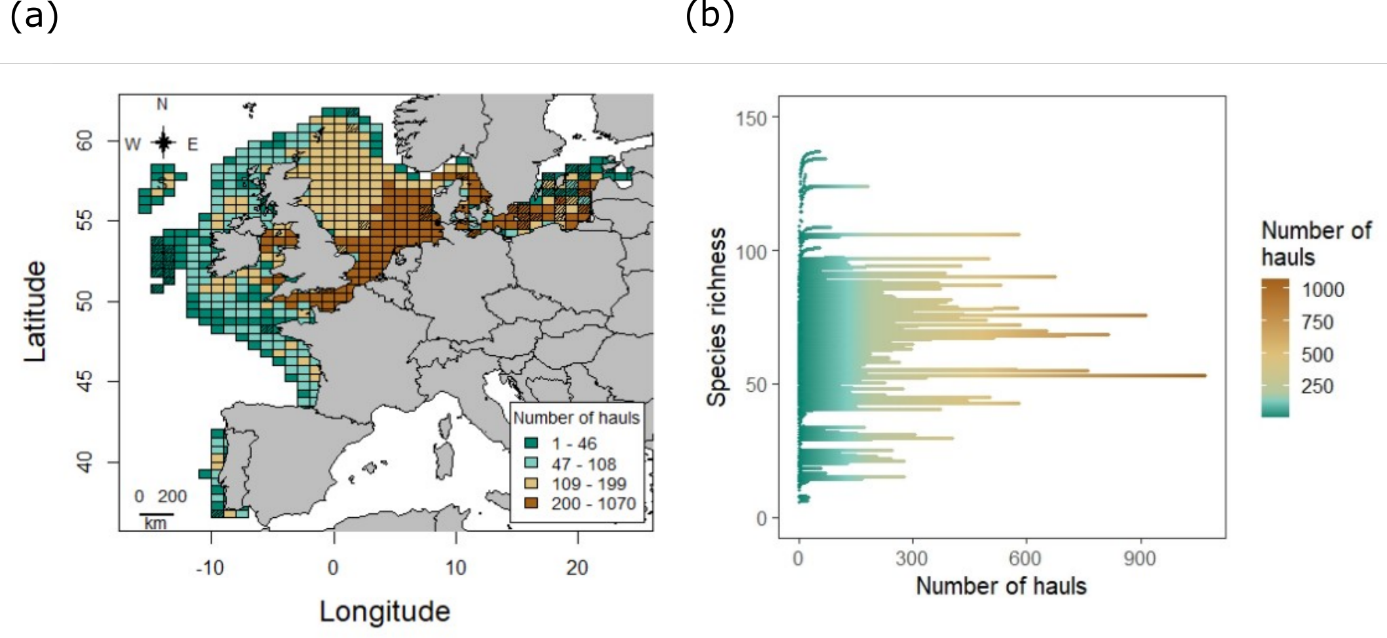
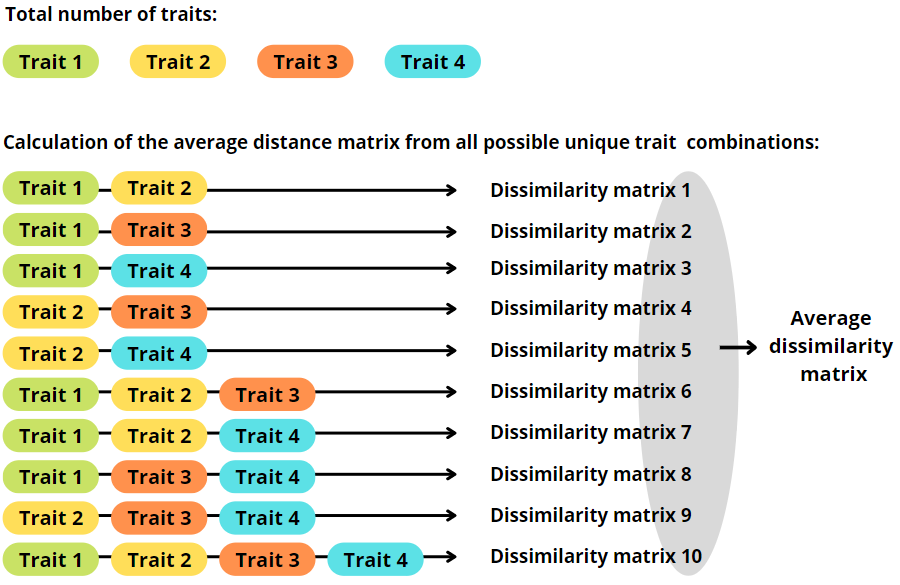
**Supporting Information:**

Threatened fish species in the Northeast Atlantic are functionally rare

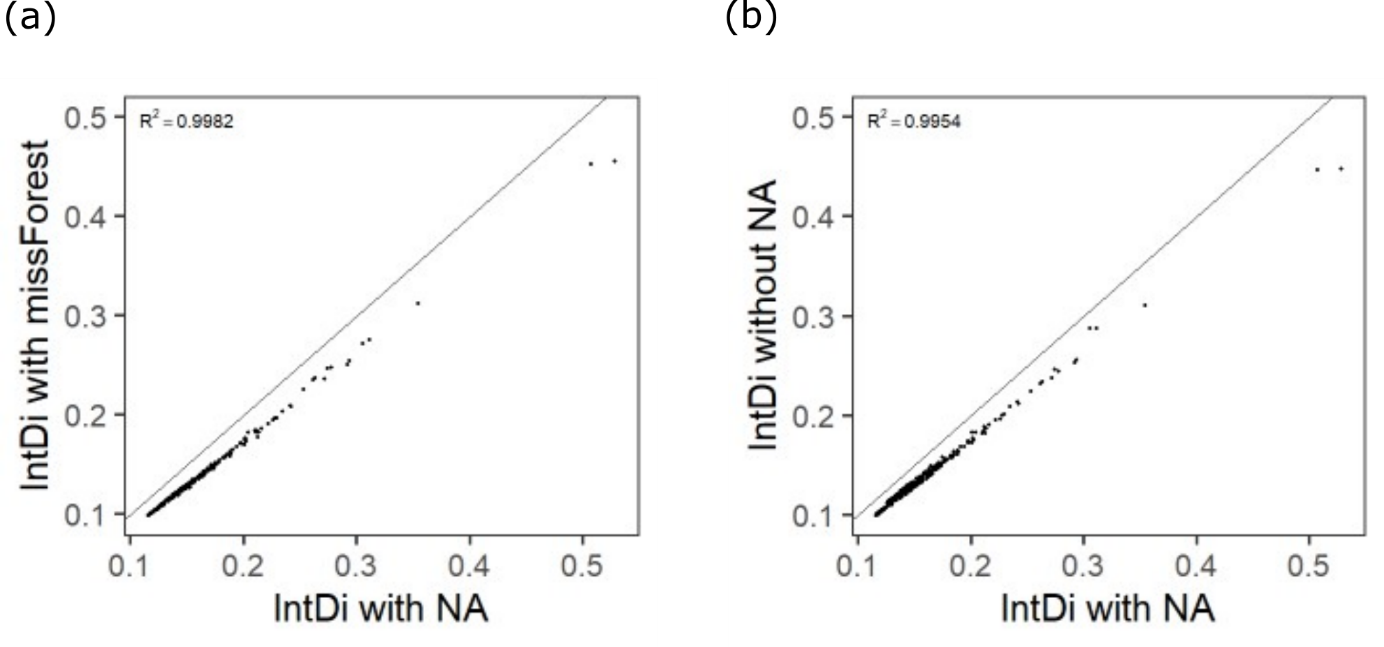
**Supplementary Appendix 2 – Figures**

****

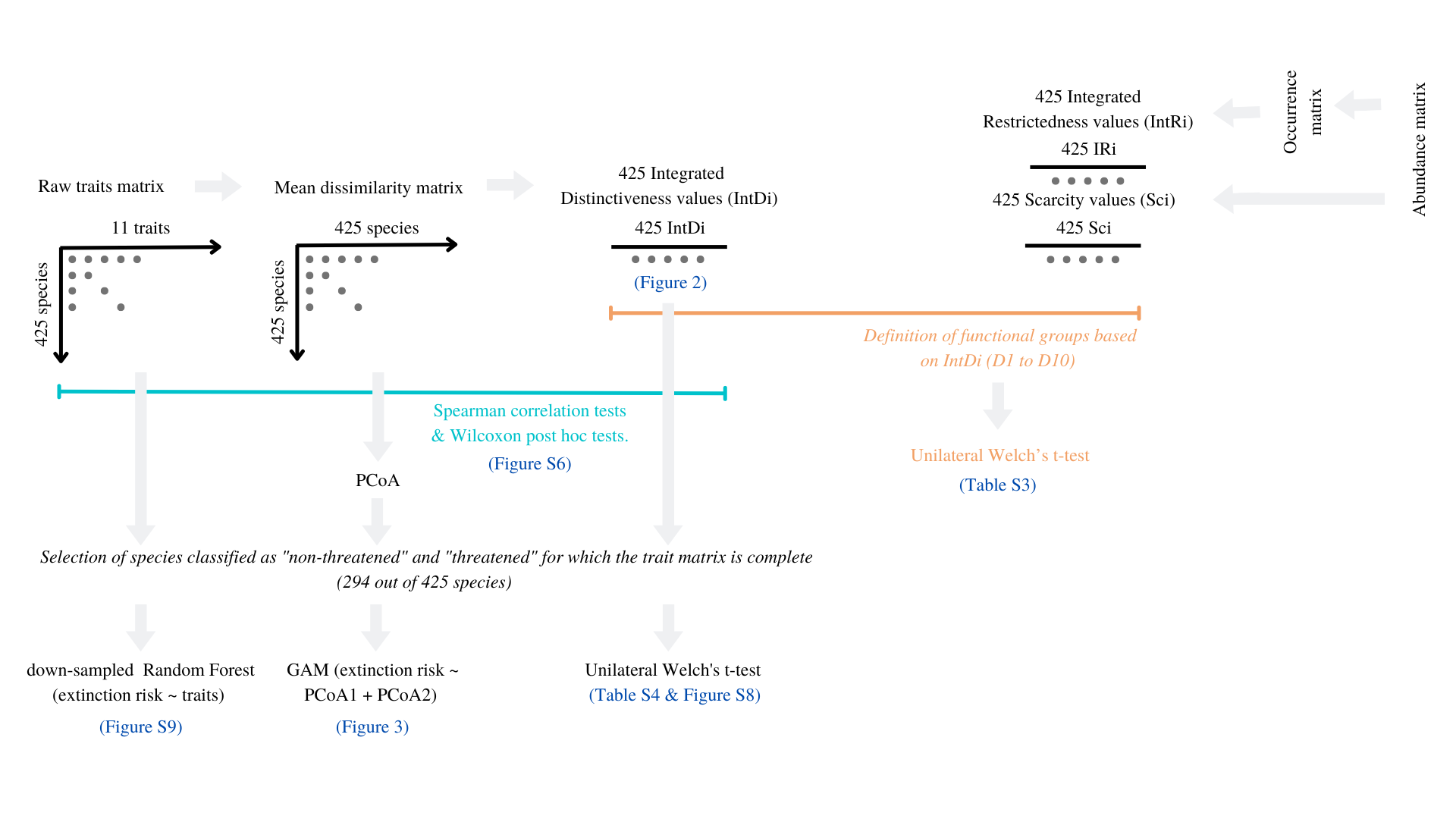
**Figure S1.** Sampling effort in the seas of the European continental shelf. **(a)** Total haul number performed from 1984 to 2020 within each ICES rectangle. Deleted rectangles due to undersampling are black striped. **(b)** Species Accumulation Curves for each rectangle. The Michaelis-Menten function is given by: 𝑓(𝑥) = 𝑆 × 𝑥 / 𝑎 + 𝑥 with *f* the number of species, *S* the asymptotic species richness estimated, *x* the number of hauls and *a* the estimated minimum number of hauls to capture half of the asymptote values. Only the rectangles covering 65% of the asymptotic number of species are included in the analysis.



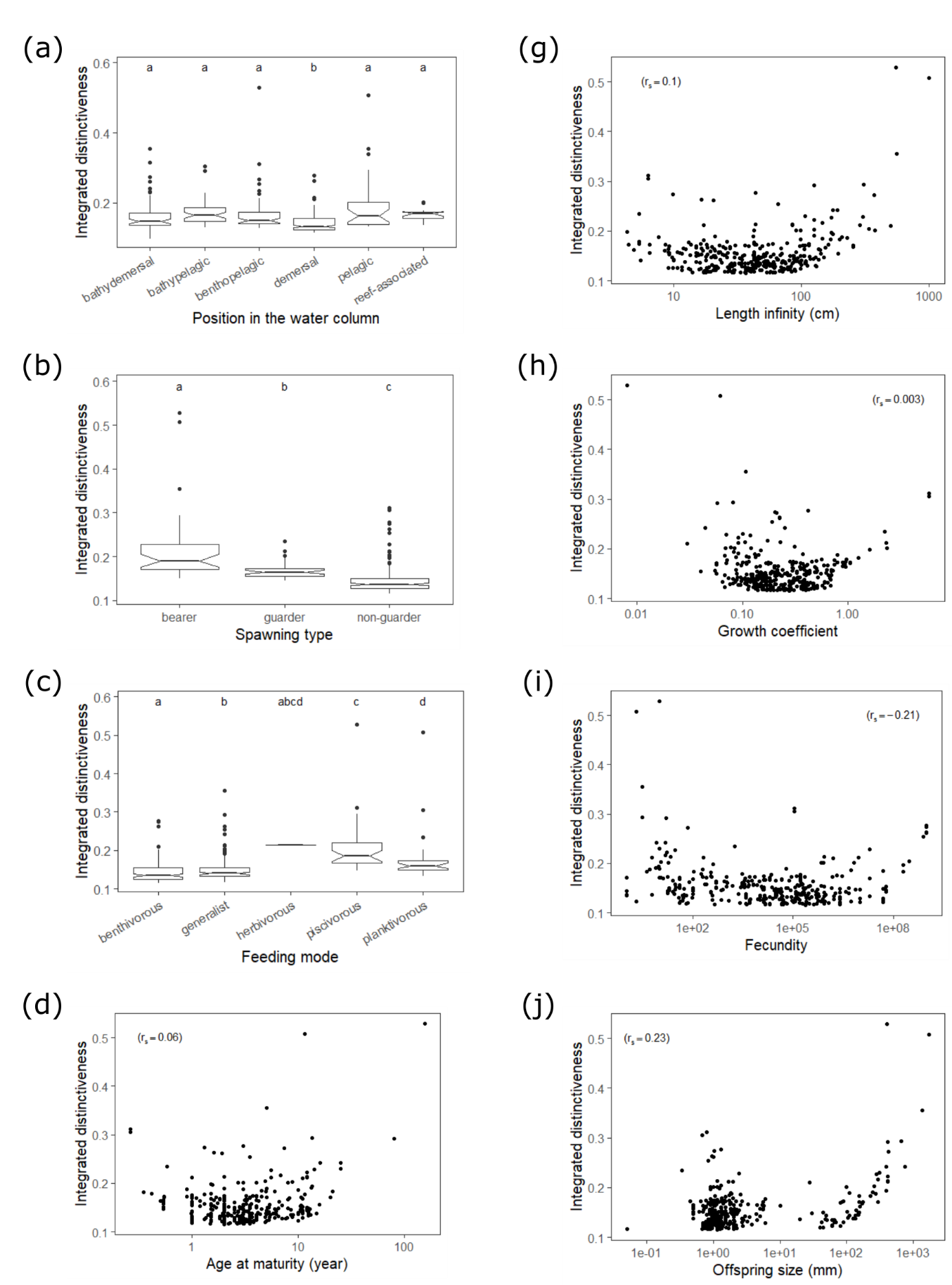
**Figure S2.** Flowchart of the methodology applied to calculate the average dissimilarity matrix on which the integrated distinctiveness index is based: To characterize the difference between two species, we constructed 10 unique trait combinations from an initial set of 4 traits, and computed the average dissimilarity matrix from 10 dissimilarity matrices from 4 traits considering that a minimum of 2 traits is needed to characterize the difference between two species.

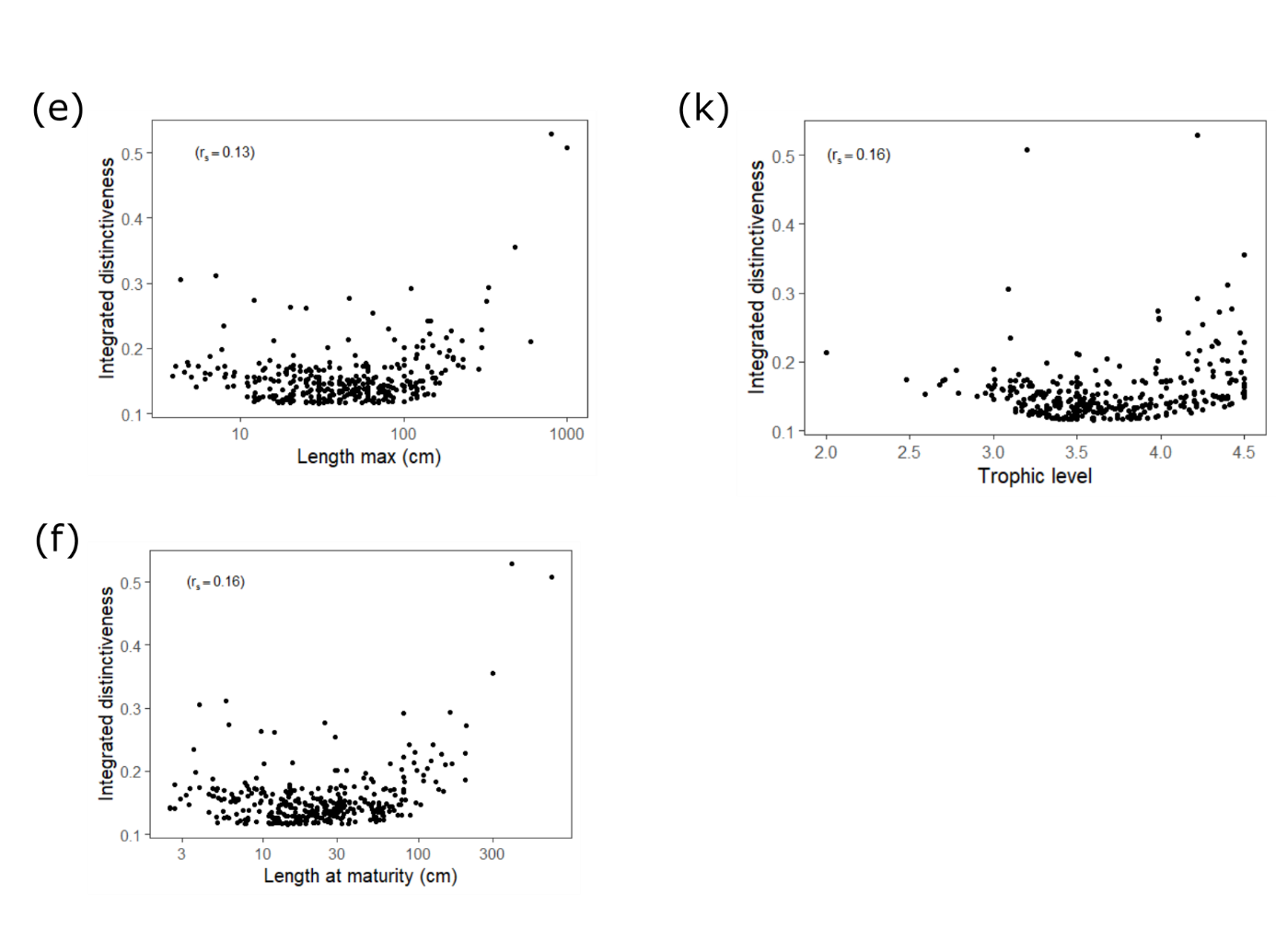
****

**Figure S3.** Robustness of theIntegrated distinctiveness index (IntDi) classification to missing traits values. The bisector x = y is plotted, with **(a)** classification of species with complete trait data compared to the one defined independently of the presence of "NA" in the traits. A total of 339 species out of 425 were considered for the calculation, witheach dot representing a species. **(b)** Classification of species after imputing missing information using the ‘missForest’ package compared to the classification defined independently of the presence of NA in the traits. A total of 425 species out of 425 were considered for the calculation, with each dot representing a species.

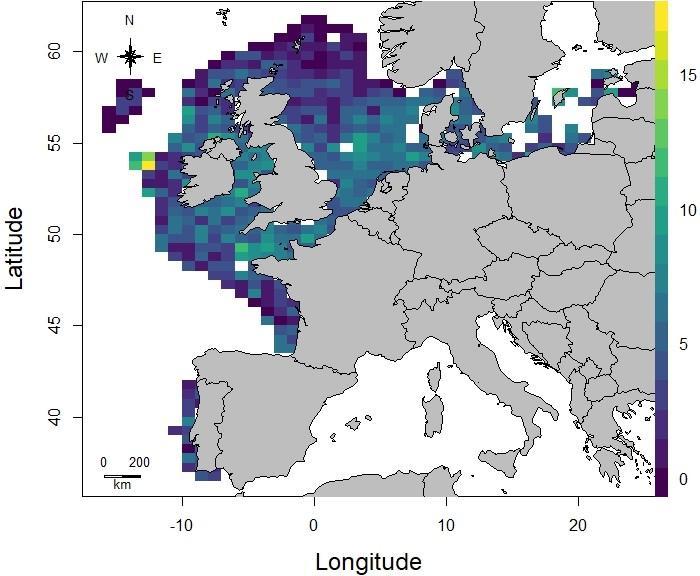


**Figure S4.** Flowchart of the methodology applied in our study

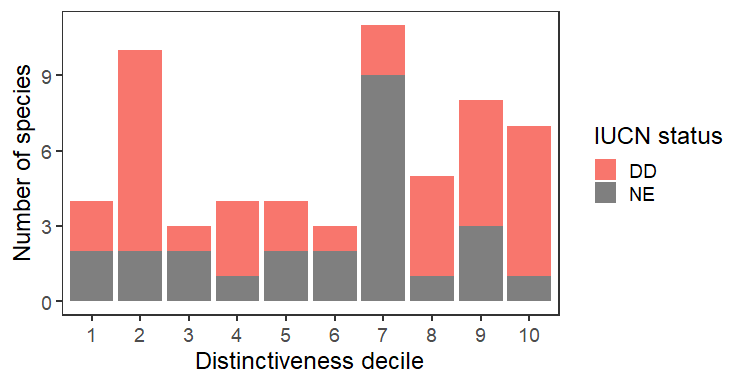




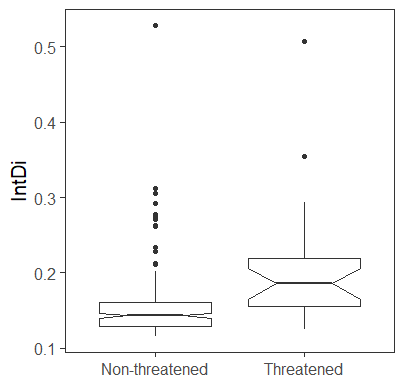
**Figure S5**. Statistical relationships between species functional distinctiveness and their ecological traits. (**a**) position in the water column, (**b**) spawning type, (**c**) feeding mode, (**d**) age at maturity (year; log10 transformed), (**e**) length at maturity (cm; log10 transformed), (**f**) infinite length (cm; log10 transformed), (**g**) maximal length at maturity (cm; log10 transformed), (**h**) growth coefficient (log10 transformed), (**i**) fecundity (log10 transformed), (**j**) offspring size (mm; log10 transformed), and (**k**) trophic level. Letters above boxplots denote significant differences between trait attributes (Wilcoxon post-hoc test).



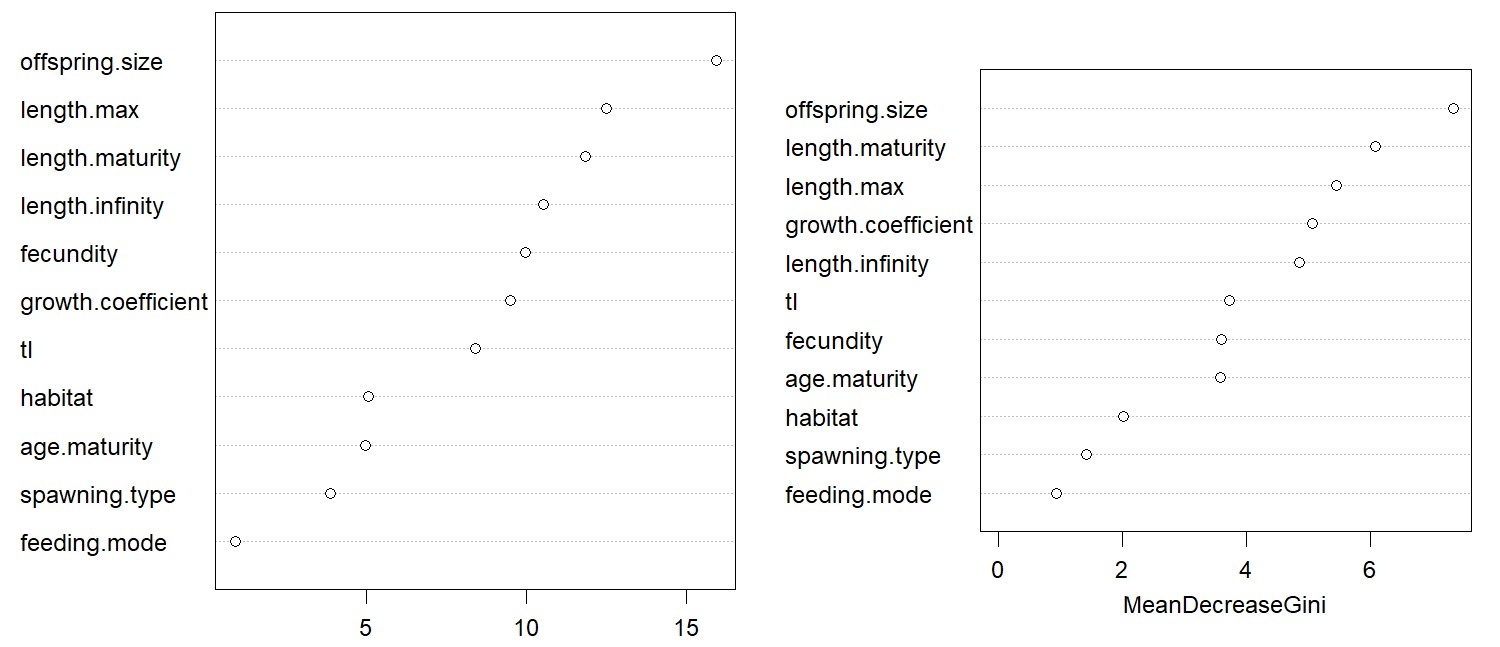
**Figure S6**. Map of the percentage of distinct species per rectangle across European Seas. The color gradient refers to the percentage of distinct species.



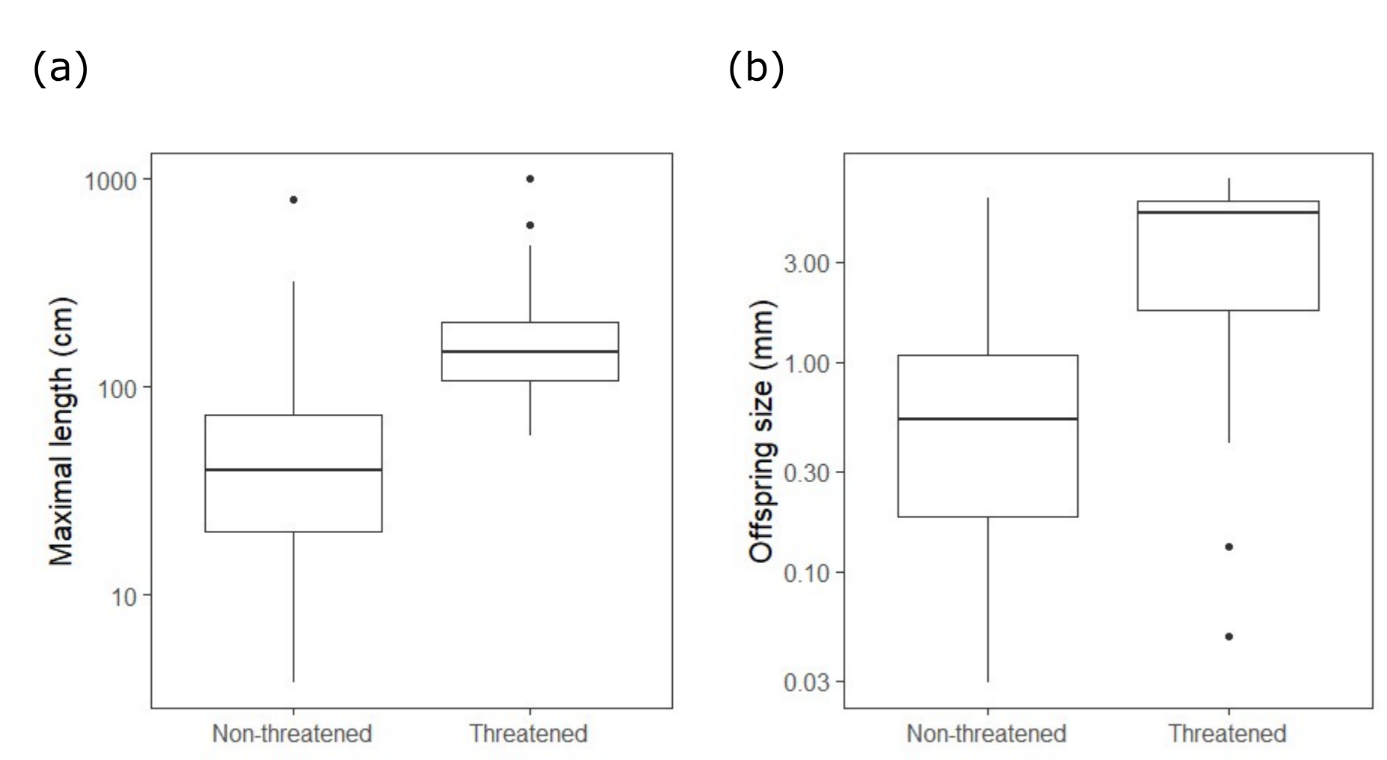
**Figure S7.** Distribution of IUCN Data Deficient (DD) and Not Assessed (NE) status across functional distinctiveness groups.



**Figure S8.** Boxplot showing the distribution of integrated distinctiveness values in the "not threatened" and "threatened" categories (unilateral Welch’s t-test; p = .003).



**Figure S9.** Dot-chart of variable importance as measured by the down-sampled random forest with species threat (1: threatened, 196 species; 0: not threatened, 17 species) as response variable and species traits values as predictors.



**Figure S10.** Boxplot showing the distribution of values of the most important traits in determining species extinction risk. **(a)** Threatened species have a larger maximal length (log10 transformed). **(b)** Threatened species have a much larger offspring size (log10 transformed).