ECOLOGICAL QUALITY ASSESSMENT OF MARINAS: AN INTEGRATIVE APPROACH COMBINING BIOLOGICAL AND ENVIRONMENTAL DATA.

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Highlights:

-An integrative method for quality assessment is developed and proposed for marinas

-Correlations between fauna and abiotic data are detected at family and order level

-Soft-bottom benthic communities are key tools for managing programmes

Abstract

The importance of marinas as infrastructures for recreational boating is increasing substantially. However, information on their soft-bottom benthic communities, a key tool for managing programmes, is still scarce. We combined environment features with macro- and meiofaunal soft-bottom community information for assessing the ecological status of marinas with an integrative approach. To address this issue, we focused on eight marinas of the Southern Iberian Peninsula. Macro- and meiofauna data revealed high benthic heterogeneity at a spatial scale. The environmental variables which correlated best with macrofauna were mainly

phosphorus, granulometry, and total organic carbon, and secondarily important variables were faecal coliforms, the biocide Irgarol, and heavy metals; total hydrocarbon concentration was also significant for meiofauna. Annelida was the dominant phylum in terms of number of species (37%) and abundance (66%) and were better descriptors of the environmental conditions than Arthropoda and Mollusca. Although identification to the species level is desirable and mandatory for assessing biological pollution, significant differences among marinas and correlations between fauna and abiotic variables were already detected at the level of family and order. This implies that biota assessment at higher levels may still be useful in monitoring programmes limited by time and budget constraints. The major novelty of this study lies in the development of an integrative assessment method based on the following selected ecological indicators: Marinas Environmental Pollution Index (MEPI), Biocontamination Index (BCI), macrofaunal biotic indices (AMBI, M-AMBI, BENTIX, MEDOCC and BENFES), macrofaunal taxa richness and Shannon-Wiener's diversity, and nematode:copepod index. This approach was able to discriminate marinas of the Southern Iberian Peninsula based on their ecological status, which ranged from poor to good. The method can be useful to design standards for assigning "sustainable quality seals" to those marinas with better values of ecological indicators.

Keywords: Marinas, ecological assessment, macrofauna, meiofauna, soft bottoms, taxonomic resolution

1. Introduction

Port areas and marinas in particular, are confined environments subjected to a number of anthropogenic activities that result in significant environmental disturbances (Tempesti et al., 2020 and references therein). The number of marinas has significantly increased during the last years, since they are essential infrastructures for the recreational boating sector, a key activity of global marine tourism in high demand (Di Franco et al., 2011). However, marinas modify ecological conditions (Rivero et al., 2013; Valdor et al., 2019) and their increasing number is recognized as an important environmental stressor in many regions (e.g. Gómez et al., 2017).

Despite the importance of marinas as hotspots of environmental and biological pollution, knowledge about these novel ecosystems is still very scarce. Previous studies

have evaluated the pollution pressure (Mali et al., 2017; Gómez et al., 2019; Guerra-García et al., 2021), but little effort has been put into proper characterization of their biological communities (Covazzi Harriague et al., 2012; Chatzinikolaou et al., 2018; Dimitrou et al., 2020). Faunistic information in marinas is mainly restricted to sessile communities and/or Non-Indigenous Species (NIS) (e.g. Di Franco et al., 2011; Oricchio et al., 2016; Kenworthy et al., 2018; Ulman et al., 2019; Ferrairo et al., 2020), and there is a lack of research targeting mobile macro- or meiofauna. Furthermore, the few studies dealing with these taxa have focused on arborescent substrates attached to floating pontoons (Ros et al., 2013; Marchini et al., 2015; Fernández-Romero et al., 2019; Gavira O'Neill et al., 2018; Martínez-Laiz et al., 2018). Meanwhile, studies on soft-bottom fauna in marinas are scarce (e.g. Chatzinikolaou et al., 2018, Dimitrou et al., 2020, Table S1) and generally limited when compared to other assemblages, such as the biofouling organisms which cause noticeable financial and ecological impacts (Ng et al., 2019 and references therein). The study of the soft bottom environment in marinas (usually corresponding to muddy sediments) is especially relevant since (i) it is the most widespread habitat there, (ii) it represents a more stable substrate for fauna than the floating structures above (which are temporally cleaned and often subjected to fluctuations in salinity and temperature), and (iii) sediments accumulate pollutants and provide more reliable information about environmental conditions than seawater, which only provides punctual information. Indeed, most of the monitoring programmes for quality assessment guidelines in marine habitats are focused on sediments (Birch, 2017; 2018; Dimitrou et al., 2020) and previous work (e.g Martínez-Lladó et al., 2007; Ondiviela et al., 2013) has already demonstrated that sediments constitute the main testimony of contaminant episodes in harbours.

To achieve the goal of "Bridging the Gap Between Policy and Science in Assessing the Health Status of Marine Ecosystems", scientists should provide policymakers with the best available and updated knowledge (Borja et al., 2016, 2017). Most of the monitoring programmes are mainly concerned with bathing water, while marinas and harbours are usually excluded. Regulations in marinas are especially challenging due to the wide range of uses, pressures and singularities of each marina (different morphology and hydrodynamic regimes, quick and unpredictable changes due to local actions, etc) (Gupta et al., 2005; Petrosillo et al., 2010). Management of marinas also involves conflicting uses by residents, visitors, boat owners, shipping, and industry

among others, thus requiring the integration of multi-disciplinary authorities and stakeholders from different sectors (e.g. engineers, biologists, economists, environmental agencies, governmental bodies) (Chatzinikolaou et al., 2018).

Several methods and models, such as the Complexity Tidal Range Index (CTRI) or the Marina Environmental Risk Assessment (MERA), have been recently applied to prioritize environmental strategies in marinas (e.g. Gómez et al., 2019; Valdor et al., 2019). However, the progress in these tools significantly contrasts with the scarce biotic and abiotic information available. This basic information is mandatory to develop an integrative assessment, which is necessary to undertake properly designed management programs in marine ecosystems (Karydis and Kitsiou, 2013; Dauner et al., 2018; Carriger and Parker, 2020; Stelzenmüller et al., 2021).

Thus, the use of appropriate and effective indicators of environmental conditions is critical to accurately conduct integrative assessments and to ensure that human activities are carried out in a sustainable manner (Birch, 2017). In this sense, benthic invertebrates are very sensitive to physical and chemical perturbations and recommended as good biological indicators of contamination for integrating environmental disturbances over time (Albano et al., 2013). Biological data have the advantage of giving an integrated view of the long-term environmental conditions, whereas chemical and physical analytical methods provide only a 'snapshot' of conditions at the time of sampling (Saiz-Salinas, 1997; de-la-Ossa-Carretero et al., 2012; Ng et al., 2019). In fact, the use of benthic communities to assess the environmental state of marine systems is strongly supported by the Water Framework Directive (WFD) of the European Union (2000/60/EC). For harbour environments, Ondiviela et al. (2013) stressed the importance of considering simultaneously abiotic and biological indicators in integrative assessments to evaluate the ecological status.

An integrative approach must, therefore, include inventories of the biodiversity, since taxonomic information is pivotal for establishing a baseline to properly address sustainable management of marinas. Ideally, the analysis of benthic communities should be based on identification to the species level but this is usually a complex and time-consuming procedure (Terlizzi et al., 2003; Sánchez-Moyano et al., 2006). Indeed, in many taxa, species identification is laborious and requires appropriate taxonomic expertise that nowadays is often lacking (Paknia et al., 2015; Chatzinikolaou et al., 2018). Furthermore, policy makers and funding agencies often demand results and

recommendations be achieved within very short timescales. These requirements prevent identification to species level and promote analyses considering higher taxa (e.g. genus, family, order). Extensive literature, including a variety of methodologies, habitats and substrate types, has been developed to explore if environmental changes can be detected above the species level (see Sánchez-Moyano et al., 2006 and references therein; De Oliveira et al., 2020; Gerwin et al., 2020). Nonetheless, the response of fauna to environmental data by considering different taxonomic levels has been scarcely studied in harbours and marinas (Chatzinikolaou et al., 2018).

To fill the gaps described above, the main objective of this study was to explore the importance of soft-bottom environments, including both biotic and abiotic information, for assessing the ecological status of marinas from an integrative approach. To address this issue we aim to: (*i*) characterize the diversity and spatial distribution patterns of soft-bottom macro- and meiofauna communities in marinas, (*ii*) identify the set of abiotic variables which better explain the biological patterns, (*iii*) explore the taxonomic sufficiency required to detect differences among marinas and environmental patterns, and, eventually, (*iv*) develop an integrative and easy-to-apply method to assess the quality status of soft-bottom environments of marinas based on selected ecological indicators. Most previous studies regarding soft bottoms of marinas have focused on abiotic parameters, and when they include biotic data, information on the macrofaunal and meiofaunal communities is neither integrated simultaneously nor do they develop integrative quality assessments based on a multiparametric approach (Table S1). The novelty of the present study lies in the integration of abiotic and biotic data for designing a quality assessment method based, concurrently, on the following selected ecological indicators: Marinas Environmental Pollution Index (MEPI), Biocontamination Index (BCI), macrofaunal biotic indices (AMBI, M-AMBI, BENTIX, MEDOCC and BENFES), macrofaunal taxa richness and Shannon-Wiener's diversity, and nematode:copepod index.

To achieve the aforementioned objectives, the Southern Iberian Peninsula was selected as the study area since it (i) represents an interesting biogeographical area which includes an horizontal gradient Atlantic-Mediterranean, (ii) encompasses a very high number of marinas along the coast and (iii) includes the Strait of Gibraltar, a hot spot for maritime traffic.

166 **2. Material and Methods**

167 *2.1. Sampling survey and laboratory processing*

168 Sampling was conducted from June 26th to July 2nd 2017. Eight marinas were
169 randomly selected along the Southern Iberian Peninsula: four in the Atlantic coast
170 (Faro, Chipiona, Puerto América, Barbate) and four in the Mediterranean (La Línea-
171 Puerto Chico, Fuengirola, Motril, Almería) (Fig. 1). Details of these marinas
172 (coordinates, depth, size, number of berths and population density of the adjacent
173 locality) can be consulted in Guerra-García et al. (2021). Within each marina, three
174 floating pontoons were randomly selected (each pontoon was considered a replicate for
175 analyses throughout the whole study; consequently, three replicates per marina were
176 taken) and the sediment below each pontoon (mostly muddy) was sampled.

177 For macrofauna, a small van Veen grab (area: 15 x 15 cm) was used. Because
178 the grab was relatively small, the replicate (i.e. pontoon) consisted of three additive
179 sediment grabs (total area: 675 cm^2). Samples were washed through a sieve with a mesh
180 size of 0.5 mm and the retained fraction was fixed in 96% ethanol stained with Rose
181 Bengal.

182 For meiofauna, only one sediment van Veen grab was collected per pontoon.
183 Once the grab was recovered, a small corer of 10 cm^2 was introduced into the
184 undisturbed sediment. Therefore, a total of three replicates (one corer per pontoon) were
185 obtained per marina and directly fixed in 96% ethanol stained with Bengal Rose.

186 In the laboratory, macrofaunal samples were rinsed with fresh water over a 0.5-
187 mm sieve, sorted, identified to species level whenever possible, and counted. For
188 macrofauna, the status of each species (N: Native, I: Introduced, C: Cryptogenic, U:
189 Undetermined) was also considered. Species names and systematic arrangement of taxa
190 follows the World Register of Marine Species (WoRMS, 2020).

191 Meiofaunal samples were sieved in the laboratory through a 0.5-mm mesh to
192 exclude macrofauna, with a 30-µm mesh below to retain meiofauna. Specimens were
193 sorted under a stereomicroscope and identified to high taxonomic levels (e.g. phylum,
194 class or order; Sedano et al., 2014, 2020)

195 Additionally, to quantify abiotic variables in sediment for each marina, three
196 sediment samples (one per pontoon) were taken from the bottom using the van Veen
197 grab. All samples were immediately frozen (-20ºC) until laboratory analyses. The
198 following environmental variables were measured: sand, silt, clay, total organic carbon

(TOC), hydrocarbons, faecal coliforms, biocide Irgarol, and major, minor and trace elements As, Cd, Co, Cr, Cu, N, Ni, P, Pb, S and Zn. Analytical procedures are detailed in Guerra-García et al. (2021).

2.2. Statistical analyses

The experimental design included two factors: 'Location' (Lo), a fixed factor with two levels (Mediterranean *vs* Atlantic) and 'Marina' [Ma(Lo)], a random factor with four levels, nested with Lo. The number of replicates was n=3, corresponding to the three pontoons randomly selected for each marina.

Regarding macrofauna, number of taxa (considering the species, genus, family, order, class and phylum levels seperately), total abundance and Shannon-Wiener's Diversity at species level (H') were calculated for each replicate (675 cm^2). Data were also calculated separately for the three main phyla, i.e. Annelida, Arthropoda and Mollusca. Total taxa richness (i.e. total number of different species) and H' were also determined for each marina. For meiofauna, number of taxa (for high taxonomic levels), abundance (individuals/10 cm^2) and the nematode:copepod ratio (Rubal et al., 2009) were also calculated.

Two-way ANOVAs with the above design were conducted to explore differences in the biological descriptive parameters of macro- and meiofauna among marinas (factor 'Marina') along the Mediterranean-Atlantic axis (factor 'Location'). Homogeneity of variances was checked using Cochran's test. When ANOVA detected significant differences for a given factor, the source of the variance was identified by applying the Student-Newman-Keuls (SNK) test (Underwood, 1997).

Non-parametric multidimensional scaling (MDS) was used to show the relationship among locations (Atlantic *vs* Mediterranean) and marinas based on macrofaunal abundances; this was done considering the data matrix for each of the six selected taxonomic levels (species, genus, family, order, class and phylum) separately and also for the three main phyla (i.e. Annelida, Arthropoda and Mollusca) considering only the species level. The Bray-Curtis similarity index was applied after transformation of abundance values by the square-root. An additional MDS was conducted using abundances of meiofaunal higher taxa.

The macrobenthic community patterns obtained from the six different taxonomic levels were compared using a second-stage MDS, by computing a weighted Spearman

rank correlation coefficient between the corresponding elements of each pair of marinas from the respective similarity matrices (Somerfield and Clarke, 1995; Chatzinikolaou et al., 2018). Similarly, a second stage MDS was conducted to compare the patterns obtained separately for Annelida, Arthropoda and Mollusca with that of the total community.

Differences in the macro- and meiofaunal assemblage among locations and marinas were tested by permutational multivariate analyses of variance (PERMANOVA), using the same experimental design explained above, and considering the aforementioned six taxonomic levels. Additional PERMANOVAs were conducted for Annelida, Arthropoda and Mollusca independently. Analyses were based on Bray-Curtis similarities and Monte Carlo tests were included. Significant P-values were obtained by computing 9999 permutations of residuals under a reduced model, as this method gives the most accurate Type I error for complex design (Anderson, 2005). Pairwise comparisons were then used. Additionally, to test the dispersion among samples for the factors 'Location' and 'Marina', a permutational analysis of multivariate dispersions (PERMDISP) was used.

Distance-based linear modelling (DistLM) was used to assess the relative contribution of abiotic parameters to the variability observed in the macro- and meiofaunal community structure (Anderson et al., 2008). The analysis was performed based on the matrix of square-root transformed abundance data. Abiotic data were transformed by log(x+1) and normalized to reduce the effects of differences in unit scales. The model was constructed using the best combination of predictors (*Best* procedure) using AIC (Akaike's Information Criteria) (Burham and Anderson, 2004; Leonardi et al., 2020; Mulik et al., 2020; Wei et al., 2020). Prior to the DistLM analysis, multicollinearity between abiotic factors and skewness of data were evaluated using Draftsman plot based on Spearman correlations. Sets of variables with Spearman's test values higher than 0.8 ($p<0.01$) were omitted (Chatzinikolaou et al., 2018). Distance-based Redundancy Analysis (dbRDA) was performed to provide a visual representation of the macrobenthic community fitted to the significant predictor variables in the multi-dimensional space (Mulik et al., 2020; Wei et al., 2020). To increase robustness of results, the BEST routine (BIO-ENV) was also employed to explore correlations between the matrix of faunal abundances and environmental predictors from a different analytical perspective (Anderson et al., 2008). The Bray-Curtis similarities matrix was

based on faunal abundances while the Euclidean distances-based matrices derived from all the possible sequential combinations of the abiotic variables. Spearman rank coefficient was used to identify the best environmental variables that explained the observed patterns on 999 permutations (Marchini et al., 2020). To explore the response to abiotic parameters of each considered taxonomic level (species to phylum) and the three main phyla, DistLM and BIO-ENV were conducted for each category.

PERMANOVA, PERMDISP, MDS, DistLM, dbRDA and BIO-ENV analyses were carried out using the PRIMER v.6+PERMANOVA package (Clarke and Gorley, 2006; Anderson et al., 2008) and ANOVA analyses were conducted on the GMAV5 software (Underwood et al., 2002).

2.3. Integrative assessment

For an integrative assessment of the ecological quality status of marinas considering biotic and abiotic information of soft-bottom environments, the following six ecological indicators were selected and calculated for each marina (Fig. 2):

A) Marinas Environmental Pollution Index (MEPI). This index was recently developed by Guerra-García et al. (2021) to characterize the environmental pollution levels in marinas based on 15 selected stressors measured in the sediments.

B) Biocontamination Index (BCI). It was developed by Arbačiauskas et al. (2008) to assess the biopollution level (in terms of exotic species) in inland waters. We have used this index here as a proxy to evaluate the contribution of NIS to the soft-bottom benthic community in each marina.

C) Macrofaunal taxa richness. The total number of species found in each marina was calculated. The number of genera, families and orders were also included for comparison.

D) Macrofaunal diversity (at species level) was measured by the Shannon-Wiener's index (H').

E) Macrofaunal biotic indices. Many biotic indices have been developed during the last years. In the present study we have used AMBI (Borja et al. 2000), M-AMBI (Muxika et al., 2007), BENTIX (Simboura and Zenetos, 2002), MEDOCC (Pinedo et al., 2015) and BENFES (Sánchez-Moyano et al., 2017).

Compiled information about the boundaries and intervals for these indices can be found in Keeley et al. (2012). Biotic indices have been considered suitable tools for assessing the ecological status of Mediterranean ports (Dimitriou et al., 2020)

F) Meiofaunal nematode:copepod index proposed by Raffaelli and Mason (1981). This ratio was proposed as a fast, easy, and reliable method to study the effects of organic matter enrichment in coastal sediments (see Rubal et al., 2009).

The intervals and boundaries assigned in the literature for MEPI, BCI, AMBI, M-AMBI, BENTIX, MEDOCC and BENFES (high, good, moderate, poor, bad) were adopted in the present study. Intervals for taxa richness, H' and nematode:copepod ratio were established in the present study according to the results obtained in the marinas from the Southern Iberian Peninsula.

The following methodological protocol was developed to assess a quality status based on the selected ecological indicators (Fig. 2):

(i) Once the six indicators were calculated, a score for each indicator was assigned according to the colour categories for each ecological status: blue (high) was scored with 4 points, green (good) with 3 points, yellow (moderate) with 2 points, orange (poor) with 1 point and red (bad) with 0 points. All parameters have the same five intervals (blue, green, yellow, orange and red), except for MEPI which includes only green (good), yellow (moderate) and red (bad) (see Guerra-García et al., 2021). In this case green was scored with 4 points, yellow with 2 points and red with 0 points.

(ii) The global score of each marina (ranging from 0 to 24) was obtained by summing the scores assigned to each of the six selected indicators (MEPI, BCI, Taxa richness, H', biotic indices and nematode:copepod ratio) based on its ecological status (i). If several biotic indices are available, as in the present study, the value used in the assessment would result from the mean of the scores obtained for each index. Although the number of species is advisable as an indicator of taxa richness, the number of genera, families or orders could also be used in the assessment.

(iii) Establishment of global quality status of each marina according to the total score. We proposed the following intervals: (0-5: bad, 6-10: poor, 11-15: moderate, 16-20: good, 21-24: high)

Additionally, the relationships between all the indicators used were explored by Spearman correlation for all datasets.

3. Results

3.1. Macrofaunal community

8339 individuals belonging to at least 166 macrofaunal species were found during the present study in sediments from eight marinas on the Southern Iberian Peninsula (Table 1 and Tables S2, S3). This included 61 annelid species (5514 specimens, mainly represented by polychaetes), 58 arthropods (1837 specimens, mainly peracarid crustaceans), 41 molluscs (789 specimens, mainly bivalves), 3 echinoderms (9 specimens) and 190 additional specimens belonging to the phyla Nematoda, Nemertea and Phoronida. In all marinas, Annelida was the dominant phylum (Fig. 3A) both in species richness and abundance, except in Almería where Arthropoda was the most abundant phylum (due to the high density of the tanaid *Apseudopsis latreilli*). The most common and abundant taxa were the annelids *Aphelochaeta marioni*, *Capitella capitata*, *Chaetozone gibber*, *Cirriformia tentaculata*, *Cirrophorus furcatus* and *Fabricia stellaris*, the crustaceans *Phtisica marina*, *Iphinoe tenella* and *A. latreillii*, and the molluscs *Abra tenuis*, *Corbula gibba* and *Parvicardium exiguum* (Table 1). Detailed information on the taxonomical categories of each species and their status (native, cryptogenic or introduced) is included in Tables S2 and S3. Most of the species inhabiting sediments from marinas can be considered native or cryptogenic, while only four were exotic species, all of them crustaceans, namely the amphipods *Caprella scaura* and *Jassa slateryi*, the isopod *Paranthura japonica* and the decapod *Alpheus* sp. (Table S2).

Regarding the total number of species per marina, Puerto América showed the highest species richness (76) followed by Almería (53), Motril (52) and La Línea (47). The marinas with the lowest number of species were Chipiona (25), Barbate (30), Fuengirola (33) and Faro (37). This pattern was also obtained for the number of species per replicate (Fig. 3B). The highest values of the Shannon-Wiener's diversity (H') (based on the global data per marina) was also measured in Puerto América (3.23) followed by La Línea (2.82), Motril (2.41) and Faro (2.03). Barbate (1.56), Chipiona (1.64), Almería (1.86) and Fuengirola (1.92) showed the lowest values.

362 The number of species, total abundance and H' differed significantly among
363 marinas, although no differences were obtained for the factor 'location' (Atlantic *vs*
364 Mediterranean) (Table 2). The highest heterogeneity among marinas was obtained for
365 the Mediterranean (see SNK tests in ANOVAs of Table 2). The two-dimensional MDS
366 plot based on species abundances showed segregation of marinas (Fig. 4A).
367 PERMANOVA confirmed significant differences for all marinas (see pair-wise tests in
368 Table 2) with no significant differences for the factor location (Table 2).
369 When each of the three main phyla (Annelida, Arthropoda and Mollusca) was
370 analysed separately, the species richness also differed significantly among marinas
371 (Table S4A, Fig. 3C). The pattern was more evident for annelids and molluscs than for
372 arthropods (Table S4A). In fact, SNK tests indicated no differences among
373 Mediterranean marinas for arthropods. At the community level, the factor 'Marina' was
374 significant for the three phyla according to PERMANOVA results (Table S5A) and
375 MDS plots graphically showed segregation among marinas again (Fig. 5A). Molluscs
376 also revealed some segregation between Mediterranean and Atlantic marinas, although
377 'Location' was not significant according to PERMANOVA (Pseudo-F=1.9178,
378 p=0.0961, Table S5A). The second stage MDS (Fig. 5B) demonstrated that the pattern
379 derived from the annelid assemblage was very similar to that considering all taxa,
380 showing that this taxon was most responsible for driving the observed pattern for the
381 whole community.
382
383 *3.2. Meiofaunal community*
384 A total of 16 higher taxa were identified (Tables 3, Table S6), 4 of which (Copepoda,
385 nauplius larvae of crustaceans, Nematoda and Polychaeta) were always present at all
386 marinas. Nematoda was the numerically dominant taxon in Faro, Chipiona, P. América,
387 Barbate and Fuengirola, while Copepoda dominated in La Línea, Motril and Almería
388 (Fig. 6A).
389 The number of taxa did not differ among marinas or among locations (Atlantic
390 *vs* Mediterranean), while total abundance values were higher in Mediterranean marinas
391 (Fig. 6A, Table 4). The nematode:copepod ratio differed significantly among marinas,
392 although these differences were mainly due to the high values measured in Fuengirola.
393 The MDS plot showed segregation of marinas and, differently from macrofauna,
394 reflected a clear pattern for the factor location, i.e. Atlantic *vs* Mediterranean marinas

(Fig. 6B). PERMANOVA confirmed significant differences for the factors 'Location' and 'Marina' (Table 4).

3.3. Influence of environmental data on faunal assemblages

A full dataset of environmental data measured in sediments of the eight studied marinas can be found in Table S7 (see also Guerra-García et al., 2021, for details on the environmental assessment).

The variables Co, N, As, S, Clay and N were correlated with other variables ($r>0.8$, $p<0.01$) and were not included in the DistLM, so the model was run with 12 variables (Sand, Silt, hydrocarbons, faecal coliforms, biocide Irgarol, Cd, Cr, Cu, Ni, P, Pb and Zn). According to DistLM, the environmental variables which significantly correlated with the whole macrofaunal community (identified at species level) were mainly P (18.2% of variation explained), sand (16.7%) and TOC (16.0%) (Table 5). Faecal coliforms and the heavy metals Cr, Cu, Pb and Zn were also significant (Table 5). The best model (AIC=180.46, R^2=0.073) was obtained for the combination of Sand, Silt, TOC, P, faecal coliforms, Irgarol, Cr, Cu and Pb (Table 5). The first two axes of the dbRDA explained 50.9 % of the total variation (Fig. 7). BIO-ENV results showed that the best model (Rho=0.820, $p<0.01$) was obtained with the combination of Sand, TOC, P, faecal coliforms, Cu, Pb and Zn, coinciding with the significant variables provided by DistLM (Table 6).

When the three main phyla (Annelida, Arthropoda and Mollusca) were analysed separately, DistLM showed similar results to those obtained with the whole community (Sand, TOC, P, faecal coliforms and heavy metals) (Table 6, Table S8). Variables explained a higher proportion of variability in annelids, followed by molluscs and finally arthropods (Table S8). In fact, BIO-ENV only provided a significant model (Rho=0.797, $p<0.05$) for Annelida (Table 6), which, therefore, turned out to be the phylum best reflecting the environmental conditions in marinas.

Regarding to meiofauna (based on higher taxa abundances), DistLM selected Sand (17.1%), Hydrocarbons (14%), Cd (13.7%) and Cu (10%) as the variables that correlated significantly with the meiofaunal assemblage (Table S9, Table 6). The best model (AIC=157.62, R^2=0.62) was obtained for the combination of Sand, Silt, TOC, faecal coliforms, Cd, Cr, Cu and Zn. BIO-ENV also showed Hydrocarbons, Cd and Cu

427 as the best combination model. However, the model was not significant (Rho=0.630,
428 p=0.130) (Table 6).
429
430 *3.4. Macrofaunal taxonomic sufficiency*
431 This study revealed the presence of 166 species, 155 genera, 105 families, 44
432 orders, 16 classes and 8 phyla inhabiting marinas of the Southern Iberian Peninsula. The
433 number of species was very similar to the number of genera in all marinas (Fig. 3B),
434 since most of the genera were represented by a single species (Table S2). Number of
435 families was also close to the number of genera and species (Fig. 3B). Regarding taxa
436 richness, ANOVAs revealed that the factor 'Marina' was significant for all taxonomic
437 levels considered, although for class and phylum these differences were only due to the
438 high number of taxa collected in P. América in comparison with other Atlantic marinas
439 (Table S4B, Fig. 3B). PERMANOVA confirmed that there were significant differences
440 in community structure among all marinas when separately considering each matrix for
441 species, genera, families or orders (Table S5B). Although significant differences in the
442 factor 'Marina' were also obtained for classes and phyla, these differences were due to
443 the influence of certain marinas, such as Faro (Atlantic) or Almería (Mediterranean)
444 (Table S5B). This pattern was supported by the corresponding MDS ordinations (Fig.
445 4A). Separation among marinas was evident at the level of species, genus, family and
446 order, while MDS based on classes and phyla showed a less defined grouping (Fig. 4A).
447 The second-stage MDS performed on the six considered taxonomic levels (Fig. 4B)
448 demonstrated that patterns showed by the species/genus levels were similar, and close to
449 that obtained for family/order levels. Conversely, they differed considerably from those
450 derived from the higher levels (i.e. phylum and class).
451 When the influence of taxonomic resolution was considered to compare the
452 environment-fauna relations, DistLM revealed a similar pattern for species, genus,
453 family and order (Table 6, Table S8). The environmental variables that were significant
454 at the species level were the same as those found at the level of genus, family and order.
455 The set of significant variables were quite different when considering classes and phyla
456 data. Indeed, BIO-ENV provided significant results with similar variables for species,
457 genus, family and order, but they were not significant for class and phylum (Table 6).
458
459 *3.5. Global assessment. Biotic indices and biocontamination*

According to the Marinas Environmental Pollution Index (MEPI), Barbate and Fuengirola were the most polluted marinas (Fig. 8). The Biocontamination Index (BCI) values were very low in all marinas due to the small number of introduced species found on sediments. Although quality intervals for MEPI, BCI and Biotic Indices were defined in the literature, those for taxa richness, diversity (H') and nematode:copepod ratio were not available so they were established during the present study, based on the data obtained for marinas of Southern Iberian Peninsula (see Table S10). The global score, obtained by summing the scores assigned to each selected indicator (MEPI, BCI, Taxa richness, H', Biotic indices and nematode:copepod ratio) ranged from 9 to 17. Fuengirola, Barbate and Chipiona got the lowest score (9 and 10 points) while La Línea, Motril and P. América showed better ecological status (16 and 17 points) (Fig. 8). Therefore, marinas of the Southern Iberian Peninsula ranged from poor (Fuengirola, Barbate and Chipiona) to moderate (Faro and Almería) and good (P. América, La Línea and Motril).

In general terms, the ecological indicators used to conduct the global assessment were in good agreement, except for punctual differences (i.e. BENTIX classified all the marinas as bad or poor, while BENFES classified them as moderate, good or high). Apart from BCI which showed low values in all marinas and was not able to discriminate among them, environmental data (MEPI) and biological information (taxa richness, H', biotic indices and nematode:copepod ratio) were more discriminant and provided similar information (Fig. 8). MEPI was correlated with richness of species and genera, the biotic index MEDOCC and the nematode:copepod ratio. Taxa richness was correlated with H' and with biotic indices (Table S11). Indeed, the marinas classified as good (P. América, La Línea and Motril) were those with the highest values of macrofauna taxa richness and Shannon-Wiener's diversity, and the lowest degree of environmental pollution. Conversely, the most polluted marinas, such as Chipiona, Barbate and Fuengirola, showed the lowest values for taxa richness, diversity, and the highest nematode:copepod ratios.

4. Discussion

4.1. Benthic communities

The present study revealed that the soft bottom of marinas from the Southern Iberian Peninsula supported a wide variety of macrobenthic taxa (166 species

493 distributed in 155 genera, 105 families, 44 orders, 16 classes and 8 phyla). The number
494 of soft-bottom macrofauna species per marina (ranging from 25 to 76) was similar to
495 that reported from marinas worldwide (e.g. McGee et al., 1995; Estacio et al., 1997;
496 Guerra-García and García-Gómez, 2004 a,b,c; Martínez-Lladó et al., 2007; Covazzi
497 Harriague et al., 2012; Chatzinikolaou et al., 2018; Ng et al., 2019).

498 Annelida (mostly polychaetes) was the dominant phylum in number of species
499 (37%) and, especially, in number of individuals (66%). In fact, the patterns of the total
500 community were mainly driven by annelids (see Fig. 3), that are usually reported as the
501 dominant macrobenthic taxon in the sediment of marinas worldwide (Moreira et al.,
502 2010; Ng et al., 2019; Chatzinikolaou et al. 2018) and, in general, in most soft-bottom
503 habitats (Hutchings, 1998). On the contrary, Arthropoda (mainly Amphipoda inhabiting
504 arborescent substrates) dominated floating pontoons in terms of abundance and species
505 richness (Gavira O'Neill et al., 2015, 2018).

506 Although all studied marinas were located across the same geographical area,
507 univariate and multivariate analyses consistently showed significant differences among
508 them based on biological data. This heterogeneity among marinas has also been
509 revealed by environmental stressors (see Guerra-García et al., 2021). Spatial variations
510 in biotic assemblages among and within marinas have been attributed to differences in
511 the local environment as well as to the marina design (Toh et al., 2017). In fact, the
512 singularity of any given marina, largely determined by a variety of local factors (e.g.
513 environmental conditions, availability of suitable substrate, level of marine traffic) has
514 proven to be a key factor affecting, for example, several stages of the NIS invasion
515 process (Martínez-Laiz et al., 2019). Hence, our results reinforce the importance of
516 considering a local scale perspective for conservation and management purposes.

517 Although significant differences in the factor 'marina' were relevant throughout
518 the whole study, the factor 'Location' (Atlantic *vs* Mediterranean) was not relevant for
519 macrofauna, only showing certain degree of segregation when considering molluscs
520 separately. However, this factor was significant for meiofauna and should also be
521 considered in management programmes.

522 The present study only considered a spatial scale, and therefore further research
523 should explore if the observed patterns remain constant through time. Although
524 epifaunal communities associated with floating pontoons suffer significant seasonal
525 fluctuations (e.g. Ros et al., 2013), Chatzinikolaou et al. (2018) did not find important

seasonal differences in soft-bottom communities of port and marinas. On the contrary, Moreira et al. (2010) detected strong fluctuations among and within seasons mostly related to recruitment of opportunistic species and some perturbations (i.e. proliferation of ephemeral algae on the sediment in summer). This again emphasizes that the environmental singularity of any given marina must be considered in management programmes. In this sense, sediment monitoring should ideally be based on previous baseline data in order to design the appropriate sampling for each marina and reduce the monetary, time and labor costs of such activities as much as possible.

4.2. Influence of environmental data on faunal assemblages

The multivariate pattern of the macrofaunal community in the present study was mainly explained by P, Sand, TOC, faecal coliforms, and heavy metals. Although hydrocarbon concentration clearly discriminated among marinas (Table S7, Guerra-García et al., 2021) and has been traditionally considered a significant factor affecting biota (Blanchard et al., 2002), it did not contribute to explain the observed macrofaunal patterns but was, in turn, relevant for meiofauna. In this sense, Covazzi Harriague et al. (2012) pointed out that the macrofaunal and meiofaunal assemblage can respond differently to human pressure.

Most explanatory variables selected by our analyses agree with those reported in previous studies in harbours and ports. Granulometry is considered one of the main factors modulating soft-bottom communities, including those inhabiting harbour areas (e.g. Moreira et al., 2005). Guerra-García et al. (2004 a,b,c) also reported granulometry, TOC, P and heavy metals as important variables to explain the distribution of molluscs, crustaceans and polychaetes in the harbour of Ceuta, while Chatzinikolaou et al. (2018) found heavy metals to be relevant explanatory variables of biotic patterns.Among the many potential sources, metal-based antifouling systems, mainly Cu and Zn, clearly play a major role in contamination in marinas (Briant et al., 2013).

When each of the three main phyla were analysed separately, Annelida was more related to the considered environmental conditions in marinas than others. Arthropods in general, and crustaceans in particular, are traditionally considered better bioindicators due to their higher sensitivity to marine pollution (Navarro-Barranco et al., 2020) and better reflect differences at the spatial scale (i.e. among localities) than molluscs and annelids (Sánchez-Moyano and García-Gómez, 1998). However, in

559 harbours and marinas, annelids (mainly polychaetes) become the best taxon to
560 discriminate between sampling sites, especially when oxygen is not a limiting factor
561 (Guerra-García and García-Gómez, 2005a).
562
563 *4.3. Taxonomic sufficiency*
564 The use of higher taxonomic levels instead of species as a proxy for
565 identification has been extensively tested in both terrestrial and marine habitats, and on
566 such taxa as insects, fish, fauna associated with algae and seagrasses, meiofauna and
567 benthic macrofauna in general (see Sánchez-Moyano et al., 2006 and references
568 therein). However, it is important to properly analyse the cost-benefits of such
569 approaches to select the appropriate level of taxonomic resolution in benthic monitoring
570 programmes (Bouchard et al., 2005).
571 Although Ferraro and Cole (1990) indicated that the species level would be the
572 most sensitive for the evaluation of pollution impacts, Sánchez-Moyano et al. (2006),
573 based on several datasets within a wide range of habitats and substrate types along the
574 southern Iberian coastline, concluded that studies at the different levels of taxonomic
575 resolution (species, family, order) led to similar results both as regards community
576 distribution and composition, and their relationship to environmental variables.
577 The present study found similar patterns to those provided by Sánchez-Moyano
578 et al. (2006) and Chatzinikolaou et al. (2018). On the one hand, differences among
579 marinas were also detected using high taxonomic levels, and on the other hand, the set
580 of environmental variables which better explained macrofaunal assemblages were the
581 same at the species, genus, family and order level, but differed at class and phylum
582 levels. The second stage MDS revealed that identification to genus provided almost
583 identical results to those obtained when considering species due to many genera being
584 represented by only one species in each marina. Family and order levels yielded similar
585 results between them but were less informative with respect to species and genus levels
586 (Fig. 4). For all these reasons, family and order levels could be an alternative in large-
587 scale monitoring programmes with significant time and budget constraints.
588 Conversely, taxonomical resolution to the species level is mandatory to
589 accurately identify NIS in marinas, and to correctly calculate biocontamination indices
590 such as BCI (Arbačiauskas et al., 2008). Indeed, early detection of NIS is often delayed
591 when taxa are taxonomically challenging, such as small-sized marine organisms which

require great taxonomic expertise (Marchini and Cardeccia, 2017; Martínez-Laiz et al., 2020). Therefore, the potential efficacy of identification to high taxonomic levels in some monitoring programmes does not replace by any means the information obtained at the species level, which is paramount for basic and applied ecological studies (de Oliveira et al., 2020).

4.4. Global assessment

The quality assessment applied in the present study and developed specifically for marinas was based on six selected ecological indicators (MEPI, BCI, Taxa Richness, H', biotic indices and nematode:copepod ratio), encompassing five of the eleven descriptors of MSFD: D1 (Biological diversity), D2 (NIS), D5 (Human-induced eutrophication), D6 (Sea floor integrity) and D8 (Concentrations of contaminants) (Berg et al., 2015; Piroddi et al., 2015). The assessment was useful for discriminating among marinas, even when they were closely located. The evaluation simultaneously combined abiotic and biotic information, integrating chemical pollution, NIS risk and attributes of the macro- and meiofaunal assemblages.

Regarding taxa richness in the assessment method, identification to the species level is advisable, but this study showed that other categories such as genus, family or even order could provide similar ecological intervals (see Fig. 8 and Table S10). Indeed, values of these four taxonomic categories were significantly correlated ($r>0.9$, $p<0.01$) (Table S11). Therefore, this global assessment for marinas can be conducted whenever the macrofauna is, at least identified to the order level.

In recent years, a variety of biotic indices dealing with the structure of macrobenthic communities have been proposed to address the objectives of European Directives (e.g., Marine Strategy Framework Directive -MSFD- 2008/56/EC, EU Biodiversity Strategy to 2020 and Water Framework Directive -WFD- 2000/60/EC). Indeed, biotic indices have been recently demonstrated to be suitable for assessing the ecological status of Mediterranean ports and marinas (Dimitrou et al., 2020).

Although a unified protocol within the EU has not yet been adopted (Dimitriou et al., 2020) and there is no agreement on what index or indices should be used by environmental managers to establish benthic quality (Borja et al., 2015), the most used ones are AMBI (AZTI's Marine Biotic Index; Borja et al., 2000), M-AMBI (multivariate AMBI; Muxika et al., 2007) and BENTIX (Simboura and Zenetos, 2002).

625 The MEDOCC index was an adaptation of the AMBI for the Mediterranean area
626 (Pinedo et al., 2015). All these indices rely on the taxonomic identification of species.
627 Recently, a new index based on identification to the family level, i.e. BENFES, was
628 developed (Sánchez-Moyano et al., 2017). The application of these indices in marinas
629 revealed important differences in the ecological status assigned (Fig. 8). BENFES was
630 the most favourable (most marinas classified as good). Conversely, BENTIX was
631 clearly more restrictive (most marinas qualified as bad or poor), coinciding with the
632 results obtained by Dimitrou et al. (2020). BENTIX did not correlate with any other
633 index, nor with other selected ecological indicators, so its use in marinas, at least in the
634 Southern Iberian Peninsula, is discouraged. MEDOCC was the only index correlating
635 with environmental pollution (MEPI), so its calculation in marinas can be useful.
636 Therefore, we recommend using the biotic indices in marinas with caution and,
637 whenever possible, calculating several to obtain mean scores and reduce potential biases
638 in the quality assessment.
639 The selected meiofaunal indicator for assessment was the nematode:copepod
640 ratio, which is relatively easy to undertake in a marina. Undoubtedly, considering the
641 difficulty and time-consuming process of taxonomic identification of nematodes and
642 copepods, the use of taxonomic sufficiency is one of the most attractive features of this
643 ratio (Rubal et al., 2019). Hence, this index has become a common method for
644 evaluating organic enrichment and chemical pollution (Rohal et al., 2020). A higher
645 ratio is usually associated to chemical and organic pollution (Raffaelli and Mason,
646 1981), because copepods, specifically harpacticoids, are more sensitive to pollutants
647 than nematodes (Elarbaoui et al., 2015). In fact, Moreno et al. (2008) found a significant
648 correlation between nematodes and concentrations of environmental contaminants in
649 tourist marinas of the Mediterranean Sea. The present study revealed that the index
650 discriminates well among marinas. It correlated with other biotic indices and, most
651 importantly, with the environmental pollution levels as defined by the MEPI.
652 Accordingly, we consider that the measure of nematode:copepod ratio in marinas can be
653 an adequate proxy for environmental pollution.
654 Concerning exotic species, recreational boating is currently considered a
655 significant vector for the introduction and secondary spread of NIS, especially at local
656 scales (e.g. Ros et al., 2013; Ashton et al., 2014; Foster et al., 2016; Ferrario et al.,
657 2017; Martínez-Laiz et al., 2018, 2019; Ulman et al., 2019). In the present study, we

658 used the Biocontamination Index (BCI) for marinas. Alternatively, a more recent index,
659 ALEX, has also been proposed to assess the impacts of alien species on benthic
660 communities (Çinar and Bakir, 2014). While BCI is based on presence and abundance
661 of alien species *sensu lato*, ALEX does not take into account abundances and its
662 calculation requires classification of alien species as 'causal', 'established' or
663 'invasive'. However, these categories are hard to assign when considering small
664 invertebrates in marinas. For this reason, we have not calculated ALEX in the present
665 study; instead, we consider BCI to be more appropriate for marinas. Despite marinas
666 being deemed 'hot spots' for exotics, the number of alien species inhabiting soft
667 bottoms was remarkably low, with only 4 NIS (all crustaceans, 3 peracarids and 1
668 decapod) out of 166 species. It should be noted though, that the native range of more
669 than a third of the reported taxa is unknown (their status remains undetermined or
670 cryptogenic), which highlights the lack of baseline information and taxonomic
671 uncertainty for many of these small mobile taxa. In any case, the low number of alien
672 species reported here contrasts considerably with the high number of NIS (both mobile
673 and sessile taxa) inhabiting floating pontoons (e.g. Martínez-Laiz et al., 2018; Tempesti
674 et al., 2020). In fact, higher numbers of NIS in hard substrates in comparison with soft
675 bottoms have been reported by other authors (Ruiz et al., 2009; Jimenez et al., 2018).
676 Our results confirm this pattern in marinas and suggest that exploring NIS only in
677 sediments is not enough to properly characterize biopollution levels in recreational
678 harbours. The contrasting invasion pattern observed between hard and soft-bottom
679 habitats also illustrates the importance of sampling across a variety of habitats (Jiménez
680 et al., 2018).
681
682 *4.5. Towards Blue-flag marinas*
683 A suitable management of marinas and ports should be a priority in the context
684 of implementation of MWFD and United Nations (UN) sustainability goals 2030. One
685 of these goals includes marine life and aims to reduce pollution in coastal waters by
686 increasing scientific knowledge and developing research capacities and transference of
687 marine technology. Therefore, monitoring anthropogenic pressure and ecological
688 quality of marinas should be an important issue for local authorities (D'Alessandro et
689 al., 2020). The assessment of quality status can allow for design of standards when
690 assigning "sustainable quality seals" to those marinas with better values of ecological

691 indicators. Environmental quality is, indeed, one of the main criteria to assign a Blue
692 Flag to a marina (http://www.banderaazul.org/puertos-y.embarcaciones-2020, accessed
693 8 August 2020). In our study, the marinas at P. América, La Línea and Motril reached
694 the 'good' status according to the global environmental assessment based on soft-
695 bottom habitats. This assessment based on sediment indicators could provide a tool for
696 marinas to be awarded a Blue Bag.
697 To reduce environmental impact and increase biological diversity, the design of
698 new marinas should allow water exchange by building more openings or having a
699 through-flow design to facilitate exchange with the adjacent open waters (Guerra-García
700 and García-Gómez 2004a,b,c, 2005a,b; Ng et al., 2019). In fact, marinas that are well
701 designed, with adequate structural complexity and good water quality, can even
702 function as nurseries for juvenile fish (Bouchoucha et al., 2016) and small invertebrates
703 (pers. observ.).
704 Marinas may support a rich and diverse marine biodiversity and are easily
705 visible to the public (Toh et al., 2017). Pontoons are full of sessile and mobile colourful
706 fauna representing different phyla, and can be visited at any time by walking (no need
707 for snorkeling or SCUBA diving). Beside hard substrates, the bottom of marinas usually
708 corresponds to muddy sediments that can easily be sampled with small grabs for macro-
709 and meiofauna. These manageable grabs can be effortlessly hand-carried and deployed
710 from the pontoon in the marina without the need of a boat or any motorized lift system.
711 For all these reasons, marinas become suitable enclaves to develop teaching activities
712 on sampling methods in hard and soft bottoms, citizenship education and biodiversity
713 conservation programmes as well as training courses (e.g. NIS identification), among
714 others. Furthermore, by using social perception surveys and media programmes, boat
715 owners can become aware of the marine life inhabiting pontoons and sediments, and get
716 involved in reaching more ecologically sustainable marinas.
717
718 **5. Conclusions**
719
720 The present study reveals that the proposed method based on selected abiotic and biotic
721 indicators [Marinas Environmental Pollution Index (MEPI), Biocontamination Index
722 (BCI), macrofaunal biotic indices (AMBI, M-AMBI, BENTIX, MEDOCC and
723 BENFES), macrofaunal taxa richness, Shannon-Wiener's diversity, and

nematode:copepod index], can be useful for integrative assignment of the ecological status of marinas. Although the consideration of several indicators is advisable in terms of scientific integrity, it could be questioned that this would be user-friendly and easy to apply for management stakeholders. As scientists, we must encourage policy makers, governments and funding agencies to invest in rigorous scientific studies to properly address specific monitoring guidelines before making any decision. Alternatively, we must provide easy tools to facilitate this work, so a reasonable commitment must be reached with a proper balance between scientific integrity and a manageable approach. Although our proposed method involves several parameters and indicators, it can be flexible according to the available data. For example, taxa can be identified to family and order instead of species, and MEPI can be adjusted based on the environmental data available (see Guerra-García et al., 2021). Similarly, species richness can be alternatively substituted by the number of genera, family or orders. Values of the nematode:copepod index are not difficult to calculate and, regarding biotic indices, the score can be calculated on the basis of the indices available, and some of them do not require species identification. The only index that requires identification at the species level is the BCI, since it needs the correct identification of exotic species. But, if necessary, under time and budget constraints, the global score can be done by eliminating some of the markers, such as BCI, and extrapolating the score to the new intervals. Future studies must be conducted to test the method proposed across different biogeographical and seasonal scales.

Declaration of competing interest.

We declare no conflict of interest.

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Appendix A. Supplementary data

Supplementary data related to this article can be found online at https://doi.org/xxxxxxxxx.

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Figure legends

Fig. 1. Map of the study area showing the location of the eight studied marinas.

Fig. 2. Flowchart showing the methodology of the assessment method proposed in the present study.

Fig. 3. A) Abundance of the three main macrofaunal phyla (Annelida, Arthropoda and Mollusca) in each marina; "others" include remaining phyla. B) Taxa richness for each considered taxonomic level (species, genus, family, order, class and phylum). C) Species richness of the three main phyla. Values represent the mean (A–C) and standard error (B–C) (n=3) per marina.

Fig. 4. A) Non-parametric multidimensional scaling (MDS) showing the relationship among locations (Atlantic *vs* Mediterranean) and marinas according to macrofauna separately for the six considered taxonomic levels (species, genus, family, order, class and phyla). B) Second stage MDS considering all macrofaunal taxonomic levels.

Fig. 5. A) Non-parametric multidimensional scaling (MDS) showing the relationship among locations (Atlantic *vs* Mediterranean) and marinas according to macrofauna (separately for Annelida, Arthropoda and Mollusca). B) Second stage MDS for the three main phyla and the total macrofauna community.

Fig. 6. A) Nematode:copepod ratio and abundance of the main meiofaunal taxa measured in each marina. B) Non-parametric multidimensional scaling (MDS) showing the relationship among locations (Atlantic *vs* Mediterranean) and marinas according to meiofauna (higher taxa abundances).

Fig. 7. Graphic representation of the dbRDA showing ordination of marinas and variables with respect to the first two axes. Only significant variables according to the DistLM (see Table 5) are included.

Fig. 8. Global assessment of ecological quality status of the marinas from southern Iberian Peninsula based on six selected indicators: Marinas Environmental Pollution Index -MEPI-, Biocontamination Index -BCI-, macrofaunal taxa richness, Shannon-Wiener's diversity (H'), macrofaunal biotic indices and meiofaunal nematode:copepod ratio. Total score for each marina (0-24) is based on the sum of the scores for each indicator.

ECOLOGICAL QUALITY ASSESSMENT OF MARINAS: AN INTEGRATIVE APPROACH COMBINING BIOLOGICAL AND ENVIRONMENTAL DATA.

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Highlights:

-An integrative method for quality assessment is developed and proposed for marinas

-Correlations between fauna and abiotic data are detected at family and order level

-Soft-bottom benthic communities are key tools for managing programmes

Abstract

The importance of marinas as infrastructures for recreational boating is increasing substantially. However, information on their soft-bottom benthic communities, a key tool for managing programmes, is still scarce. We combined environment features with macro- and meiofaunal soft-bottom community information for assessing the ecological status of marinas with an integrative approach. To address this issue, we focused on eight marinas of the Southern Iberian Peninsula. Macro- and meiofauna data revealed high benthic heterogeneity at a spatial scale. The environmental variables which correlated best with macrofauna were mainly

phosphorus, granulometry, and total organic carbon, and secondarily important variables were faecal coliforms, the biocide Irgarol, and heavy metals; total hydrocarbon concentration was also significant for meiofauna. Annelida was the dominant phylum in terms of number of species (37%) and abundance (66%) and were better descriptors of the environmental conditions than Arthropoda and Mollusca. Although identification to the species level is desirable and mandatory for assessing biological pollution, significant differences among marinas and correlations between fauna and abiotic variables were already detected at the level of family and order. This implies that biota assessment at higher levels may still be useful in monitoring programmes limited by time and budget constraints. The major novelty of this study lies in the development of an integrative assessment method based on the following selected ecological indicators: Marinas Environmental Pollution Index (MEPI), Biocontamination Index (BCI), macrofaunal biotic indices (AMBI, M-AMBI, BENTIX, MEDOCC and BENFES), macrofaunal taxa richness and Shannon-Wiener's diversity, and nematode:copepod index. This approach was able to discriminate marinas of the Southern Iberian Peninsula based on their ecological status, which ranged from poor to good. The method can be useful to design standards for assigning "sustainable quality seals" to those marinas with better values of ecological indicators.

Keywords: Marinas, ecological assessment, macrofauna, meiofauna, soft bottoms, taxonomic resolution

1. Introduction

Port areas and marinas in particular, are confined environments subjected to a number of anthropogenic activities that result in significant environmental disturbances (Tempesti et al., 2020 and references therein). The number of marinas has significantly increased during the last years, since they are essential infrastructures for the recreational boating sector, a key activity of global marine tourism in high demand (Di Franco et al., 2011). However, marinas modify ecological conditions (Rivero et al., 2013; Valdor et al., 2019) and their increasing number is recognized as an important environmental stressor in many regions (e.g. Gómez et al., 2017).

Despite the importance of marinas as hotspots of environmental and biological pollution, knowledge about these novel ecosystems is still very scarce. Previous studies

have evaluated the pollution pressure (Mali et al., 2017; Gómez et al., 2019; Guerra-García et al., 2021), but little effort has been put into proper characterization of their biological communities (Covazzi Harriague et al., 2012; Chatzinikolaou et al., 2018; Dimitrou et al., 2020). Faunistic information in marinas is mainly restricted to sessile communities and/or Non-Indigenous Species (NIS) (e.g. Di Franco et al., 2011; Oricchio et al., 2016; Kenworthy et al., 2018; Ulman et al., 2019; Ferrairo et al., 2020), and there is a lack of research targeting mobile macro- or meiofauna. Furthermore, the few studies dealing with these taxa have focused on arborescent substrates attached to floating pontoons (Ros et al., 2013; Marchini et al., 2015; Fernández-Romero et al., 2019; Gavira O'Neill et al., 2018; Martínez-Laiz et al., 2018). Meanwhile, studies on soft-bottom fauna in marinas are scarce (e.g. Chatzinikolaou et al., 2018, Dimitrou et al., 2020, Table S1) and generally limited when compared to other assemblages, such as the biofouling organisms which cause noticeable financial and ecological impacts (Ng et al., 2019 and references therein). The study of the soft bottom environment in marinas (usually corresponding to muddy sediments) is especially relevant since (i) it is the most widespread habitat there, (ii) it represents a more stable substrate for fauna than the floating structures above (which are temporally cleaned and often subjected to fluctuations in salinity and temperature), and (iii) sediments accumulate pollutants and provide more reliable information about environmental conditions than seawater, which only provides punctual information. Indeed, most of the monitoring programmes for quality assessment guidelines in marine habitats are focused on sediments (Birch, 2017; 2018; Dimitrou et al., 2020) and previous work (e.g Martínez-Lladó et al., 2007; Ondiviela et al., 2013) has already demonstrated that sediments constitute the main testimony of contaminant episodes in harbours.

To achieve the goal of "Bridging the Gap Between Policy and Science in Assessing the Health Status of Marine Ecosystems", scientists should provide policymakers with the best available and updated knowledge (Borja et al., 2016, 2017). Most of the monitoring programmes are mainly concerned with bathing water, while marinas and harbours are usually excluded. Regulations in marinas are especially challenging due to the wide range of uses, pressures and singularities of each marina (different morphology and hydrodynamic regimes, quick and unpredictable changes due to local actions, etc) (Gupta et al., 2005; Petrosillo et al., 2010). Management of marinas also involves conflicting uses by residents, visitors, boat owners, shipping, and industry

among others, thus requiring the integration of multi-disciplinary authorities and stakeholders from different sectors (e.g. engineers, biologists, economists, environmental agencies, governmental bodies) (Chatzinikolaou et al., 2018).

Several methods and models, such as the Complexity Tidal Range Index (CTRI) or the Marina Environmental Risk Assessment (MERA), have been recently applied to prioritize environmental strategies in marinas (e.g. Gómez et al., 2019; Valdor et al., 2019). However, the progress in these tools significantly contrasts with the scarce biotic and abiotic information available. This basic information is mandatory to develop an integrative assessment, which is necessary to undertake properly designed management programs in marine ecosystems (Karydis and Kitsiou, 2013; Dauner et al., 2018; Carriger and Parker, 2020; Stelzenmüller et al., 2021).

Thus, the use of appropriate and effective indicators of environmental conditions is critical to accurately conduct integrative assessments and to ensure that human activities are carried out in a sustainable manner (Birch, 2017). In this sense, benthic invertebrates are very sensitive to physical and chemical perturbations and recommended as good biological indicators of contamination for integrating environmental disturbances over time (Albano et al., 2013). Biological data have the advantage of giving an integrated view of the long-term environmental conditions, whereas chemical and physical analytical methods provide only a 'snapshot' of conditions at the time of sampling (Saiz-Salinas, 1997; de-la-Ossa-Carretero et al., 2012; Ng et al., 2019). In fact, the use of benthic communities to assess the environmental state of marine systems is strongly supported by the Water Framework Directive (WFD) of the European Union (2000/60/EC). For harbour environments, Ondiviela et al. (2013) stressed the importance of considering simultaneously abiotic and biological indicators in integrative assessments to evaluate the ecological status.

An integrative approach must, therefore, include inventories of the biodiversity, since taxonomic information is pivotal for establishing a baseline to properly address sustainable management of marinas. Ideally, the analysis of benthic communities should be based on identification to the species level but this is usually a complex and time-consuming procedure (Terlizzi et al., 2003; Sánchez-Moyano et al., 2006). Indeed, in many taxa, species identification is laborious and requires appropriate taxonomic expertise that nowadays is often lacking (Paknia et al., 2015; Chatzinikolaou et al., 2018). Furthermore, policy makers and funding agencies often demand results and

recommendations be achieved within very short timescales. These requirements prevent identification to species level and promote analyses considering higher taxa (e.g. genus, family, order). Extensive literature, including a variety of methodologies, habitats and substrate types, has been developed to explore if environmental changes can be detected above the species level (see Sánchez-Moyano et al., 2006 and references therein; De Oliveira et al., 2020; Gerwin et al., 2020). Nonetheless, the response of fauna to environmental data by considering different taxonomic levels has been scarcely studied in harbours and marinas (Chatzinikolaou et al., 2018).

To fill the gaps described above, the main objective of this study was to explore the importance of soft-bottom environments, including both biotic and abiotic information, for assessing the ecological status of marinas from an integrative approach. To address this issue we aim to: (*i*) characterize the diversity and spatial distribution patterns of soft-bottom macro- and meiofauna communities in marinas, (*ii*) identify the set of abiotic variables which better explain the biological patterns, (*iii*) explore the taxonomic sufficiency required to detect differences among marinas and environmental patterns, and, eventually, (*iv*) develop an integrative and easy-to-apply method to assess the quality status of soft-bottom environments of marinas based on selected ecological indicators. Most previous studies regarding soft bottoms of marinas have focused on abiotic parameters, and when they include biotic data, information on the macrofaunal and meiofaunal communities is neither integrated simultaneously nor do they develop integrative quality assessments based on a multiparametric approach (Table S1). The novelty of the present study lies in the integration of abiotic and biotic data for designing a quality assessment method based, concurrently, on the following selected ecological indicators: Marinas Environmental Pollution Index (MEPI), Biocontamination Index (BCI), macrofaunal biotic indices (AMBI, M-AMBI, BENTIX, MEDOCC and BENFES), macrofaunal taxa richness and Shannon-Wiener's diversity, and nematode:copepod index.

To achieve the aforementioned objectives, the Southern Iberian Peninsula was selected as the study area since it (i) represents an interesting biogeographical area which includes an horizontal gradient Atlantic-Mediterranean, (ii) encompasses a very high number of marinas along the coast and (iii) includes the Strait of Gibraltar, a hot spot for maritime traffic.

2. Material and Methods

2.1. Sampling survey and laboratory processing

Sampling was conducted from June 26th to July 2nd 2017. Eight marinas were randomly selected along the Southern Iberian Peninsula: four in the Atlantic coast (Faro, Chipiona, Puerto América, Barbate) and four in the Mediterranean (La Línea-Puerto Chico, Fuengirola, Motril, Almería) (Fig. 1). Details of these marinas (coordinates, depth, size, number of berths and population density of the adjacent locality) can be consulted in Guerra-García et al. (2021). Within each marina, three floating pontoons were randomly selected (each pontoon was considered a replicate for analyses throughout the whole study; consequently, three replicates per marina were taken) and the sediment below each pontoon (mostly muddy) was sampled.

For macrofauna, a small van Veen grab (area: 15 x 15 cm) was used. Because the grab was relatively small, the replicate (i.e. pontoon) consisted of three additive sediment grabs (total area: 675 cm^2). Samples were washed through a sieve with a mesh size of 0.5 mm and the retained fraction was fixed in 96% ethanol stained with Rose Bengal.

For meiofauna, only one sediment van Veen grab was collected per pontoon. Once the grab was recovered, a small corer of 10 cm^2 was introduced into the undisturbed sediment. Therefore, a total of three replicates (one corer per pontoon) were obtained per marina and directly fixed in 96% ethanol stained with Bengal Rose.

In the laboratory, macrofaunal samples were rinsed with fresh water over a 0.5-mm sieve, sorted, identified to species level whenever possible, and counted. For macrofauna, the status of each species (N: Native, I: Introduced, C: Cryptogenic, U: Undetermined) was also considered. Species names and systematic arrangement of taxa follows the World Register of Marine Species (WoRMS, 2020).

Meiofaunal samples were sieved in the laboratory through a 0.5-mm mesh to exclude macrofauna, with a 30-µm mesh below to retain meiofauna. Specimens were sorted under a stereomicroscope and identified to high taxonomic levels (e.g. phylum, class or order; Sedano et al., 2014, 2020)

Additionally, to quantify abiotic variables in sediment for each marina, three sediment samples (one per pontoon) were taken from the bottom using the van Veen grab. All samples were immediately frozen (-20ºC) until laboratory analyses. The following environmental variables were measured: sand, silt, clay, total organic carbon

(TOC), hydrocarbons, faecal coliforms, biocide Irgarol, and major, minor and trace elements As, Cd, Co, Cr, Cu, N, Ni, P, Pb, S and Zn. Analytical procedures are detailed in Guerra-García et al. (2021).

2.2. Statistical analyses

The experimental design included two factors: 'Location' (Lo), a fixed factor with two levels (Mediterranean *vs* Atlantic) and 'Marina' [Ma(Lo)], a random factor with four levels, nested with Lo. The number of replicates was n=3, corresponding to the three pontoons randomly selected for each marina.

Regarding macrofauna, number of taxa (considering the species, genus, family, order, class and phylum levels seperately), total abundance and Shannon-Wiener's Diversity at species level (H') were calculated for each replicate (675 cm^2). Data were also calculated separately for the three main phyla, i.e. Annelida, Arthropoda and Mollusca. Total taxa richness (i.e. total number of different species) and H' were also determined for each marina. For meiofauna, number of taxa (for high taxonomic levels), abundance (individuals/10 cm^2) and the nematode:copepod ratio (Rubal et al., 2009) were also calculated.

Two-way ANOVAs with the above design were conducted to explore differences in the biological descriptive parameters of macro- and meiofauna among marinas (factor 'Marina') along the Mediterranean-Atlantic axis (factor 'Location'). Homogeneity of variances was checked using Cochran's test. When ANOVA detected significant differences for a given factor, the source of the variance was identified by applying the Student-Newman-Keuls (SNK) test (Underwood, 1997).

Non-parametric multidimensional scaling (MDS) was used to show the relationship among locations (Atlantic *vs* Mediterranean) and marinas based on macrofaunal abundances; this was done considering the data matrix for each of the six selected taxonomic levels (species, genus, family, order, class and phylum) separately and also for the three main phyla (i.e. Annelida, Arthropoda and Mollusca) considering only the species level. The Bray-Curtis similarity index was applied after transformation of abundance values by the square-root. An additional MDS was conducted using abundances of meiofaunal higher taxa.

The macrobenthic community patterns obtained from the six different taxonomic levels were compared using a second-stage MDS, by computing a weighted Spearman

rank correlation coefficient between the corresponding elements of each pair of marinas from the respective similarity matrices (Somerfield and Clarke, 1995; Chatzinikolaou et al., 2018). Similarly, a second stage MDS was conducted to compare the patterns obtained separately for Annelida, Arthropoda and Mollusca with that of the total community.

Differences in the macro- and meiofaunal assemblage among locations and marinas were tested by permutational multivariate analyses of variance (PERMANOVA), using the same experimental design explained above, and considering the aforementioned six taxonomic levels. Additional PERMANOVAs were conducted for Annelida, Arthropoda and Mollusca independently. Analyses were based on Bray-Curtis similarities and Monte Carlo tests were included. Significant P-values were obtained by computing 9999 permutations of residuals under a reduced model, as this method gives the most accurate Type I error for complex design (Anderson, 2005). Pairwise comparisons were then used. Additionally, to test the dispersion among samples for the factors 'Location' and 'Marina', a permutational analysis of multivariate dispersions (PERMDISP) was used.

Distance-based linear modelling (DistLM) was used to assess the relative contribution of abiotic parameters to the variability observed in the macro- and meiofaunal community structure (Anderson et al., 2008). The analysis was performed based on the matrix of square-root transformed abundance data. Abiotic data were transformed by log(x+1) and normalized to reduce the effects of differences in unit scales. The model was constructed using the best combination of predictors (*Best* procedure) using AIC (Akaike's Information Criteria) (Burham and Anderson, 2004; Leonardi et al., 2020; Mulik et al., 2020; Wei et al., 2020). Prior to the DistLM analysis, multicollinearity between abiotic factors and skewness of data were evaluated using Draftsman plot based on Spearman correlations. Sets of variables with Spearman's test values higher than 0.8 ($p<0.01$) were omitted (Chatzinikolaou et al., 2018). Distance-based Redundancy Analysis (dbRDA) was performed to provide a visual representation of the macrobenthic community fitted to the significant predictor variables in the multi-dimensional space (Mulik et al., 2020; Wei et al., 2020). To increase robustness of results, the BEST routine (BIO-ENV) was also employed to explore correlations between the matrix of faunal abundances and environmental predictors from a different analytical perspective (Anderson et al., 2008). The Bray-Curtis similarities matrix was

265 based on faunal abundances while the Euclidean distances-based matrices derived from
266 all the possible sequential combinations of the abiotic variables. Spearman rank
267 coefficient was used to identify the best environmental variables that explained the
268 observed patterns on 999 permutations (Marchini et al., 2020). To explore the response
269 to abiotic parameters of each considered taxonomic level (species to phylum) and the
270 three main phyla, DistLM and BIO-ENV were conducted for each category.
271 PERMANOVA, PERMDISP, MDS, DistLM, dbRDA and BIO-ENV analyses
272 were carried out using the PRIMER v.6+PERMANOVA package (Clarke and Gorley,
273 2006; Anderson et al., 2008) and ANOVA analyses were conducted on the GMAV5
274 software (Underwood et al., 2002).
275
276 *2.3. Integrative assessment*
277 For an integrative assessment of the ecological quality status of marinas
278 considering biotic and abiotic information of soft-bottom environments, the following
279 six ecological indicators were selected and calculated for each marina (Fig. 2):
280
281 A) Marinas Environmental Pollution Index (MEPI). This index was recently
282 developed by Guerra-García et al. (2021) to characterize the environmental
283 pollution levels in marinas based on 15 selected stressors measured in the
284 sediments.
285 B) Biocontamination Index (BCI). It was developed by Arbačiauskas et al. (2008)
286 to assess the biopollution level (in terms of exotic species) in inland waters. We
287 have used this index here as a proxy to evaluate the contribution of NIS to the
288 soft-bottom benthic community in each marina.
289 C) Macrofaunal taxa richness. The total number of species found in each marina
290 was calculated. The number of genera, families and orders were also included
291 for comparison.
292 D) Macrofaunal diversity (at species level) was measured by the Shannon-Wiener's
293 index (H').
294 E) Macrofaunal biotic indices. Many biotic indices have been developed during the
295 last years. In the present study we have used AMBI (Borja et al. 2000), M-
296 AMBI (Muxika et al., 2007), BENTIX (Simboura and Zenetos, 2002),
297 MEDOCC (Pinedo et al., 2015) and BENFES (Sánchez-Moyano et al., 2017).

Compiled information about the boundaries and intervals for these indices can be found in Keeley et al. (2012). Biotic indices have been considered suitable tools for assessing the ecological status of Mediterranean ports (Dimitriou et al., 2020)

F) Meiofaunal nematode:copepod index proposed by Raffaelli and Mason (1981). This ratio was proposed as a fast, easy, and reliable method to study the effects of organic matter enrichment in coastal sediments (see Rubal et al., 2009).

The intervals and boundaries assigned in the literature for MEPI, BCI, AMBI, M-AMBI, BENTIX, MEDOCC and BENFES (high, good, moderate, poor, bad) were adopted in the present study. Intervals for taxa richness, H' and nematode:copepod ratio were established in the present study according to the results obtained in the marinas from the Southern Iberian Peninsula.

The following methodological protocol was developed to assess a quality status based on the selected ecological indicators (Fig. 2):

(i) Once the six indicators were calculated, a score for each indicator was assigned according to the colour categories for each ecological status: blue (high) was scored with 4 points, green (good) with 3 points, yellow (moderate) with 2 points, orange (poor) with 1 point and red (bad) with 0 points. All parameters have the same five intervals (blue, green, yellow, orange and red), except for MEPI which includes only green (good), yellow (moderate) and red (bad) (see Guerra-García et al., 2021). In this case green was scored with 4 points, yellow with 2 points and red with 0 points.

(ii) The global score of each marina (ranging from 0 to 24) was obtained by summing the scores assigned to each of the six selected indicators (MEPI, BCI, Taxa richness, H', biotic indices and nematode:copepod ratio) based on its ecological status (i). If several biotic indices are available, as in the present study, the value used in the assessment would result from the mean of the scores obtained for each index. Although the number of species is advisable as an indicator of taxa richness, the number of genera, families or orders could also be used in the assessment.

(iii) Establishment of global quality status of each marina according to the total score. We proposed the following intervals: (0-5: bad, 6-10: poor, 11-15: moderate, 16-20: good, 21-24: high)

Additionally, the relationships between all the indicators used were explored by Spearman correlation for all datasets.

3. Results

3.1. Macrofaunal community

8339 individuals belonging to at least 166 macrofaunal species were found during the present study in sediments from eight marinas on the Southern Iberian Peninsula (Table 1 and Tables S2, S3). This included 61 annelid species (5514 specimens, mainly represented by polychaetes), 58 arthropods (1837 specimens, mainly peracarid crustaceans), 41 molluscs (789 specimens, mainly bivalves), 3 echinoderms (9 specimens) and 190 additional specimens belonging to the phyla Nematoda, Nemertea and Phoronida. In all marinas, Annelida was the dominant phylum (Fig. 3A) both in species richness and abundance, except in Almería where Arthropoda was the most abundant phylum (due to the high density of the tanaid *Apseudopsis latreilli*). The most common and abundant taxa were the annelids *Aphelochaeta marioni*, *Capitella capitata*, *Chaetozone gibber*, *Cirriformia tentaculata*, *Cirrophorus furcatus* and *Fabricia stellaris*, the crustaceans *Phtisica marina*, *Iphinoe tenella* and *A. latreillii*, and the molluscs *Abra tenuis*, *Corbula gibba* and *Parvicardium exiguum* (Table 1). Detailed information on the taxonomical categories of each species and their status (native, cryptogenic or introduced) is included in Tables S2 and S3. Most of the species inhabiting sediments from marinas can be considered native or cryptogenic, while only four were exotic species, all of them crustaceans, namely the amphipods *Caprella scaura* and *Jassa slateryi*, the isopod *Paranthura japonica* and the decapod *Alpheus* sp. (Table S2).

Regarding the total number of species per marina, Puerto América showed the highest species richness (76) followed by Almería (53), Motril (52) and La Línea (47). The marinas with the lowest number of species were Chipiona (25), Barbate (30), Fuengirola (33) and Faro (37). This pattern was also obtained for the number of species per replicate (Fig. 3B). The highest values of the Shannon-Wiener's diversity (H') (based on the global data per marina) was also measured in Puerto América (3.23) followed by La Línea (2.82), Motril (2.41) and Faro (2.03). Barbate (1.56), Chipiona (1.64), Almería (1.86) and Fuengirola (1.92) showed the lowest values.

362 The number of species, total abundance and H' differed significantly among
363 marinas, although no differences were obtained for the factor 'location' (Atlantic *vs*
364 Mediterranean) (Table 2). The highest heterogeneity among marinas was obtained for
365 the Mediterranean (see SNK tests in ANOVAs of Table 2). The two-dimensional MDS
366 plot based on species abundances showed segregation of marinas (Fig. 4A).
367 PERMANOVA confirmed significant differences for all marinas (see pair-wise tests in
368 Table 2) with no significant differences for the factor location (Table 2).
369 When each of the three main phyla (Annelida, Arthropoda and Mollusca) was
370 analysed separately, the species richness also differed significantly among marinas
371 (Table S4A, Fig. 3C). The pattern was more evident for annelids and molluscs than for
372 arthropods (Table S4A). In fact, SNK tests indicated no differences among
373 Mediterranean marinas for arthropods. At the community level, the factor 'Marina' was
374 significant for the three phyla according to PERMANOVA results (Table S5A) and
375 MDS plots graphically showed segregation among marinas again (Fig. 5A). Molluscs
376 also revealed some segregation between Mediterranean and Atlantic marinas, although
377 'Location' was not significant according to PERMANOVA (Pseudo-F=1.9178,
378 p=0.0961, Table S5A). The second stage MDS (Fig. 5B) demonstrated that the pattern
379 derived from the annelid assemblage was very similar to that considering all taxa,
380 showing that this taxon was most responsible for driving the observed pattern for the
381 whole community.
382
383 *3.2. Meiofaunal community*
384 A total of 16 higher taxa were identified (Tables 3, Table S6), 4 of which (Copepoda,
385 nauplius larvae of crustaceans, Nematoda and Polychaeta) were always present at all
386 marinas. Nematoda was the numerically dominant taxon in Faro, Chipiona, P. América,
387 Barbate and Fuengirola, while Copepoda dominated in La Línea, Motril and Almería
388 (Fig. 6A).
389 The number of taxa did not differ among marinas or among locations (Atlantic
390 *vs* Mediterranean), while total abundance values were higher in Mediterranean marinas
391 (Fig. 6A, Table 4). The nematode:copepod ratio differed significantly among marinas,
392 although these differences were mainly due to the high values measured in Fuengirola.
393 The MDS plot showed segregation of marinas and, differently from macrofauna,
394 reflected a clear pattern for the factor location, i.e. Atlantic *vs* Mediterranean marinas

(Fig. 6B). PERMANOVA confirmed significant differences for the factors 'Location' and 'Marina' (Table 4).

3.3. Influence of environmental data on faunal assemblages

A full dataset of environmental data measured in sediments of the eight studied marinas can be found in Table S7 (see also Guerra-García et al., 2021, for details on the environmental assessment).

The variables Co, N, As, S, Clay and N were correlated with other variables ($r>0.8$, $p<0.01$) and were not included in the DistLM, so the model was run with 12 variables (Sand, Silt, hydrocarbons, faecal coliforms, biocide Irgarol, Cd, Cr, Cu, Ni, P, Pb and Zn). According to DistLM, the environmental variables which significantly correlated with the whole macrofaunal community (identified at species level) were mainly P (18.2% of variation explained), sand (16.7%) and TOC (16.0%) (Table 5). Faecal coliforms and the heavy metals Cr, Cu, Pb and Zn were also significant (Table 5). The best model (AIC=180.46, R^2=0.073) was obtained for the combination of Sand, Silt, TOC, P, faecal coliforms, Irgarol, Cr, Cu and Pb (Table 5). The first two axes of the dbRDA explained 50.9 % of the total variation (Fig. 7). BIO-ENV results showed that the best model (Rho=0.820, $p<0.01$) was obtained with the combination of Sand, TOC, P, faecal coliforms, Cu, Pb and Zn, coinciding with the significant variables provided by DistLM (Table 6).

When the three main phyla (Annelida, Arthropoda and Mollusca) were analysed separately, DistLM showed similar results to those obtained with the whole community (Sand, TOC, P, faecal coliforms and heavy metals) (Table 6, Table S8). Variables explained a higher proportion of variability in annelids, followed by molluscs and finally arthropods (Table S8). In fact, BIO-ENV only provided a significant model (Rho=0.797, $p<0.05$) for Annelida (Table 6), which, therefore, turned out to be the phylum best reflecting the environmental conditions in marinas.

Regarding to meiofauna (based on higher taxa abundances), DistLM selected Sand (17.1%), Hydrocarbons (14%), Cd (13.7%) and Cu (10%) as the variables that correlated significantly with the meiofaunal assemblage (Table S9, Table 6). The best model (AIC=157.62, R^2=0.62) was obtained for the combination of Sand, Silt, TOC, faecal coliforms, Cd, Cr, Cu and Zn. BIO-ENV also showed Hydrocarbons, Cd and Cu

as the best combination model. However, the model was not significant (Rho=0.630, p=0.130) (Table 6).

3.4. Macrofaunal taxonomic sufficiency

This study revealed the presence of 166 species, 155 genera, 105 families, 44 orders, 16 classes and 8 phyla inhabiting marinas of the Southern Iberian Peninsula. The number of species was very similar to the number of genera in all marinas (Fig. 3B), since most of the genera were represented by a single species (Table S2). Number of families was also close to the number of genera and species (Fig. 3B). Regarding taxa richness, ANOVAs revealed that the factor 'Marina' was significant for all taxonomic levels considered, although for class and phylum these differences were only due to the high number of taxa collected in P. América in comparison with other Atlantic marinas (Table S4B, Fig. 3B). PERMANOVA confirmed that there were significant differences in community structure among all marinas when separately considering each matrix for species, genera, families or orders (Table S5B). Although significant differences in the factor 'Marina' were also obtained for classes and phyla, these differences were due to the influence of certain marinas, such as Faro (Atlantic) or Almería (Mediterranean) (Table S5B). This pattern was supported by the corresponding MDS ordinations (Fig. 4A). Separation among marinas was evident at the level of species, genus, family and order, while MDS based on classes and phyla showed a less defined grouping (Fig. 4A). The second-stage MDS performed on the six considered taxonomic levels (Fig. 4B) demonstrated that patterns showed by the species/genus levels were similar, and close to that obtained for family/order levels. Conversely, they differed considerably from those derived from the higher levels (i.e. phylum and class).

When the influence of taxonomic resolution was considered to compare the environment-fauna relations, DistLM revealed a similar pattern for species, genus, family and order (Table 6, Table S8). The environmental variables that were significant at the species level were the same as those found at the level of genus, family and order. The set of significant variables were quite different when considering classes and phyla data. Indeed, BIO-ENV provided significant results with similar variables for species, genus, family and order, but they were not significant for class and phylum (Table 6).

3.5. Global assessment. Biotic indices and biocontamination

According to the Marinas Environmental Pollution Index (MEPI), Barbate and Fuengirola were the most polluted marinas (Fig. 8). The Biocontamination Index (BCI) values were very low in all marinas due to the small number of introduced species found on sediments. Although quality intervals for MEPI, BCI and Biotic Indices were defined in the literature, those for taxa richness, diversity (H') and nematode:copepod ratio were not available so they were established during the present study, based on the data obtained for marinas of Southern Iberian Peninsula (see Table S10). The global score, obtained by summing the scores assigned to each selected indicator (MEPI, BCI, Taxa richness, H', Biotic indices and nematode:copepod ratio) ranged from 9 to 17. Fuengirola, Barbate and Chipiona got the lowest score (9 and 10 points) while La Línea, Motril and P. América showed better ecological status (16 and 17 points) (Fig. 8). Therefore, marinas of the Southern Iberian Peninsula ranged from poor (Fuengirola, Barbate and Chipiona) to moderate (Faro and Almería) and good (P. América, La Línea and Motril).

In general terms, the ecological indicators used to conduct the global assessment were in good agreement, except for punctual differences (i.e. BENTIX classified all the marinas as bad or poor, while BENFES classified them as moderate, good or high). Apart from BCI which showed low values in all marinas and was not able to discriminate among them, environmental data (MEPI) and biological information (taxa richness, H', biotic indices and nematode:copepod ratio) were more discriminant and provided similar information (Fig. 8). MEPI was correlated with richness of species and genera, the biotic index MEDOCC and the nematode:copepod ratio. Taxa richness was correlated with H' and with biotic indices (Table S11). Indeed, the marinas classified as good (P. América, La Línea and Motril) were those with the highest values of macrofauna taxa richness and Shannon-Wiener's diversity, and the lowest degree of environmental pollution. Conversely, the most polluted marinas, such as Chipiona, Barbate and Fuengirola, showed the lowest values for taxa richness, diversity, and the highest nematode:copepod ratios.

4. Discussion

4.1. Benthic communities

The present study revealed that the soft bottom of marinas from the Southern Iberian Peninsula supported a wide variety of macrobenthic taxa (166 species

493 distributed in 155 genera, 105 families, 44 orders, 16 classes and 8 phyla). The number
494 of soft-bottom macrofauna species per marina (ranging from 25 to 76) was similar to
495 that reported from marinas worldwide (e.g. McGee et al., 1995; Estacio et al., 1997;
496 Guerra-García and García-Gómez, 2004 a,b,c; Martínez-Lladó et al., 2007; Covazzi
497 Harriague et al., 2012; Chatzinikolaou et al., 2018; Ng et al., 2019).

498 Annelida (mostly polychaetes) was the dominant phylum in number of species
499 (37%) and, especially, in number of individuals (66%). In fact, the patterns of the total
500 community were mainly driven by annelids (see Fig. 3), that are usually reported as the
501 dominant macrobenthic taxon in the sediment of marinas worldwide (Moreira et al.,
502 2010; Ng et al., 2019; Chatzinikolaou et al. 2018) and, in general, in most soft-bottom
503 habitats (Hutchings, 1998). On the contrary, Arthropoda (mainly Amphipoda inhabiting
504 arborescent substrates) dominated floating pontoons in terms of abundance and species
505 richness (Gavira O'Neill et al., 2015, 2018).

506 Although all studied marinas were located across the same geographical area,
507 univariate and multivariate analyses consistently showed significant differences among
508 them based on biological data. This heterogeneity among marinas has also been
509 revealed by environmental stressors (see Guerra-García et al., 2021). Spatial variations
510 in biotic assemblages among and within marinas have been attributed to differences in
511 the local environment as well as to the marina design (Toh et al., 2017). In fact, the
512 singularity of any given marina, largely determined by a variety of local factors (e.g.
513 environmental conditions, availability of suitable substrate, level of marine traffic) has
514 proven to be a key factor affecting, for example, several stages of the NIS invasion
515 process (Martínez-Laiz et al., 2019). Hence, our results reinforce the importance of
516 considering a local scale perspective for conservation and management purposes.

517 Although significant differences in the factor 'marina' were relevant throughout
518 the whole study, the factor 'Location' (Atlantic *vs* Mediterranean) was not relevant for
519 macrofauna, only showing certain degree of segregation when considering molluscs
520 separately. However, this factor was significant for meiofauna and should also be
521 considered in management programmes.

522 The present study only considered a spatial scale, and therefore further research
523 should explore if the observed patterns remain constant through time. Although
524 epifaunal communities associated with floating pontoons suffer significant seasonal
525 fluctuations (e.g. Ros et al., 2013), Chatzinikolaou et al. (2018) did not find important

seasonal differences in soft-bottom communities of port and marinas. On the contrary, Moreira et al. (2010) detected strong fluctuations among and within seasons mostly related to recruitment of opportunistic species and some perturbations (i.e. proliferation of ephemeral algae on the sediment in summer). This again emphasizes that the environmental singularity of any given marina must be considered in management programmes. In this sense, sediment monitoring should ideally be based on previous baseline data in order to design the appropriate sampling for each marina and reduce the monetary, time and labor costs of such activities as much as possible.

4.2. Influence of environmental data on faunal assemblages

The multivariate pattern of the macrofaunal community in the present study was mainly explained by P, Sand, TOC, faecal coliforms, and heavy metals. Although hydrocarbon concentration clearly discriminated among marinas (Table S7, Guerra-García et al., 2021) and has been traditionally considered a significant factor affecting biota (Blanchard et al., 2002), it did not contribute to explain the observed macrofaunal patterns but was, in turn, relevant for meiofauna. In this sense, Covazzi Harriague et al. (2012) pointed out that the macrofaunal and meiofaunal assemblage can respond differently to human pressure.

Most explanatory variables selected by our analyses agree with those reported in previous studies in harbours and ports. Granulometry is considered one of the main factors modulating soft-bottom communities, including those inhabiting harbour areas (e.g. Moreira et al., 2005). Guerra-García et al. (2004 a,b,c) also reported granulometry, TOC, P and heavy metals as important variables to explain the distribution of molluscs, crustaceans and polychaetes in the harbour of Ceuta, while Chatzinikolaou et al. (2018) found heavy metals to be relevant explanatory variables of biotic patterns.Among the many potential sources, metal-based antifouling systems, mainly Cu and Zn, clearly play a major role in contamination in marinas (Briant et al., 2013).

When each of the three main phyla were analysed separately, Annelida was more related to the considered environmental conditions in marinas than others. Arthropods in general, and crustaceans in particular, are traditionally considered better bioindicators due to their higher sensitivity to marine pollution (Navarro-Barranco et al., 2020) and better reflect differences at the spatial scale (i.e. among localities) than molluscs and annelids (Sánchez-Moyano and García-Gómez, 1998). However, in

559 harbours and marinas, annelids (mainly polychaetes) become the best taxon to
560 discriminate between sampling sites, especially when oxygen is not a limiting factor
561 (Guerra-García and García-Gómez, 2005a).
562
563 *4.3. Taxonomic sufficiency*
564 The use of higher taxonomic levels instead of species as a proxy for
565 identification has been extensively tested in both terrestrial and marine habitats, and on
566 such taxa as insects, fish, fauna associated with algae and seagrasses, meiofauna and
567 benthic macrofauna in general (see Sánchez-Moyano et al., 2006 and references
568 therein). However, it is important to properly analyse the cost-benefits of such
569 approaches to select the appropriate level of taxonomic resolution in benthic monitoring
570 programmes (Bouchard et al., 2005).
571 Although Ferraro and Cole (1990) indicated that the species level would be the
572 most sensitive for the evaluation of pollution impacts, Sánchez-Moyano et al. (2006),
573 based on several datasets within a wide range of habitats and substrate types along the
574 southern Iberian coastline, concluded that studies at the different levels of taxonomic
575 resolution (species, family, order) led to similar results both as regards community
576 distribution and composition, and their relationship to environmental variables.
577 The present study found similar patterns to those provided by Sánchez-Moyano
578 et al. (2006) and Chatzinikolaou et al. (2018). On the one hand, differences among
579 marinas were also detected using high taxonomic levels, and on the other hand, the set
580 of environmental variables which better explained macrofaunal assemblages were the
581 same at the species, genus, family and order level, but differed at class and phylum
582 levels. The second stage MDS revealed that identification to genus provided almost
583 identical results to those obtained when considering species due to many genera being
584 represented by only one species in each marina. Family and order levels yielded similar
585 results between them but were less informative with respect to species and genus levels
586 (Fig. 4). For all these reasons, family and order levels could be an alternative in large-
587 scale monitoring programmes with significant time and budget constraints.
588 Conversely, taxonomical resolution to the species level is mandatory to
589 accurately identify NIS in marinas, and to correctly calculate biocontamination indices
590 such as BCI (Arbačiauskas et al., 2008). Indeed, early detection of NIS is often delayed
591 when taxa are taxonomically challenging, such as small-sized marine organisms which

592 require great taxonomic expertise (Marchini and Cardeccia, 2017; Martínez-Laiz et al.,
593 2020). Therefore, the potential efficacy of identification to high taxonomic levels in
594 some monitoring programmes does not replace by any means the information obtained
595 at the species level, which is paramount for basic and applied ecological studies (de
596 Oliveira et al., 2020).
597
598 *4.4. Global assessment*
599 The quality assessment applied in the present study and developed specifically
600 for marinas was based on six selected ecological indicators (MEPI, BCI, Taxa Richness,
601 H', biotic indices and nematode:copepod ratio), encompassing five of the eleven
602 descriptors of MSFD: D1 (Biological diversity), D2 (NIS), D5 (Human-induced
603 eutrophication), D6 (Sea floor integrity) and D8 (Concentrations of contaminants) (Berg
604 et al., 2015; Piroddi et al., 2015). The assessment was useful for discriminating among
605 marinas, even when they were closely located. The evaluation simultaneously combined
606 abiotic and biotic information, integrating chemical pollution, NIS risk and attributes of
607 the macro- and meiofaunal assemblages.
608 Regarding taxa richness in the assessment method, identification to the species
609 level is advisable, but this study showed that other categories such as genus, family or
610 even order could provide similar ecological intervals (see Fig. 8 and Table S10). Indeed,
611 values of these four taxonomic categories were significantly correlated ($r>0.9$, $p<0.01$)
612 (Table S11). Therefore, this global assessment for marinas can be conducted whenever
613 the macrofauna is, at least identified to the order level.
614 In recent years, a variety of biotic indices dealing with the structure of
615 macrobenthic communities have been proposed to address the objectives of European
616 Directives (e.g., Marine Strategy Framework Directive -MSFD- 2008/56/EC, EU
617 Biodiversity Strategy to 2020 and Water Framework Directive -WFD- 2000/60/EC).
618 Indeed, biotic indices have been recently demonstrated to be suitable for assessing the
619 ecological status of Mediterranean ports and marinas (Dimitrou et al., 2020).
620 Although a unified protocol within the EU has not yet been adopted (Dimitriou
621 et al., 2020) and there is no agreement on what index or indices should be used by
622 environmental managers to establish benthic quality (Borja et al., 2015), the most used
623 ones are AMBI (AZTI's Marine Biotic Index; Borja et al., 2000), M-AMBI
624 (multivariate AMBI; Muxika et al., 2007) and BENTIX (Simboura and Zenetos, 2002).

625 The MEDOCC index was an adaptation of the AMBI for the Mediterranean area
626 (Pinedo et al., 2015). All these indices rely on the taxonomic identification of species.
627 Recently, a new index based on identification to the family level, i.e. BENFES, was
628 developed (Sánchez-Moyano et al., 2017). The application of these indices in marinas
629 revealed important differences in the ecological status assigned (Fig. 8). BENFES was
630 the most favourable (most marinas classified as good). Conversely, BENTIX was
631 clearly more restrictive (most marinas qualified as bad or poor), coinciding with the
632 results obtained by Dimitrou et al. (2020). BENTIX did not correlate with any other
633 index, nor with other selected ecological indicators, so its use in marinas, at least in the
634 Southern Iberian Peninsula, is discouraged. MEDOCC was the only index correlating
635 with environmental pollution (MEPI), so its calculation in marinas can be useful.
636 Therefore, we recommend using the biotic indices in marinas with caution and,
637 whenever possible, calculating several to obtain mean scores and reduce potential biases
638 in the quality assessment.
639 The selected meiofaunal indicator for assessment was the nematode:copepod
640 ratio, which is relatively easy to undertake in a marina. Undoubtedly, considering the
641 difficulty and time-consuming process of taxonomic identification of nematodes and
642 copepods, the use of taxonomic sufficiency is one of the most attractive features of this
643 ratio (Rubal et al., 2019). Hence, this index has become a common method for
644 evaluating organic enrichment and chemical pollution (Rohal et al., 2020). A higher
645 ratio is usually associated to chemical and organic pollution (Raffaelli and Mason,
646 1981), because copepods, specifically harpacticoids, are more sensitive to pollutants
647 than nematodes (Elarbaoui et al., 2015). In fact, Moreno et al. (2008) found a significant
648 correlation between nematodes and concentrations of environmental contaminants in
649 tourist marinas of the Mediterranean Sea. The present study revealed that the index
650 discriminates well among marinas. It correlated with other biotic indices and, most
651 importantly, with the environmental pollution levels as defined by the MEPI.
652 Accordingly, we consider that the measure of nematode:copepod ratio in marinas can be
653 an adequate proxy for environmental pollution.
654 Concerning exotic species, recreational boating is currently considered a
655 significant vector for the introduction and secondary spread of NIS, especially at local
656 scales (e.g. Ros et al., 2013; Ashton et al., 2014; Foster et al., 2016; Ferrario et al.,
657 2017; Martínez-Laiz et al., 2018, 2019; Ulman et al., 2019). In the present study, we

658 used the Biocontamination Index (BCI) for marinas. Alternatively, a more recent index,
659 ALEX, has also been proposed to assess the impacts of alien species on benthic
660 communities (Çinar and Bakir, 2014). While BCI is based on presence and abundance
661 of alien species *sensu lato*, ALEX does not take into account abundances and its
662 calculation requires classification of alien species as 'causal', 'established' or
663 'invasive'. However, these categories are hard to assign when considering small
664 invertebrates in marinas. For this reason, we have not calculated ALEX in the present
665 study; instead, we consider BCI to be more appropriate for marinas. Despite marinas
666 being deemed 'hot spots' for exotics, the number of alien species inhabiting soft
667 bottoms was remarkably low, with only 4 NIS (all crustaceans, 3 peracarids and 1
668 decapod) out of 166 species. It should be noted though, that the native range of more
669 than a third of the reported taxa is unknown (their status remains undetermined or
670 cryptogenic), which highlights the lack of baseline information and taxonomic
671 uncertainty for many of these small mobile taxa. In any case, the low number of alien
672 species reported here contrasts considerably with the high number of NIS (both mobile
673 and sessile taxa) inhabiting floating pontoons (e.g. Martínez-Laiz et al., 2018; Tempesti
674 et al., 2020). In fact, higher numbers of NIS in hard substrates in comparison with soft
675 bottoms have been reported by other authors (Ruiz et al., 2009; Jimenez et al., 2018).
676 Our results confirm this pattern in marinas and suggest that exploring NIS only in
677 sediments is not enough to properly characterize biopollution levels in recreational
678 harbours. The contrasting invasion pattern observed between hard and soft-bottom
679 habitats also illustrates the importance of sampling across a variety of habitats (Jiménez
680 et al., 2018).
681
682 *4.5. Towards Blue-flag marinas*
683 A suitable management of marinas and ports should be a priority in the context
684 of implementation of MWFD and United Nations (UN) sustainability goals 2030. One
685 of these goals includes marine life and aims to reduce pollution in coastal waters by
686 increasing scientific knowledge and developing research capacities and transference of
687 marine technology. Therefore, monitoring anthropogenic pressure and ecological
688 quality of marinas should be an important issue for local authorities (D'Alessandro et
689 al., 2020). The assessment of quality status can allow for design of standards when
690 assigning "sustainable quality seals" to those marinas with better values of ecological

indicators. Environmental quality is, indeed, one of the main criteria to assign a Blue Flag to a marina (http://www.banderaazul.org/puertos-y.embarcaciones-2020, accessed 8 August 2020). In our study, the marinas at P. América, La Línea and Motril reached the 'good' status according to the global environmental assessment based on soft-bottom habitats. This assessment based on sediment indicators could provide a tool for marinas to be awarded a Blue Bag.

To reduce environmental impact and increase biological diversity, the design of new marinas should allow water exchange by building more openings or having a through-flow design to facilitate exchange with the adjacent open waters (Guerra-García and García-Gómez 2004a,b,c, 2005a,b; Ng et al., 2019). In fact, marinas that are well designed, with adequate structural complexity and good water quality, can even function as nurseries for juvenile fish (Bouchoucha et al., 2016) and small invertebrates (pers. observ.).

Marinas may support a rich and diverse marine biodiversity and are easily visible to the public (Toh et al., 2017). Pontoons are full of sessile and mobile colourful fauna representing different phyla, and can be visited at any time by walking (no need for snorkeling or SCUBA diving). Beside hard substrates, the bottom of marinas usually corresponds to muddy sediments that can easily be sampled with small grabs for macro- and meiofauna. These manageable grabs can be effortlessly hand-carried and deployed from the pontoon in the marina without the need of a boat or any motorized lift system. For all these reasons, marinas become suitable enclaves to develop teaching activities on sampling methods in hard and soft bottoms, citizenship education and biodiversity conservation programmes as well as training courses (e.g. NIS identification), among others. Furthermore, by using social perception surveys and media programmes, boat owners can become aware of the marine life inhabiting pontoons and sediments, and get involved in reaching more ecologically sustainable marinas.

5. Conclusions

The present study reveals that the proposed method based on selected abiotic and biotic indicators [Marinas Environmental Pollution Index (MEPI), Biocontamination Index (BCI), macrofaunal biotic indices (AMBI, M-AMBI, BENTIX, MEDOCC and BENFES), macrofaunal taxa richness, Shannon-Wiener's diversity, and

nematode:copepod index], can be useful for integrative assignment of the ecological status of marinas. Although the consideration of several indicators is advisable in terms of scientific integrity, it could be questioned that this would be user-friendly and easy to apply for management stakeholders. As scientists, we must encourage policy makers, governments and funding agencies to invest in rigorous scientific studies to properly address specific monitoring guidelines before making any decision. Alternatively, we must provide easy tools to facilitate this work, so a reasonable commitment must be reached with a proper balance between scientific integrity and a manageable approach. Although our proposed method involves several parameters and indicators, it can be flexible according to the available data. For example, taxa can be identified to family and order instead of species, and MEPI can be adjusted based on the environmental data available (see Guerra-García et al., 2021). Similarly, species richness can be alternatively substituted by the number of genera, family or orders. Values of the nematode:copepod index are not difficult to calculate and, regarding biotic indices, the score can be calculated on the basis of the indices available, and some of them do not require species identification. The only index that requires identification at the species level is the BCI, since it needs the correct identification of exotic species. But, if necessary, under time and budget constraints, the global score can be done by eliminating some of the markers, such as BCI, and extrapolating the score to the new intervals. Future studies must be conducted to test the method proposed across different biogeographical and seasonal scales.

Declaration of competing interest.

We declare no conflict of interest.

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Appendix A. Supplementary data

Supplementary data related to this article can be found online at https://doi.org/xxxxxxxxx.

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Figure legends

Fig. 1. Map of the study area showing the location of the eight studied marinas.

Fig. 2. Flowchart showing the methodology of the assessment method proposed in the present study.

Fig. 3. A) Abundance of the three main macrofaunal phyla (Annelida, Arthropoda and Mollusca) in each marina; "others" include remaining phyla. B) Taxa richness for each considered taxonomic level (species, genus, family, order, class and phylum). C) Species richness of the three main phyla. Values represent the mean (A–C) and standard error (B–C) (n=3) per marina.

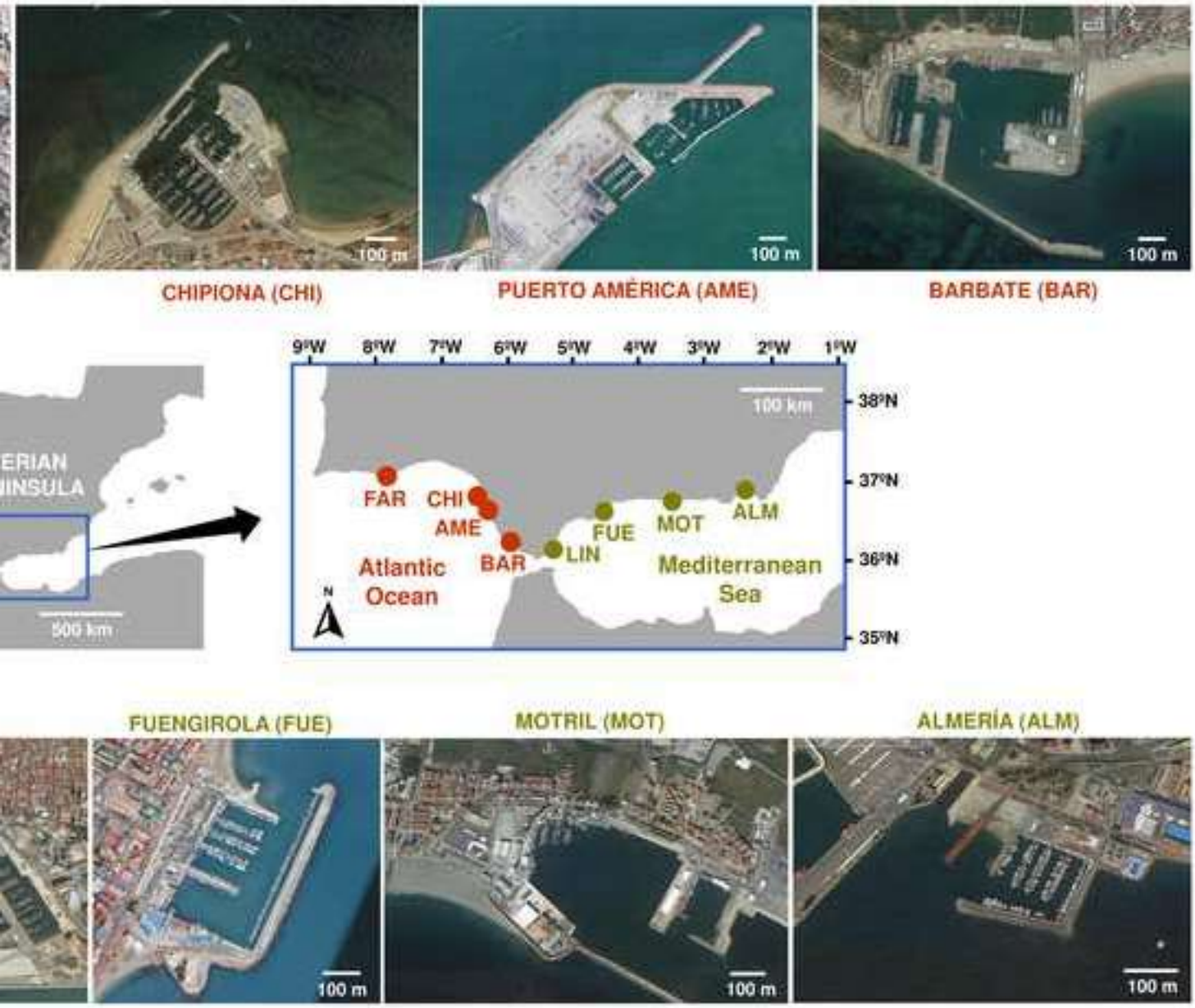
Fig. 4. A) Non-parametric multidimensional scaling (MDS) showing the relationship among locations (Atlantic *vs* Mediterranean) and marinas according to macrofauna separately for the six considered taxonomic levels (species, genus, family, order, class and phyla). B) Second stage MDS considering all macrofaunal taxonomic levels.

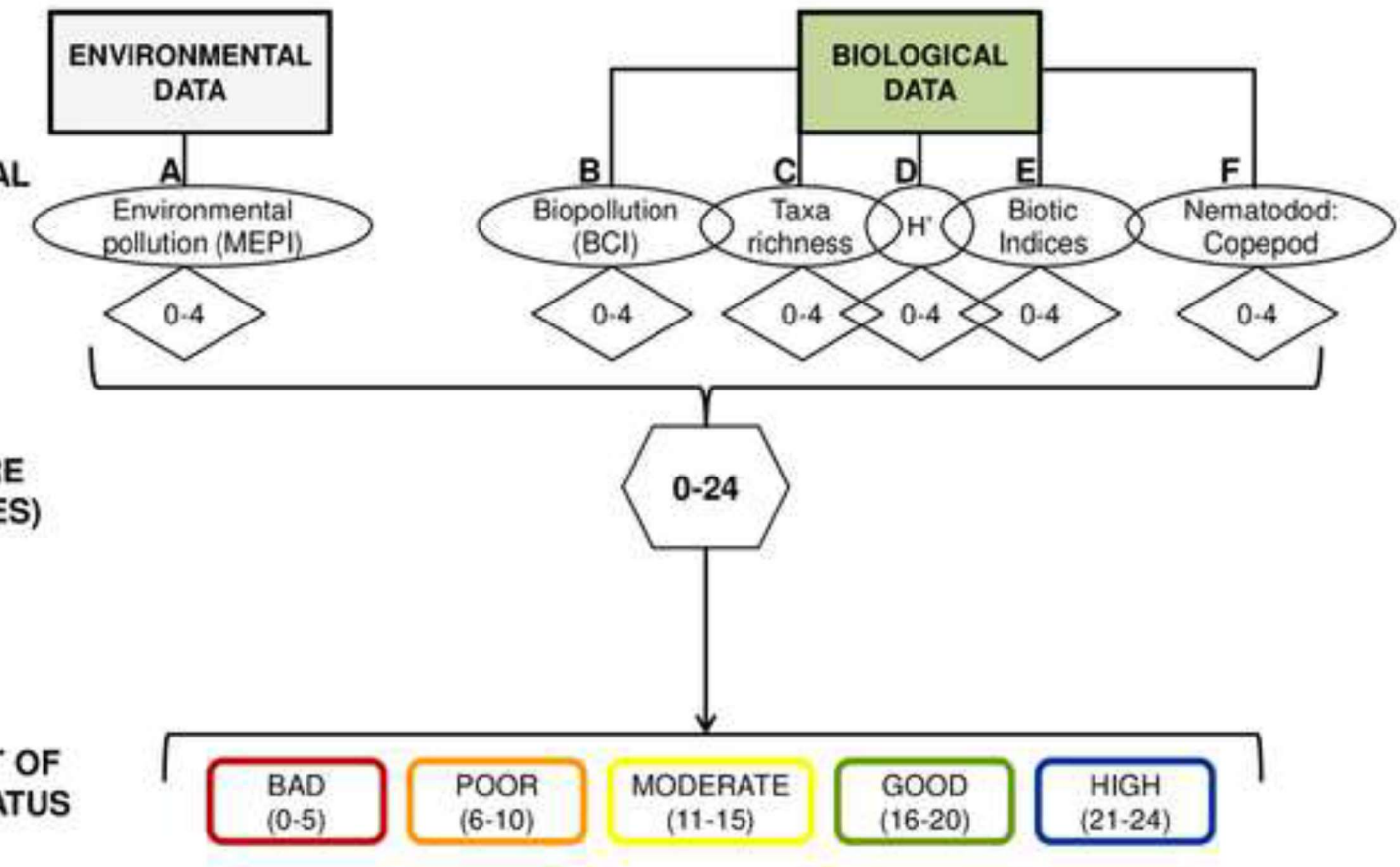
Fig. 5. A) Non-parametric multidimensional scaling (MDS) showing the relationship among locations (Atlantic *vs* Mediterranean) and marinas according to macrofauna (separately for Annelida, Arthropoda and Mollusca). B) Second stage MDS for the three main phyla and the total macrofauna community.

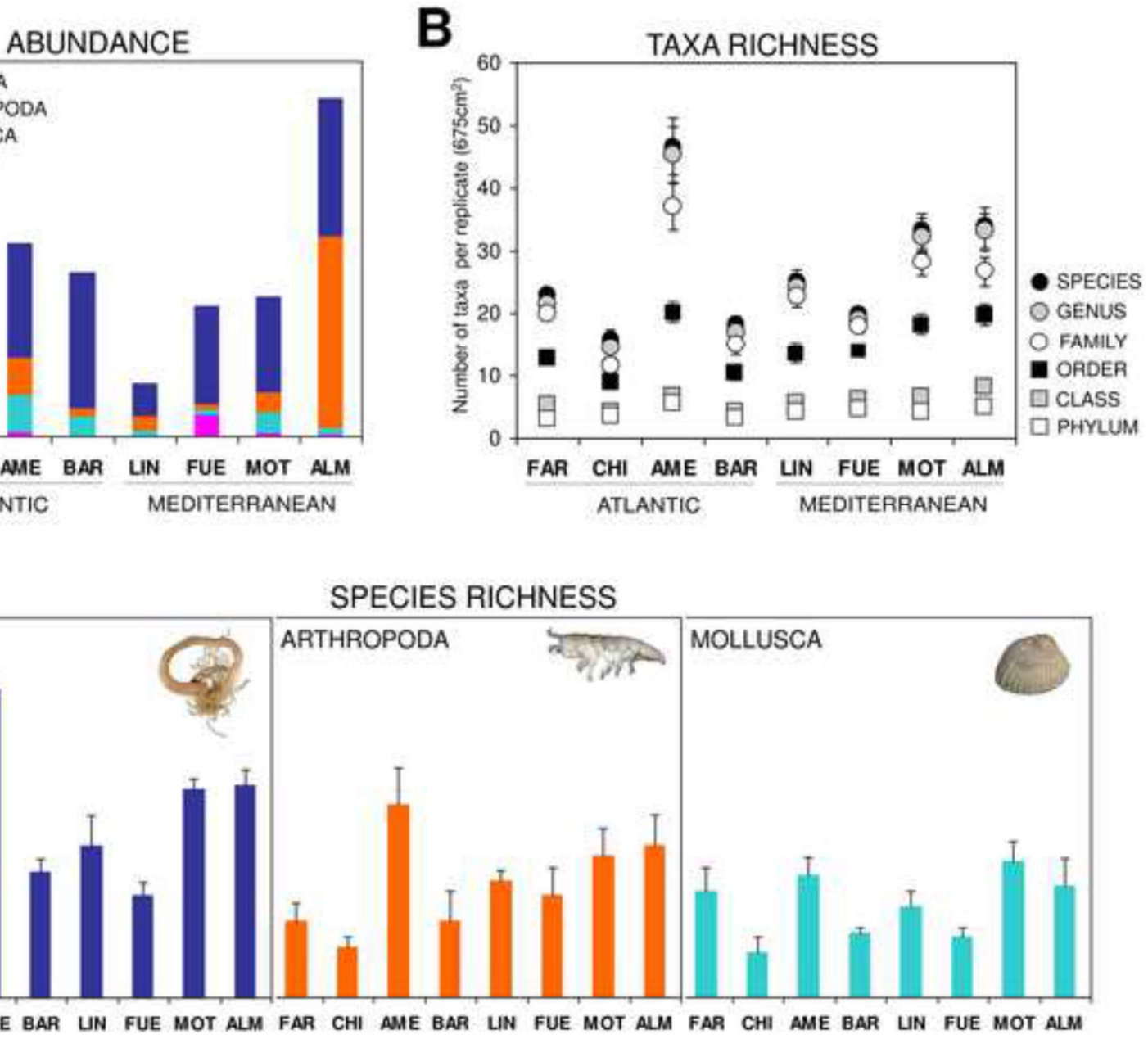
Fig. 6. A) Nematode:copepod ratio and abundance of the main meiofaunal taxa measured in each marina. B) Non-parametric multidimensional scaling (MDS) showing the relationship among locations (Atlantic *vs* Mediterranean) and marinas according to meiofauna (higher taxa abundances).

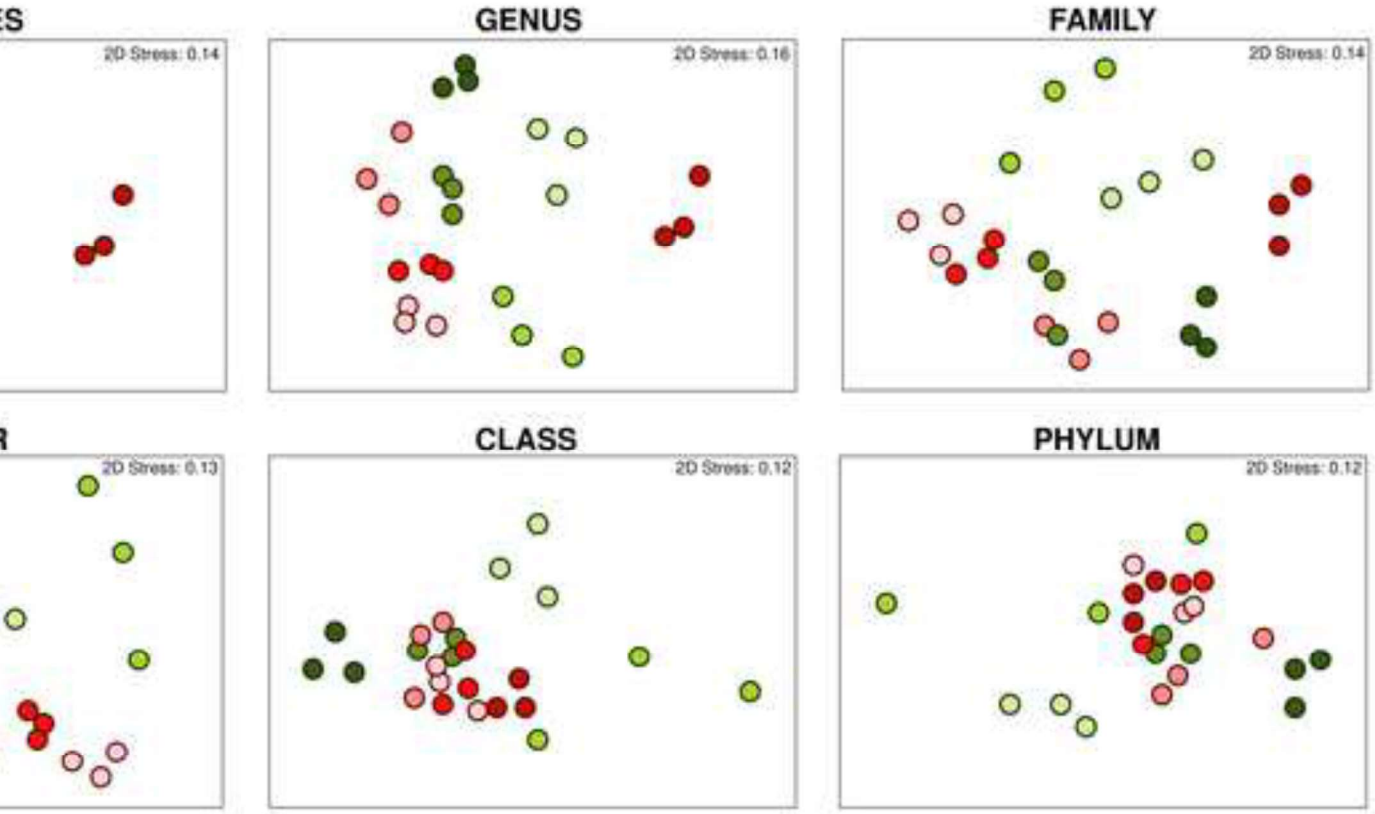
Fig. 7. Graphic representation of the dbRDA showing ordination of marinas and variables with respect to the first two axes. Only significant variables according to the DistLM (see Table 5) are included.

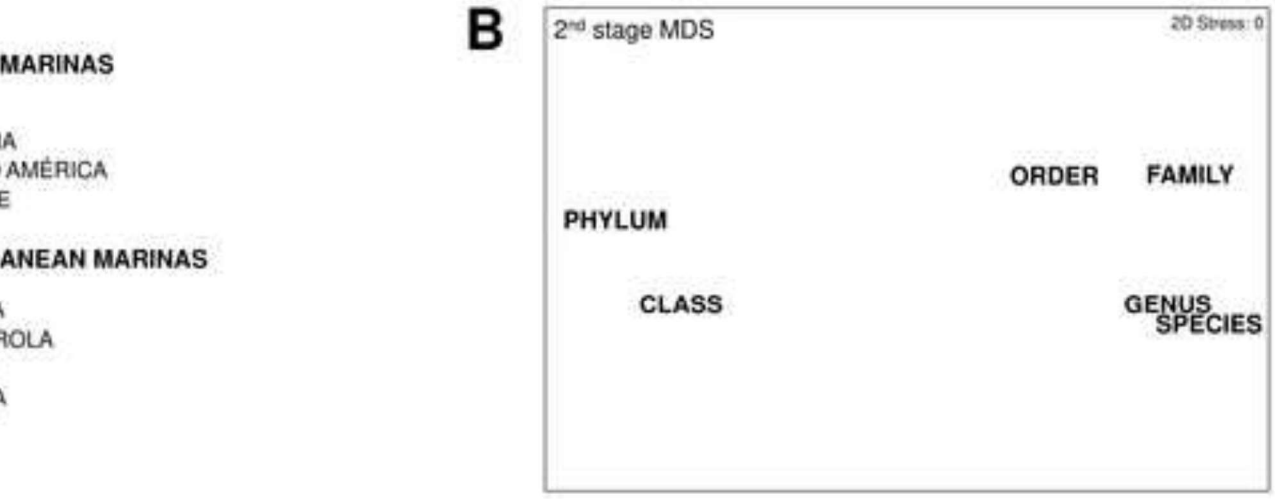
Fig. 8. Global assessment of ecological quality status of the marinas from southern Iberian Peninsula based on six selected indicators: Marinas Environmental Pollution Index -MEPI-, Biocontamination Index -BCI-, macrofaunal taxa richness, Shannon-Wiener's diversity (H'), macrofaunal biotic indices and meiofaunal nematode:copepod ratio. Total score for each marina (0-24) is based on the sum of the scores for each indicator.

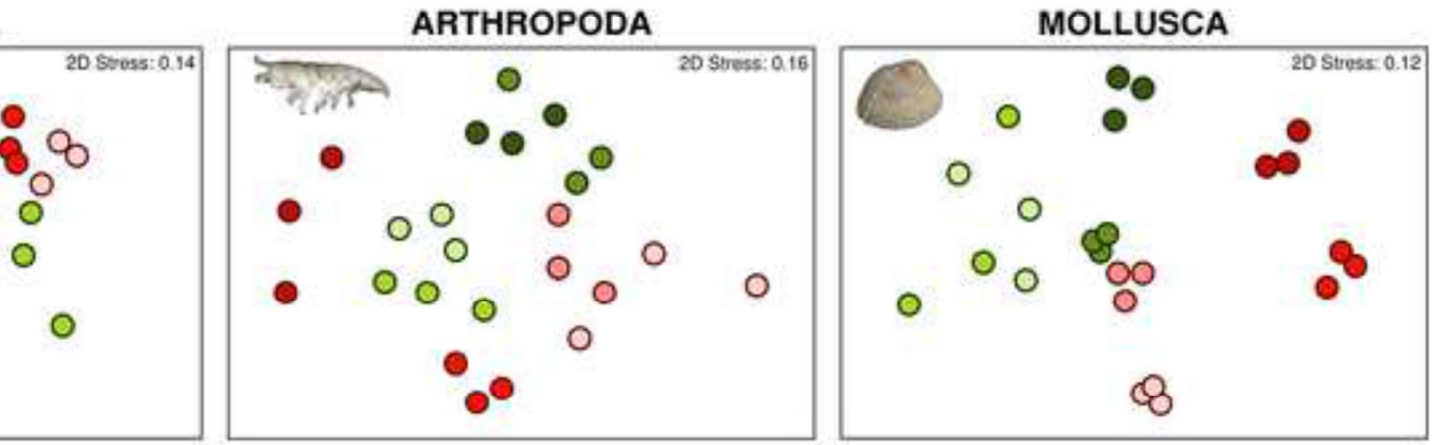












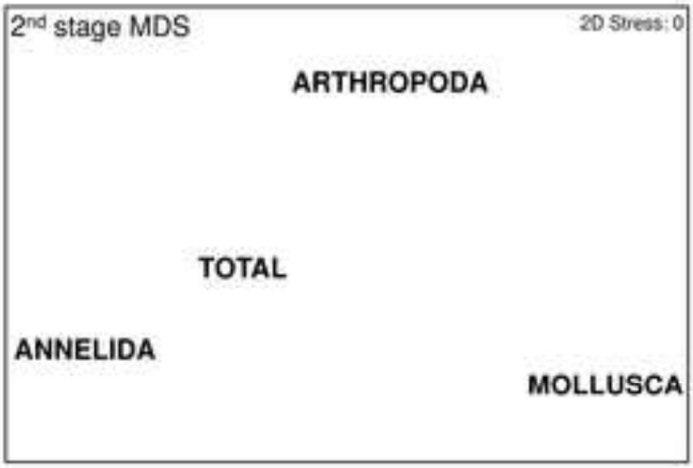
RINAS

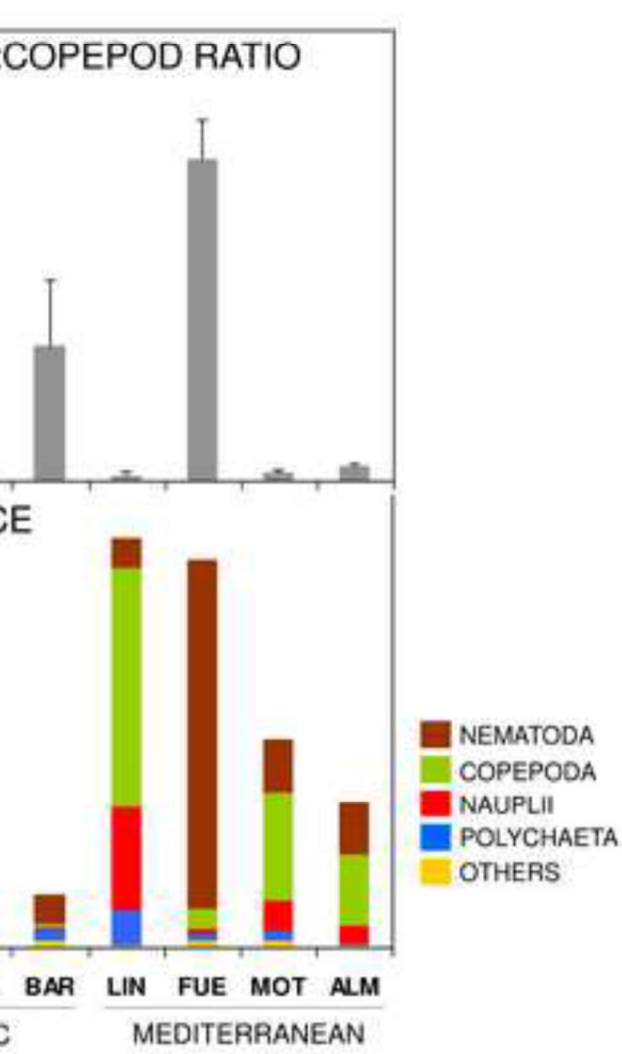
ÉRICA

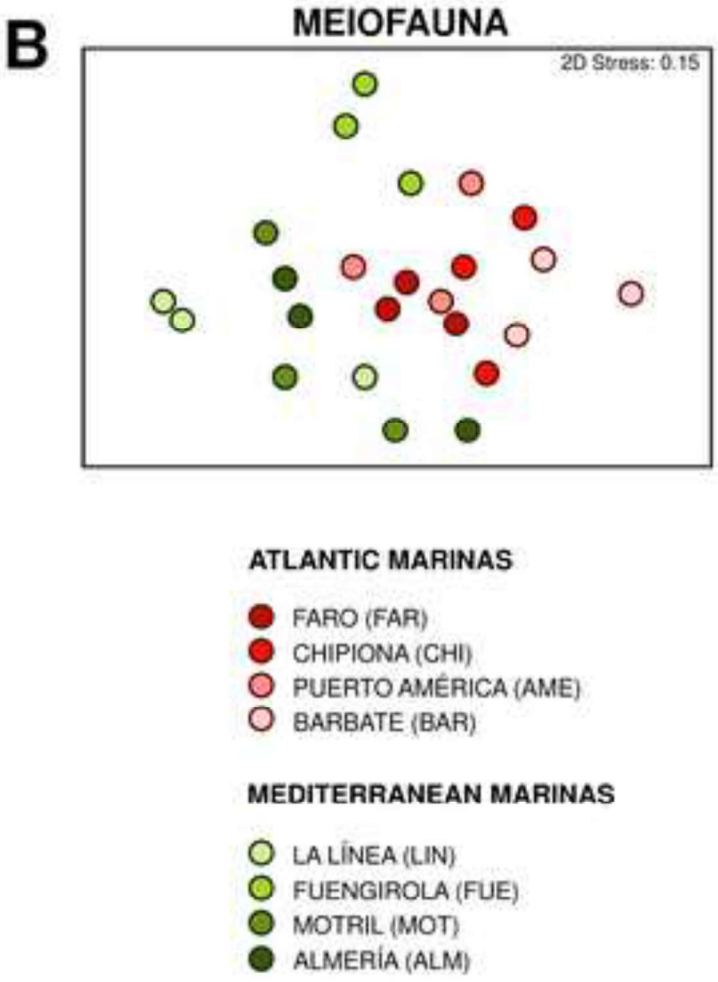
EAN MARINAS

A

B







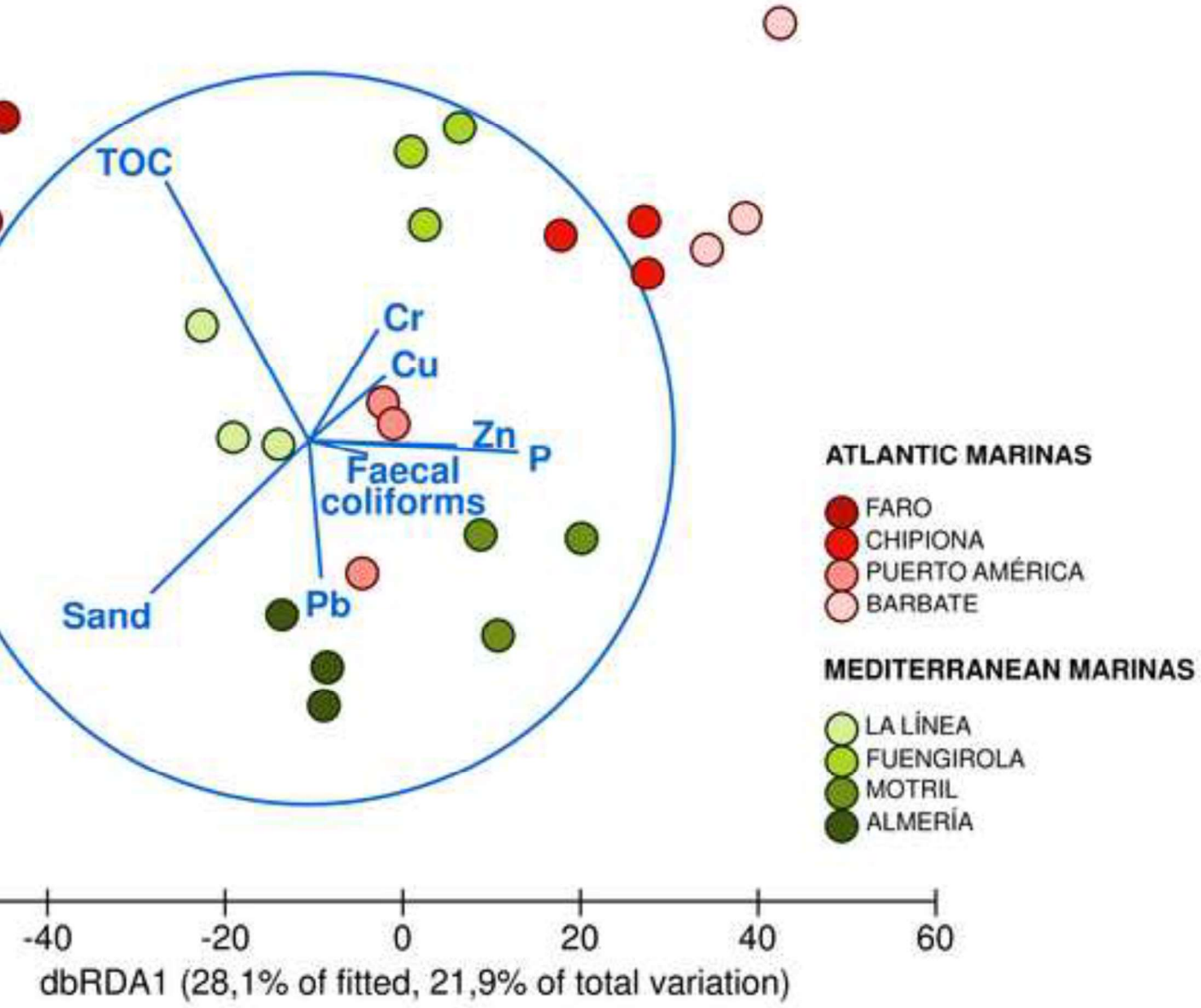


Figure 8

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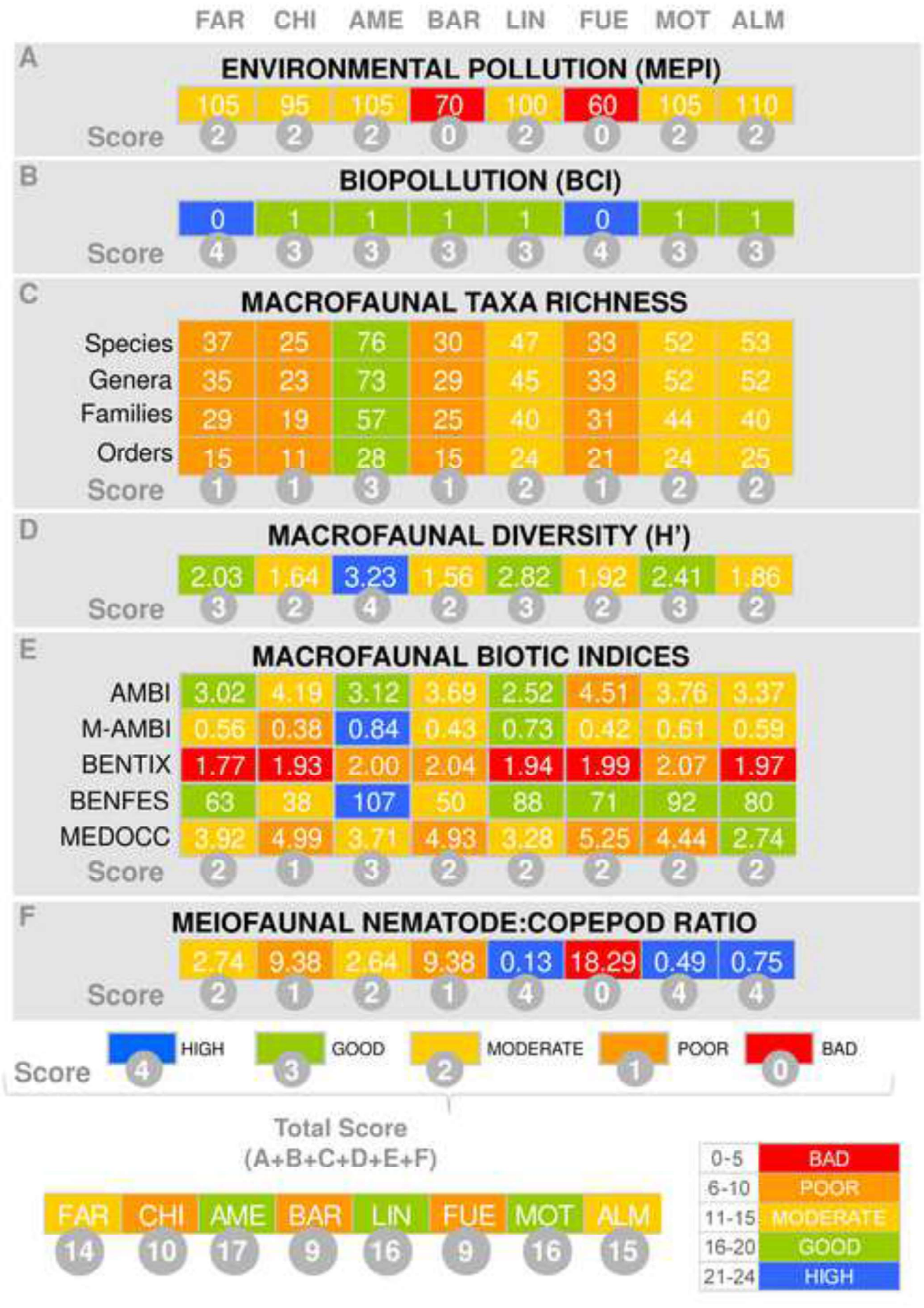

Table 1. List of macrofaunal species with average abundance higher than 1% of the total abundance at each marina. Dark blue: 1-100 ind/m^2; medium blue: 101-1000 ind/m^2; light blue: 1001-10,000 ind/m^2. The whole list of species and abundances per replicate are detailed in Table S1 and S2 (Supplementary material). FAR: Faro, CHI: Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería.

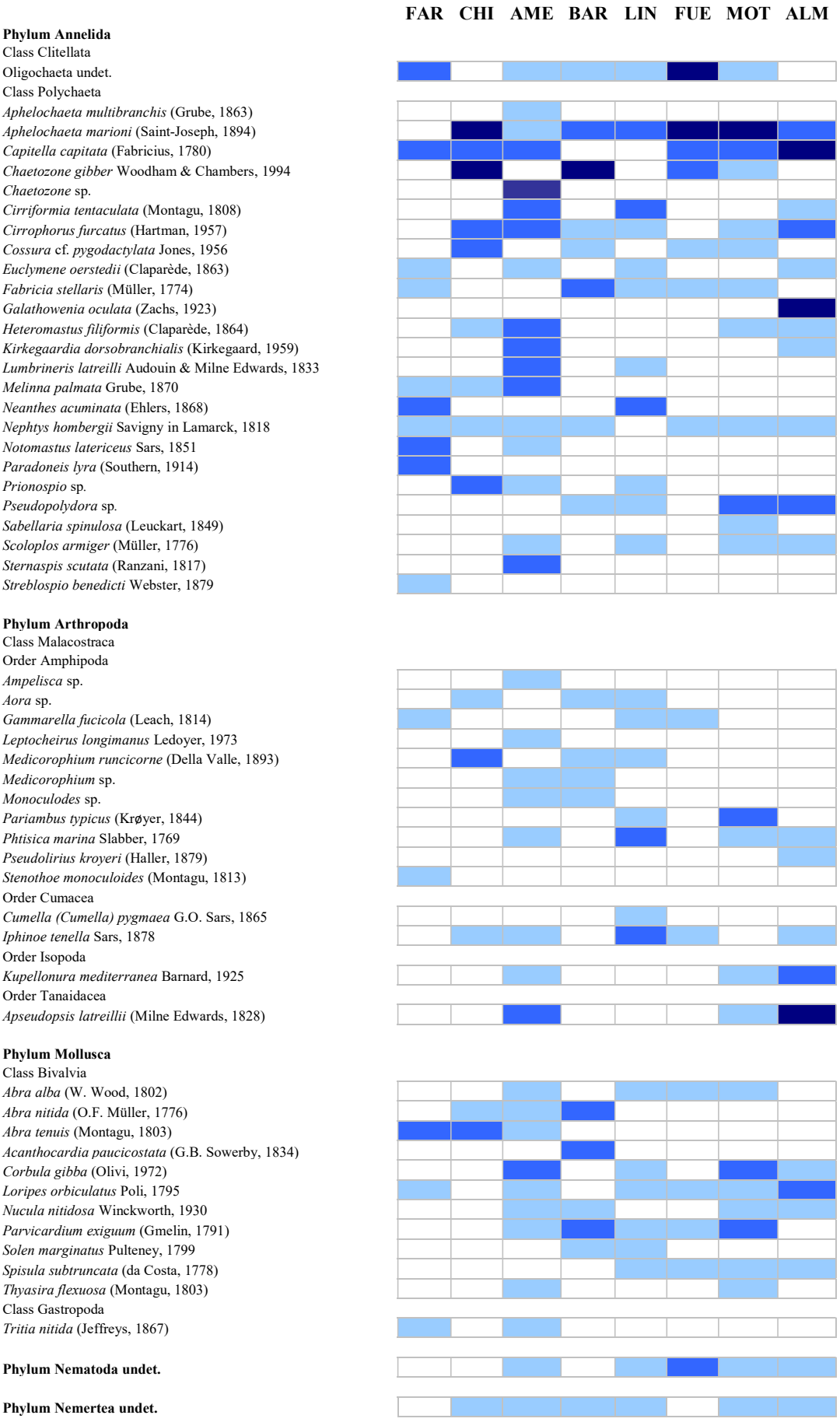

Table 2. Summary of results of the two-way ANOVAs for number of species, total macrofaunal abundance and Shannon-Wiener's diversity, and two-way PERMANOVA for macrofaunal community (species abundances). Lo: Location (Atl: Atlantic, Med: Mediterranean); Ma(Lo): Marina nested within location (FAR: Faro, CHI: Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería). df: degrees of freedom, MS: mean squares, MC: Montecarlo, p: level of significance. *: p<0.05, ***: p <0.001, n.s. not significant. PERMDISP results for the factors Lo and Ma(Lo) are also included.

ANOVAs		**Number of species**			**Total Abundance**			**Shannon-Wiener Diversity**		
Source of variation	**df**	**MS**	**F**	**p**	**MS**	**F**	**p**	**MS**	**F**	**p**
Lo	1	24.0000	0.06	0.8098 n.s.	630.37	0.01	0.9412 n.s.	0.0030	0.04	0.8462 n.s.
Ma(Lo)	6	379.5278	20.29	0.0000***	106706.59	13.64	0.0000***	0.0739	15.34	0.0000***
Residual	16	18.7083			7824.75			0.0048		
Total	23									
Cochran's test		C=0.4031 n.s.			C=0.2631 n.s.			C=0.5662 p<0.05		
Transformation		None			None			Sqrt (x+1)		
SNK tests:										
Lo		Atl=Med			Atl=Med			Atl=Med		
Ma(Lo)		Atl: (FAR=CHI=BAR)<AME Med: LIN=FUE, LIN<MOT, LIN=ALM, FUE<(MOT=ALM)			Atl: FAR=CHI=AME=BAR Med: LIN<FUE, LIN=MOT, LIN<ALM, (FUE=MOT)<ALM			Atl: (FAR=CHI=BAR)<AME Med: LIN>FUE, LIN=MOT, LIN>ALM, FUE<MOT, FUE=ALM, MOT=ALM		

PERMANOVA		**Macrofaunal community**				**PERMDISP**
Source of variation	**df**	**MS**	**Pseudo-F**	**p(MC)**	**Unique permutations**	**Deviations from centroid**
Lo	1	8574.9	1.0052	0.4327 n.s.	35	F=2.4940, p=0.1599 n.s.
Ma(Lo)	6	8531.0	10.894	0.0001***	9876	F=5.0242, p=0.1406 n.s.
Residual	16	783.1				
Total	23					
Pair-wise tests:						
Lo		Atl=Med				
Ma(Lo)		Atl: FAR≠CHI≠AME≠BAR Med: LIN≠FUE≠MOT≠ALM				

Table 3. Average abundance of meiofaunal higher taxa. Dark blue: 1-10 ind/10 cm^2; medium blue: 11-100 ind/10cm^2; light blue: 101-1000 ind/10cm^2. The full list of taxa and abundances are detailed in Table S3 (Supplementary material). FAR: Faro, CHI: Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería.

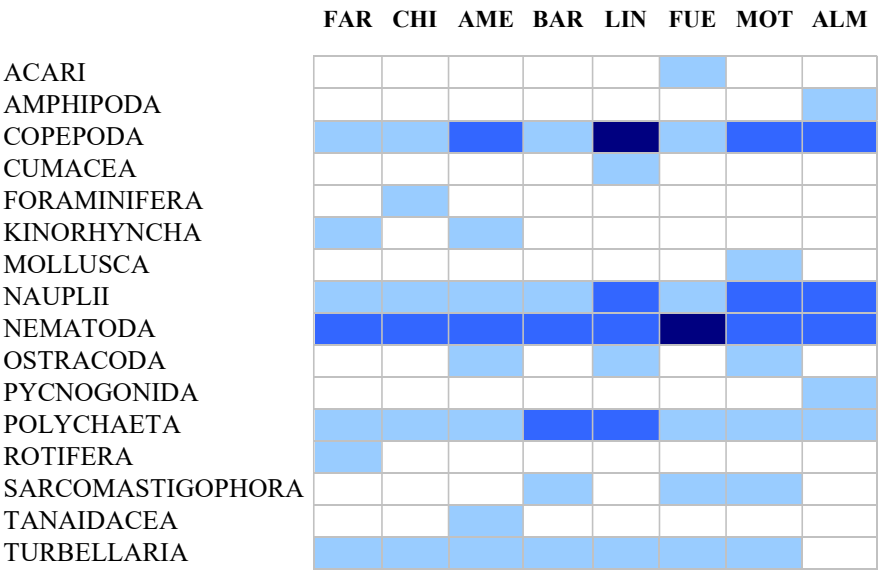

Table 4. Summary results of the two-way ANOVAs for number of meiofaunal taxa, total meiofaunal abundance and nematode:copepod ratio, and two-way PERMANOVA for meiofaunal community (based on higher taxa abundances). Lo: Location (Atl: Atlantic, Med: Mediterranean); Ma(Lo): Marina nested within location (FAR: Faro, CHI: Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería). df: degrees of freedom, MS: mean squares, MC: Montecarlo, p: level of significance. *: p<0.05, ***: p <0.001, n.s. not significant. PERMDISP results for the factors Lo and Ma(Lo) are also included.

ANOVAs		**Number of taxa**			**Total Abundance**			**Nematode:copepod ratio**		
Source of variation	**df**	**MS**	**F**	**p**	**MS**	**F**	**p**	**MS**	**F**	**p**
Lo	1	0.6667	0.67	0.4454 n.s.	279.1699	13.27	0.0108*	13.1092	0.10	0.7594 n.s.
Ma(Lo)	6	1.0000	1.50	0.2405 n.s.	21.0432	1.23	0.2405 n.s.	127.6104	9.36	0.0002***
Residual	16	0.6667			17.0490			13.6349		
Total	23									
Cochran's test		C=0.2500 n.s.			C=0.5966 p<0.05			C=0.5053 n.s.		
Transformation		None			Sqrt (x+1)			None		
SNK tests:										
Lo		Atl=Med			Atl<Med			Atl=Med		
Ma(Lo)		Atl: FAR=CHI=AME=BAR			Atl: FAR=CHI=AME=BAR			Atl: FAR=CHI=AME=BAR		
		Med: LIN=FUE=MOT=ALM			Med: LIN=FUE=MOT=ALM			Med: FUE>(LIN=MOT=ALM)		

PERMANOVA		**Meiofaunal community**				**PERMDISP**
Source of variation	**df**	**MS**	**Pseudo-F**	**p (MC)**	**Unique permutations**	**Deviations from centroid**
Lo	1	4776.6	3.3032	0.0246*	35	F=4.7188, p=0.0541 n.s.
Ma(Lo)	6	1446.1	2.9222	0.0003***	9903	F=1.3130, p=0.7926 n.s.
Residual	16	494.8				
Total	23					
Pair-wise tests:						
Lo		Atl≠Med				
Ma(Lo)		Atl: FAR≠CHI≠BAR, FAR=AME, CHI=AME, AME=BAR				
		Med: FUE≠(LIN=MOT=ALM)				

Table 5. Results of DistLM (distance-based linear modelling) analysis. The variables explaining macrofaunal community (species abundances) are included. Table shows significance levels for each predictor variable and the proportion of variation explained. Only variables with significant results ($p<0.05$) in marginal tests are shown. Overall best models are also included. AIC: Akaike information criterion; SS (trace): sum of squares of sequential test, Prop.: proportion of variability explained by each factor (in the marginal tests without coaction of factors), TOC: Total Organic Carbon, F. colif.: faecal coliforms, *: $p<0.05$, ***: $p<0.001$.

Variables	SS (trace)	Pseudo-F	p	Prop. (%)
P	13181	4.91	0.0001***	18.2
Sand	12057	4.40	0.0001***	16.7
TOC	11571	4.19	0.0001***	16.0
Zn	11121	3.99	0.0002***	15.3
Cr	10068	3.56	0.0004***	13.9
Cu	9833	3.46	0.0001***	13.6
F. colif.	6916	2.33	0.0156*	9.5
Pb	6880	2.31	0.0122*	9.5

AIC	R^2	Variables
180.46	0.73	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Cu, Pb
180.60	0.75	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Cu, Pb, Zn
180.73	0.73	Sand, Silt, TOC, P, F. colif., Cr, Cu, Pb, Zn

Table 6

Table 6. Summary results of BIO-ENV and DistLM analysis for macrofauna (separately for each of six considered meiofauna (higher taxa). The variables included in the best BIO-ENV model are shaded. Significance levels for eac Only variables with significant results ($p<0.05$) in marginal tests are shown. TOC: Total Organic Carbon, Hydr.: p<0.05, **: p<0.01, ***: p <0.001.

			BIO-ENV														
Macrofauna:	Rho	p	Sand	Silt	TOC	P	Hydr.	F.colif.	Cd	Cr	Cu	Pb	Zn	Sand	Silt	TOC	P
Species	0.820	0.002**	■		■	■		■			■	■	■	***		***	***
Genus	0.802	0.006**				■			■		■	■	■	***		***	***
Family	0.777	0.006**	■	■	■	■					■	■	■	***		**	***
Order	0.742	0.007**		■	■	■			■	■	■	■	■	***		***	***
Class	0.411	0.710 n.s.			■				■						*	**	
Phylum	0.385	0.870 n.s.			■		■			■						***	
Annelida	0.797	0.010**			■	■		■			■	■		***		***	***
Arthropoda	0.594	0.090 n.s.	■	■	■	■							■	***		***	**
Mollusca	0.591	0.220 n.s.	■						■			■		**		*	**
Meiofauna	0.630	0.130 n.s.					■		■		■			**			

SUPPLEMENTARY MATERIAL

ECOLOGICAL QUALITY ASSESSMENT OF MARINAS: AN INTEGRATIVE APPROACH COMBINING BIOLOGICAL AND ENVIRONMENTAL DATA

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Table S1. Previous studies addressing sediments (biotic and abiotic data) from worldwide marinas.

References	Topics addressed
Albanis et al., 2002	Antifouling biocides in Greek marinas
Batista-Andrade et al., 2018	Antifouling biocides in marinas from Panama Canal
Biselli et al., 2020	Antifouling biocides in marinas from North and Baltic Sea, Germany
Bowman et al., 2003	Antifouling biocides in Brighton Marina, UK
Boxall et al., 2000	Antifouling biocides in Orwell and Hamble marinas, UK
Briant et al., 2013	Trace elements and butyltin concentrations in Port Camargue marina, France
Cassi et al., 2008	Antifouling biocides in French marinas
Chatzinikolaou et al., 2018 (sta. C1, E1-E3, H1)	Sediment pollutants and macrobenthic biodiversity in touristic harbours of Italy, Greece and Tunisia
Covazzi Harrriague et al., 2012	Macro and meiofaunal communities, and enviromental data of the touristic harbour of Rapallo, Italy
Dimitriou et al., 2020	Benthic indices and ecological assessment in touristic harbours of Italy, Greece and Tunisia
Egardt et al., 2017	Biocides and trace metals in Swedish marinas
Estacio et al., 1997 (stations 1-7)	Macrobenthic communities and environmental data of Saladillo harbour, Algeciras, Southern Spain
García et al., 2020	Antifouling biocides in marinas of SW Spain
Gatidou et al., 2007	Antifouling biocides in Shoreham Harbour and Brighton Marina, UK
Gómez et al., 2017	Atlas of susceptibility to pollution of 320 Spanish marinas
Gómez et al., 2019	Environmental risks of 320 Spanish marinas
Guerra-García et al., 2004 a,b,c (sta 1 and 2)	Polychaetes, Crustaceans and Molluscs of marina of Ceuta, northern Africa
Guerra-García and García-Gómez, 2005 a,b (sta 1 and 2)	Macrobenthic communities and environmental data of marina of Ceuta, northern Africa
Guerra-García et al., in press	Development of MEPI (Marinas Environmental Pollution Index) based on environmental data of marinas from Southern Spain
Hinkey and Zaidi, 2007	Trace metals in marinas from Virgin Islands, USA
Jupp et al., 2017	Heavy metals and hydrocarbon pollution in Oman marinas
Kenworthy et al., 2018	Pollutants in Brest marinas, France
Mali et al., 2017 (suppl. material)	Heavy metals and PHAs in marinas of the Apulia region, Italy
Martínez and Barceló, 2001	Antifouling biocides in marinas from Catalonia, NE Spain
McGee et al., 1995 (sta. BR1-BR4)	Sediment contamination and biological effects in a Chesapeake Bay marina
Moreira et al., 2005 (sta. 19, 20)	Mollusc assemblages and sediment characteristics of Baiona marina, NW Spain
Moreira et al., 2010	Temporal dynamics (one year) of the benthic assemblage of Baiona marina, NW Spain
Moreno et al., 2009	Nematode response to metal and organic enrichment, including PHAs in touristic marinas of Ligurian Sea, Italy
Neira et al., 2017	PHAs in San Diego Bay marinas, USA
Neira et al., 2018	PCBs in recreational marina of Southern California, USA
Norén et al., 2020	Integrated assessment of management strategies for metal-contaminated dredged sediments
Sapozhnikova et al., 2013	Antifouling biocides in California marinas, USA
Sedano et al., 2014 a,b	Meiofaunal communities from Marina del Este, Southeastern Spain
Shakkas et al. 2002	Antifouling biocides in Greek marinas
Sim et al., 2015	Sediment contaminats and infauna in marinas from Clyde Estuary, Australia
Tamburini et al., 2020	Sediment pollutants and prokaryotic biodiversity in touristic harbours of Italy, Greece and Tunisia
Thomas et al., 2000, 2001, 2002	Antifouling biocides in UK marinas
Viana et al., 2009	Antifouling biocides in marinas from São Luís Island, Brazil
Voudrias and Smith, 1986	Hydrocarbon pollution in marinas from USA
Zhang et al., 2019	Spatiotemporal characterization of metals in harbours, including marinas from Nova Scotia, Canada
Zhou, 2008	Antifouling biocides in marinas of Southern UK

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Table S2. Average abundance of the macrofaunal species found during the present study. Dark blue: 1-100 ind/m^2; medium blue: 101-1000 ind/m^2; light blue: 1001-10,000 ind/m^2. Status of each species is indicated (N: Native, I: Introduced, C: Cryptogenic, U: Undetermined). Information of the status taken from Gofas and Zenetos, 2003; Çinar, 2013; López and Richter, 2017; Marchini and Cardeccia, 2017; Bonifazi et al., 2018; Martínez-Laiz et al., 2018; WORMS (http://www.marinespecies.org/). FAR: Faro, CHI: Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería.

	STATUS	FAR	CHI	AME	BAR	LIN	FUE	MOT	ALM
Phylum Annelida									
Class Clitellata									
Oligochaeta undet.	U								
Class Polychaeta									
Ampharete santillani Parapar et al., 2017	N								
Amphitrite sp.	U								
Aonides oxycephala (Sars, 1862)	N								
Aphelochaeta marioni (Saint-Joseph, 1894)	C								
Aphelochaeta multibranchis (Grube, 1863)	N								
Aponuphis bilineata (Baird, 1870)	N								
Aricidea (Acmira) catherinae (Laubier, 1967)	N								
Branchiomma sp.	U								
Capitella capitata (Fabricius, 1780)	C								
Chaetozone gibber Woodham & Chambers, 1994	N								
Chaetozone sp.	U								
Cirriformia tentaculata (Montagu, 1808)	N								
Cirrophorus furcatus (Hartman, 1957)	N								
Cossura cf. *pygodactylata* Jones, 1956	U								
Diopatra sp.	N								
Drilonereis filum (Claparède, 1868)	N								
Euclymene oerstedii (Claparède, 1863)	C								
Eumida sanguinea (Örsted, 1843)	C								
Eunice sp.	U								
Fabricia stellaris (Müller, 1774)	N								
Galathowenia oculata (Zachs, 1923)	N								
Glycera tridactyla Schmarda, 1861	N								
Harmothoe sp.	U								
Heteromastus filiformis (Claparède, 1864)	C								
Kirkegaardia dorsobranchialis (Kirkegaard, 1959)	C								
Lagis koreni Malmgren, 1866	N								
Leiochone leiopygos (Grube, 1860)	N								
Lumbrineris latreilli Audouin & Milne Edwards, 1833	N								
Magelona alleni Wilson, 1958	N								
Magelona minuta Eliason, 1962	N								
Melinna palmata Grube, 1870	N								
Naineris laevigata (Grube, 1855)	N								
Neanthes acuminata (Ehlers, 1868)	N								
Nephtys hombergii Savigny in Lamarck, 1818	N								
Nereididae undet.	U								
Notomastus latericeus Sars, 1851	N								
Paradoneis armata Glémarec, 1966	N								
Paradoneis lyra (Southern, 1914)	N								
Parexogone hebes (Webster & Benedict, 1884)	N								
Perkinsyllis anophthalma (Capaccioni & San Martín, 1990)	N								
Pholoe inornata Johnston, 1839	N								
Pista cristata (Müller, 1776)	N								
Podarkeopsis capensis (Day, 1963)	C								
Polycirrus sp.	U								
Polydora sp.	U								
Prionospio sp.	U								
Pseudopolydora sp.	U								
Sabellaria spinulosa (Leuckart, 1849)	N								
Sabellidae undet.	U								
Schistomeringos rudolphi (Delle Chiaje, 1828)	C								
Scoloplos armiger (Müller, 1776)	N								
Serpulidae undet.	U								
Sigambra parva (Day, 1963)	C								
Spionidae sp. 1	U								
Spionidae sp. 2	U								
Sternaspis scutata (Ranzani, 1817)	C								
Streblospio benedicti Webster, 1879	N								
Syllidia armata Quatrefages, 1866	N								
Syllis gracilis Grube, 1840	C								
Terebellides stroemii Sars, 1835	C								

Table S2. (Cont.)

	STATUS	FAR	CHI	AME	BAR	LIN	FUE	MOT	ALM
Phyllum Arthropoda									
Class Hexanauplia, Subclass Copepoda									
Order Harpacticoida undet.	U								
Order Cyclopoida undet.	U								
Class Malacostraca									
Order Amphipoda									
Ampelisca sp.	U								
Amphilochus neapolitanus Della Valle, 1893	N								
Aora sp.	U								
Apocorophium acutum (Chevreux, 1908)	C								
Caprella acanthifera Leach, 1814	N								
Caprella scaura Templeton, 1836	I								
Dexamine spinosa (Montagu, 1813)	N								
Elasmopus sp.	U								
Ericthonius sp.	U								
Gammarella fucicola (Leach, 1814)	N								
Harpinia pectinata Sars, 1891	N								
Iphimedia sp.	U								
Jassa slatteryi Conlan, 1990	I								
Leptocheirus longimanus Ledoyer, 1973	N								
Leucothoe oboa Karaman, 1971	N								
Liljeborgia dellavallei Stebbing, 1906	N								
Medicorophium runcicorne (Della Valle, 1893)	N								
Medicorophium sp.	U								
Megaluropus sp.	U								
Microdeutopus sp.	U								
Monoculodes sp.	U								
Pariambus typicus (Krøyer, 1844)	N								
Perioculodes longimanus (Bate & Westwood, 1868)	N								
Phtisica marina Slabber, 1769	N								
Pontocrates arenarius (Spence Bate, 1858)	N								
Pseudolirius kroyeri (Haller, 1879)	N								
Stenothoe monoculoides (Montagu, 1813)	N								
Order Cumacea									
Cumella (Cumella) pygmaea G.O.Sars, 1865	N								
Eocuma sp.	U								
Iphinoe tenella Sars, 1878	N								
Pseudocuma sp.	U								
Order Decapoda									
Alpheus sp.	I								
Athanas nitescens (Leach, 1814)	N								
Brachynotus sp.	U								
Carcinus maenas (Linnaeus, 1758)	N								
Paguroidea sp.	U								
Philocheras bispinosus (Hailstone, 1835)	N								
Sirpus zariquieyi Gordon, 1953	N								
Upogebia pusilla (Petagna, 1972)	N								
Upogebia sp.	U								
Oder Isopoda									
Cyathura carinata (Krøyer, 1847)	N								
Dynamene edwardsi (Lucas, 1849)	N								
Dynamene magnitorata Holdich, 1968	N								
Eurydice pulchra Leach, 1815	N								
Gnathia cf. *maxillaris* (Montagu, 1804)	U								
Kupellonura mediterranea Barnard, 1925	N								
Neohyssura sp.	U								
Paranthura japonica Richardson, 1909	I								
Order Leptostraca									
Nebalia strausi Risso, 1826	N								
Order Tanaidacea									
Apseudopsis latreillii (Milne Edwards, 1828)	N								
Chondrochelia dubia (Krøyer, 1842) *sensu lato*	C								
Zeuxo sp.	U								
Class Insecta									
Order Diptera undet.	U								
Class Ostracoda									
Ostracoda sp. 1	U								
Ostracoda sp. 2	U								
Class Pycnogonida									
Anoplodactylus angulatus (Dohrn, 1881)	N								

Table S2. (Cont.)

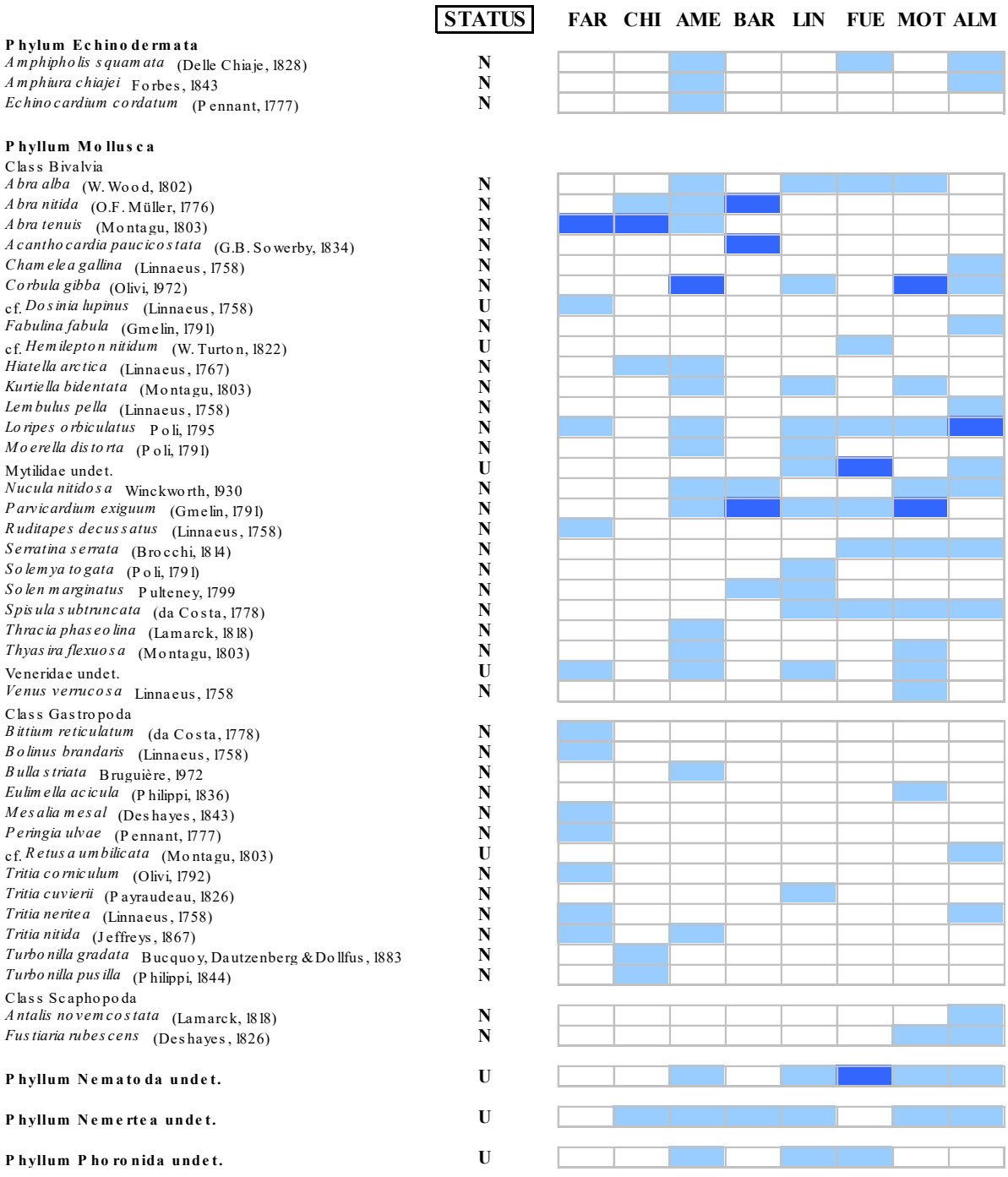

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Table S3. Abundance (individuals/225cm^2) of the 72 samples (9 for each marina) collected during the present study. Each replicate (1.1., 1.2 and 1.3) taken from the same pontoon (see Material and Methods section). Detailed information about the taxonomical cat Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería.

Atlantic marinas

PHYL.	CLASS	ORDER	FAMILY	SPECIES	FAR 1			FAR 2			FAR 3			CHI 1			CHI 2			CHI 3			AME	
					1.1	1.2	1.3	2.1	2.2	2.3	3.1	3.2	3.3	1.1	1.2	1.3	2.1	2.2	2.3	3.1	3.2	3.3	1.1	1.2
ANN	Clitellata			Oligochaeta undet.	0	11	15	2	4	7	1	2	4	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Ampharetidae	*Ampharete santillani*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
ANN	Polychaeta	Terebellida	Terebellidae	*Amphitrite* sp.	0	0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Spionida	Spionidae	*Aonides oxycephala*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Cirratulidae	*Aphelochaeta multibranchis*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Eunicida	Onuphidae	*Aponuphis bilineata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Cirratulidae	*Aphelochaeta marioni*	0	0	0	0	0	0	0	0	0	108	25	35	3	35	21	57	69	64	0	0
ANN	Polychaeta	Scolecida	Capitellidae	*Capitella capitata*	0	2	2	0	0	0	0	1	1	1	0	1	0	0	2	0	0	0	0	0
ANN	Polychaeta	Terebellida	Cirratulidae	*Chaetozone gibber*	0	0	2	0	0	0	0	1	0	29	24	27	64	45	26	32	56	31	0	0
ANN	Polychaeta	Terebellida	Cirratulidae	*Chaetozone* sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5
ANN	Polychaeta	Terebellida	Cirratulidae	*Cirriformia tentaculata*	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	26	3
ANN	Polychaeta	Scolecida	Paraonidae	*Cirrophorus furcatus*	0	0	0	0	0	0	0	0	0	1	7	0	1	2	3	0	20	7	18	19
ANN	Polychaeta	Scolecida	Cossuridae	*Cossura* cf *pygodactylata*	0	0	0	0	0	0	0	0	0	8	4	4	15	1	0	0	1	1	0	0
ANN	Polychaeta	Eunicida	Onuphidae	*Diopatra* sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Maldanidae	*Euclymene oerstedi*	2	0	0	1	1	3	0	1	1	0	0	0	0	0	0	0	0	0	8	1
ANN	Polychaeta	Sabellida	Fabriciidae	*Fabricia stellaris*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Glyceridae	*Glycera tridactyla*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	1	2
ANN	Polychaeta	Phyllodocida	Polynoidae	*Harmothoe* sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
ANN	Polychaeta	Scolecida	Capitellidae	*Heteromastus filiformis*	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	6	9
ANN	Polychaeta	Terebellida	Cirratulidae	*Kirkegaardia dorsobranchialis*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	3
ANN	Polychaeta	Terebellida	Pectinariidae	*Lagis koreni*	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Maldanidae	*Leiopygos clypeatus*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	3
ANN	Polychaeta	Eunicida	Lumbrineridae	*Lumbrineris latreilli*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	3
ANN	Polychaeta		Magelonidae	*Magelona alleni*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta		Magelonidae	*Magelona minuta*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Ampharetidae	*Melinna palmata*	0	1	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1
ANN	Polychaeta	Phyllodocida	Nereididae	*Neanthes acuminata*	61	18	28	19	31	54	49	25	13	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Nephtyidae	*Nephtys hombergii*	0	2	0	0	0	0	0	1	0	0	1	1	1	0	1	0	0	0	0	0
ANN	Polychaeta	Scolecida	Capitellidae	*Notomastus latericeus*	7	0	32	46	0	0	0	68	20	0	0	0	0	0	0	0	0	0	1	0
ANN	Polychaeta	Scolecida	Paraonidae	*Paradoneis lyra*	3	6	10	0	4	2	0	1	33	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Syllidae	*Perkinsyllis anophthalma*	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Terebellidae	*Pista cristata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Hesionidae	*Podarkeopsis capensis*	0	0	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Terebellidae	*Polycirrus* sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Spionida	Spionidae	*Prionospio* sp.	0	0	0	0	0	0	0	0	0	5	3	6	2	3	5	28	15	23	0	0
ANN	Polychaeta	Spionida	Spionidae	*Pseudopolydora* sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Eunicida	Dorvilleidae	*Schistomeringos rudolphi*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Orbiniidae	*Scoloplos armiger*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S3 (Cont.)

Atlantic marinas (cont.)

PHYIL.	CLASS	ORDER	FAMILY	SPECIES	FAR 1			FAR 2			FAR 3			CHI 1			CHI 2			CHI 3			AME
ANN	Polychaeta	Sabellida	Serpulidae	Serpulidae undet.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Pilargidae	*Sigambra parva*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
ANN	Polychaeta	Spionida	Spionidae	Spionidae sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	1
ANN	Polychaeta	Spionida	Spionidae	Spionidae sp. 2	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Sternaspidae	*Sternaspis scutata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Spionida	Spionidae	*Streblospio benedicti*	0	0	0	0	0	3	0	0	9	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Hesionidae	*Syllidia armata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
ANN	Polychaeta	Phyllodocida	Syllidae	*Syllis gracilis*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Hexanauplia	Harpacticoida		Order Harpacticoida undet.	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Hexanauplia	Cyclopoida		Order Cyclopoida undet.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Malacostraca	Amphipoda	Ampeliscidae	*Ampelisca sp.*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Amphilochidae	*Amphilochus neapolitanus*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Aoridae	*Aora sp.*	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Corophiidae	*Apocorophium acutum*	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Caprellidae	*Caprella scaura*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Dexaminidae	*Dexamine spinosa*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3
ART	Malacostraca	Amphipoda	Maeridae	*Elasmopus sp.*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Ischyroceridae	*Ericthonius sp.*	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Nuuanuidae	*Gammarella fucicola*	0	0	1	1	7	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Iphimediidae	*Iphimedia sp.*	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Ischyroceridae	*Jassa slatteryi*	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Corophiidea	*Leptocheirus longimanus*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
ART	Malacostraca	Amphipoda	Leucothoidae	*Leucothoe oboa*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Corophiidae	*Medicorophium runcicorne*	0	0	0	0	0	0	0	0	0	3	0	0	6	11	1	6	2	1	0	0
ART	Malacostraca	Amphipoda	Corophiidae	*Medicorophium sp.*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Aoridae	*Microdeutopus sp.*	2	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Oedicerotidae	*Monoculodes sp.*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0
ART	Malacostraca	Amphipoda	Caprellidae	*Phtisica marina*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2
ART	Malacostraca	Amphipoda	Oedicerotidae	*Pontocrates arenarius*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
ART	Malacostraca	Amphipoda	Stenothoidae	*Stenothoe monoculoides*	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Cumacea	Bodotriidae	Eocuma sp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
ART	Malacostraca	Cumacea	Bodotriidae	*Iphinoe tenella*	0	0	0	0	0	0	0	0	0	1	0	0	3	0	2	1	0	0	1	0
ART	Malacostraca	Decapoda	Alpheidae	*Alpheus pontederiae*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0
ART	Malacostraca	Decapoda	Alpheidae	*Athanas nitescens*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Decapoda	Varunidae	*Brachynothus* sp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
ART	Malacostraca	Decapoda	Carcinidae	*Carcinus maenas*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3
ART	Malacostraca	Decapoda	Crangonidae	*Philocheras bispinosus*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Isopoda	Anthuridae	*Cyathura carinata*	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
ART	Malacostraca	Isopoda	Sphaeromatidae	*Dynamene edwardsi*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S3 (Cont.)

Atlantic marinas (cont.)

PHYIL.	CLASS	ORDER	FAMILY	SPECIES	FAR 1			FAR 2			FAR 3			CHI 1			CHI 2			CHI 3			AME	
ART	Malacostraca	Isopoda	Sphaeromatidae	*Dynamene magnitorata*	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Isopoda	Cirolanidae	*Eurydice pulchra*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Isopoda	Gnathiidae	*Gnathia cf. maxillaris*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Isopoda	Hyssuridae	*Kupellonura mediterranea*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
ART	Malacostraca	Isopoda	Hyssuridae	*Neohyssura sp*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Isopoda	Paranthuridae	*Paranthura japonica*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Tanaidacea	Apseudidae	*Apseudopsis latreillii*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Tanaidacea	Tanaididae	*Zeuxo sp*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Insecta	Diptera		Order Diptera undet.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ECH	Ophiuroidea	Amphilepidida	Amphiuridae	*Amphiura chiajei*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
ECH	Echinoidea	Spatangoida	Loveniidae	*Echinocardium cordatum*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Cardiida	Semelidae	*Abra alba*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0
MOL	Bivalvia	Cardiida	Semelidae	*Abra nitida*	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	1	0	3	2
MOL	Bivalvia	Cardiida	Semelidae	*Abra tenuis*	20	27	25	11	3	2	1	6	13	8	2	2	2	1	4	15	0	7	0	1
MOL	Bivalvia	Cardiida	Cardiidae	*Acanthocardia paucicostata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Myida	Corbulidae	*Corbula gibba*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	14	8	0
MOL	Bivalvia	Venerida	Veneridae	cf. *Dosinia lupinus*	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Galeommatida	Lasaeidae	*cf. Hemilepton nitidum*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Adapedonta	Hiatellidae	*Hiatella arctica*	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Galeommatida	Lasaeidae	*Kurtiella bidentata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0	0
MOL	Bivalvia	Lucinida	Lucinidae	*Loripes orbiculatus*	1	1	1	2	0	0	0	4	2	0	0	0	0	0	0	0	0	0	2	0
MOL	Bivalvia	Cardiida	Tellinidae	*Moerella distorta*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
MOL	Bivalvia	Nuculida	Nuculidae	*Nucula nitidosa*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Cardiida	Cardiidae	*Parvicardium exiguum*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	3	0
MOL	Bivalvia	Venerida	Veneridae	*Ruditapes decussatus*	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Adapedonta	Solenidae	Solen marginatus	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Anomalodesmata	Thraciidae	*Thracia phaseolina*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0
MOL	Bivalvia	Lucinida	Thyasiridae	Thyasira flexuosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	1	0
MOL	Bivalvia	Venerida	Veneridaa	Veneridae undet.	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0
MOL	Gastropoda	Caenogastropoda	Cerithiidae	*Bittium reticulatum*	0	0	0	0	1	1	0	1	1	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Neogastropoda	Muricidae	*Bolinus brandaris*	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Cephalaspidea	Bullidae	*Bulla striata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0
MOL	Gastropoda	Caenogastropoda	Turritellidae	*Mesalia mesal*	0	0	0	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Littorinimorpha	Hydrobiidae	*Peringia ulvae*	0	0	0	0	1	0	1	3	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Neogastropoda	Nassariidae	*Tritia corniculum*	0	0	3	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Neogastropoda	Nassariidae	*Tritia neritea*	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Neogastropoda	Nassariidae	*Tritia nitida*	0	0	0	1	0	2	0	0	0	0	0	0	0	0	0	0	0	1	0	0
MOL	Gastropoda	Pylopulmonata	Pyramidellidae	*Turbonilla gradata*	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Pylopulmonata	Pyramidellidae	*Turbonilla pusilla*	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
NEM				Phyllum Nematoda undet.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	2	0
NET				Phyllum Nemertea undet.	0	0	0	0	0	0	0	0	0	2	0	0	0	2	1	1	0	2	3	4
PHO				Phyllum Phoronida undet.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S3 (Cont.)

Mediterranean marinas

PHYL.	CLASS	ORDER	FAMILY	SPECIES	LIN 1			LIN 2			LIN 3			FUE 1			FUE 2			FUE 3			MOT	
					1.1	1.2	1.3	2.1	2.2	2.3	3.1	3.2	3.3	1.1	1.2	1.3	2.1	2.2	2.3	3.1	3.2	3.3	1.1	1.2
ANN	Clitellata			Oligochaeta undet.	0	0	0	0	0	0	0	3	0	11	7	13	35	91	0	40	10	11	0	0
ANN	Polychaeta	Spionida	Spionidae	*Aonides oxycephala*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Paraonidae	*Aricidea (Acmira) catterinae*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Cirratulidae	*Aphelochaeta marioni*	2	5	8	14	4	6	9	5	2	0	0	0	1	1	7	0	140	105	71	42
ANN	Polychaeta	Sabellida	Sabellidae	*Branchiomma* sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Capitellidae	*Capitella capitata*	0	0	0	0	0	0	1	0	0	1	2	1	4	6	0	3	4	5	0	2
ANN	Polychaeta	Terebellida	Cirratulidae	*Chaetozone gibber*	0	0	0	0	0	0	0	0	0	8	7	1	12	16	20	1	36	20	1	2
ANN	Polychaeta	Terebellida	Cirratulidae	*Chaetozone* sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Cirratulidae	*Cirriformia tentaculata*	0	1	1	4	9	2	4	6	6	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Paraonidae	*Cirrophorus furcatus*	0	3	6	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	1
ANN	Polychaeta	Scolecida	Cossuridae	*Cossura* cf *pygodactylata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	2	0	4
ANN	Polychaeta	Eunicida	Oenonidae	*Drilonereis filum*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Maldanidae	*Euclymene oerstedi*	0	1	2	0	1	1	0	2	1	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Phyllodocidae	*Eumida sanguinea*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Eunicida	Eunicidae	*Eunice* sp.	0	1	0	0	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0
ANN	Polychaeta	Sabellida	Fabriciidae	*Fabricia stellaris*	0	0	0	0	0	0	1	1	0	0	0	0	1	3	0	0	0	0	1	0
ANN	Polychaeta		Oweniidae	*Galathowenia oculata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Capitellidae	*Heteromastus filiformis*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
ANN	Polychaeta	Terebellida	Cirratulidae	*Kirkegaardia dorsobranchialis*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Maldanidae	*Leiopygos clypeatus*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Eunicida	Lumbrineridae	*Lumbrineris latreilli*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Orbiniidae	*Naineris laevigata*	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Nereididae	*Neanthes acuminata*	11	20	12	1	4	0	14	5	6	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Nephtyidae	*Nephtys hombergii*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1
ANN	Polychaeta	Phyllodocida	Nereididae	Nereididae undet.	0	0	0	0	0	0	0	0	0	0	0	1	0	2	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Paraonidae	*Paradoneis armata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Syllidae	*Parexogone hebes*	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Phyllodocida	Pholoidae	*Pholoe inornata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Spionida	Spionidae	*Polydora* sp.	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Spionida	Spionidae	*Prionospio* sp.	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
ANN	Polychaeta	Spionida	Spionidae	*Pseudopolydora* sp.	0	0	0	2	0	2	2	2	0	0	0	0	0	0	0	0	0	0	0	7
ANN	Polychaeta	Canalipalpata	Sabellariidae	*Sabellaria spinulosa*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Sabellida	Sabellidae	Sabellidae undet.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Eunicida	Dorvilleidae	*Schistomeringos rudolphi*	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Scolecida	Orbiniidae	*Scoloplos armiger*	1	0	1	2	0	0	2	2	0	0	0	0	0	0	0	0	0	0	0	1
ANN	Polychaeta	Phyllodocida	Pilargidae	*Sigambra parva*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Spionida	Spionidae	Spionidae sp. 1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
ANN	Polychaeta	Terebellida	Trichobranchidae	*Terebelllides stroemii*	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0

Table S3 (Cont.)

Mediterranean marinas (cont.)

PHYL.	CLASS	ORDER	FAMILY	SPECIES	LIN 1			LIN 2			LIN 3			FUE 1			FUE 2			FUE 3			MOT
ART	Hexanauplia	Harpacticoida		Order Harpacticoida undet.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1
ART	Hexanauplia	Cyclopoida		Order Cyclopoida undet.	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Aoridae	*Aora sp.*	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Corophiidae	*Apocorophium acutum*	0	0	0	0	2	0	0	0	0	0	0	1	0	1	0	0	0	1	0	0
ART	Malacostraca	Amphipoda	Caprellidae	*Caprella acanthifera*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Caprellidae	*Caprella scaura*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0
ART	Malacostraca	Amphipoda	Maeridae	*Elasmopus sp.*	0	0	0	0	0	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Ischyroceridae	*Ericthonius sp.*	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Nuuanuidae	*Gammarella fucicola*	0	0	0	0	0	0	0	2	0	0	0	0	1	1	0	0	0	2	0	0
ART	Malacostraca	Amphipoda	Phoxocephalidae	*Harpinia pectinata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
ART	Malacostraca	Amphipoda	Ischyroceridae	*Jassa slatteryi*	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Leucothoidae	*Leucothoe oboa*	0	0	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Liljeborgiidae	*Liljeborgia dellavallei*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Corophiidae	*Medicorophium runcicorne*	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Aoridae	*Microdeutopus sp.*	4	1	1	1	1	2	2	5	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Caprellidae	*Pariambus typicus*	3	3	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	2	1
ART	Malacostraca	Amphipoda	Oedicerotidae	*Perioculodes longimanus*	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Caprellidae	*Phtisica marina*	9	2	1	0	1	2	5	2	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Oedicerotidae	*Pontocrates arenarius*	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Amphipoda	Caprellidae	*Pseudolirius kroyeri*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Cumacea	Nannastacidae	*Cumella pygmaea*	1	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Cumacea	Bodotriidae	*Iphinoe tenella*	1	3	2	2	4	4	3	10	2	1	0	0	0	0	2	0	3	0	0	0
ART	Malacostraca	Cumacea	Pseudocumatidae	*Pseudocuma sp*	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Decapoda		*Paguroidea* sp	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Decapoda	Carcinidae	*Sirpus zariquiey*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Decapoda	Upogebiidae	*Upogebia pusilla*	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0
ART	Malacostraca	Decapoda	Upogebiidae	*Upogebia* sp	0	0	0	0	0	0	0	0	0	0	0	1	1	1	2	2	0	0	0	1
ART	Malacostraca	Isopoda	Gnathiidae	*Gnathia cf. maxillaris*	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0
ART	Malacostraca	Isopoda	Hyssuridae	*Kupellonura mediterranea*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4	4
ART	Malacostraca	Leptostraca	Nebaliidae	*Nebalia strausi* Risso, 1826	0	0	0	0	0	0	0	0	0	0	0	0	0	4	0	0	0	0	0	0
ART	Malacostraca	Tanaidacea	Apseudidae	*Apseudopsis latreillii*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Malacostraca	Tanaidacea	Leptocheliidae	*Chondrochelia dubia sensu lato*	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0
ART	Malacostraca	Tanaidacea	Tanaididae	*Zeuxo sp*	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Ostracoda			Ostracoda sp. 1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Ostracoda			Ostracoda sp. 2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ART	Pycnogonida	Pantopoda	Phoxichilidiidae	*Anoplodactylus angulatus*	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
ECH	Ophiuroidea	Amphilepidida	Amphiuridae	*Amphipholis squamata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0
ECH	Ophiuroidea	Amphilepidida	Amphiuridae	*Amphiura chiajei*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

Table S3 (Cont.)

Mediterranean marinas (cont.)

PHYL.	CLASS	ORDER	FAMILY	SPECIES	LIN 1			LIN 2			LIN 3			FUE 1			FUE 2			FUE 3			MOT
MOL	Bivalvia	Cardiida	Semelidae	*Abra alba*	1	1	0	0	1	0	3	1	0	0	0	1	0	0	0	0	1	0	1	0
MOL	Bivalvia	Venerida	Veneridae	*Chamelea gallina*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Myida	Corbulidae	*Corbula gibba*	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	9	7
MOL	Bivalvia	Cardiida	Tellinidae	*Fabulina fabula*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Galeommatida	Lasaeidae	*cf. Hemilepton nitidum*	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	1	0	0	0
MOL	Bivalvia	Galeommatida	Lasaeidae	*Kurtiella bidentata*	0	0	0	0	1	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Nuculanida	Nuculanidae	*Lembulus pella*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Lucinida	Lucinidae	*Loripes orbiculatus*	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0
MOL	Bivalvia	Cardiida	Tellinidae	*Moerella distorta*	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Mytilida	Mytilidae	Mytilidae undet.	0	0	0	0	0	0	1	0	0	0	0	2	0	2	12	2	0	4	0	0
MOL	Bivalvia	Nuculida	Nuculidae	*Nucula nitidosa*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	4
MOL	Bivalvia	Cardiida	Cardiidae	*Parvicardium exiguum*	0	0	0	0	1	0	1	0	0	0	1	1	1	0	0	0	0	0	5	0
MOL	Bivalvia	Cardiida	Tellinidae	*Serratina serrata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0
MOL	Bivalvia	Solemyida	Solemyidae	Solemya togata	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Adapedonta	Solenidae	Solen marginatus	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Venerida	Mactridae	*Spisula subtruncata*	4	1	0	0	1	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0
MOL	Bivalvia	Lucinida	Thyasiridae	Thyasira flexuosa	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Venerida	Veneridaa	Veneridae undet.	1	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Bivalvia	Venerida	Veneridaa	*Venus verrucosa*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0
MOL	Gastropoda	Pylopulmonata	Pyramidellidae	*Eulimella acicula*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Cephalaspidea	Retusidae	*cf. Retusa umbilicata*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Neogastropoda	Nassariidae	*Tritia cuvierii*	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0
MOL	Gastropoda	Neogastropoda	Nassariidae	*Tritia neritea*	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Scaphopoda	Dentaliida	Dentaliidae	Antalis novemcostata	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
MOL	Scaphopoda	Dentaliida	Fustiariidae	Fustiaria rubescens	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
NEM				Phyllum Nematoda undet.	0	1	0	0	0	0	1	0	0	53	3	48	6	16	0	0	1	4	2	0
NET				Phyllum Nemertea undet.	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	5	0
PHO				Phyllum Phoronida undet.	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0

Table S4. Summary of the two-way ANOVA results for number of species of Annelida, Arthropoda and Mollusca (A), and for global taxa richness for each taxonomical level (species, genera, families, orders, classes and phyla) (B). Lo: Location (Atl: Atlantic, Med: Mediterranean); Ma(Lo): Marina nested with location (FAR: Faro, CHI: Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería). df: degrees of freedom, MS: mean squares, p: level of significance. *: p<0.05, **: p<0.01, ***: p <0.001, n.s. not significant.

A

		Number of annelid species			Number of arthropod species			Number of mollusc species		
Source of variation	**df**	**MS**	**F**	**p**	**MS**	**F**	**p**	**MS**	**F**	**p**
Lo	1	4.17	0.06	0.8113 n.s.	22.04	0.74	0.4225 n.s.	0.67	0.03	0.8727n.s.
Ma(Lo)	6	66.97	17.86	0.0000***	29.76	3.57	0.0194*	23.86	5.97	0.0020**
Residual	16	3.75			8.33			4.00		
Total	23									
Cochran's test		C=0.4000 n.s			C=0.2600 n.s			C=0.2917 n.s.		
Transformation		None			None			None		
SNK tests										
Lo		Atl=Med			Atl=Med			Atl=Med		
Ma(Lo)		Atl: (FAR=CHI=BAR)<AME Med: (MOT=ALM)>LIN>FUE			Atl: (FAR=CHI=BAR)<AME Med: LIN=FUE=MOT=ALM			Atl: (FAR=CHI=BAR)<AME Med: LIN=FUE=ALM, FUE<MOT, LIN=MOT=ALM		

B

		Number of species			Number of genera			Number of families		
Source of variation	**df**	**MS**	**F**	**p**	**MS**	**F**	**p**	**MS**	**F**	**p**
Lo	1	24.00	0.06	0.8098 n.s.	42.67	0.12	0.7453 n.s.	51.04	0.23	0.6492 n.s.
Ma(Lo)	6	379.52	20.29	0.0000***	368.78	21.85	0.0000***	222.88	20.42	0.0000***
Residual	16	18.71			16.87			10.92		
Total	23									
Cochran's test		C=0.4031 n.s			C=0.4321 n.s			C=0.4466 n.s.		
Transformation		None			None			None		
SNK tests										
Lo		Atl=Med			Atl=Med			Atl=Med		
Ma(Lo)		Atl: (FAR=CHI=BAR)<AME Med: LIN=FUE, LIN<MOT LIN=ALM, FUE<(MOT=ALM)			Atl: (FAR=CHI=BAR)<AME Med: (LIN=FUE)<(MOT=ALM)			Atl: (FAR=CHI=BAR)<AME Med: (LIN=FUE)<(MOT=ALM)		
		Number of orders			**Number of classes**			**Number of phyla**		
Source of variation	**df**	**MS**	**F**	**p**	**MS**	**F**	**p**	**MS**	**F**	**p**
Lo	1	66.67	1..31	0.2955 n.s.	9.38	2.57	0.1603 n.s.	2.04	0.90	0.3790 n.s.
Ma(Lo)	6	50.78	11.95	0.0000***	3.65	3.51	0.0208*	2.26	3.88	0.0139*
Residual	16	4.25			1.04			0.58		
Total	23									
Cochran's test		C=0.3039 n.s			C=0.2800 n.s			C=0.5000 n.s.		
Transformation		None			None			None		
SNK tests										
Lo		Atl=Med			Atl=Med			Atl=Med		
Ma(Lo)		Atl: (FAR=CHI=BAR)<AME Med: (LIN=FUE)<(MOT=ALM)			Atl: (FAR=CHI=BAR)<AME Med: LIN=FUE=MOT=ALM			Atl: (FAR=CHI=BAR)<AME Med: LIN=FUE=MOT=ALM		

Table S5. Summary of the two-way PERMANOVA results for Annelida, Arthropoda and Mollusca (at species level) (A) and for total macrofaunal community of each considered taxonomic level (species, genus, family, order, class, phylum) (B). Lo: Location (Atl: Atlantic, Med: Mediterranean); Ma(Lo): Marina nested with location (FAR: Faro, CHI: Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería). df: degrees of freedom, MS: mean squares, MC: Montecarlo, p: level of significance. ***: p <0.001, n.s. not significant.

A

		Annelida			Arthropoda			Mollusca		
Source of variation	**df**	**MS**	**Pseudo-F**	**p (MC)**	**MS**	**Pseudo-F**	**p (MC)**	**MS**	**Pseudo-F**	**p (MC)**
Lo	1	6692.7	0.7945	0.5615 n.s.	8538.4	0.9668	0.4712 n.s.	16313.0	1.9178	0.0961 n.s.
Ma(Lo)	6	8424.0	12.716	0.0001***	8831.7	5.4811	0.0001***	8506.1	9.581	0.0001***
Residual	16	662.4			494.8			887.8		
Total	23				1611.3					
Pair-wise tests										
Lo		Atl=Med			Atl=Med			Atl=Med		
Ma(Lo)		Atl: FAR≠CHI≠AME≠BAR			Atl: FAR≠CHI≠(AME=BAR)			Atl: FAR≠CHI≠AME≠BAR		
		Med: LIN≠FUE≠MOT≠ALM			Med: LIN≠FUE≠MOT≠ALM			Med: (LIN=FUE=MOT)≠ALM		

B

		Species			Genus			Family		
Source of variation	**df**	**MS**	**Pseudo-F**	**p (MC)**	**MS**	**Pseudo-F**	**p (MC)**	**MS**	**Pseudo-F**	**p (MC)**
Lo	1	8574.9	1.0052	0.4327 n.s.	9172.5	1.195	0.3110 n.s.	5552.2	0.8856	0.5197
Ma(Lo)	6	8531	10.894	0.0001***	7675.8	9.996	0.0001***	6269.5	9.3464	0.0001***
Residual	16	783.1			767.9			670.7		
Total	23									
Pair-wise tests										
Lo		Atl=Med			Atl=Med			Atl=Med		
Ma(Lo)		Atl: FAR≠CHI≠AME≠BAR			Atl: FAR≠CHI≠AME≠BAR			Atl: FAR≠CHI≠AME≠BAR		
		Med: LIN≠FUE≠MOT≠ALM			Med: LIN≠FUE≠MOT≠ALM			Med: LIN≠FUE≠MOT≠ALM		
		Order			**Class**			**Phyllum**		
Source of variation	**df**	**MS**	**Pseudo-F**	**p (MC)**	**MS**	**Pseudo-F**	**p (MC)**	**MS**	**Pseudo-F**	**p (MC)**
Lo	1	3651.7	0.9081	0.4845 n.s.	2023.0	1.2739	0.2951 n.s.	1454.3	1.453	0.2480n.s.
Ma(Lo)	6	4021.0	9.503	0.0001***	1588.1	7.7824	0.0001***	1000.9	6.8949	0.0001***
Residual	16	423.1			204.1			145.2		
Total	23									
Pair-wise tests										
Lo		Atl=Med			Atl=Med			Atl=Med		
Ma(Lo)		Atl: FAR≠CHI≠AME≠BAR			Atl: FAR≠(CHI=AME=BAR)			Atl: FAR≠(CHI=AME=BAR)		
		Med: LIN≠FUE≠MOT≠ALM			Med: LIN≠FUE≠MOT≠ALM			Med: (LIN=FUE=MOT)≠ALM		

Table S6. Abundance of meiofaunal taxa per replicate (10 cm^2). Three replicates (1, 2, 3) per marina were studied. FAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería.

	FAR			CHI			AME			BAR			LIN			FUE			M	
	1	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	**2**	**3**	**1**	2
ACARI	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	2	-	-
AMPHIPODA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
COPEPODA	6	22	14	3	3	2	35	10	8	3	5	-	22	342	244	22	11	16	32	9
CUMACEA	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-	-	-	-	-	-
FORAMINIFERA	-	-	-	-	-	4	-	-	-	-	-	-	-	-	-	-	-	-	-	-
KINORHYNCHA	3	-	-	-	-	-	1	-	-	-	-	-	-	-	-	-	-	-	-	-
MOLLUSCA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	-
NAUPLII	5	6	11	10	12	1	16	8	-	-	3	-	22	69	175	5	6	1	3	4
NEMATODA	29	42	44	8	32	35	47	22	71	36	15	24	15	25	37	406	151	339	10	1
OSTRACODA	-	-	-	-	-	-	2	-	-	-	-	-	-	-	2	-	-	-	-	-
PYCNOGONIDA	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
POLYCHAETA	4	4	4	3	10	10	10	9	6	17	12	4	1	32	57	3	12	1	2	4
ROTIFERA	-	6	1	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
SARCOMASTIGOPHORA	-	-	-	-	-	-	-	-	-	3	5	5	-	-	-	-	3	2	2	2
TANAIDACEA	-	-	-	-	-	-	-	-	2	-	-	-	-	-	-	-	-	-	-	-
TURBELLARIA	-	-	1	5	12	10	5	1	1	-	-	2	-	1	-	4	6	-	-	2

Table S7. Environmental variables measured in each marina (3 replicates). TOC: Total Organic Carbon, N: total Nitrogen, Kjeldahl method, FAR: Faro, CHI: Chipiona, AME: Puerto América, BAR: Barbate, LIN: La Línea, FUE: Fuengirola, MOT: Motril, ALM: Almería.

Atlantic marinas

	FAR 1	FAR 2	FAR 3	CHI 1	CHI 2	CHI 3	AME 1	AME 2	AME 3	BAR 1	BAR 2	BAR 3
Sand (%)	55.0	52.7	56.6	4.0	5.0	2.5	60.7	56.8	13.6	17.9	4.5	6.4
Silt (%)	28.9	29.8	26.1	34.4	34.0	32.5	16.1	21.7	35.8	18.2	21.4	23.7
Clay (%)	16.1	17.5	17.3	61.6	61.0	65.4	23.2	21.5	50.6	63.9	74.1	69.9
TOC (%)	2.64	2.91	3.80	1.40	1.51	1.35	0.91	0.99	2.15	1.88	2.18	2.07
N (%)	0.13	0.15	0.18	0.13	0.14	0.13	0.09	0.08	0.18	0.14	0.16	0.15
P (ppm)	388.09	429.46	380.66	925.46	931.37	893.36	527.12	571.53	856.06	1016.37	1212.61	1112.78
S (ppm)	11251.58	10523.38	11605.33	2026.03	2260.33	1495.59	1787.70	2283.34	5968.11	3277.29	3172.06	3123.43
Hydrocarbons (ppm)	2000	1600	4300	4600	300	400	3400	1200	1200	1800	200	2500
Faecal coliforms (cfu/g)	50	200	50	850	1600	1300	50	50	350	2000	1500	950
Irganol (ppb)	0.00	0.00	3.93	2.01	0.00	2.57	0.00	0.00	1.85	6.70	7.52	5.86
As (ppm)	10.58	12.23	13.54	18.71	16.13	17.37	6.77	10.30	13.20	12.75	17.91	19.79
Cd (ppm)	0.07	0.43	0.03	0.21	0.11	0.09	0.25	0.18	0.18	0.08	0.30	0.00
Co (ppm)	3.40	3.79	3.35	8.52	8.72	8.73	4.37	4.96	8.25	9.09	11.21	10.69
Cr (ppm)	20.75	24.40	22.37	47.97	51.10	49.86	23.99	24.85	51.13	74.32	88.57	82.79
Cu (ppm)	51.52	69.13	65.90	92.03	95.95	91.56	41.85	41.99	136.83	119.65	153.06	135.14
Ni (ppm)	11.35	13.19	11.86	25.05	25.54	25.93	10.78	11.65	23.26	28.02	32.17	30.08
Pb (ppm)	18.91	15.24	13.07	34.35	34.78	36.43	39.38	14.86	47.73	17.75	36.13	16.89
Zn (ppm)	59.80	71.37	70.64	151.63	153.34	140.14	153.28	82.19	152.65	141.72	191.69	165.94

Mediterranean marinas

	LIN 1	LIN 2	LIN 3	FUE 1	FUE 2	FUE 3	MOT 1	MOT 2	MOT 3	ALM 1	ALM 2	ALM 3
Sand (%)	20.5	55.1	50.6	26.5	9.5	21.6	23.4	37.1	75.2	82.2	76.7	72.6
Silt (%)	42.0	25.2	26.2	46.8	63.9	38.5	71.6	59.8	24.0	16.4	21.1	25.3
Clay (%)	37.5	19.7	23.2	26.7	26.6	39.9	5.0	3.1	0.8	1.4	2.2	2.1
TOC (%)	2.33	1.58	1.77	4.10	3.10	2.83	0.97	1.00	0.84	0.65	0.76	0.89
N (%)	0.13	0.21	0.14	0.19	0.24	0.20	0.07	0.07	0.07	0.08	0.15	0.05
P (ppm)	624.99	583.39	638.00	1453.42	1105.56	936.14	1074.95	1068.04	1039.58	647.86	750.74	708.84
S (ppm)	9768.70	4676.37	5982.53	7810.35	6800.35	6354.08	1523.83	1562.98	1400.23	1097.45	1158.91	1238.93
Hydrocarbons (ppm)	1600	9600	8200	1700	1400	2800	2400	3900	7400	1700	2200	2600
Faecal coliforms (cfu/g)	650	1000	1400	2000	800	350	50	1000	650	1500	1100	1300
Irganol (ppb)	1.96	0.00	2.09	0.00	0.00	0.61	0.00	0.00	10.93	2.12	1.98	0.00
As (ppm)	12.79	8.23	5.54	20.50	23.62	25.08	18.37	17.87	13.14	17.64	13.76	17.11
Cd (ppm)	0.72	0.43	0.32	0.24	0.34	0.48	0.21	0.34	0.43	0.26	0.49	0.24
Co (ppm)	5.91	3.47	4.57	15.92	18.83	19.10	9.85	10.22	8.70	7.47	6.75	7.54
Cr (ppm)	77.71	47.01	57.99	113.27	117.17	115.14	15.71	16.94	11.80	8.83	6.17	7.07
Cu (ppm)	56.89	67.29	83.31	187.55	145.51	129.78	136.93	82.87	53.89	51.94	51.49	70.64
Ni (ppm)	51.37	29.54	34.93	193.71	219.43	220.67	24.72	24.08	22.48	17.42	16.23	18.86
Pb (ppm)	25.48	19.46	21.80	44.47	34.02	32.16	33.69	33.66	28.98	32.95	40.87	43.06
Zn (ppm)	83.83	78.14	111.00	216.99	167.48	190.35	153.26	136.70	118.10	122.86	125.46	151.94

Table S8. Results of DistLM (distance-based linear modelling) analysis for macrofauna. The variables explaining macrofaunal community (based on identifications at genus, family, order, class and phylum level) are included. Analyses were conducted also for Annelida, Arthropoda and Mollusca separately. Table shows significance levels for each predictor variable and the proportion of variation explained for any faunal assemblage. Only variables with significant results ($p<0.05$) in marginal tests are shown. Overall best models are also included. AIC: Akaike information criterion; SS (trace): sum of squares of sequential test, Prop.: proportion of variability explained by each factor (in the marginal tests without coaction of factors), TOC: Total Organic Carbon, F. colif.: faecal coliforms,
*: $p<0.05$, **: $p<0.01$, ***: $p<0.001$.

Genus level:

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
Sand	11610	4.56	0.0001***	17.2
TOC	19888	4.26	0.0001***	16.3
P	12213	4.85	0.0001***	18.1
F. colif.	5994	2.14	0.0237*	8.9
Cr	9902	3.78	0.0004***	14.7
Cu	9197	3.46	0.0001***	13.6
Pb	6924	2.51	0.0085**	10.3
Zn	10559	4.08	0.0002***	15.6

AIC	R^2	Variables
178.10	0.74	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Cu, Pb
178.43	0.76	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Cu, Pb, Zn
178.53	0.74	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Cu, Zn

Family level:

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
Sand	10788	5.50	0.0001***	20.0
TOC	7438	3.52	0.0015**	13.8
P	11115	5.71	0.0001***	20.6
F. colif.	4759	2.13	0.0299*	8.8
Cr	9834	4.91	0.0001***	18.2
Cu	9118	4.48	0.0003***	16.9
Pb	4076	1.80	0.0691*	7.5
Zn	8916	4.36	0.0002***	16.5

AIC	R^2	Variables
172.45	0.74	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Cu, Pb
172.63	0.74	Sand, Silt, TOC, P, F. colif., Cr, Cu, Pb, Zn
172.67	0.72	Sand, Silt, TOC, P, F. colif., Cr, Cu, Pb

Table S8 (Cont.)

Order level:

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
Sand	6958	5.54	0.0001***	20.1
TOC	5759	4.40	0.0007***	16.7
P	6760	5.35	0.0001***	19.5
F. colif.	3185	2.23	0.0308*	9.2
Cr	7978	6.61	0.0001***	23.1
Cu	6308	4.91	0.0004***	18.3
Pb	3315	2.33	0.0237*	9.6
Zn	5560	4.21	0.0004***	16.1

AIC	R^2	Variables
160.94	0.73	Sand, Silt, TOC, P, F. colif., Cr, Cu, Pb
161.09	0.75	Sand, Silt, TOC, P, F. colif., Cr, Cu, Pb, Zn
161.23	0.77	Sand, TOC, P, Hydrocarbons, F. colif., Irgarol, Cr, Cu, Pb, Zr

Class level:

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
Silt	1472	2.42	0.0464*	9.9
TOC	3968	8.05	0.0001**	26.8
Cr	2833	5.20	0.0006***	19.1
Cu	1445	2.38	0.0466*	9.7

AIC	R^2	Variables
142.34	0.73	Sand, Silt, TOC, P, Hydrocarbons, F. colif., Irgarol, Cr, Zn
142.40	0.69	Sand, Silt, TOC, F. colif., Cr, Pb, Zn
142.51	0.71	Sand, TOC, P, F. colif., Irgarol, Cr, Pb, Zn

Phylum level:

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
TOC	1918	5.36	0.0007***	19.6
Cr	1710	4.66	0.0021**	17.5
Pb	1069	2.70	0.0334*	10.9

AIC	R^2	Variables
134.27	0.69	Sand, TOC, P, F.colif, Irgarol, Cr, Pb, Zn
134.29	0.66	Sand, Silt, TOC, F. colif., Cr, Pb, Zn
134.59	0.71	Sand, TOC, P, F. colif., Irgarol, Cr, Cu, Pb, Zn

Table S8 (Cont.)

ANNELIDA:

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
Sand	12493	4.97	0.0003***	18.4
TOC	12793	5.11	0.0001***	18.8
P	15331	6.42	0.0001***	22.6
F. colif.	8001	2.94	0.0078**	11.8
Cr	9182	3.44	0.0029**	13.5
Cu	11905	4.68	0.0001***	17.6
Pb	7164	2.59	0.0157*	10.6
Zn	12664	5.05	0.0001***	18.7

AIC	R^2	Variables
177.55	0.75	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Cu, Pb
177.93	0.72	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Pb
178.04	0.76	Sand, Silt, TOC, P, F. colif., Irgarol, Cd, Cr, Cu, Zn

ARTHROPODA:

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
Sand	9755	2.76	0.0006***	11.1
TOC	10945	3.15	0.0002***	12.5
P	9071	2.55	0.0013**	10.3
Cr	10769	3.09	0.0005***	12.3
Pb	8166	2.27	0.0067*	9.4
Zn	8124	2.26	0.0072**	9.3

AIC	R^2	Variables
191.66	0.62	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Pb
191.84	0.58	Sand, Silt, TOC, P, F. colif., Cr, Pb
192.07	0.64	Sand, Silt, TOC, P, F. colif., Irgarol, Cr, Pb, Zn

MOLLUSCA:

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
Sand	11913	3.76	0.0011**	14.6
TOC	7692	2.29	0.0283*	9.4
P	9638	2.94	0.0062**	11.8
Cd	10108	3.11	0.0033**	12.4
Cr	11254	3.52	0.0019**	13.8
Cu	7916	2.36	0.00272*	9.7
Zn	6949	2.05	0.0488*	8.5

AIC	R^2	Variables
183.92	0.73	Sand, Silt, TOC, P, F. colif., Cr, Cu, Pb, Zn
184.00	0.70	Sand, Silt, TOC, P, F. colif., Cr, Cu, Zn
184.06	0.75	Sand, Silt, TOC, P, F. colif., Cd, Cr, Cu, Pb, Zn

Table S9. Results of DistLM (distance-based linear modelling) analysis for meiofauna. The variables explaining meiofaunal community (based on identifications at high taxonomic levels) are included. Table shows significance levels for each predictor variable and the proportion of variation in the community explained. Only variables with significant results ($p<0.05$) in marginal tests are shown. Overall best models are also included. AIC: Akaike information criterion; SS (trace): sum of squares of sequential test, Prop.: the proportion of variability which explained each factor (in the marginal tests without coaction of factors), TOC: Total Organic Carbon, F. colif.: faecal coliforms, *: $p<0.05$, **: $p<0.01$.

Variables	SS (trace)	Pseudo-F	P	Prop. (%)
Sand	3656	4.54	0.0012**	17.1
Hydrocarbons	2998	3.59	0.0053**	14.0
Cd	2929	3.49	0.0059**	13.7
Cu	2148	2.46	0.0333*	10.0

AIC	R^2	Variables
157.62	0.62	Sand, Silt, TOC, F. colif., Cd, Cr, Cu, Zn
157.76	0.65	Sand, Silt, TOC, F. colif., Cd, Cr, Cu, Pb, Zn
157.86	0.65	Sand, TOC, Hydrocarbons, F. colif., Cd, Cr, Cu, Pb, Zn

Table S10. Intervals established to assign ecological quality status for taxa richness (species, genus, family and order level), Shannon-Wiener diversity (H') and the nematode:copepod ratio (Nem:Cop). This information has been used to conduct the global assessment (see Fig. 7).

Taxa richness						
Species	Genera	Families	Orders	H'	Nem:Cop	
<25	<20	<15	<10	<1.0	>15	BAD
25-44	20-44	15-34	10-22	1.0-1.4	7-15	POOR
45-74	45-69	35-49	23-27	1.5-1.9	3-6	MODERATE
75-100	70-80	50-60	28-32	2.0-3.0	1-2	GOOD
>100	>80	>60	>32	>3.0	<1	HIGH

Table S11. Spearman correlations among ecological indicators selected for global assessment (see Fig. 7). *: $p<0.05$, **: $p<0.01$.

	MEPI	BCI	Species	Genera	Families	Orders	H'	AMBI	M-AMBI	BENTIX	BENFES	MEDOCC
MEPI												
BCI												
Species	0.781*											
Genera	0.761*		0.994**									
Families			0.934**	0.958**								
Orders			0.952**	0.939**	0.939**							
H'			0.714*	0.755*	0.814**	0.663*						
AMBI												
M-AMBI			0.881**	0.898**	0.886**	0.843**	0.833**	-0.690*				
BENTIX												
BENFES			0.905**	0.934**	0.994**	0.916**	0.857**		0.905**			
MEDOCC	-0.805**		-0.762*	-0.719*		-0.687*		-0.810**	-0.762*			
Nem:Cop	-0.675*		-0.683*	-0.699*	-0.699*			-0.647*	-0.814**		-0.683*	-0.802**

CRediT author statement

José M. Guerra-García: Conceptualization, Sampling, Methodology, Formal analysis, Investigation, Writing-original draft, Funding acquisition

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Declaration of interests

x The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

☐The authors declare the following financial interests/personal relationships which may be considered as potential competing interests:
