 0.5 % of average abundances); dots (samples) are shaped and coloured in

748 relation to three temporal phases and batches (legend).

749

750 **Supplementary Tables:**

751

752 **Supplementary Table 1.** The fifty-two VOCs detected in the headspace of vacuum packaged hamburger
753 during the thirty days of storage at 4 °C. Data are the means of three replicates (n=3; ± std error mean)
754 and reported as µg/g. Asterisk are highlighting significant differences between batches at each day of
755 sampling (T-test), *P*-value: *= < 0.05 , **= < 0.01 , ***= < 0.001 . Different letters indicate significant
756 differences (ANOVA and Tukey's post hoc tests; *P*-value < 0.05) between sampling days (0, 4, 8, 15,
757 30) in the batch A (a, b, c) and B (x, y, z), respectively.

758

759 **Supplementary Table 2.** Variance in biological dissimilarity explained by each categorical variable
760 (batch, time, or their interactions) in the core bacterial and fungal communities. Variance explained (R^2)
761 and statistical significance (*P*-value) quantified by Permutational Analysis of Variance (PERMANOVA)
762 test with Bray–Curtis dissimilarity.

763

764 **Supplementary Table 3.** Summary of positive and negative SparCC correlations detected among
765 bacterial and fungal ASVs.

766

767 **Supplementary Table 4.** Correlation coefficients (Pearson's moment correlation) of *l* variables (VOCs
768 and taxa) with NMDS ordination.

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772 **Supplementary Figures:**

773 **Supplementary Figure 1.** Box plots displaying Log-transformed abundances and alpha-diversity
774 metrics significantly different (Wilcoxon's test; P -value [FDR adjusted]: <0.05) between batch A and B
775 (all sampling points considered together).

776

777

778 **Supplementary Figure 2. Correlation between metataxonomic and volatilomic data.** Tile plots
779 showing existing correlation between VOCs and ASVs merged at the species/genus level. Colours
780 represents level of Spearman's Rho correlation (from -1 to 1; caption) and significant positive and
781 negative correlations are highlighted with asterisks (FDR: $*= P < 0.05$; $**= P < 0.01$; $***= P < 0.001$).

782

783 **Supplementary Figure 3.** Metabolic pathways differentially represented in the two batches on the base
784 of inferred bacterial metagenomes; box plots show the results of pathways enrichment analysis (*gage*
785 Bioconductor) with all metabolic pathways significantly (*gage* enrichment statistic: $P < 0.001$)
786 overrepresented in batch A and B.

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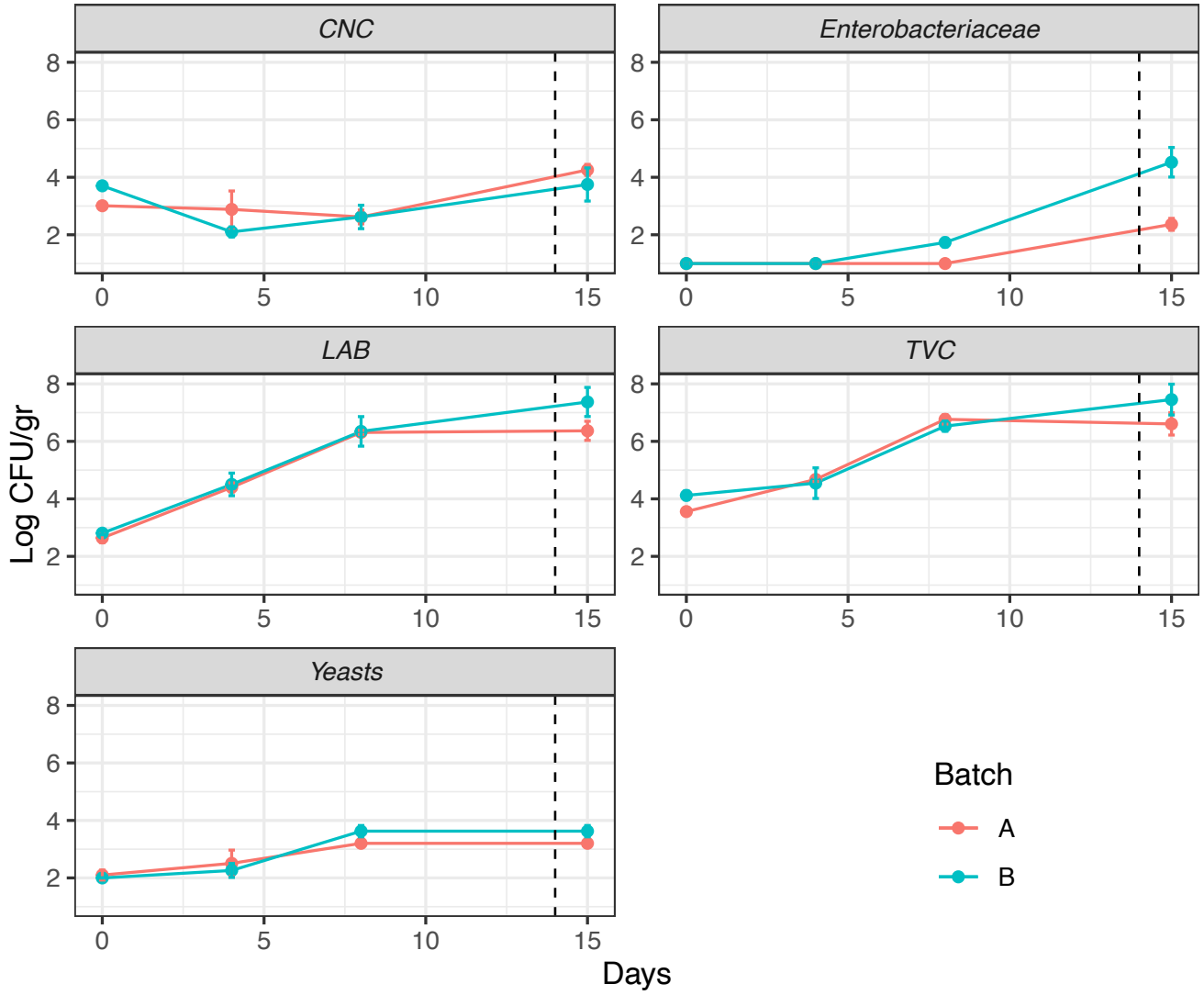
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791 **Fig. 1**

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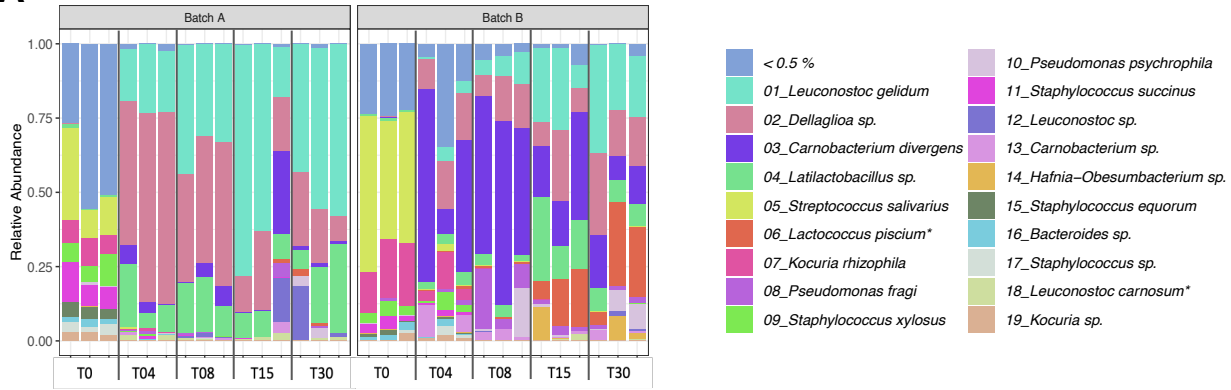
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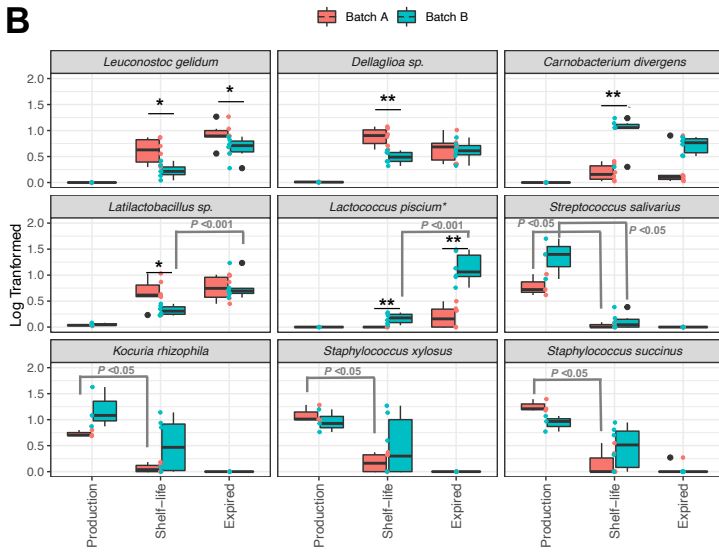
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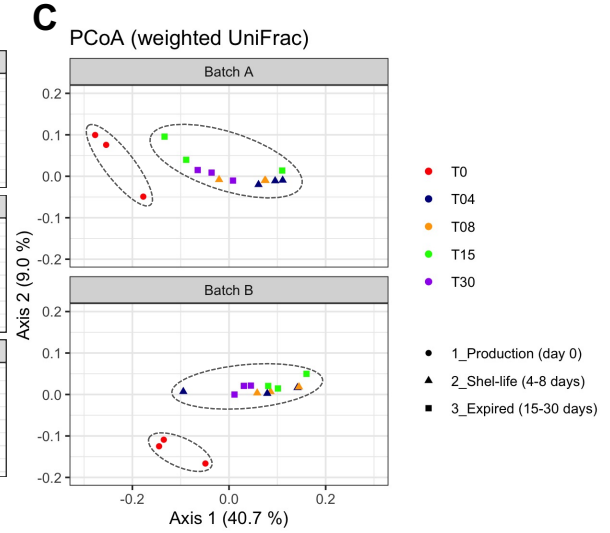
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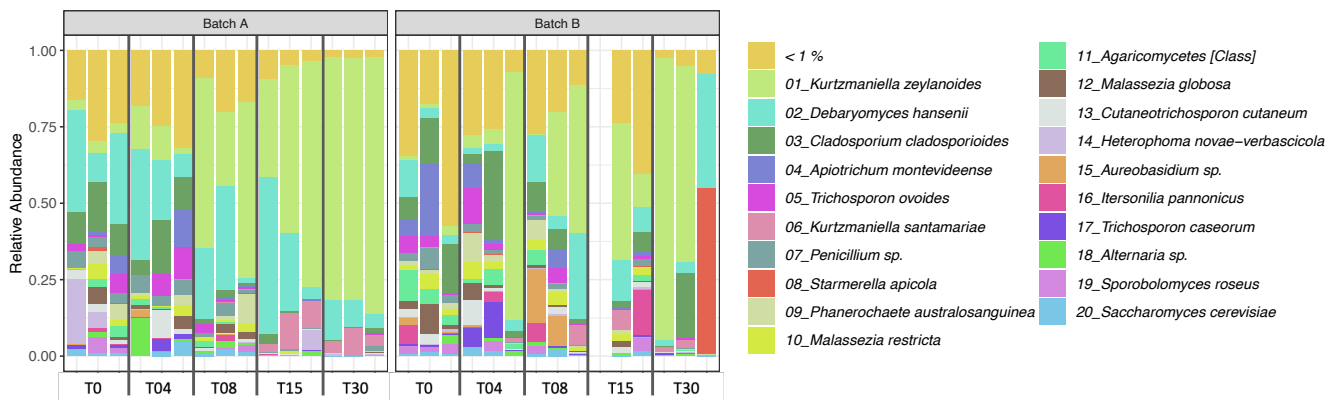
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819 Fig. 4

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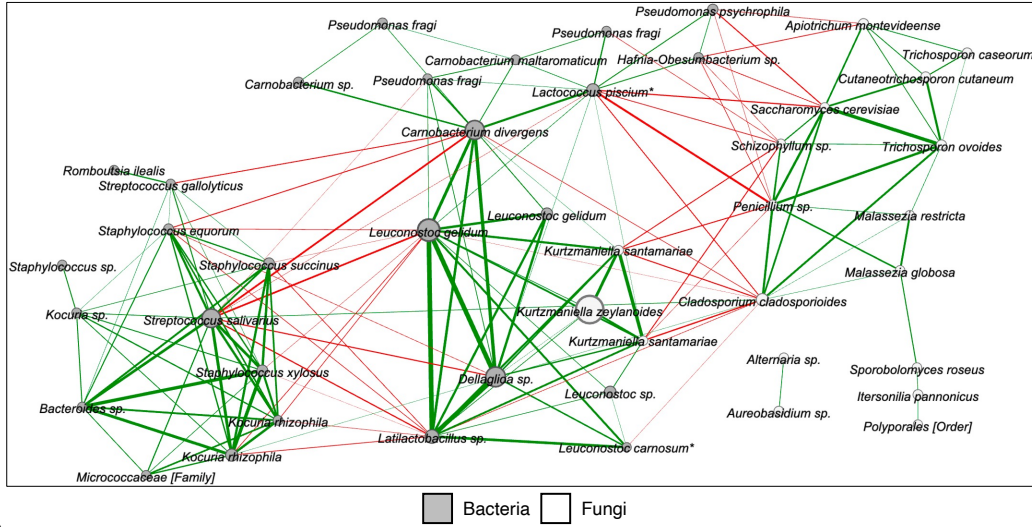


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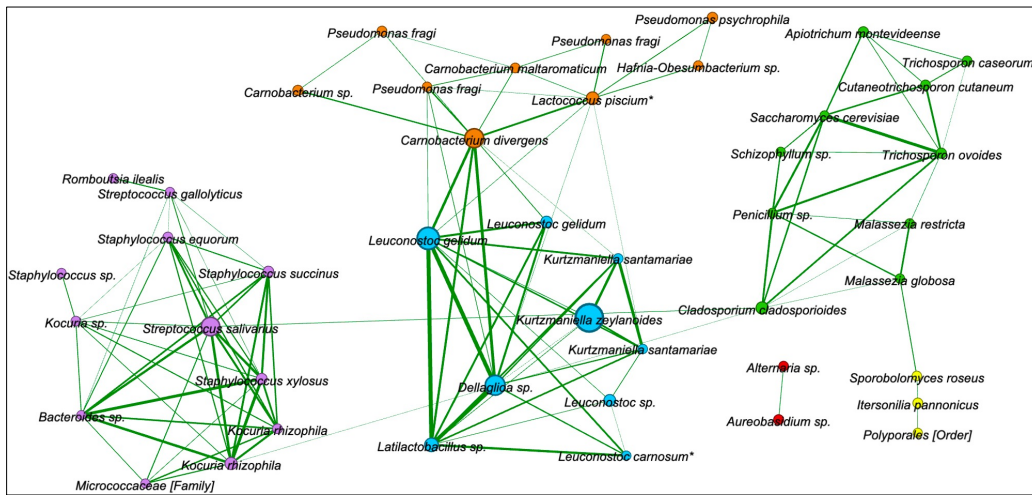
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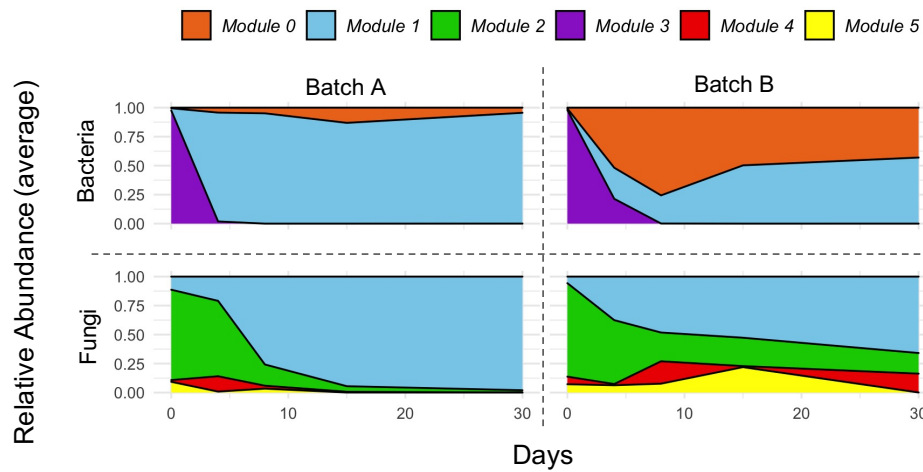
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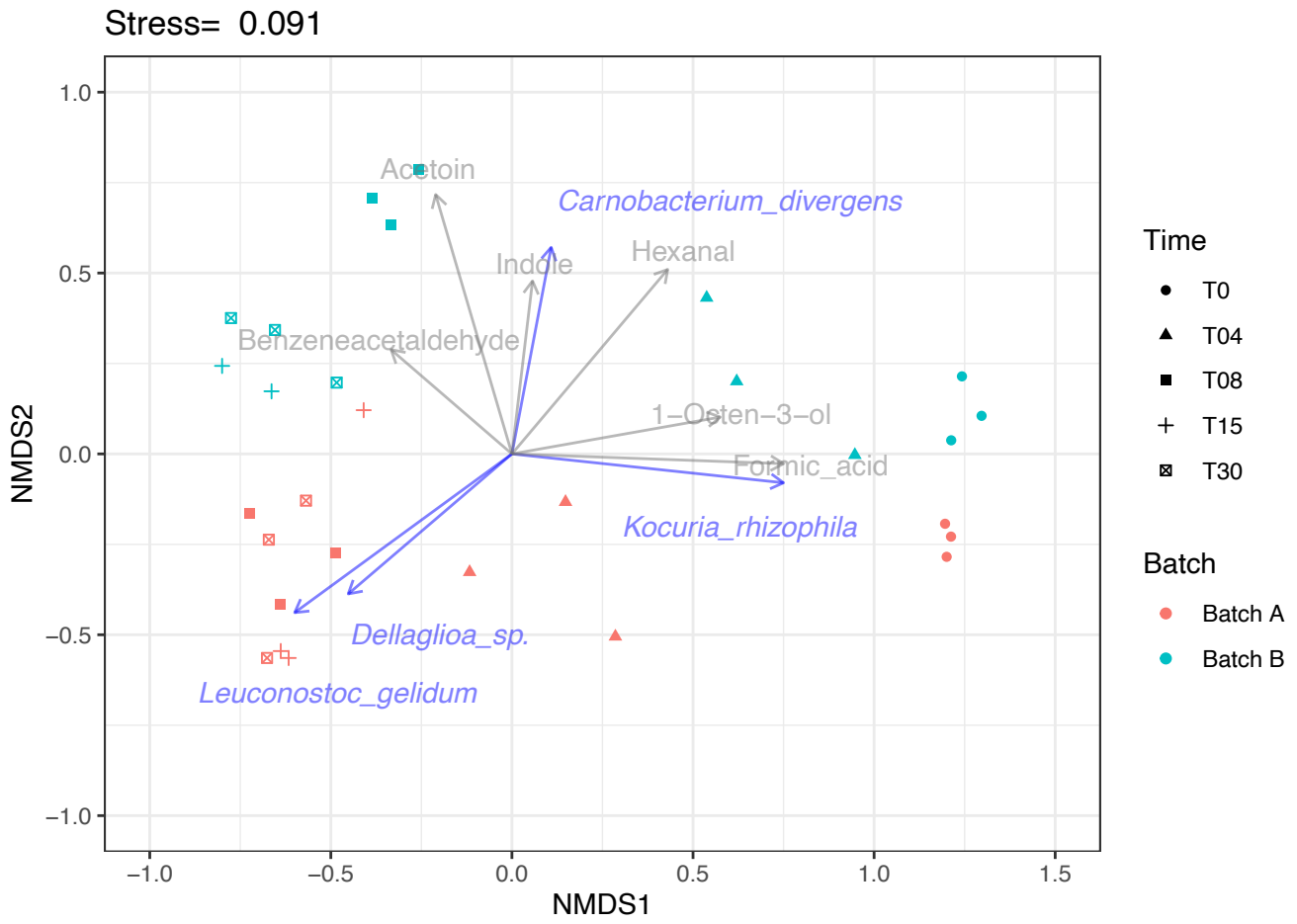


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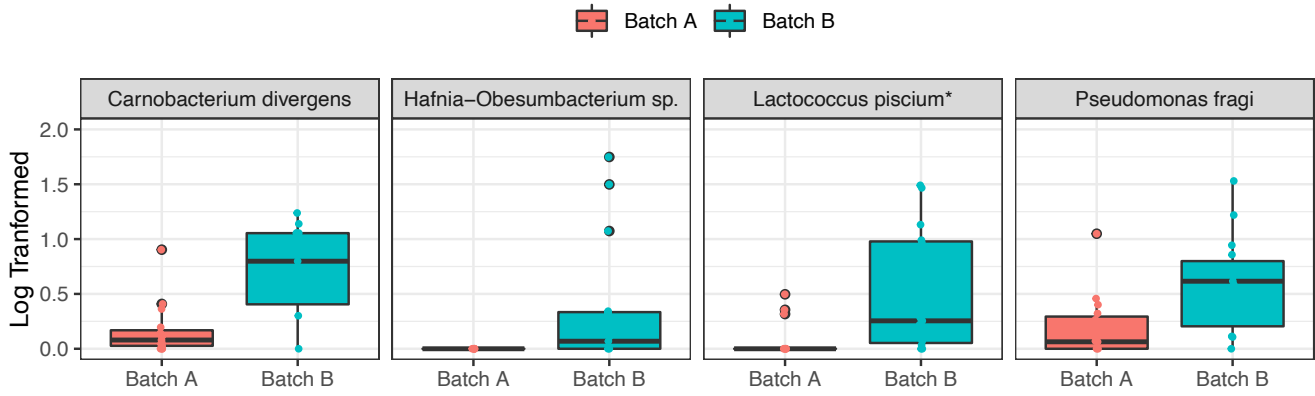
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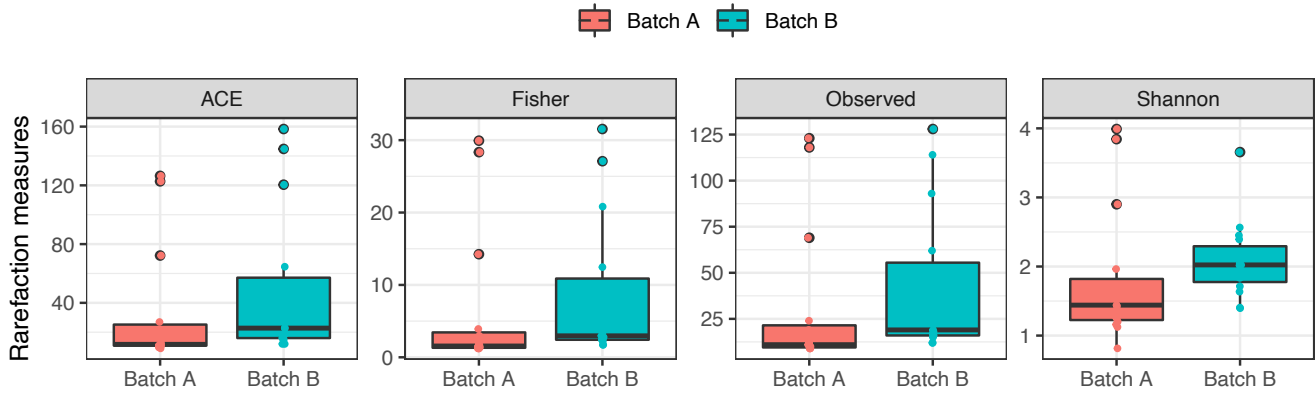
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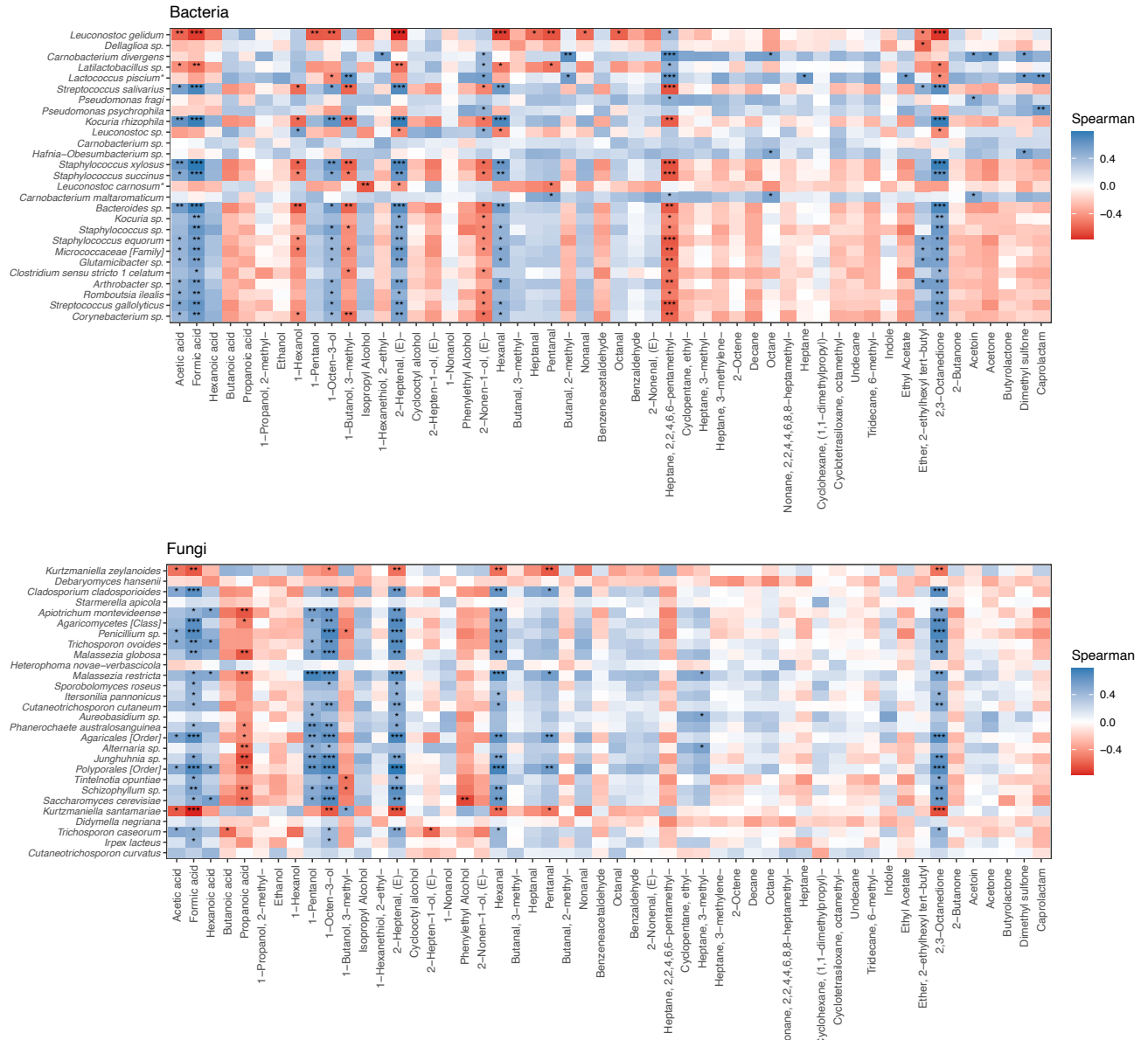
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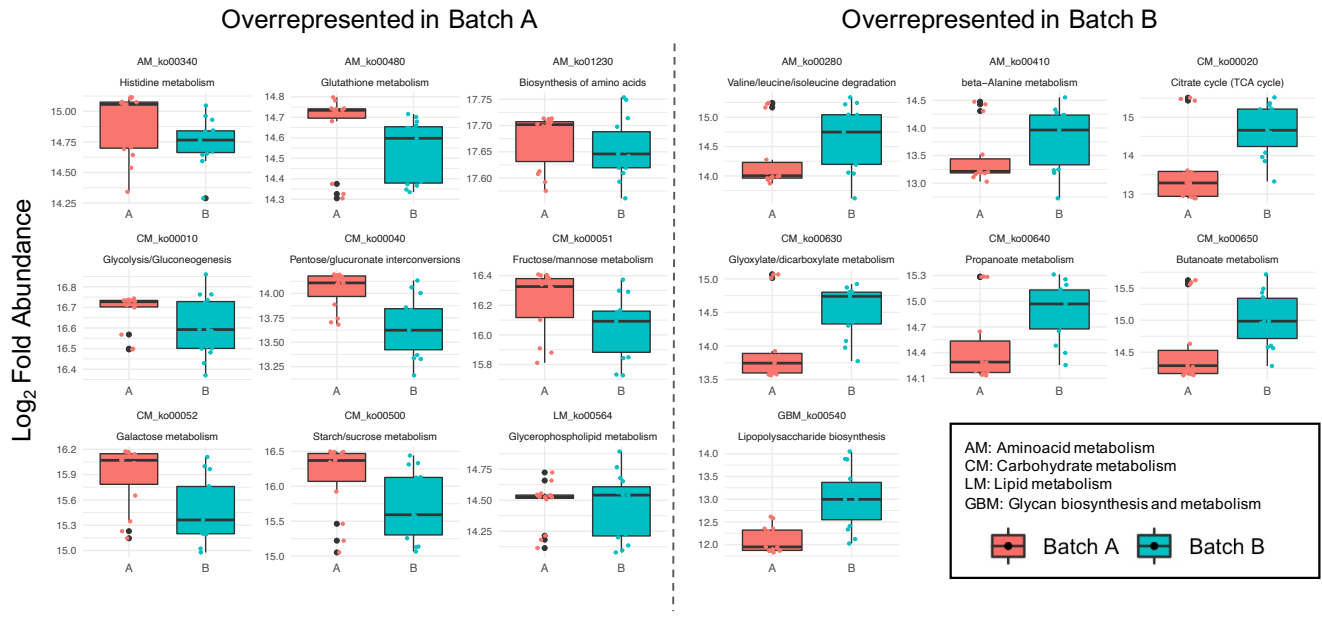
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