

## SUPPLEMENTARY INFORMATIONS:

### Insights on the drivers of genetic divergence in the European anchovy

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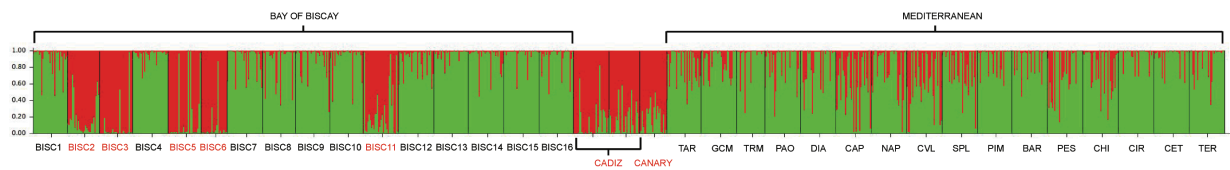
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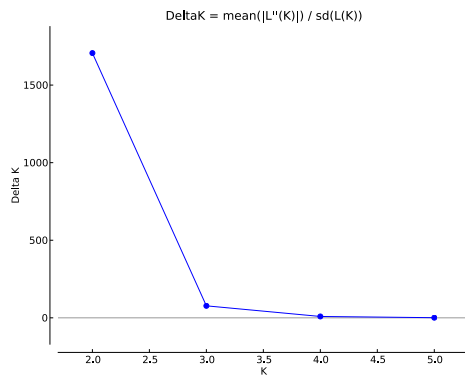
**Figure S1** STRUCTURE ANALYSIS. The number of sub-populations ( $\Delta K$ ) was determined using the method of Evanno<sup>39</sup> based on the rate change in the log probability of data between successive K values, and implemented in Structure Harvester.  $\Delta K$  reached its maximum value when K = 2

a) Proportional membership (Q) of each accession at K=2. Atlantic sampling sites considered as coastal in Montes *et al.*<sup>20</sup> are labelled with red letters. b) Plot of  $\Delta K$ .

a)

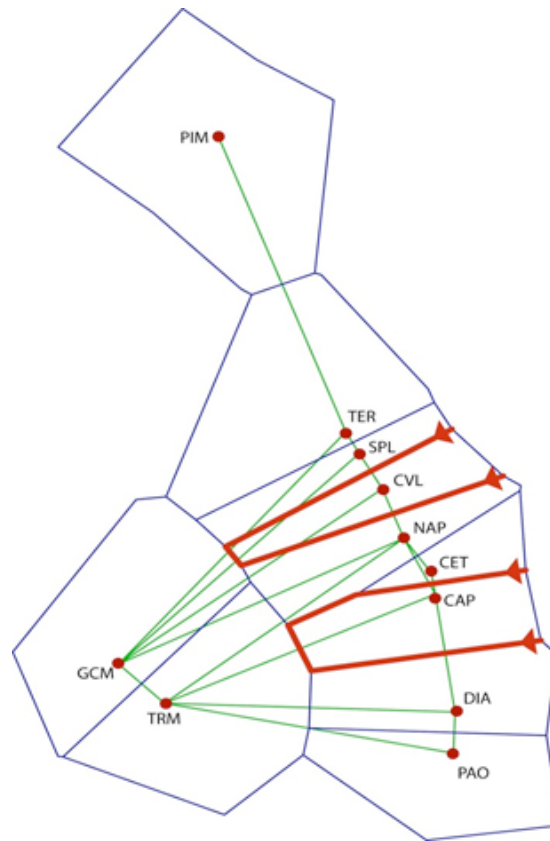


b)



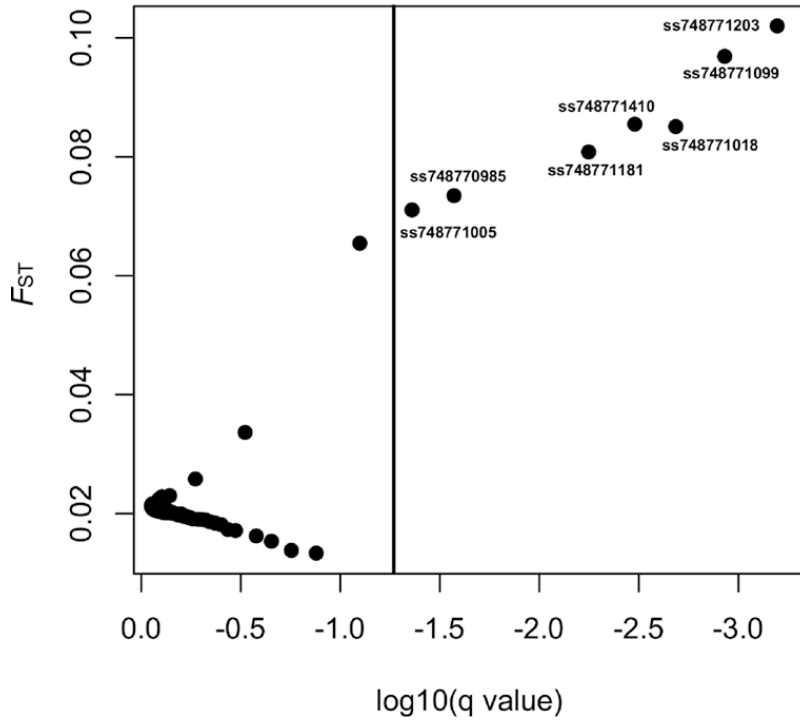
K	Reps	Mean LnP(K)	Stdev LnP(K)	Ln'(K)	Ln''(K)	Delta K
1	10	-108190.500000	0.081650	-	-	-
2	10	-98576.225000	4.594471	9614.275000	7839.500000	1706.289900
3	10	-96801.450000	13.433416	1774.775000	1037.975000	77.268135
4	10	-96064.650000	7.079313	736.800000	62.325000	8.803821
5	10	-95390.175000	616.9046025	674.475000	552.100000	0.894952
6	10	-94163.600000	107.309583	1226.575000	-	-

**Figure S2** Genetic barriers predicted by BARRIER (version 2.2), employing Monmonier's maximum difference algorithm to highlight geographical features corresponding to pronounced genetic discontinuity in Tyrrhenian Sea (red bold lines with arrows). Sampling sites (red points) are shown.

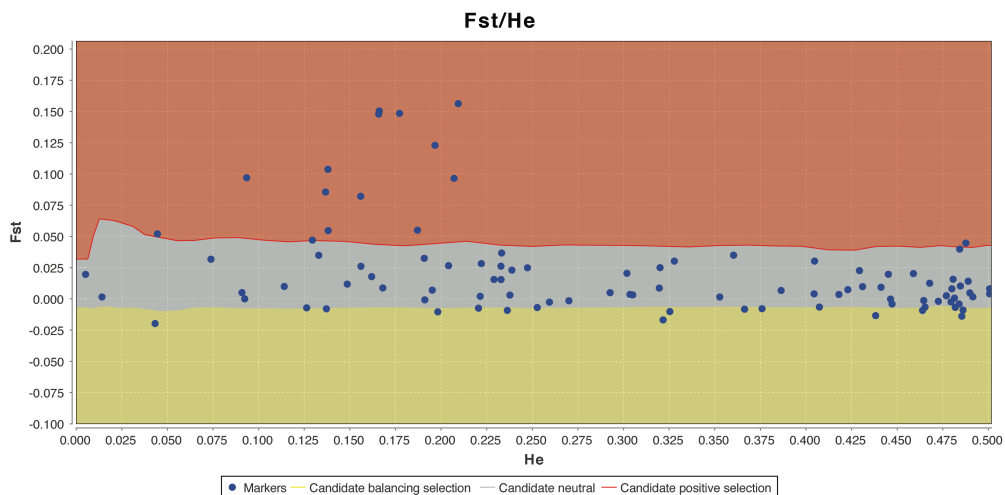


**Figure S3** Detection of outlier SNPs. a) BayeScan Log<sub>10</sub>(q value) are shown on the x-axis and  $F_{ST}$ -values on the y axis. Log<sub>10</sub>(q-value): decision factor in logarithmic scale (base 10) to determine selection; b) Lositan graphical output with the simulated confidence area for neutral loci (grey color band) with loci from the original empirical dataset represented as dots. Candidate positive selection outliers are situated in the red band.

a)

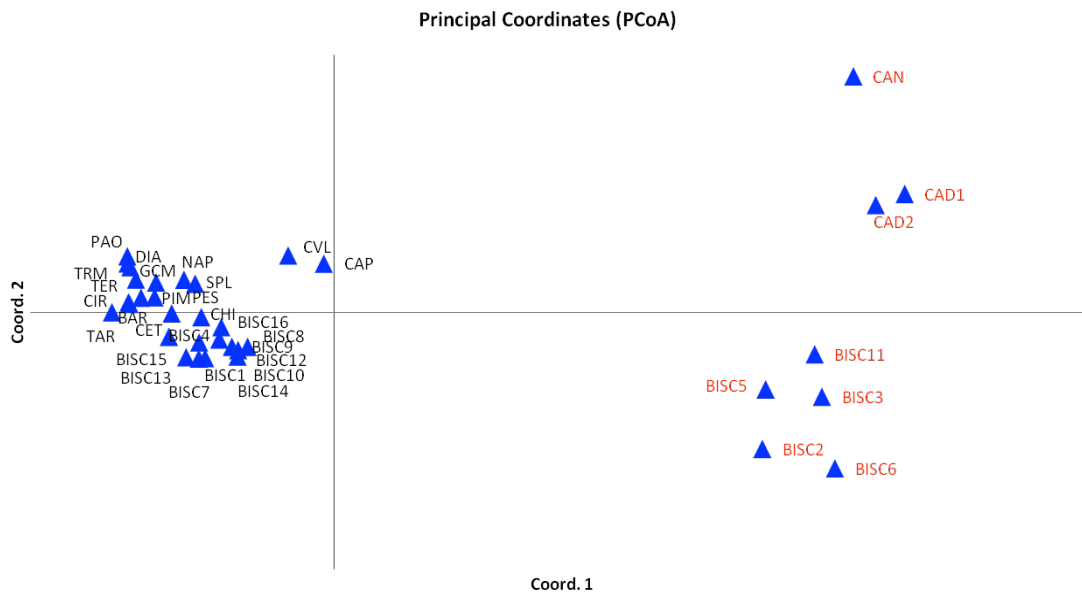


b)

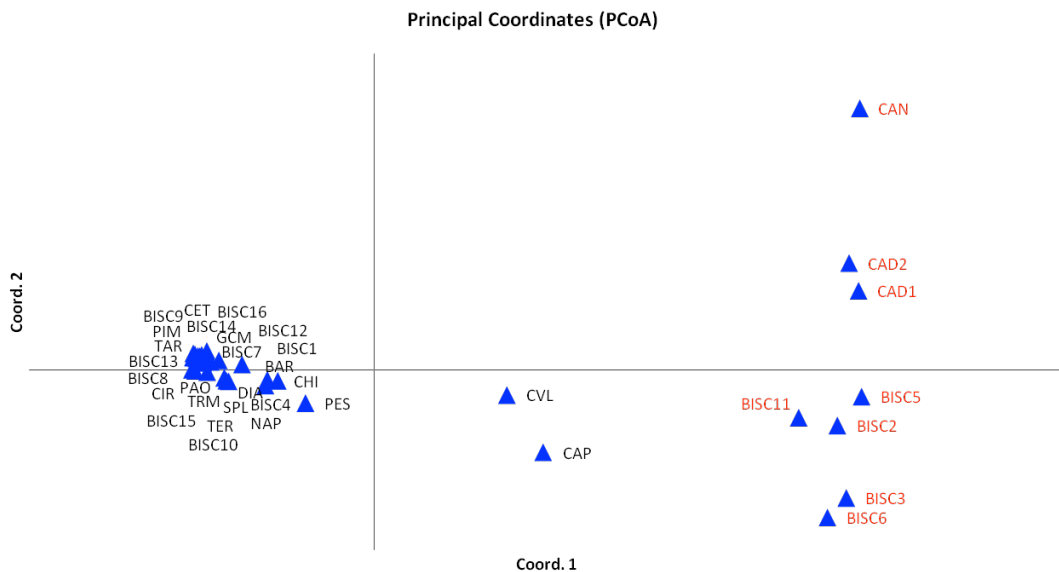


**Figure S4** PCoA of Mediterranean and Atlantic samples with (a) only putative neutral markers (variance of axis 1: 65.11%; variance of axis 2: 13.27%); and (b) with putative outliers markers (variance of axis 1: 98.58%; variance of axis 2: 0.85%). Atlantic coastal populations are labelled with red letters. PCoA of the Mediterranean and Atlantic samples grouped by sampling locality with (c) only putative neutral markers (variance of axis 1: 63.2%; variance of axis 2: 18%); and (d) with putative outliers markers (variance of axis 1: 94.9%; variance of axis 2: 3.8%). In circles we highlighted the different ecotypes. PCoA of Tyrrhenian adult anchovies and eggs sample sites (e) with putative neutral markers (variance of axis 1: 24.41%; variance of axis 2: 9.20%) and (f) putative outlier markers (variance of axis 1: 84.5%; variance of axis 2: 8.44%).

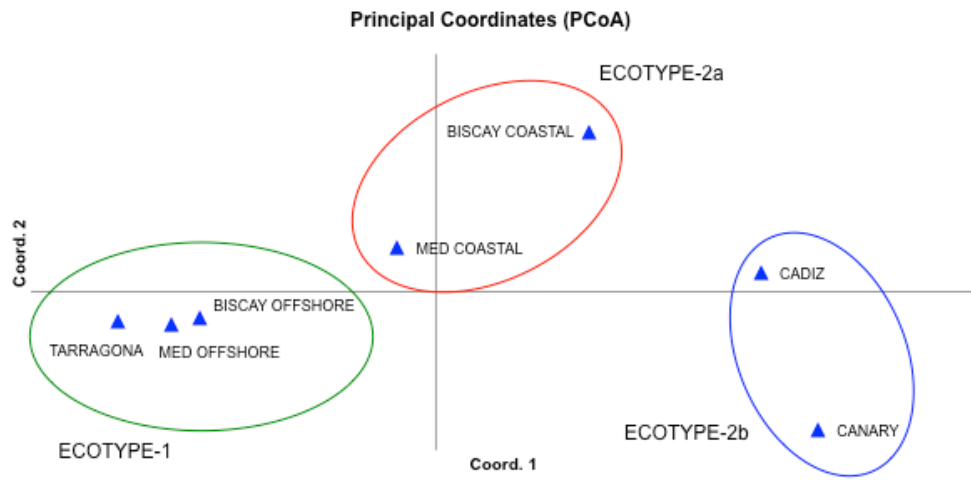
a)



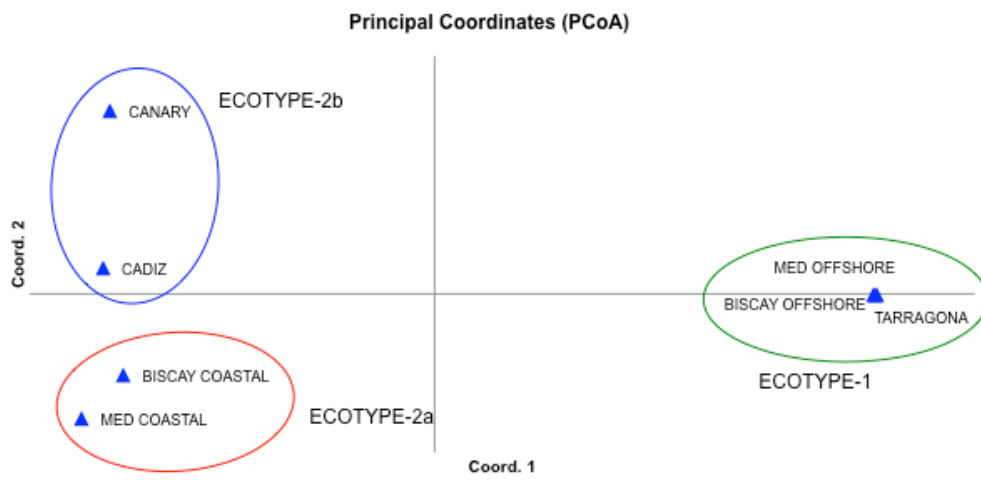
b)



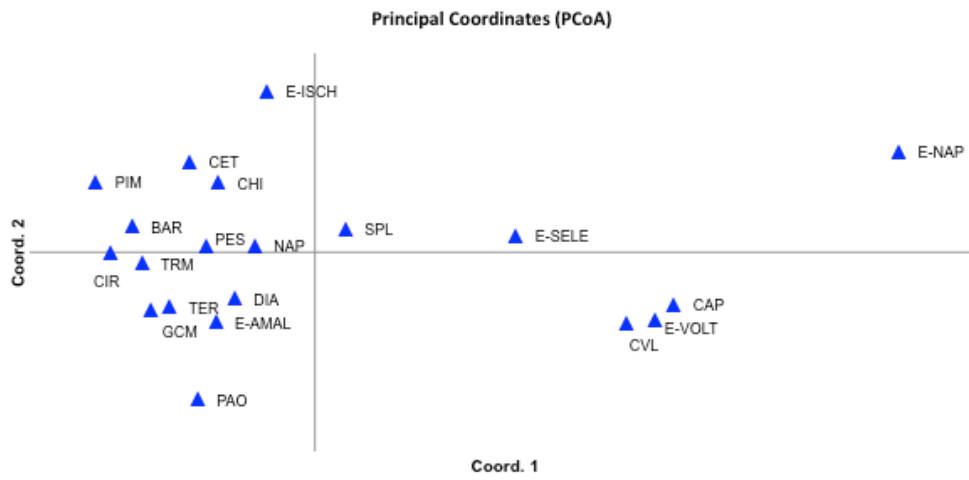
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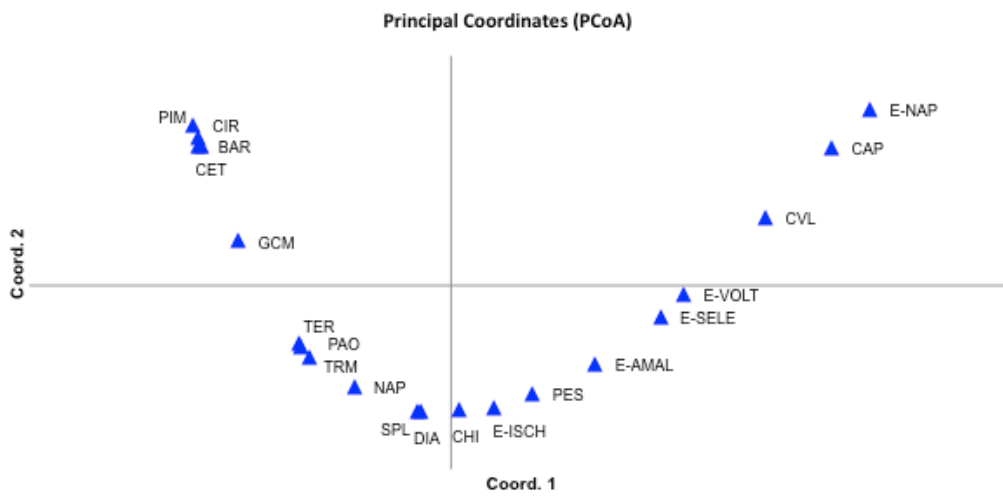
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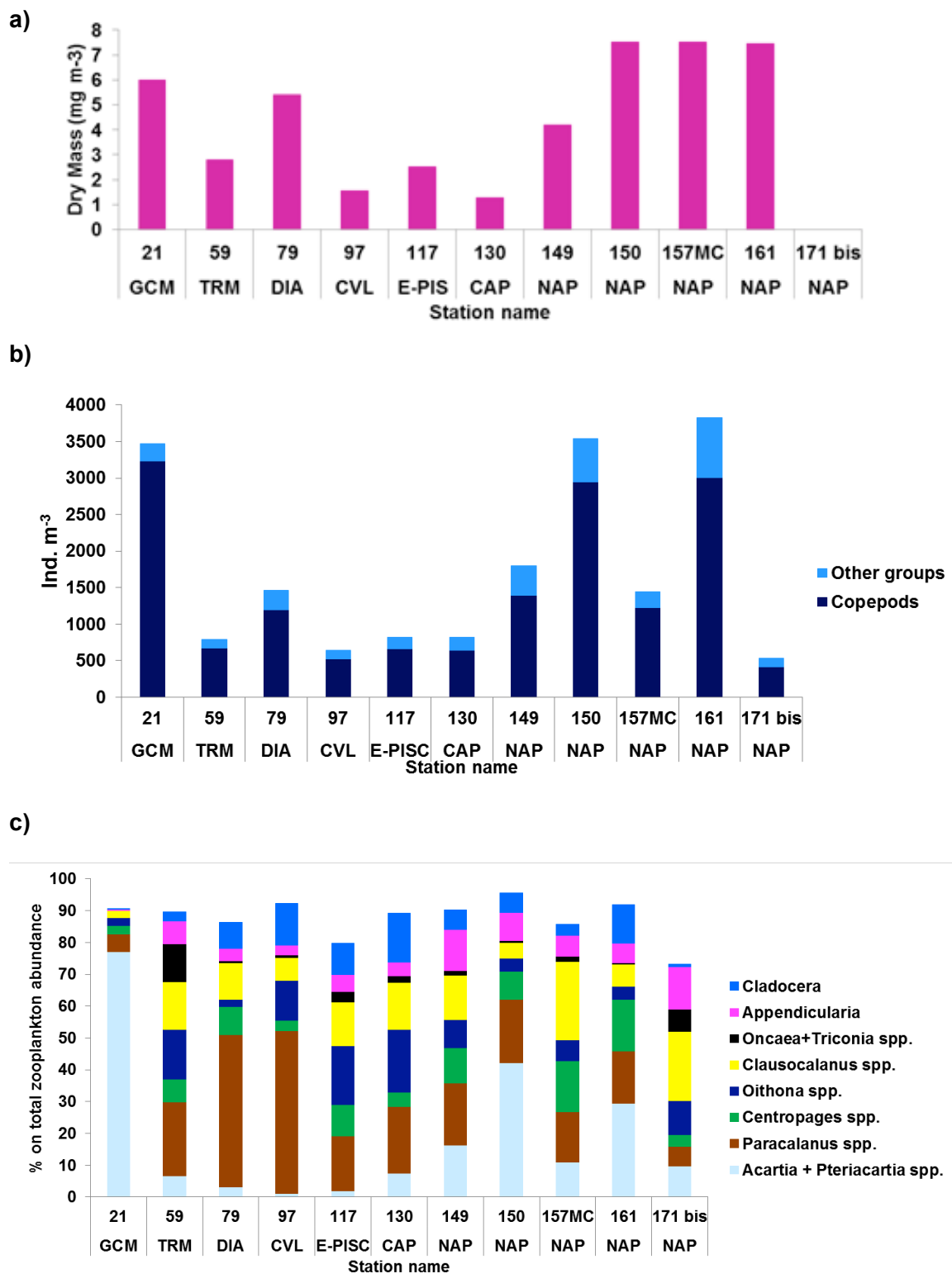
e)



f)



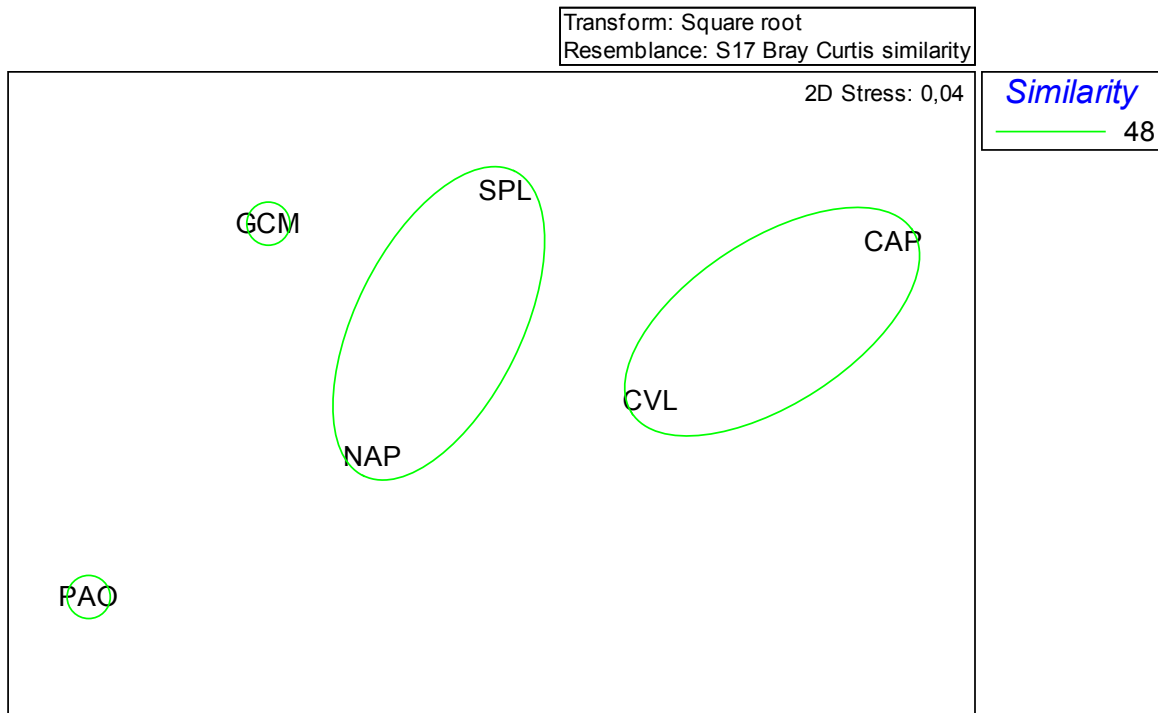
**Figure S5.** Characterization of the zooplankton community in a sub-set of stations in which anchovies were collected; a) total zooplankton biomass; b) relative abundance of copepods; c) abundance of most representative groups



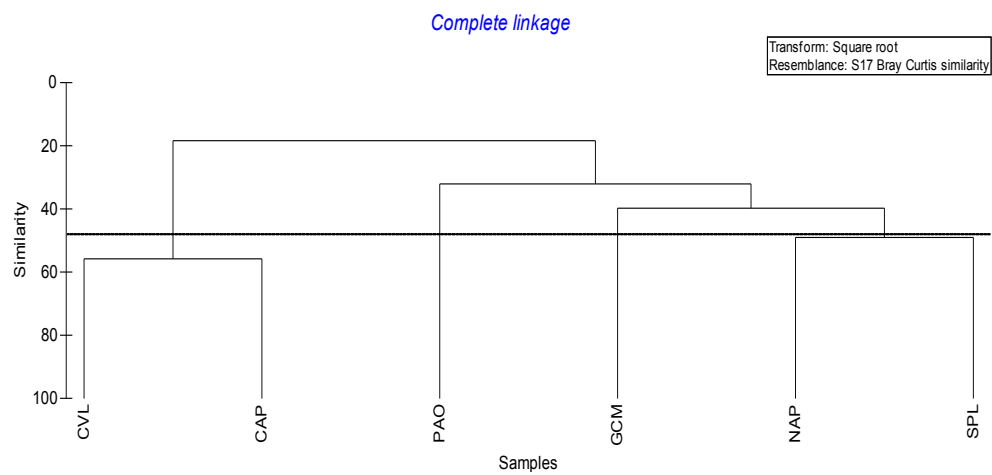


**Figure S6** (a) Clustering of the different areas obtained using the diet of anchovy as descriptor, (b) MDS representation of the similarity among areas obtained using the diet of anchovy as descriptor.

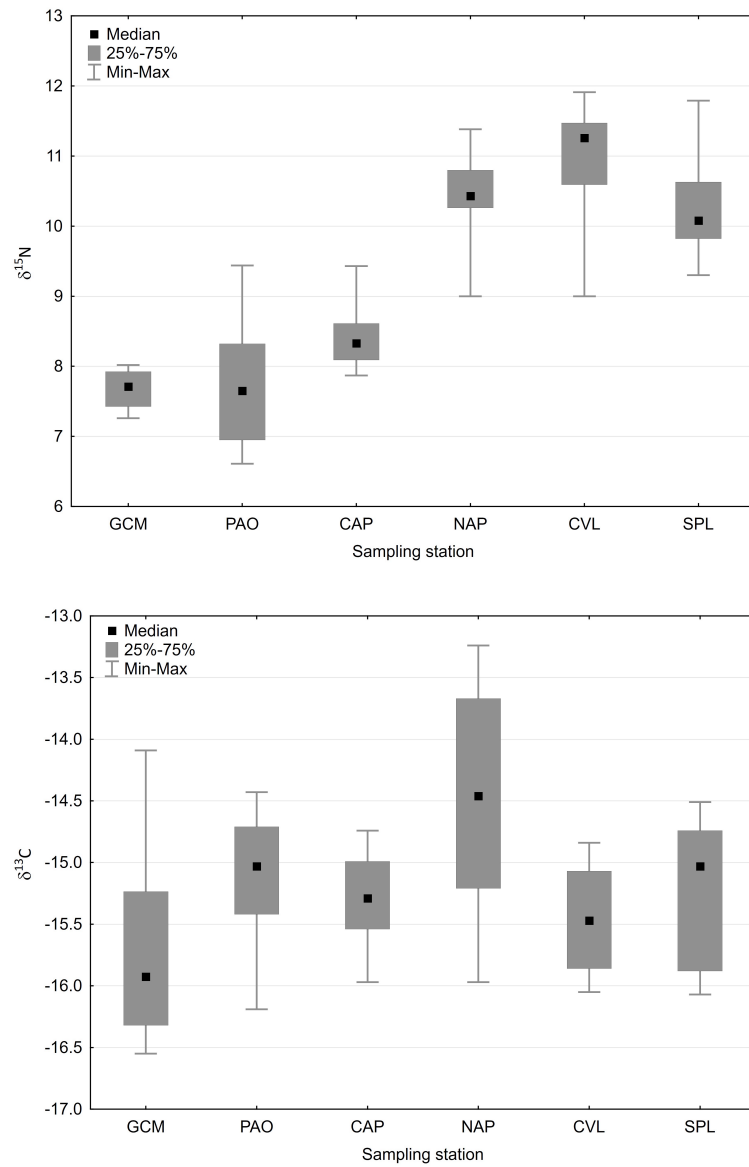
a)



b)



**Figure S7:** Boxplot of  $\delta^{15}\text{N}$  (top panel) and  $\delta^{13}\text{C}$  (bottom panel) values recorded in each considered station.



**Table.S1** Anchovy diet composition expressed by percentage.

Group	Prey item	SPL	CVL	NAP	CAP	PAO	GCM
BACILLARIOPHYCEAE	<i>Coscinodiscus</i> spp.	0.0	0.8	0.0	0.8	0.0	0.0
DINOPHYCEAE	<i>Dinophysis fortii</i>	0.0	0.0	0.6	0.0	0.0	0.0
	<i>Phalacroma rotundatum</i>	0.0	0.0	0.0	0.0	0.4	0.0
MOLLUSCA	Atlantidae indet.	0.0	0.4	1.8	5.5	2.8	0.0
	Bivalvia veliger	0.0	3.1	0.0	1.6	0.0	0.0
POLYCHAETA	Polychaeta larvae	0.0	0.4	0.0	0.0	0.0	2.3
CLADOCERA	<i>Podon intermedius</i>	0.0	0.0	0.0	0.8	0.4	0.0
OSTRACODA	Ostracoda indet.	0.0	0.0	0.0	0.0	6.8	0.0
Calanoida	<i>Acartia clausi</i>	0.0	0.4	0.0	0.0	0.0	0.0
	<i>Acartia</i> spp.	0.0	1.5	0.0	0.8	0.0	0.0
	<i>Calanus helgolandicus</i>	0.0	0.0	0.0	0.0	0.4	0.0
	<i>Candacia giesbrechti</i>	1.3	0.0	8.6	0.0	0.0	0.0
	<i>Candacia</i> spp.	6.7	0.8	12.3	0.0	1.1	2.3
	<i>Centropages typicus</i>	13.4	3.8	16.6	0.8	1.8	2.3
	<i>Centropages</i> spp.	0.0	3.5	5.5	0.8	0.0	0.0
	<i>Clausocalanus</i> sp.	0.0	1.5	1.8	0.0	1.1	0.0
	<i>Euchaeta</i> sp.	0.0	0.0	0.0	0.0	0.4	0.0
	<i>Heterorhabdus</i> spp.	0.0	0.0	0.0	0.0	0.7	0.0
	<i>Isias clavipes</i>	0.0	0.0	0.0	0.0	0.4	0.0
	<i>Lucicutia</i> spp.	0.0	0.0	1.8	0.0	0.0	0.0
	<i>Paracalanus</i> spp.	0.0	1.5	1.2	1.6	0.0	0.0
	<i>Pleuromamma abdominalis</i>	0.0	0.0	0.6	0.0	0.4	0.0
	<i>Pleuromamma gracilis</i>	0.0	0.0	0.0	0.0	0.4	0.0
	<i>Pleuromamma</i> sp.	0.0	0.4	0.6	0.0	0.4	0.0
	<i>Temora stylifera</i>	5.3	0.0	2.5	0.0	0.0	0.0
	Calanoida prosoma<500	0.0	1.9	0.0	0.0	0.0	0.0
	Calanoida 500<prosoma<1000	0.0	9.6	3.1	15.6	0.4	6.9
	Calanoida 1000<prosoma<1500	2.7	6.2	6.8	0.8	2.1	18.4
	Calanoida 1500<prosoma<2000	1.3	1.2	0.6	0.0	1.4	0.0
	Calanoida prosoma>2000	0.0	0.0	3.1	0.0	0.0	0.0
Cyclopoida	<i>Oithona</i> cf. <i>nana</i>	0.0	1.5	0.0	0.0	0.0	0.0
	<i>Oithona</i> cf. <i>plumifera</i>	1.3	1.9	0.6	0.8	0.0	0.0
	<i>Oithona setigera</i>	0.0	0.0	0.0	0.0	0.7	0.0
	<i>Oithona</i> cf. <i>similis</i>	0.0	0.4	0.0	0.8	0.0	0.0
	<i>Oithona</i> spp.	0.0	0.8	0.0	0.0	0.0	0.0
Poecilostomatoida	<i>Corycaeus typicus</i>	1.3	2.3	0.0	0.0	0.0	0.0
	<i>Corycaeus</i> spp.	5.3	0.4	0.0	0.0	0.7	0.0
	<i>Farranula</i> sp.	1.3	5.0	0.6	25.8	0.0	0.0
	<i>Urocorycaeus</i> sp.	0.0	0.0	0.6	0.0	0.0	0.0
	<i>Vetтория</i> sp.	0.0	0.0	0.0	0.0	0.4	2.3
	Corycaeidae indet.	2.7	0.0	1.2	0.0	0.0	0.0
	<i>Oncaea venusta</i>	0.0	0.0	0.0	0.0	0.4	0.0

	<i>Oncaea</i> prosoma<350	6.7	2.7	1.2	7.0	1.4	20.7
	<i>Oncaea</i> 350<prosoma<600	20.0	5.8	4.9	5.5	27.7	25.3
	<i>Oncaea</i> prosoma>650	1.3	0.0	0.6	0.0	3.9	2.3
	<i>Triconia conifera</i>	0.0	0.0	2.5	0.0	12.4	2.3
Harpacticoida	<i>Euterpina acutifrons</i>	4.0	31.9	0.0	25.8	0.0	0.0
	<i>Microsetella</i> spp.	14.7	4.6	1.8	0.0	2.5	11.5
	Harpacticoida indet.	0.0	0.0	0.0	0.0	0.4	0.0
	Copepoda nauplius	0.0	0.4	0.0	1.6	0.0	0.0
	Copepoda (not Calanoida)	0.0	0.4	0.0	0.0	0.0	0.0
AMPHIPODA	Caprellidae indet.	0.0	0.0	0.0	0.0	0.4	0.0
DECAPODA	Decapoda zoea	1.3	0.0	1.2	0.8	0.0	0.0
	Decapoda mysis	0.0	0.0	0.6	0.0	0.0	0.0
	Decapoda megalopa	0.0	0.0	0.6	0.0	0.0	0.0
	Decapoda indet.	0.0	0.0	8.3	0.0	0.2	3.4
APPENDICULARIA	<i>Oikopleura</i> spp.	0.0	0.4	2.5	0.0	26.7	0.0
	Appendicularia indet.	0.0	0.4	0.0	2.3	0.0	0.0
CHAETOGNATHA	Sagittoidea indet.	2.5	0.3	3.3	0.1	0.6	0.1
TELEOSTEA	Teleostea larvae indet.	0.0	0.0	0.0	0.0	0.4	0.0
others	Invertebrata eggs spheric	2.7	1.5	0.0	0.8	0.0	0.0
	Invertebrata eggs elliptical	2.7	1.2	0.6	0.0	0.0	0.0
	Invertebrata eggs irregular	0.0	0.0	0.6	0.0	0.0	0.0
	Pollen grains	0.0	0.8	0.6	0.0	0.4	0.0
	Carabidae indet.	1.3	0.0	0.0	0.0	0.0	0.0
	Insecta indet.	0.0	0.4	0.0	0.0	0.0	0.0