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**Effects of Plastic Ingestion on Blood Chemistry, Gene Expression and Body Condition in Wedge-Tailed Shearwaters (*Ardenna Pacifica*)**

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46 **ABSTRACT**

47       Plastic pollution is a global threat and affects almost every marine ecosystem. The  
48 amount of plastic in the ocean has increased substantially over the past decade, posing a  
49 mounting threat to biodiversity. Seabirds, typically top predators in marine food chains, have  
50 been negatively affected by plastic pollution. Here we focused on documenting the sublethal  
51 effects of plastic in Wedge-tailed Shearwaters (*Ardenna pacifica*, WTSH) on the island of Maui,  
52 Hawai'i. Through analyses of blood chemistry, gene expression, morphometrics and stomach  
53 contents, we documented the effects of plastic ingestion on adult WTSH from 3 established  
54 colonies. We detected a negative relationship between body weight and the presence of plastic in  
55 regurgitated stomach contents. Genes associated with metabolic, biosynthetic pathways,  
56 inflammatory responses and ribosome function were upregulated in lighter birds. Birds that had  
57 ingested plastic tended to be lighter in weight, in comparison to birds that did not have plastic  
58 and tended to weight more. Furthermore, there were 43 genes differentiating males and females  
59 that did not have plastic compared to only 11 genes differentiating males and females that had  
60 ingested plastic. There was also a marginal negative relationship between lighter birds and blood  
61 urea nitrogen levels. We also hope that the morphometric measurements, blood parameters and  
62 gene expression data we collected contributes to a database that will be used for future studies on  
63 understanding anthropogenic effects on seabird body condition.

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## 66 INTRODUCTION

67           Plastics are the most common form of marine debris. It is estimated that in 2010,  
68 approximately 8 million metric tons of plastic entered the ocean (NOAA, 2022). This number  
69 has continued to grow exponentially over the past decade as the worldwide production has  
70 increased nearly 200-fold since the 1950s (Ritchie & Roser, 2018). The composition of plastic  
71 products leads to detrimental environmental consequences because, unlike plant products, they  
72 do not biodegrade quickly. Estimates of plastic decomposition range up from decades to several  
73 hundreds of years, causing accumulation of plastic in the natural environment (Barnes et al.,  
74 2009).

### 75 *Plastics in the environment*

76           Plastic has several properties that cause it to amass toxins on its surface through physical  
77 interactions such as physisorption and non-covalent bonds (Verla, 2019). Microplastics have a  
78 low-density and can be found on the surface microlayer of the ocean where they interact with  
79 heavy metals and organic chemicals. They also serve as good sorbents for heavy metals and  
80 organic chemicals due to a large surface area-to-volume ratio and hydrophobic surfaces. The  
81 substantial amount of toxins on the surface of microplastics can serve as vectors for transport of  
82 toxins to organisms (Koelmans et al., 2016).

83           One of the main pathways through which microplastics enter the environment is ingestion  
84 by organisms (Gallo et al., 2018). Approximately 43-100% of the world's marine mammals,  
85 seabirds, and turtle species are at risk of ingesting plastic (Lavers et al., 2019). Ingestion  
86 endangers these organisms to perforations, entanglements, and other non-visible effects. Many  
87 marine organisms ingest microplastics through filter- or deposit-feeding, mistaking them for prey  
88 when foraging or by consuming prey that have ingested microplastics (Gallo et al., 2018).

89           Studies suggest that ingested plastics may cause harm to an organism because of their  
90   ability to break down in the body and leach toxins into the bloodstream. There was marked  
91   bioaccumulation of the toxins in the digestive glands and gills of mussels and lugworms that  
92   were exposed to microplastics contaminated with toxins (polyaromatic hydrocarbons,  
93   nonylphenol and phenanthrene, Browne et al., 2013, Gallo et al., 2018). Research shows that  
94   exposure to these chemicals disrupt endogenous hormones, a process that can cause reproductive  
95   complications (Gallo et al., 2018). Toxins absorbed by plastic have also been linked to  
96   neurological or behavioral changes in organisms (Gallo et al., 2018). A study that aimed at  
97   assessing the effects of polyethylene microplastics in amphibians, exposed *Physalaemus cuvieri*  
98   to 60 mg/dL of polyethylenes for just 7 days and reported visible mutagenic (da Costa Araújo et  
99   al., 2020). Other effects included accumulation of polyethylene in the gills, gastrointestinal tract,  
100   gastrointestinal tract and in the blood as well as several external morphological changes (da  
101   Costa Araújo et al., 2020).

102           It is acknowledged that plastic pollution has more negative effects on seabird health when  
103   compared to other marine vertebrates (Thiel, 2018). Examples of negative effects of plastics on  
104   marine vertebrates include nutritional deprivation, reduced body mass, reduced appetite and  
105   damage or obstruction to the gut (Wang et al., 2021). In a study conducted in Lord Howe Island,  
106   Lavers *et al.* (2019) found that plastic ingestion had “significant negative effect(s) on bird  
107   morphometrics and blood calcium levels and a positive relationship with the concentration of  
108   uric acid, cholesterol, and amylase” (Lavers et al., 2019). Despite these findings, few  
109   experiments have further examined sublethal effects of plastic on physiology, gene expression  
110   and overall seabird health and living species. There is a limited understanding of the effects of  
111   microplastic exposure on gene expression, particularly in vertebrates. However, experiments

112 have shown possible effects of exposure on gene expression in Zebrafish (*Danio rerio*).  
113 Disruptions in reproduction were shown in breeding groups of Zebrafish that were exposed to  
114 environmentally significant concentrations of Bisphenol - A, a chemical used in plastic  
115 production, for 15 days (Liang et al., 2016). More studies are needed on natural populations to  
116 understand the mechanistic connections between plastic pollution and gene expression in the  
117 affected organisms.

118 In this study, we focused on detecting possible effects of microplastic exposure on gene  
119 expression, morphometrics, and blood analytics in three established colonies of Wedge-tailed  
120 Shearwaters (*Ardenna pacifica*, WTSH, Fig.1A). WTSH, highly pelagic seabirds that range  
121 across the tropical and subtropical areas of the Pacific and Indian Ocean, engage in feeding  
122 behaviors such as contact dipping and surface-seizing (Adams et al., 2020). It is predicted that  
123 WTSH and other seabirds with similar feeding behavior are susceptible to ingesting the floating  
124 pieces of plastic on the surface of the ocean (Boersma & Groom, 1993). Plastic ingestion by  
125 WTSH in Hawai  $\square$  i has been documented; however, sub-lethal effects were not evaluated  
126 (NOAA). To evaluate possible sub-lethal effects of plastic ingestion in WTSH, we collected  
127 morphometric data and blood samples to measure the health of the seabird. Blood chemistry can  
128 be used as an indicator for overall health and morphometric data are widely used in ecological  
129 studies to determine body condition (Harr, 2002, Mallory et al., 2010, Labocha & Hayes, 2012).  
130 While ornithologists debate over which morphometrics provide the best estimates for body  
131 condition, literature suggests gathering multiple proxies to fully understand body condition in  
132 seabirds (Mallory et al., 2010, Labocha & Hayes, 2012). Along with collecting several  
133 morphometric measurements such as weight and blood chemistry, we used transcriptome  
134 analysis to characterize activity of actively expressed genes under various conditions. More

135 specifically, transcriptome analysis provided a mechanism to compare snapshots of which genes  
136 were turned on or off in seabirds that had ingested plastic and those that did not have ingested  
137 plastic. Knowledge gaps and questions remain about the intrinsic aspects of plastic, severity of  
138 impact on human health and marine organisms, effective mitigation measures, and  
139 biomagnification across the food webs (Bonanno & Orlando-Bonaca, 2018, Galloway, 2020).  
140 Therefore, the aim of this project is to provide more information to this overarching question of  
141 how plastic debris affects marine organisms.

## 142 **Materials and Methods**

### 143 *Study site*

144 The collection of blood samples occurred at three different sites on the island of Maui,  
145 Hawai'i. These sites were chosen based on known established colonies of WTSH at these  
146 locations (Fig. 1B). Although all populations are located in protected areas, the three sites were  
147 on the seashore near frequently visited beaches. Kamaole Park III is located on the southern part  
148 of the island. Ho'okipa Beach located on the northern part of the island. Finally, Hawea Point is  
149 located on the western part of the island; this location also had the largest WTSH colony.

150 These populations of WTSH along with other seabird populations are vulnerable to  
151 microplastic exposure given that there are significant centers of plastic accumulation around the  
152 Hawaiian archipelago. Andrés Cózar et al. (2014) synthesized data to create a global map that  
153 approximates the magnitude of plastic pollution in the open ocean. Using the coordinates and  
154 data from Cózar et al. (2014), we mapped the magnitude of plastic pollution near the island of  
155 Maui (Fig. 1B). The concentration near Maui is sizeable compared to other sampled locations,  
156 with a non-adjusted concentration of 225,115 items per km<sup>3</sup>. Despite our collection of samples  
157 from three different locations, we do not expect any significant genetic differentiation between

158 the populations. Whereas marked genetic differentiation has been found in WTSH in populations  
159 breeding in different islands and archipelagos along the Pacific coast of North America, there is  
160 no evidence for deep evolutionary divergences (Herman et al., 2022). The three WTSH colonies  
161 were treated as one population when we analyzed the data.

### 162 *Gut Sample Testing*

163 We used the procedure outlined by Duffy et al. (1986) for gut sample testing to collect  
164 possible ingested plastic. The procedure outlined by Duffy et al., involves a stomach pump  
165 system where the seabird is filled with seawater through a gavage and then tipped over a bowl to  
166 promote and collect regurgitation. We completed sampling of the gut contents for 28 out of the  
167 29 birds.

### 168 *Blood Sampling*

169 We collected blood samples first to avoid a signal of stress response in the analyses of  
170 gene expression and blood chemistry from being handled. Blood sample collection was possible  
171 in 28 out of the 29 birds for gene expression analysis, and in 25 out of the 29 birds for chemical  
172 analysis. This lack was due to not enough blood collection during sampling.

173 We collected approximately 200 $\mu$ l of blood using a syringe from the medial metatarsal  
174 vein. We used styptic powder to stop bleeding when necessary. We added 100 $\mu$ l of blood to a  
175 vial containing RNAlater buffer. We stored 20 $\mu$ l of blood in heparin tubes for iStat cartridge  
176 analysis. The iStat Chem8+ provided us with the following blood analytics; sodium (Na  
177 mmol/L), potassium (K mmol/L), chloride (Cl mmol/L), ionized calcium (iCa mmol/L), total  
178 carbon dioxide (TCO<sub>2</sub>), glucose (Glu mg/dL), urea nitrogen/urea (BUN mg/dL), creatinine (Crea  
179 mg/dL), hematocrit (Hct %PCU), hemoglobin (Hb g/dL), anion gap (AnGap mmol/L). We used  
180 Qiagen QiAMP DNA Blood kit for DNA purification to proceed to the PCR reaction. We

181 used the universal method outlined by Fridolfsson and Ellegren (1999) for sexing in birds with  
182 PCR reaction. The 2- primer system is as follows:

183 2550F: 5'-GTTACTGATTCGTCTACGAGA-3'

184 2718R: 5'-ATTGAAATGATCCAGTGCTTG-3'

185 Using this primer system, we employed standard PCR on the templates of DNA extracted  
186 from unknown-sex *A. pacifica* species. The PCR mixture (15 µl) contained 1.5 µl of 10X buffet,  
187 0.5 µl of dNTP (10 pmol), 0.5 µl of forward primer (10 pmol), 0.5 µl of reverse primer (10  
188 pmol), 0.1 µl of NEB Ta1 (5U/uL), and 9.4 µl of H<sub>2</sub>O. 2.5 µl of the DNA extraction was used.  
189 The PCR program was as follows: 94°C for 5 min, 94°C for 30 sec, 60°C for 30 sec  
190 \*touchdown, -1.0°C/cycle x 10 cycles, 72°C for 30sec, 94°C for 30 sec, 50°C for 30 sec x 30  
191 cycles, 72°C for 30 sec, 72°C for 5 min, 4°C hold. We used molecular graded H<sub>2</sub>O as a negative  
192 control. A negative control was essential for possible misinterpretation due to contamination or  
193 other factors. We separated the PCR product through electrophoresis on a 2% agarose gel at 90  
194 V for about 1 hour. We stained the gel with *GelRed*<sup>TM</sup> - a fluorescent nucleic acid gel stain that  
195 replaces the highly toxic ethidium bromide (EtBr) - and we used a gel imaging camera.

#### 196 *Morphometric Data*

197 We completed collection of morphometric measurements for 28 out of 29 of the birds,  
198 using a Pesola scale. We measured tarsus length, bill length, nares depth and width using calipers  
199 and we measured wing chord length using a ruler. We banded each bird and recorded the number  
200 if the bird was a recapture.

#### 201 *RNA Isolation and Sequencing*

202 Before initiating RNA isolation, we removed RNA later through centrifuging  
203 aliquots at 20,800 x g (RCF). We removed supernatants from the remaining pellets containing



204 cell material. We used a Qiagen RNeasy Plus Universal Mini Kit for blood isolation. At the  
205 Harvard Bauer Sequencing Core Facility, we used KAPA mRNA Hyperprep kit and a  
206 NOVASeq SP platform to sequence paired end reads of 150 bp length, yielding between 20 and  
207 30 million reads per sample.

#### 208 *Data analysis*

209 We calculated several values to assess the quality of the RNA. We analyzed RNA  
210 integrity score (RIN) values, and calculated Phred Scores to assess the quality of our sequencing.  
211 RIN values assign a numerical value to the quality of the RNA that we worked with to evaluate  
212 the integrity of 18S and 28S rRNAs (Puchta et al., 2020). A RIN value of 8 and above indicated  
213 higher quality and integrity of RNA and values below 5 indicated some levels of RNA  
214 degradations. Phred scores are similar in that they assess the quality of sequences. Similar to RIN  
215 value, a high Phred score (90% and above) indicated better quality sequences (Scholz, 2021).

216 We aligned sequences to the publicly available reference genome of Cory's Shearwater  
217 (*Calonectris borealis*, accession # PRJNA545868, Feng et al., 2019) with the RNA sequence  
218 mapper STAR (Spliced Transcripts Alignment to a Reference) (Dobin et al. 2013). Followed by  
219 a transcript quantification with RSEM (Li & Dewey, 2011) and a differential gene expression  
220 analysis with DESeq2 (Love et al., 2014) in R programming. We created heatmaps to determine  
221 if there were observable patterns between gene expression and presence of plastic. Combined  
222 with clustering methods, heatmaps can help determine there are similar changes in gene  
223 expression based on their activity. In all of the tests, we used both a conservative p-value of 0.05  
224 and a less conservative p-value of 0.1 to determine the significance of results. The summary of  
225 all tests we ran can be seen in supplementary table 1.

226 We conducted gene ontology analysis using R 3.5.1 (R Core Team 2018) and the package  
227 *ggprofiler2* with *Gallus gallus*, *Taeniopygia guttata* and *Mus musculus* as the model systems in  
228 the search database. We used *Ggplot2* and *plotly* for plotting as outlined in Kolberg et al. (2021).  
229 We separated terms into Gene Ontology, KEGG pathways and Reactome databases.

230 We ran multiple tests to analyze possible relationships between the variables of sex,  
231 presence of plastic and blood chemistry levels. We ran all analyses using R 3.5.1 (R Core Team  
232 2018). We used a t-test to compare the means between blood analytes of birds that had ingested  
233 plastic and those that had no. All blood parameters were analyzed independently. Parameters  
234 were plotted against the presence of plastic. Differences were considered statistically significant  
235 when  $p < 0.07$ . We ran principal component analysis (PCA) to determine if the categories of  
236 plastic and sex were clustering together according to the morphometric, blood chemical and  
237 genetic data. We first ran PCA in relation to sex to control for possible differences in sex. We  
238 then ran PCA in relation to the presence of plastic to determine if individuals would cluster due  
239 to physiological differences caused by the presence of plastic. Packages used for these analyses  
240 included *devtools*, *ggplot2* and *ggbiplot*. Finally, we used a general linear model (*glm*) to study  
241 the association between the variables, such as the morphometric measurements and blood  
242 parameters, and the conditions, which was either presence or absence of plastic. Differences  
243 were considered statistically significant when  $p < 0.05$ . and we considered effect size as well.

## 244 **Results**

### 245 *Gut samples*

246 Plastic or other unidentified hard pieces were found in 12 of the 28 birds sampled for  
247 plastic (Fig. 1C). These included fishing line and pieces of microplastics. A summary of which  
248 birds contained plastic, their sex and what blood samples were available for each bird can be

249 found in Fig. 2. Four out of the ten males contained plastic or other unidentified hard pieces.  
250 Seven out of 17 females contained plastic or other unidentified hard pieces. Bird N004 contained  
251 plastic or other unidentified hard pieces, but the sex of this bird was unknown due to insufficient  
252 blood sample to carry out analyses (Fig. 2).

### 253 *Sex Determination through PCR*

254 Our sample consisted of 10 males and 17 females. Bird N001 was a female, but gut  
255 samples were not collected for this bird (Fig. 2).

### 256 *Blood Analytics, Morphometric and Gut Sampling*

257 We found minimal relationships between the presence of plastic and the measurements  
258 listed above. Significant values from t-test analyses included levels TCO<sub>2</sub> (Fig. 3e.) in the  
259 presence of plastic. There were no other significant values for other blood analytes in our t-tests  
260 and t-values ranged from .05789 to .87 (Fig. 3).

261 Our PCA results showed minimal relationships for both blood chemistry and  
262 morphometric measurements when the independent variable is set as either sex or presence of  
263 plastic (Fig. 4). The absence of clustering when using blood chemistry and morphometrics  
264 provides a control for sexual dimorphism in our samples. Wedge-tailed Shearwaters are not  
265 sexually dimorphic, which is consistent with our results.

266 Weight deviated from the other variables in the presence or absence of plastic under PCA  
267 3 and 4 (Fig. 4b). There was a negative relationship between weight and presence of plastic when  
268 using a general linear model; birds that had ingested plastic tended to weigh less whereas birds  
269 that did not have ingested plastic tended to weigh more (Fig. 5a). When weight was the  
270 independent variable, urea nitrogen/urea, hematocrit and potassium demonstrated significant p-

271 values (Fig. 6). A summary of the averages, standard deviation and p-values from t-tests is found  
272 in Supplementary figure S2.

### 273 *R NA Isolation and Sequencing*

274 The RIN value used to assess RNA integrity during isolation was around 8.4 - 6 for most  
275 samples (Supplementary figure S9). Sample N005 had a lower RIN value of 4.8. Phred Scores  
276 were used to assess sequencing quality (Supplementary figure S4). On average, all samples  
277 reached > 30 Phred Score, which indicated good quality for downstream analyses.

278 Supplementary figure S4 depicts reads per sample, which fell between 48,000,000 and  
279 80,000,000 reads per sample. Uniquely mapped reads were all above 40%, with the highest being  
280 slightly above 60% (Supplementary figure S5). Low values could be due to the rate of  
281 degradation of blood RNA (Dobin & Gingeras, 2015) or because we are not using a species-  
282 specific reference genome for the transcriptome alignment. Multiple mapped reads, which read  
283 mapping to multiple locations in the genome, occurred at a rate of 1.3% to 2.7% (Supplementary  
284 figure S6, Pantano, 2018). We were able to distinguish four genes that separate the samples into  
285 two groups, discernible by upregulation and downregulation activity. Shades of blue represent  
286 downregulation activity while shades of red indicate upregulation of the gene (Fig. 7A).

287 There were no discernible differences in gene expression under the presence and absence  
288 of plastic. These results suggested that the clustering by presence of plastic does not explain the  
289 differential gene expression profiles (see Fig. 7A). We did not obtain significant results with  
290 either the conservative p-value or less conservative p-value.

291 We divided the analysis into sex; females in one analysis and males in the other with and  
292 without plastic as the variable (Supplementary figure S7). In this analysis we identified one gene  
293 that differentiated females with and without plastic when using the less conservative p-value.

294 Fourteen genes differentiated males with and without plastic under the more conservative p-  
295 value. The presence of plastic in males was associated with the upregulation of the top four  
296 genes. Eleven genes differentiated males and females that contained plastic (Supplementary  
297 figure S8A). Forty-three genes differentiated males and females that did not have plastic  
298 (Supplementary figure S8B).

299 We analyzed DE genes that examined weight with and without plastic. We divided  
300 weight into 3 factors: low, medium and high. Birds that did have ingested plastic, tended to be  
301 heavier and showed a downregulation in the expression of the top 18 differentiating genes  
302 (Figure 8A). Birds that had ingested plastic, tended to be lighter and showed an upregulation in  
303 the expression of the same genes. These distinctions were able to be made while using a  
304 conservative p-value for the top four genes and marginal p-value for the remaining genes. The  
305 genes responsible for differentiation when the samples were not separated into variables were  
306 associated with transcriptional activation, body fluid secretion and protein transportation activity  
307 (Fig. 7B). The top two genes responsible for weight differentiation, Ankrd11\_1 and Hsph 1  
308 (Supplementary figure S10A), were upregulated in heavier birds. Genes that were upregulated in  
309 heavier birds were associated with trimethylation and cell cycle function (Supplementary figure  
310 S10B). The top twelve genes that were upregulated in lighter birds (Fig. 8A) have been  
311 associated with several metabolic and biosynthetic processes, ribosome function and pathway  
312 response associated with COVID-19 (Supplementary figure S10).

## 313 **DISCUSSION**

314 Our overarching question was whether ingested plastics from the environment have a  
315 sublethal effect in seabirds, gut samples, morphometric measurements and blood samples from  
316 Wedge-tailed Shearwaters in Maui, Hawai'i as a test case. Using PCA analysis, general linear

317 models and analysis of DE genes, we quantified the effect of microplastic load on the overall  
318 health of the birds. We found a marginal, negative correlation between body weight and plastic.  
319 When using body weight as an indirect measure for the effect of plastic on the bird, we found  
320 associations between upregulation of metabolic and biologic pathways and lighter birds. Birds  
321 with lower weight tended to contain plastic.

322         The main effects to gene expression were attributed to i) upregulation of biosynthetic and  
323 metabolic pathways in lighter birds and ii) downregulation of biosynthetic pathways in heavier  
324 birds. Analysis of DE genes showed an upregulation of genes involved in biosynthetic processes  
325 in lighter birds. Biosynthetic and metabolic processes are responsible for body mass  
326 accumulation. Disruptions to energy and lipid metabolism pathways have been documented in  
327 Zebrafish (*D. rerio*) (Limonta et al., 2019, Lu et al., 2016), and African Catfish that were  
328 exposed to microplastics (*Clarias gariepinus*) (Karami et al., 2016). Toxins found in  
329 microplastics, such as BPA and BP, are associated with disruption of metabolic and biosynthetic  
330 pathways (Sun et al., 2022). Sprague-Dawley Rats exposed to BPA experienced weight loss (Sun  
331 et al., 2022). Adult Zebrafish, also exposed to BPA, experienced a decrease in oxidative stress  
332 and body weight change (Jordan et al., 2012, Lu et al., 2014, Huang et al., 2019, Sun et al.,  
333 2022). Previous physiological suggestions in seabirds include reduction in the functional volume  
334 of the gizzard; this reduces digestive capability causing weight loss (Furness & Monaghan,  
335 1987).

336         Lighter birds also displayed upregulation of genes involved in organonitrogen compound  
337 metabolic processes. This process is associated with the formation of compounds that are directly  
338 linked to a nitrogen atom. Our general linear model revealed a marginal relationship between  
339 lighter birds and higher BUN (blood urea nitrogen) levels. Higher BUN levels have been used to

340 infer dehydration in birds (Hochleither). Higher urea levels were associated with European pond  
341 turtles (*Emys orbicularis*) exposed to varying doses of microplastics (Banaee et al., 2020). These  
342 results could suggest a possible relationship between the presence of plastic, and disruption of  
343 genes involved in metabolic and biosynthetic processes.

344         There were only 11 genes that differentiated females and males among individuals with  
345 plastic (Supplementary figure S8A). Meanwhile, there were 43 genes that differentiated females  
346 and males among individuals without plastic (Supplementary figure S8B). Several studies have  
347 found that when bisphenol-a (BPA), a chemical used in plastic, is leached from plastic, it can  
348 activate estrogen receptors in mammals (Bittner et al., 2009, Gao et al., 2015). These findings  
349 suggest that males would present a detectable level of estrogen, causing the genetic  
350 differentiation to be less defined between males and females. More research is needed on the  
351 effects of plastic toxins on sex hormones to support this hypothesis.

352         One of our significant findings included genes associated with a pathway in response to a  
353 COVID-19 infection (Supplementary figure S10B). This pathway is associated with an  
354 inflammatory response, organ failure, and hypercoagulability (Harrison et al., 2020). We cannot  
355 be sure that this has to do with a Sars-CoV-2 infection in birds, but this pathway response in  
356 birds may be associated with a similar infection leading to an inflammatory response. Male mice  
357 exposed to PCBs, DDE (dichlorodiphenyldichloroethylene) and HCB (hexachlorobenzene),  
358 suffered liver injury and systemic inflammation (Deng et al., 2019). PCBs, DDE and HCB are  
359 chemicals found in plastic. Presence of microplastics in zebrafish have been linked to enhanced  
360 immune responses (Limonta et al., 2019), and other disruptions to the immune system (Powell et  
361 al., 2010).

362

363 *Challenges in study design*

364           One significant challenge in our study was the possibility of false negative results. All  
365 bird populations we sampled are on the island near a big source of plastic. It could be the case  
366 that those birds without plastic in their gut at the moment of sampling, were already exposed at  
367 some level to plastic and we were not able to detect it. The flushing technique for gut sampling  
368 we used does not allow for full collection of gut samples. Other methods of obtaining sampling  
369 might be more effective but could also increase the risk of death and injury to the birds. A study  
370 that does not rely on destructive sampling also allows for repeated sampling and continued  
371 monitoring of bird health. Destructive sampling only allows for a single observation (Provencher  
372 et al., 2019).

373 *Using weight as an indirect metric*

374           With a marginal p-value, lighter birds tended to be associated with the presence of plastic  
375 while heavier birds tended to be associated with the absence of plastic (Fig. 5a). More  
376 importantly, the relationships that we detected have been noted in previous studies examining  
377 plastic load and its effect on different organisms (Ryan 1986, Sievert & Sileo 1993, Pierce et al.  
378 2004). A study on *Physalaemus cuvieri* tadpoles that were exposed to polyethylene microplastics  
379 at significant concentrations for 7 days reported accumulation of microplastics in the internal  
380 organs of which led to morphological and mutagenic changes; these changes can have effects on  
381 health and development (da Costa Araújo et al., 2020). In the same study, abnormalities were  
382 observed in nuclear erythrocytes and on external morphological traits such as mouth-cloaca  
383 distance.

384           Despite the challenges presented by experimental design, we were able to detect marginal  
385 indications of possible effects of microplastic toxins in relation to genetic expression, weight and



386 blood analytes. Perhaps the challenges of conducting an ecological study in the field cause the  
387 associations to not be as strong as they could have been in a laboratory setting.

388  
389 **CONCLUSIONS**

390 Our results indicate that there are signs of sublethal effects of ingested plastic in Wedge-  
391 tailed Shearwaters. We were able to detect a negative relationship between the presence of  
392 plastic and weight. When using weight as an indirect measurement for the effect of ingested  
393 microplastics, there is some evidence that plastic affects metabolic and biosynthetic processes in  
394 Wedge-tailed Shearwaters. Whereas there was no direct relationship between load of plastic  
395 collected and DE genes, there was upregulation of genes involved in biosynthetic processes and  
396 ribosome function in lighter birds. Birds that had ingested plastic tended to be lighter. There  
397 were more genes that differentiated females and males that had not ingested plastic than females  
398 and males that had ingested plastic. Furthermore, there is the possibility of false negatives (in  
399 absence of plastic loads during gut sampling). The experiment contributes to an understanding of  
400 the relationship between plastic and sublethal effects in seabirds. Given the finding of a COVID-  
401 19 response pathway, we can further ask more questions on how anthropogenic diseases are  
402 translating into wildlife. In seabirds specifically, this raises the question of whether ingested  
403 plastic is having an impact on seabirds' immune system.

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424 **Data Availability Statement**

425   The sequence data will be available upon publication. Data sets associated with this paper will be  
426 available upon acceptance.

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- 674

675 **Figure Legends**

676 **Fig. 1.** (A) Wedge-tailed Shearwater (*Ardenna pacifica*) in Hawai'i. From U.S. Fish and Wildlife  
677 Service by Ian Jones. (B) Sampling Sites. Three sampling sites on the island of Maui in the  
678 Hawaiian Islands represented by triangles. Colored circle represents concentrations of plastic  
679 (items km<sup>-2</sup>) found around the Hawaiian Islands based on data from Cózar et al. 2014). (C)  
680 Plastic samples. Plastic collected from gut samples from WTSH.

681 **Fig. 2.** Bird ID and data available for each specimen. An ID was appointed for each specimen.  
682 The sex is indicated for each specimen. Plastic refers to if that particular specimen had ingested  
683 plastic; (+) indicates presence of plastic and (-) indicated that that specimen did not have  
684 ingested plastic. Blood sample refers to what information was obtained from the collected blood.  
685 Specimens where only genetic information is available is denoted by "Gene only". Specimens  
686 where only a chemical blood panel is available is denoted by "Chem only". Specimens where  
687 both genetic information and chemical blood panels are available is denoted by "both".

688 **Fig. 3.** Individual t-test analysis of each blood analyte and weight. (a-k) Blood analyte plotted  
689 against presence and absence of plastic with error bars. Any test that showed a slight significance  
690 value is noted on the right-hand corner of the individual chart. (l) Weight plotted against  
691 presence or absence of plastic.

692 **Fig. 4.** PCA analyses of morphometrics and blood analytes. (a) Morphometric measurements  
693 with variables of presence of plastic using PCA 1 and PCA 2. (b) Morphometric measurements  
694 with variables of presence of plastic using PCA 3 and PCA 4. (c) Morphometrics measurements  
695 with variables of sex using PCA 1 and PCA 2. (d) Morphometric measurements with variables of  
696 sex using PCA 3 and PCA 4. (e) Blood analytes with variables of presence of plastic using PCA  
697 1 and PCA 2. (f) Blood analytes with variables of presence of plastic using PCA 3 and PCA 4.

698 (g) Blood analytes with variables of sex using PCA 1 and PCA 2. (h) Blood analytes with  
699 variables of sex using PCA 3 and PCA 4.

700 **Fig. 5.** Significant relationships from general linear model. (a) Relationship between presence or  
701 absence of plastic and weight of bird. (b) Relationship between presence or absence of plastic  
702 and total carbon dioxide.

703 **Fig. 6.** Significant results from general linear model of blood analytes with weight as the  
704 variable. (a) Hematocrit as percentage with weight as variable. (b) Urea nitrogen/urea with  
705 weight as the variable. (c) Potassium with weight as the variable.

706 **Fig. 7.** DE genes and enrichment analysis for the entire data set. (A) Heatmap showing that  
707 plastic and size factor of libraries do not explain the DE gene profiles. The heatmap shows the  
708 top 20 genes with the highest statistical power. (B) Enrichment analysis and significant terms for  
709 the 6 DE genes shown on the heatmap above.

710 **Fig. 8.** DE genes with three categories of weight; low, medium and high. (A) Heatmap showing  
711 the 18 significantly DE genes. (B) Normalize count in the two top genes showing differences in  
712 counts between the three weight categories.

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718 **Supporting Information**

719

720 List of Supplementary figures and Tables. Tables. Supporting Information, Tables are both in the

721 Supporting Information, File (pdf) and in the Supporting Information.

722 **Supporting Information, Fig. S1.** Table summarizing differential genetic expression analyses

723 run. The test/experiment column describes the three main analyses that we conducted and the

724 variables that were used for each test. Transcripts represent the count of transcripts that were

725 aligned with the reference genome. Net transcripts represent the count of transcripts that were

726 represented or quantifiable in all of the samples. Outlier transcripts and outlier genes represent

727 the count of transcripts that differentiated within the respective test. P-value represents the two p-

728 values we used to determine significance of the results. We used both a marginal p-value (0.1)

729 and a standard value (0.05).

730 **Supporting Information, Fig. S2.** Summary of values from blood analytes. This table provides

731 the mean, standard deviation and p-values from the t-tests for each of the blood chemistry

732 analytes and weight. The plus sign (+) indicated the values for individuals with plastic. The

733 minus sign (-) indicates the values for individuals without plastic. The blood analytes measured

734 were sodium (Na mmol/L), potassium (K mmol/L), chloride (Cl mmol/L), ionized calcium (iCa

735 mmol/L), total carbon dioxide (TCO<sub>2</sub>), glucose (Glu mg/dL), Urea nitrogen/urea (BUN mg/dL),

736 creatine (Crea mg/dL), hematocrit (Hct% PCU), hemoglobin (Hb g/dL), anion gap (AnGap

737 mmol/L) and are ordered respectively in the table.

738 **Supporting Information, Fig. S3.** Reads per sample. This measurement assesses an inferred

739 sequence of base pairs that correspond to a single DNA fragment.

740 **Supporting Information, Fig. S4.** Phred score for samples. Phred score is used for quality

741 assessment of sequencing.

742 **Supporting Information, Fig. S5.** Uniquely mapped reads. Uniquely mapped reads have one  
743 exact location within the reference genome which they map to. This is the number of uniquely  
744 mapped reads from the prepared library that are aligned to the Cory Shearwater reference  
745 genome.

746 **Supporting Information, Fig. S6.** Multiple mapped reads. Multiple mapped reads describe  
747 reads that map more than once in the genome. This is the number of multiple mapped reads from  
748 the prepared library that are aligned to the Cory Shearwater reference genome.

749 **Supporting Information, Fig. S7.** DE genes for plastic and sex. (A) Heatmap showing the 14  
750 significantly expressed genes in males. (B) Heatmap showing the 4 significant DE genes in  
751 females.

752 **Supporting Information, Fig. S8.** DE genes divided into samples that had ingested plastic and  
753 samples that did not have plastic. (A) Heatmap showing the 11 significant DE genes in all of the  
754 samples containing plastic separated by sex. (B) Heatmap showing the 43 significant DE genes  
755 in all samples that do not contain plastic separated by sex.

756 **Supporting Information, Fig. S9.** RIN values. RIN values assign a numerical value to the  
757 quality of the RNA that we worked with. A RIN value of 8 and above indicated higher quality  
758 and integrity of RNA and values below 5 indicated some levels of RNA degradations.

759 **Supporting Information, Fig. S10.** Gene enrichment analysis results for bird weight. (A)  
760 Manhattan plot showing results of enrichment analysis and the databases used. (B) Terms with  
761 significant values from the enrichment analysis in the DE genes between weight categories

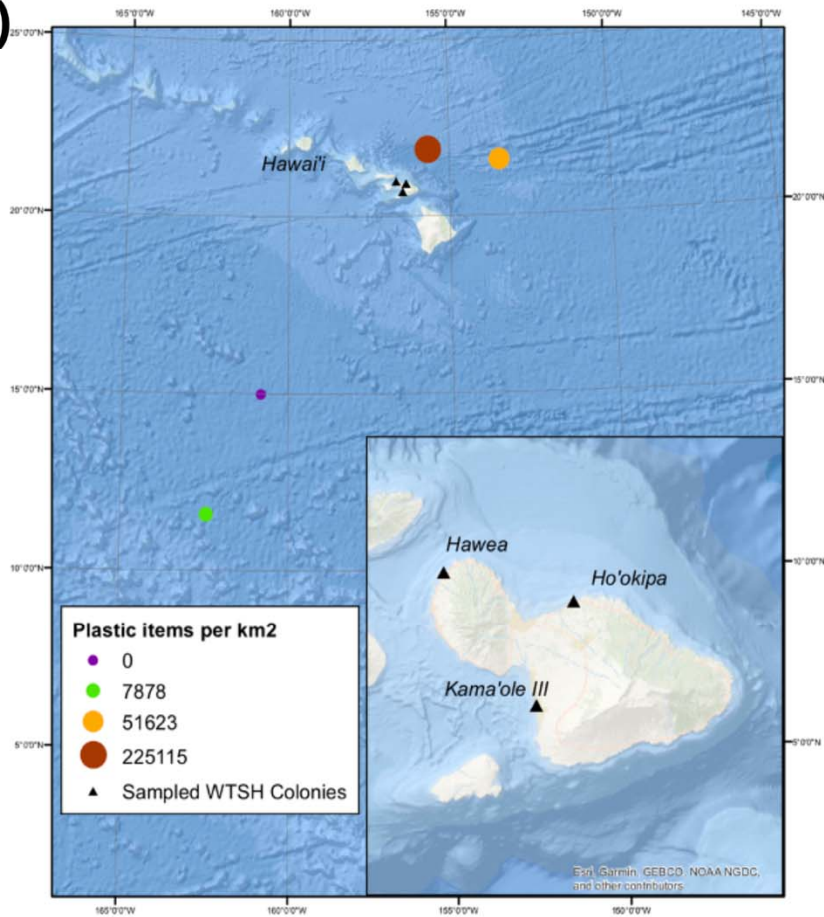
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A)



B)



C)

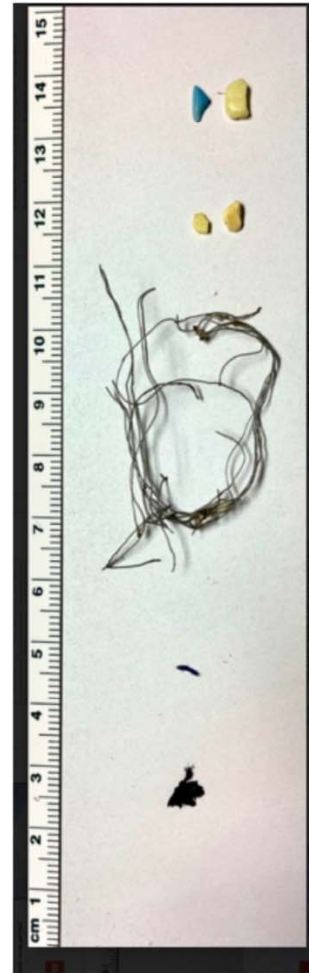


Fig. 1

<b>Bird ID</b>	<b>Sex</b>	<b>Plastic</b>	<b>Blood Sample</b>
N001	F	NA	Gene only
N002	F	(+)	Both
N003	F	(-)	Gene only
N004	NA	(+)	Chem only
N005	M	(+)	Both
N006	F	(-)	Both
N007	F	(+)	Both
N008	F	(-)	Both
N009	F	(-)	Both
N010	M	(+)	Both
N011	M	(+)	Both
N012	F	(-)	Both
N013	F	(-)	Both
N014	M	(-)	Both
N015	F	(+)	Both
N015	M	(-)	Both
N017	M	(+)	Both
N018	F	(-)	Both
N019	M	(-)	Both
N020	F	(+)	Both
N021	M	(-)	Both
N022	F	(-)	Both
N023	F	(-)	Both
N024	F	(+)	Gene only
N025	F	(+)	Both
N026	M	(-)	Both
N027	M	(-)	Both
N028	F	(+)	Both
N029	F	(-)	Gene only

Fig. 2

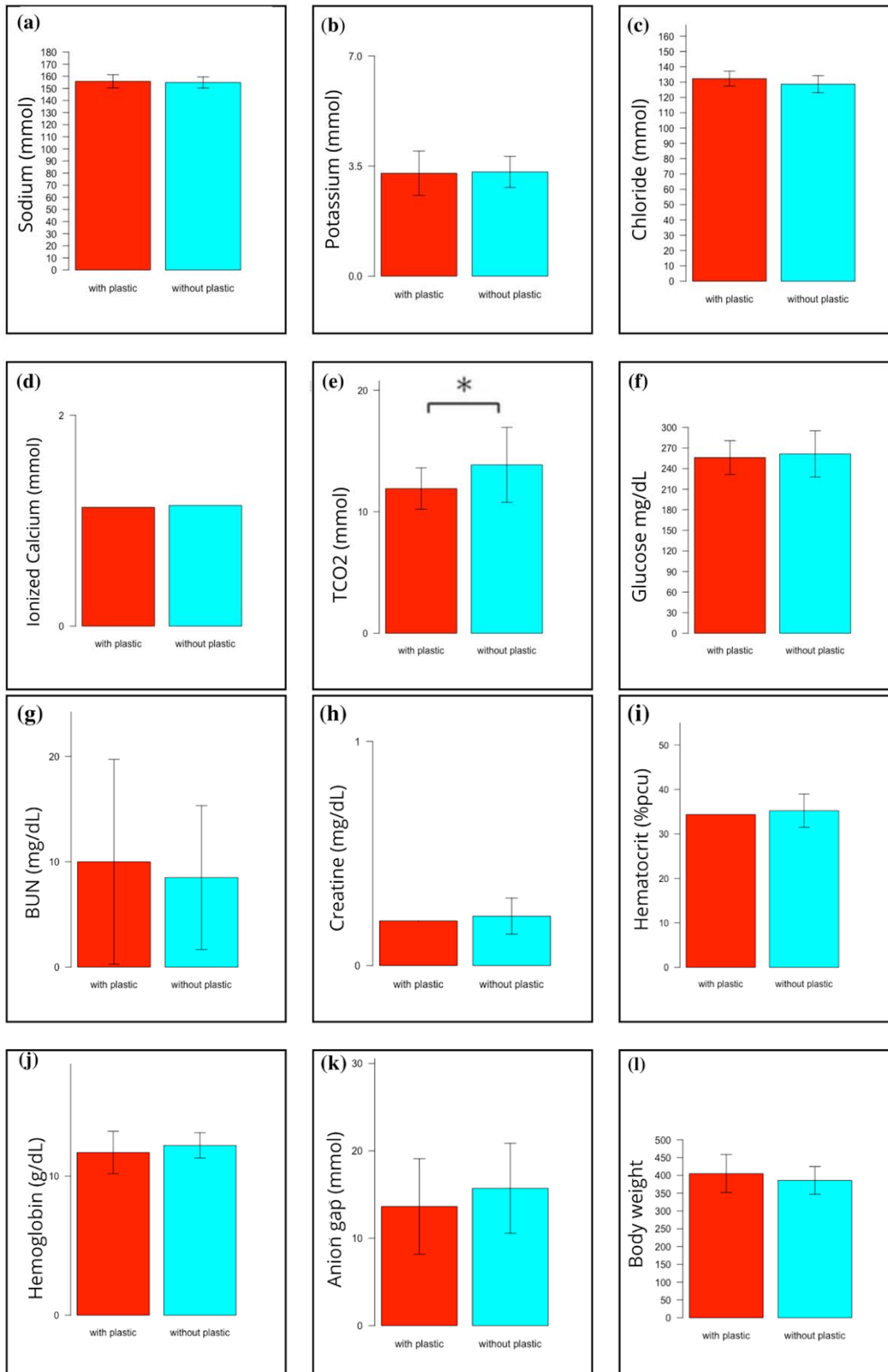


Fig. 3



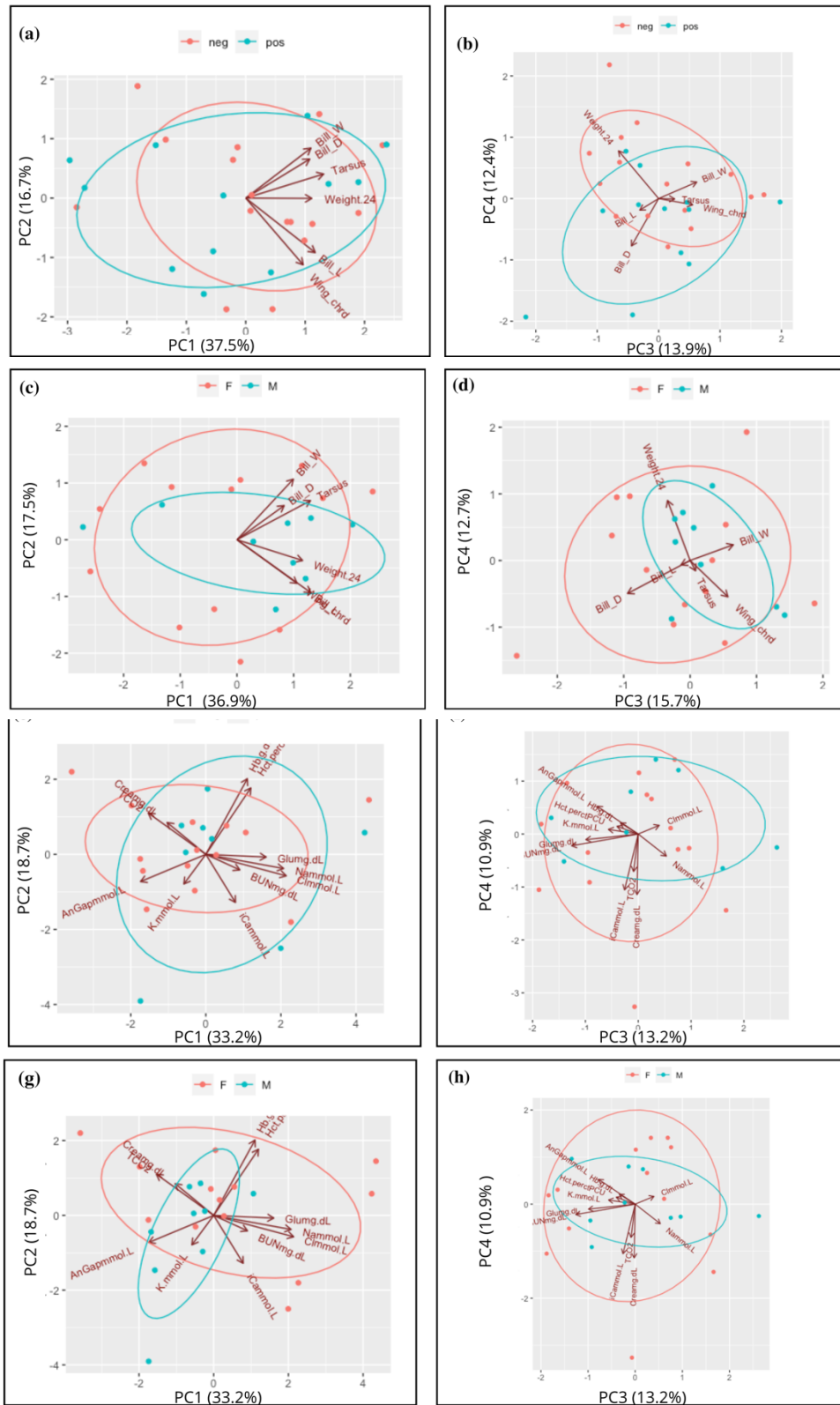


Fig. 4

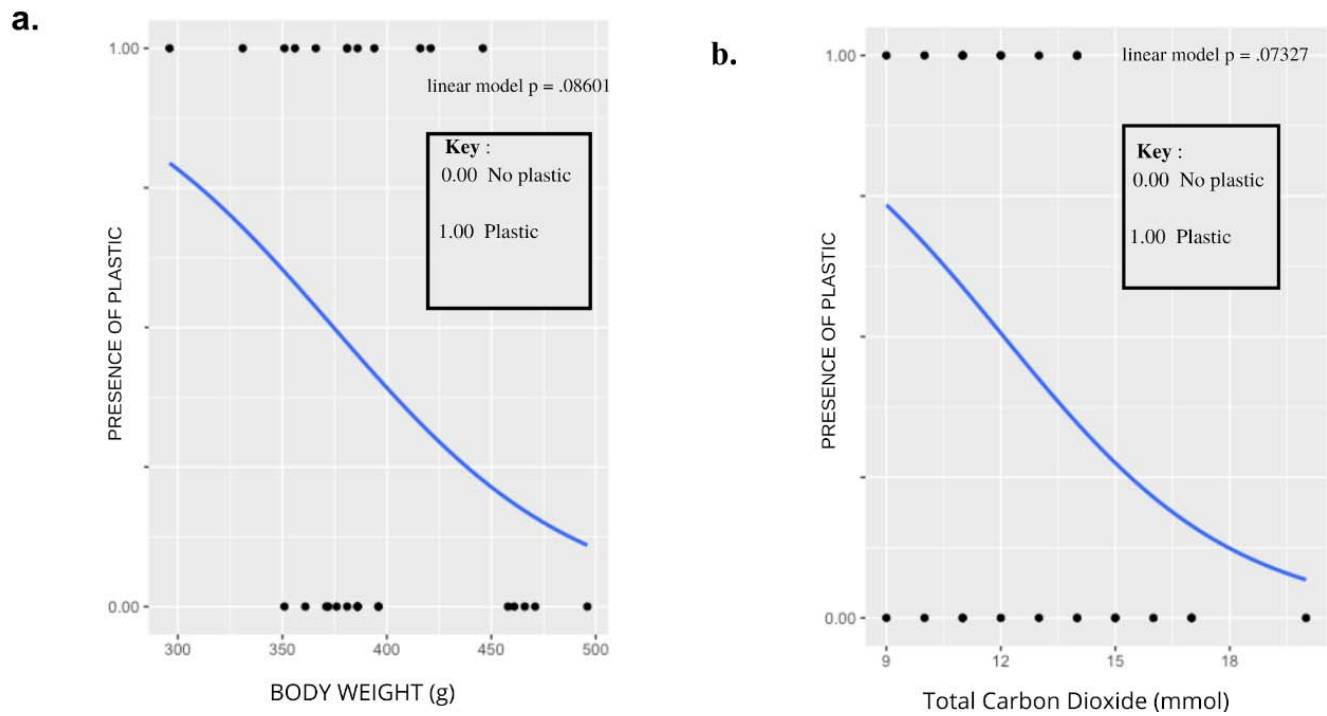


Fig. 5

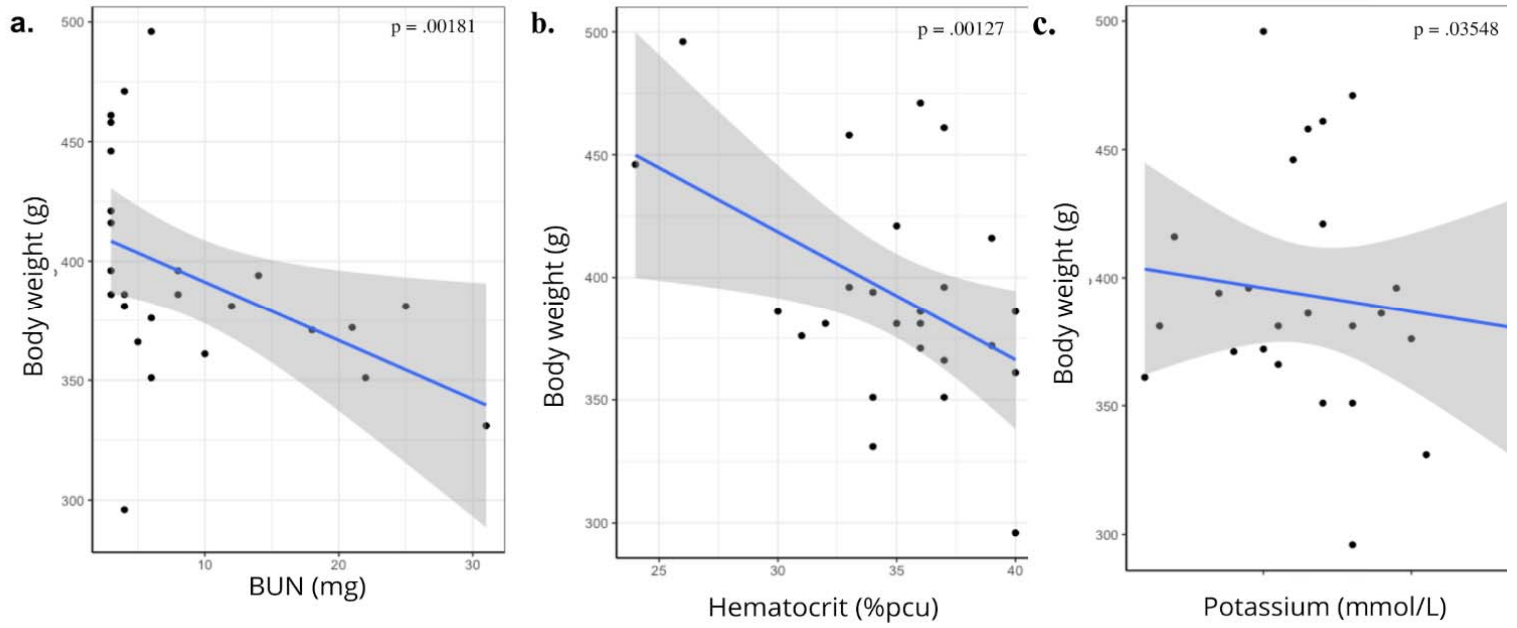


Fig. 6

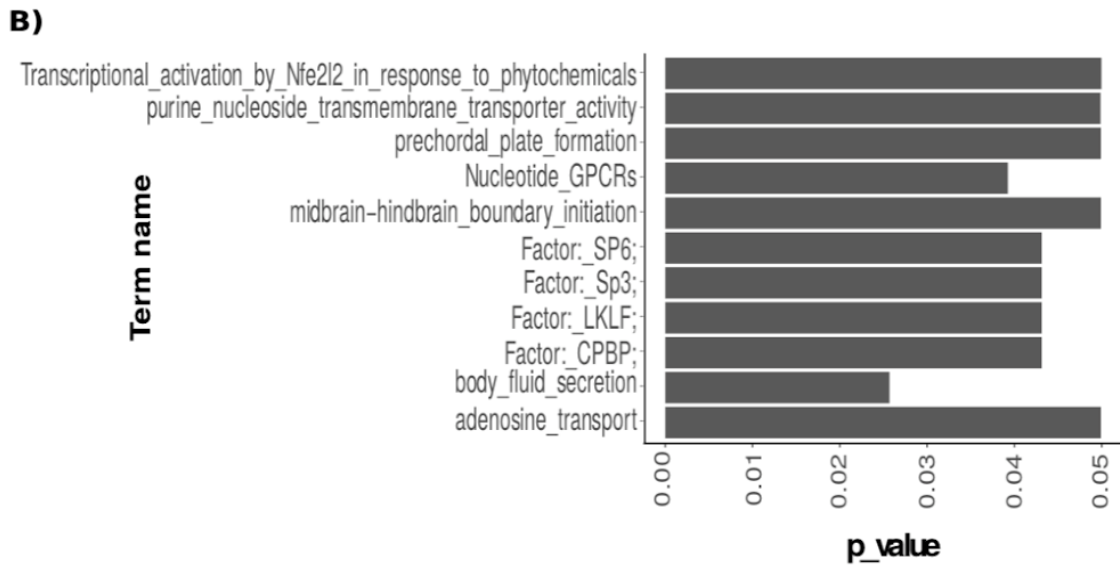
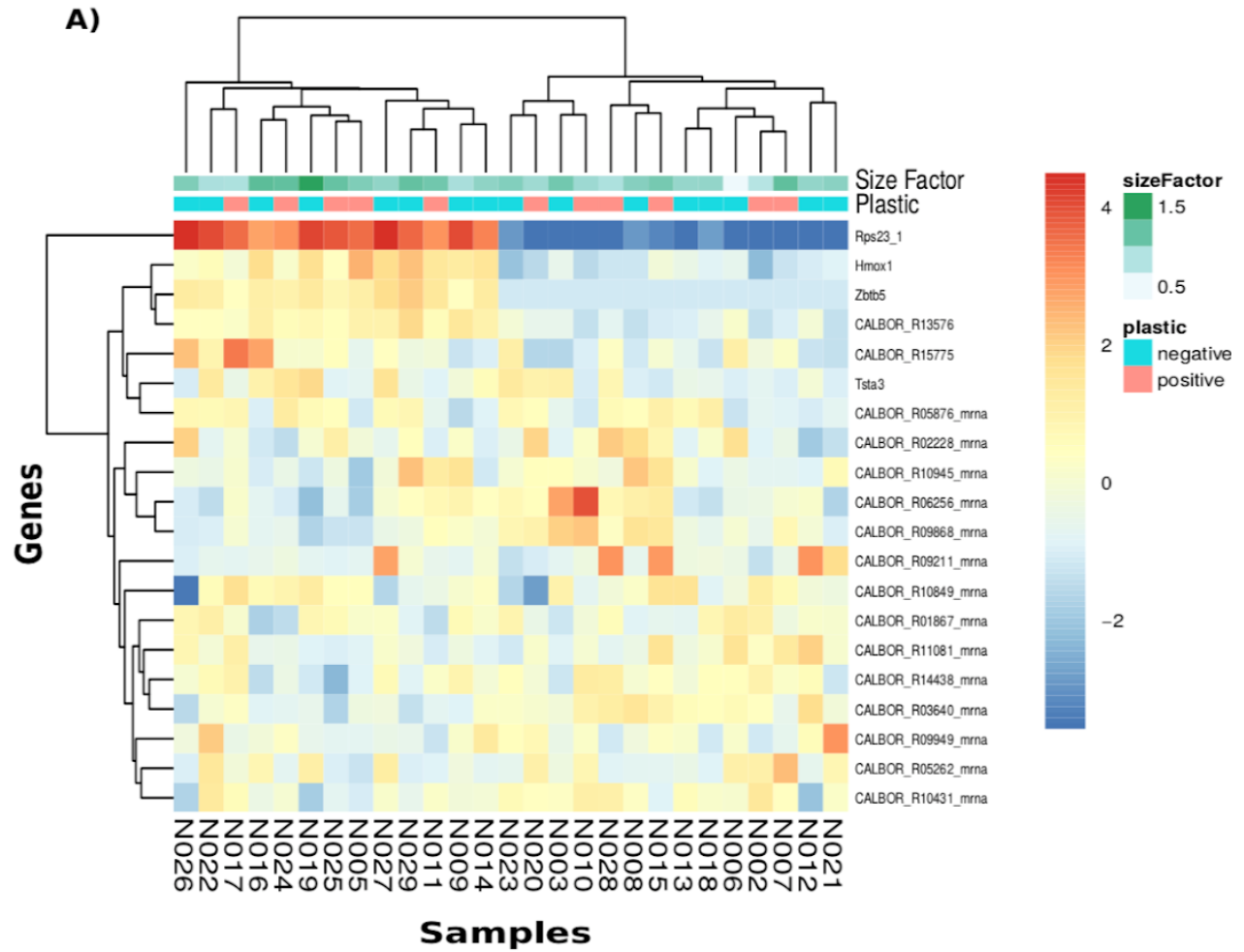


Fig. 7

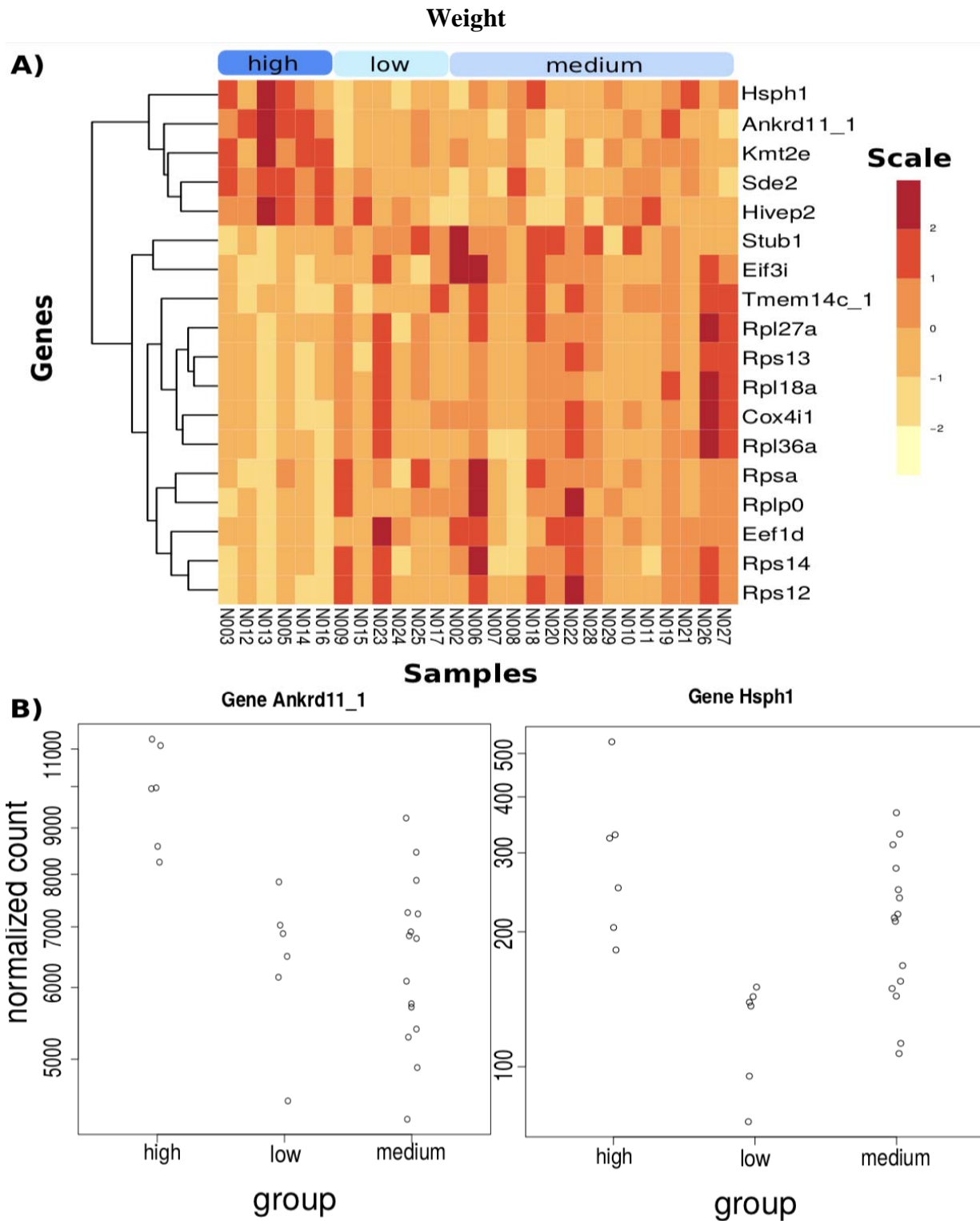


Fig. 8

## Supporting Information

### Effects of Plastic Ingestion on Blood Chemistry, Gene Expression and Body Condition in Wedge-Tailed Shearwaters (*Ardenna Pacifica*)

Nicole Mejia<sup>1,2</sup>, Flavia Termignoni Garcia<sup>1,2</sup>, Jennifer Learned<sup>3</sup>, Jay Penniman<sup>3</sup>, Scott V. Edwards<sup>1,2</sup>

<b>Supporting Text</b> .....	2
Fig. S1. Table summarizing differential genetic expression analyses run.....	5
Fig. S2. Summary of values from blood analytes.....	6
Fig. S3. Reads per sample.....	7
Fig. S4. Phred score for samples.....	8
Fig. S5. Uniquely mapped reads.....	9
Fig. S6. Multiple mapped reads.....	10
Figure S7. Differential gene expression analysis for plastic and sex.....	11
Fig. S8. Differential gene expression analysis divided into samples that had ingested plastic and samples that did not have plastic.....	12
Fig. S9. RIN values.....	13
Fig. S10. Gene enrichment analysis results for bird weight.....	14
<b>Supporting references</b> .....	15

## Supporting Text

*Heavy metals and organic pollutants.* Heavy metals, metals with density greater than 5 g/cm<sup>3</sup>, find their way into the environment both through natural means and as cause of human activity (Briffa et al., 2020). Weathering of earth's crust, urban runoff, industrial waste, pesticides, sewage runoff and many other anthropogenic sources introduce heavy metals into the environment. Heavy metals are found in significant concentrations near areas of anthropogenic activity such as harbors and marinas (Bighiu, 2017). Conversely, these are also areas where there are significant amounts of microplastics (Claessens et al. 2011). Heavy metals then attach to the surface of microplastics due to the strong physical interactions. In excess quantities, heavy metals are toxic to organisms (Furness & Monaghan, 1987).

Organic chemicals, pollutants containing carbon bonded with other compounds, include persistent organic pollutants (or POPs) (Liu et al., 2021). POP's are resistant to degradation and can bioaccumulate to toxin levels. Bioaccumulation refers to the accumulation of a contaminant in an organism. Similar to heavy metals, POPs can be traced back to both natural and anthropogenic activities. These activities include volcanic eruptions or synthesis of chemicals. POPs are known to be easily transported from the source and easily absorbed in a new environment (Ashraf, 2017). Due to the low solubility in water, they are also easily absorbed by microplastics (Verla et al., 2019). Some well-known examples of POPs include the insecticide DDT, PCBs (Polychlorinated biphenyls) and BPAs (Bisphenol A) (Verla et al., 2019).

*Wedge-tailed Shearwater (A. pacifica) Biology.* Wedge-tailed Shearwater are pelagic seabirds that are monogamous and are known to be natal philopatric. Shearwater pairs often form a long-term pair bond which lasts several years. They have extensive feeding ranges, with a mean maximum range of 615 km (Adams et al., 2020). Although not endangered, global

numbers are in decline. When it is not breeding season, Wedge-tailed Shearwaters take long migrations and use specific migratory routes that take advantage of the oceanic wind patterns (Schaffer et al., 2006) It has been documented that the birds sometimes make long dispersive movements (Weimerskirch et al. 2020).

*Science of plastic accumulation in the ocean.* Due to ocean circulation patterns, there are certain regions in the open ocean where there is a greater concern for ocean pollution, such as the Great Pacific Garbage Patch in the Northern Pacific that stretches from the west coast of North America (Cózar et al., 2014). These garbage patches form because of gyres, large systems of circulating water in the ocean. Five gyres in particular play an important role in circulating water around the globe: North Atlantic, South Atlantic, North Pacific, South Pacific and Indian (NOAA). Plastic congregates around these slow-moving whirlpools, forming massive areas of circulating plastic (NOAA).

*Gut sampling from the proventriculus.* The flushing technique empties out gut contents from the proventriculus of a bird, but we cannot be assured that it empties out gut contents from the ventriculus in Procellariids (Duffy & Jackson, 1986). Procellariids' stomachs can be divided into two sections: the proventriculus and the gizzard. A lack of plastic content in the proventriculus often means that it is either regurgitated or emptied quicker than the gizzard (Nania & Shugart, 2021). This creates the possibility that the proventriculus of birds we sampled had been already cleared of plastic and we did not fully capture the plastic load.

*Challenges of gene expression with blood.* Using whole blood to create a genetic profile is a relatively new approach, especially in non-model organisms and livestock (Désert et al., 2016). Most gene profiles use tissue samples for a particular study because the composition and content of RNA, responsible for genetic activity that we are able to investigate, is specific to the tissue



activity (Jax et al., 2018). Target tissues also provide information on specific adverse effects specially in response to toxic exposure (Lobenhofer et al., 2008).

The use of whole blood for genetic profiling is a rising and useful tool (Désert et al., 2016). It could be used as a new approach in conservation to assess the health status of natural populations of species in threatened status. Studies with whole blood transcriptome have quantified immune response in birds and identifying sex chromosome evolution in two rare species of kiwi birds (Désert et al. 2016, Ekblom et al. 2014, Ramstad et al. 2016, Sandford et al. 2012). It is worthy to note the importance of continuing to advocate for these procedures which may provide a less invasive way of conducting data collection.

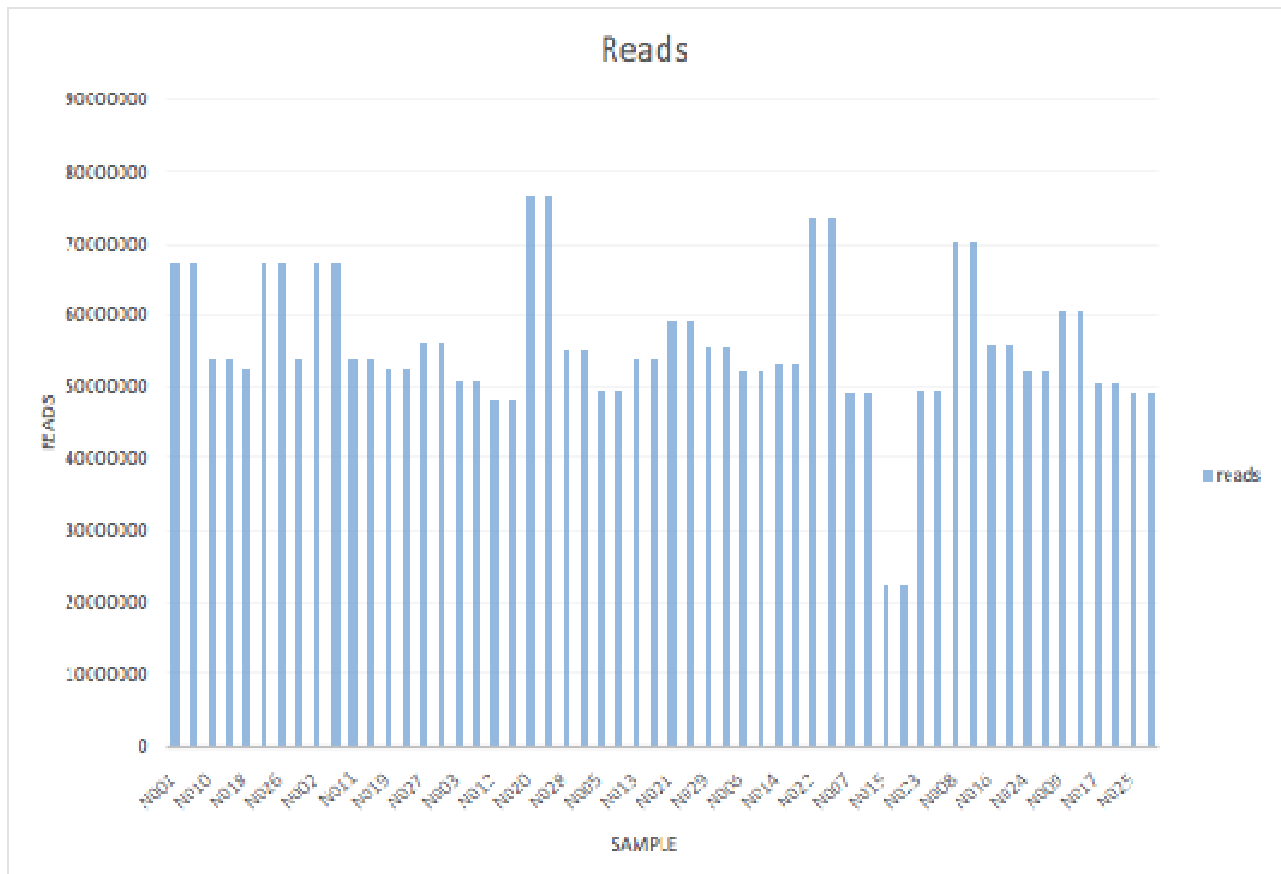
## Figures

<i>Test-experiment</i>	Total Transcripts	Net Transcripts	Outlier Transcripts	Outlier genes	Pvalue_used
<b>PLASTIC</b>					
-all samples	15799	12842	0	0	0.05,0.1
-males	15799	8824	4,14	4,14	0.05,0.1
-females	15799	12503	1,1	1,1	0.05,0.1
<b>SEX</b>					
-all samples	15799	12853	2,3	2,3	0.05,0.1
-plastic	15799	12177	1,10		0.05,0.1
-no plastic	15799	12477	12,43		0.05,0.1
<b>WEIGHT 3 factor</b>					
-all samples	15799	12842	5,17		0.05,0.1
-males (just 2 factor)	15799	12048	1,2		0.05,0.1
-females	15799	12507	5,14		0.05,0.1

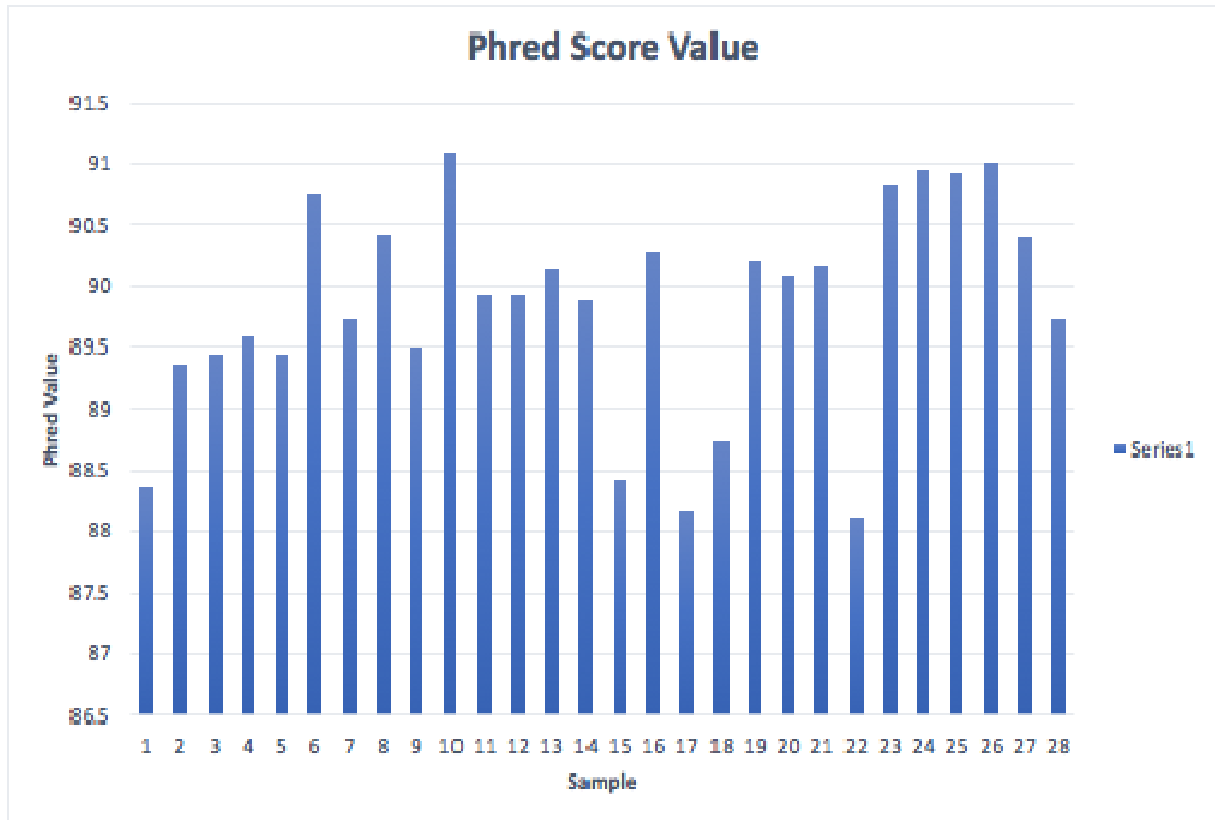
**Fig. S1. Table summarizing differential genetic expression analyses.** The test/experiment column describes the three main analyses that we conducted and the variables that we used for each test. Transcripts represent the count of transcripts that were aligned with the reference genome. Net transcripts represent the count of transcripts that were represented or quantifiable in all of the samples. Outlier transcripts and outlier genes represent the count of transcripts that differentiated within the respective test. P-value represents the two p-values we used to determine significance of the results. We used both a marginal p-value (0.1) and a standard value (0.05).

	Na	K	Cl	iCa	TCO2	Glucose	BUN	Crea	Hct	Hb	AnGap	Weight
<b>MN</b> +	155.8 182	3.2727 27	132.2 727	1.12727 3	11.90 909	256	9.998 182	0.199	34.36 364	11.7	13.63 636	405.2 5
<b>MN</b> -	154.8 571	3.3142 86	128.6 429	1.145	13.85 714	261.3 571	8.497 857	0.2205	35.21 429	1.5244 67	15.71 429	3386
<b>SD</b> +	5.473 905	0.7044 017	4.900 835	0.09360 458	13.85 714	24.62 113	9.727 693	0	4.500 505	1.5244 67	5.463 931	53.36 176
<b>SD</b> -	4.588 567	0.4943 638	5.583 039	0.09920 841	3.084 88	33.69 685	6.826 59	0.08044 563	3.745 327	0.9110 132	5.150 483	39.02 99
<b>T-test</b> (p-value)	0.645 4	0.87	0.097 5	0.6516	0.057 89*	0.650 6	0.669 4	0.3356	0.619 6	0.3446	0.344 1	0.651 6

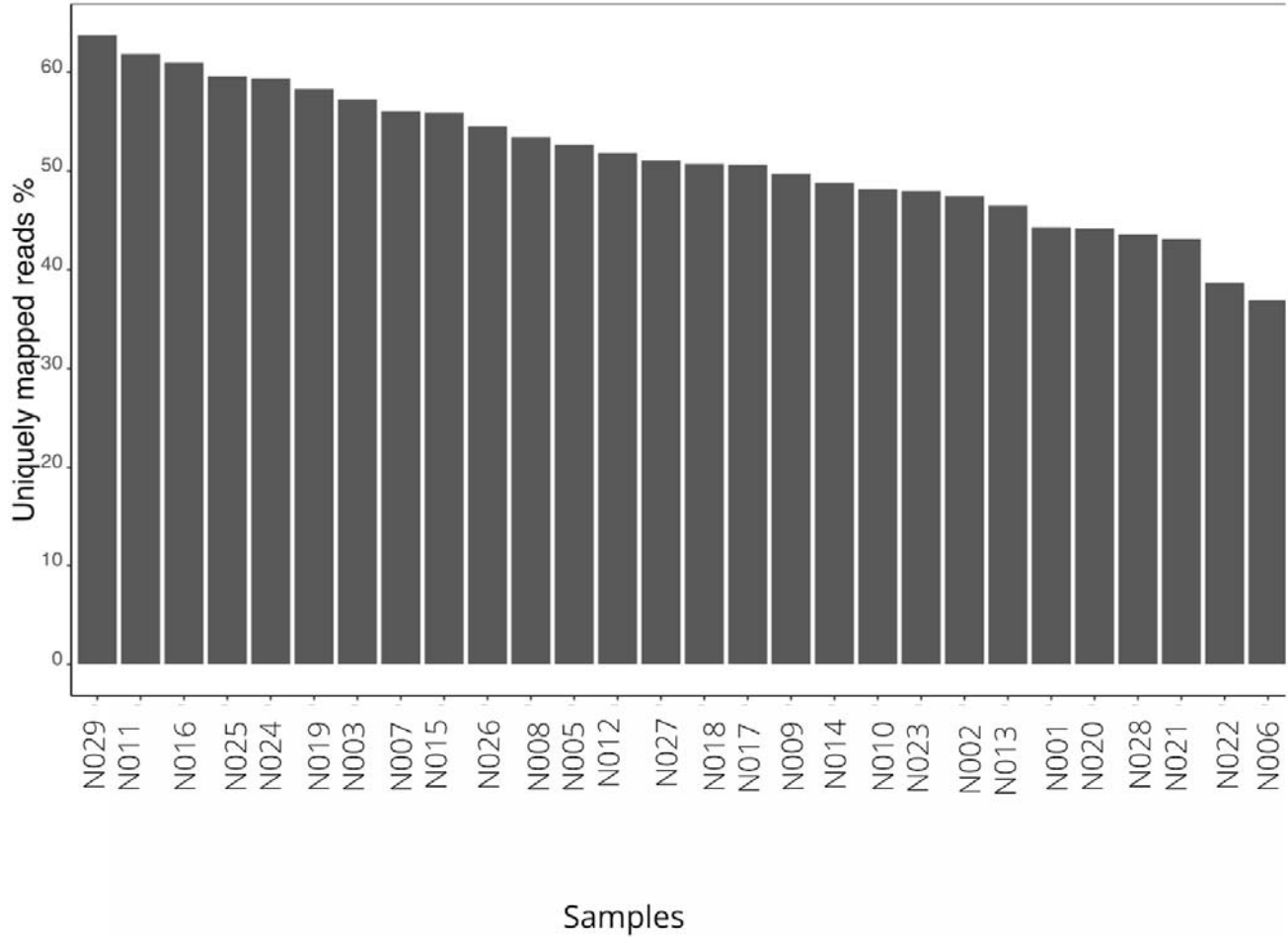
**Fig. S2. Summary of values from blood analytes and weight.** This table provides the mean, standard deviation and p-values from the t-tests for each of the blood chemistry analytes and weight. The plus sign (+) indicates the values for individuals with plastic. The minus sign (-) indicates the values for individuals without plastic. The blood analytes measured were sodium (Na mmol/L), potassium (K mmol/L), chloride (Cl mmol/L), ionized calcium (iCa mmol/L), total carbon dioxide (TCO2), glucose (Glu mg/dL), Urea nitrogen/urea (BUN mg/dL), creatinine (Crea mg/dL), hematocrit (Hct %PCU), hemoglobin (Hb g/dL), anion gap (AnGap mmol/L) and are ordered respectively in the table. Differences were considered statistically significant when  $p < 0.07$ .



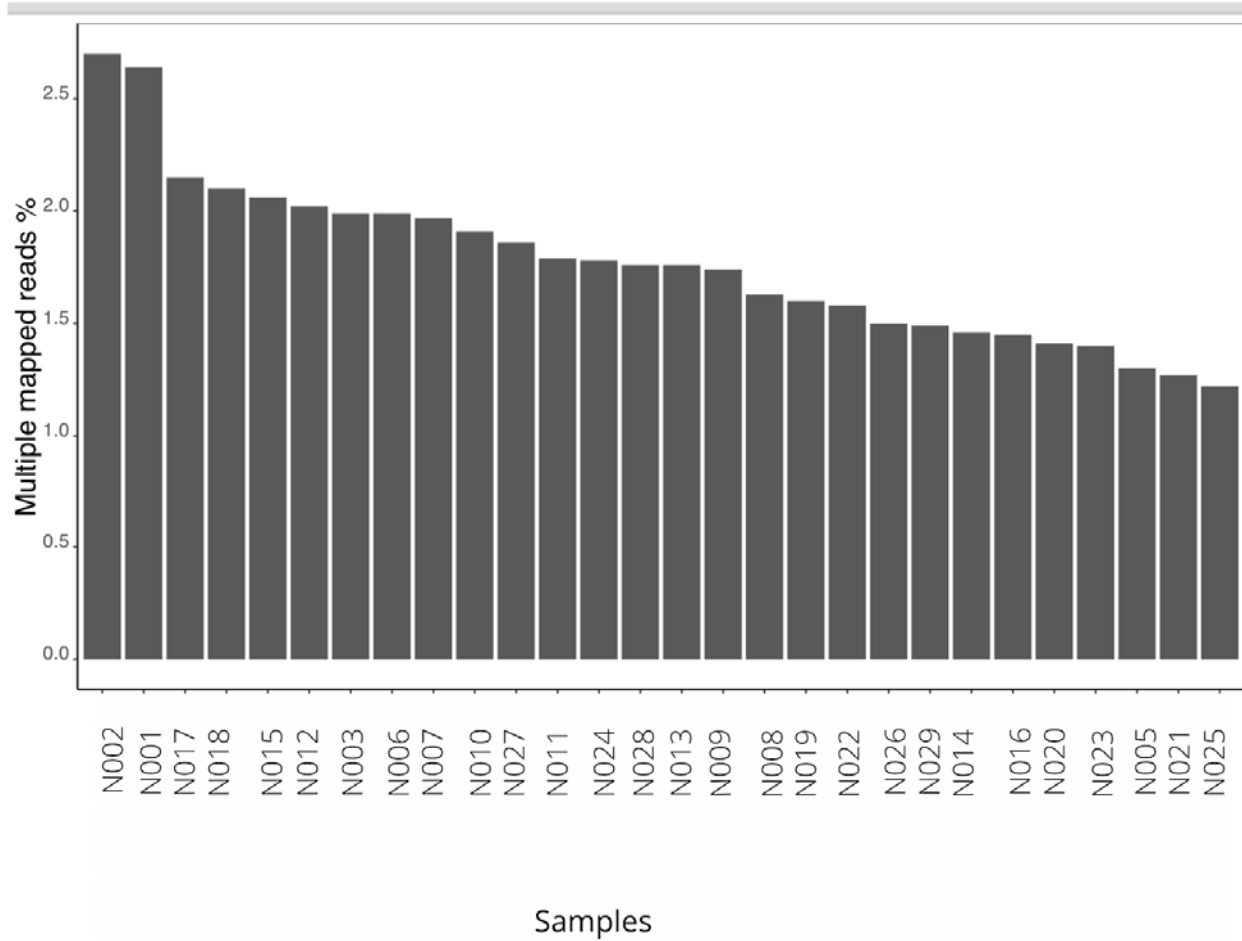
**Fig. S3. Reads per sample.** This measurement assesses inferred sequence of base pairs that correspond to a single DNA fragment.



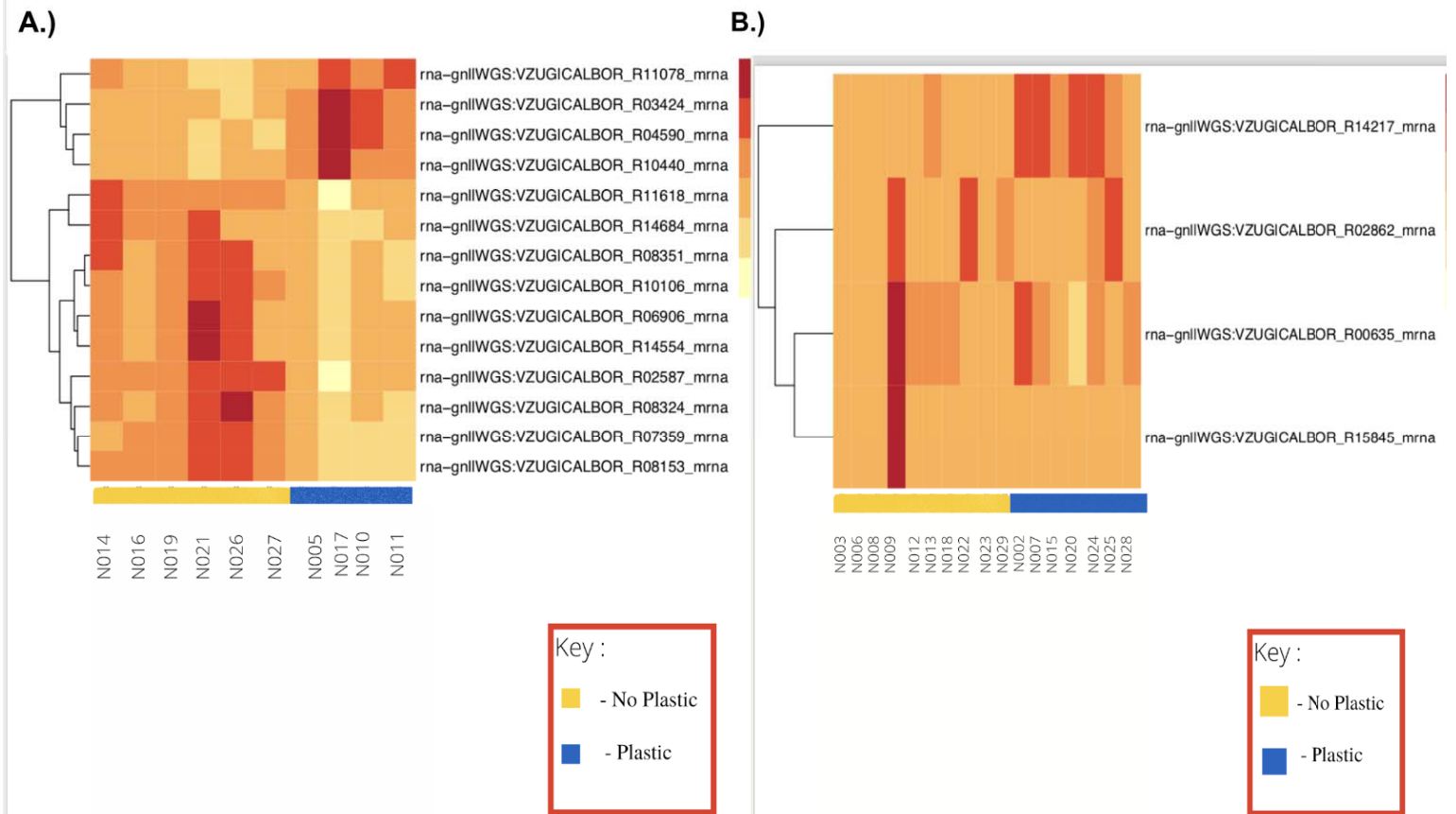
**Fig. S4. Phred score of samples.** Phred score is used for quality assessment of sequencing



**Fig. S5. Uniquely mapped reads.** Uniquely mapped reads have one exact location within the reference genome which they map to. This is the number of uniquely mapped reads from the prepared library that are aligned to the Cory Shearwater reference genome.



**Fig. S6. Multiply mapped reads.** Multiple mapped reads are reads that map more than once in the genome. This is the number of multiple mapped reads from the prepared library that are aligned to the Cory Shearwater reference genome.



**Fig. S7. Differential gene expression analysis for plastic and sex.** (A) Heatmap showing the 14 significantly differentially expressed genes in males. (B) Heatmap showing the 4 significant differentially expressed genes in females.

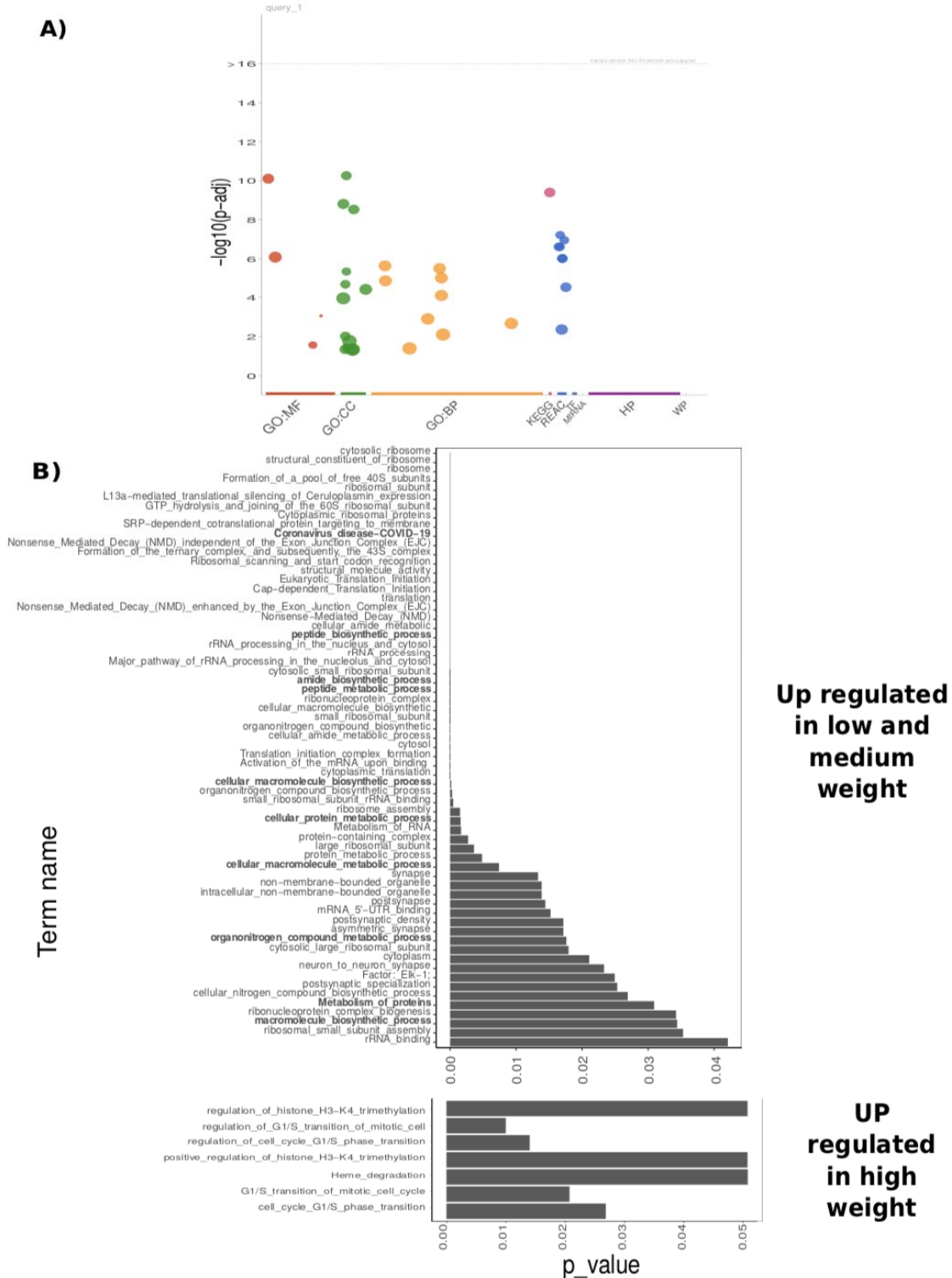




<b>Sample ID</b>	<b>RIN Score</b>
<b>N001</b>	<b>7.4</b>
<b>N002</b>	<b>7.6</b>
<b>N003</b>	<b>7.4</b>
<b>N005</b>	<b>4.8</b>
<b>N006</b>	<b>7.7</b>
<b>N007</b>	<b>7.8</b>
<b>N008</b>	<b>7.5</b>
<b>N009</b>	<b>7.1</b>
<b>N010</b>	<b>8.4</b>
<b>N011</b>	<b>7.7</b>
<b>N012</b>	<b>8.4</b>
<b>N013</b>	<b>7.3</b>
<b>N014</b>	<b>6.7</b>
<b>N015</b>	<b>8.3</b>
<b>N016</b>	<b>7.3</b>
<b>N017</b>	<b>8</b>
<b>N018</b>	<b>8</b>
<b>N019</b>	<b>6.4</b>
<b>N020</b>	<b>7.2</b>

<b>N021</b>	<b>7.3</b>
<b>N022</b>	<b>7.3</b>
<b>N023</b>	<b>6.6</b>
<b>N024</b>	<b>7.6</b>
<b>N025</b>	<b>6.1</b>
<b>N026</b>	<b>6.7</b>
<b>N027</b>	<b>7.4</b>
<b>N028</b>	<b>8.3</b>
<b>N029</b>	<b>7</b>

**Fig. S9. RIN Values.** RIN values assign a numerical value to the quality of the RNA that we worked with. A RIN value of 8 and above indicated higher quality and integrity of RNA and values below 5 indicated some levels of RNA degradations.



**Fig. S10. Gene enrichment analysis results for bird weight.** (A) Manhattan plot showing results of enrichment analysis and the databases used. (B) Terms with significant values from the enrichment analysis in the differentially expressed genes between weight categories.

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