Table S1. Pairs of sequencing replicates (with grey background) and of samples separated by *p distance* similar or lower than distances observed for replicates (on the basis of 51 439 RAD loci obtained with ipyrad; see table S3). The numbers in the column 'Reads' correspond to the number of reads after the Kraken analysis. For each sample pair, we retained the sample with the highest number of reads for further analyses. See main text for details. PCCOF: Catchoff – Stn A; PCODF: Yeux de chat; PCIMP: Impérial du large; PCGCO: Grand Congloue

Sample 1	Reads	Sample 2	Reads	*p distance*
PCCOF58-17	7708166	PCCOF58-17-2	6,380,908	0.018
PCCOF58-8	6733912	PCCOF58-8-2	9,117,315	0.022
PCODC30-25	5057861	PCODC30-25-2	4,444,312	0.027
PCODC30-9	6613213	PCODC30-9-2	4,153,968	0.022
PCODC30-21-2	4365254	PCODC30-5	6,556,789	0.020
PCODC30-18	9148556	PCODC30-20-2	5,220,776	0.018
PCIMP54-18	6264317	PCIMP54-13	5,090,699	0.020
PCGCO33-8	6548623	PCGCO33-4	6,513,661	0.025

Table S2. Number of loci retained at each filtering step for all populations, with the software used at each step. The final dataset included 49,215 SNPs for 82 samples

	retained loci	software
total_prefiltered_loci	109,1960	ipyrad
filtered_by_rm_duplicates	109,1960	ipyrad
filtered_by_max_indels	109,1960	ipyrad
filtered_by_max_SNPs	109,1081	ipyrad
filtered_by_max_shared_het	108,7331	ipyrad
filtered_by_min_sample	51,439	ipyrad
max 75 % of missing data, 2 alleles per SNP, no LD, one SNP per locus	49,215	vcftools and GBS_SNP_filter

Table S3. Number of loci retained at each filtering step for the analysis of the two sites in the north of the Bay of Marseille, with the software used at each step. The last two lines correspond to the dataset Mars_1 and Mars_2 respectively, with 55 samples in both cases.

	retained loci	software
total_prefiltered_loci	757,308	ipyrad
filtered_by_rm_duplicates	757,308	ipyrad
filtered_by_max_indels	757,308	ipyrad
filtered_by_max_SNPs	756,695	ipyrad
filtered_by_max_shared_het	751,168	ipyrad
filtered_by_min_sample	62,313	ipyrad
max 75% missing data per locus, 2 alleles per SNP, no LD, one SNP per locus	49,215	vcftools and GBS_SNP_filter
no missing data per locus, 2 alleles perSNP, no LD, one SNP per locus	7,653	Vcftools and GBS_SNP_filter

Table S4. Demographic inferences for the ODC (Yeux de chat) and COF (Catchoff–Stn A) populations. The model used for inferences is presented in Figure S2. The estimated parameters are effective sizes N_COF and N_ODC for COF and ODC, respectively; the gene flows M_ODC_COF (from ODC to COF in forward time) and M_COF_ODC (from COF to ODC); and the divergence time (TDIV in generations). The first line presents the value estimated for the best run (over 100 replicates) for the analysis of observed data. The following lines indicate the statistics describing the distribution of the parameters over 50 non-parametric bootstraps: median, standard deviation, minimum and maximum values. The computation was performed with a mutation rate of 2.9×10^{-8} / site / generation as estimated in *Acropora* corals by Mao et al. (2018)

	N_COF	N_ODC	M_ODC_COF	M_COF_ODC	TDIV
Best run	5,378	1,247,133	0.0041	< 0.0001	1987
Median	12,507	1,710,848	0.0018	< 0.0001	5004
Standard deviation	5,879	714,299	0.0053	< 0.0001	2161
Minimum	954	183,719	0.0010	< 0.0001	384
Maximun	20,015	2,651,810	0.0251	< 0.0001	7815

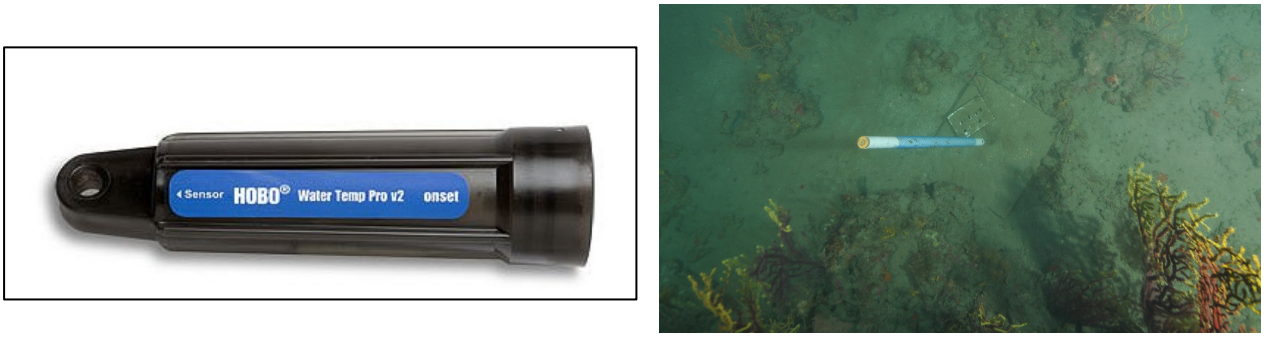

Fig. S1. Temperature sensor (left) and current meter (right) used to characterize the environment in the Catchoff site (Annex)

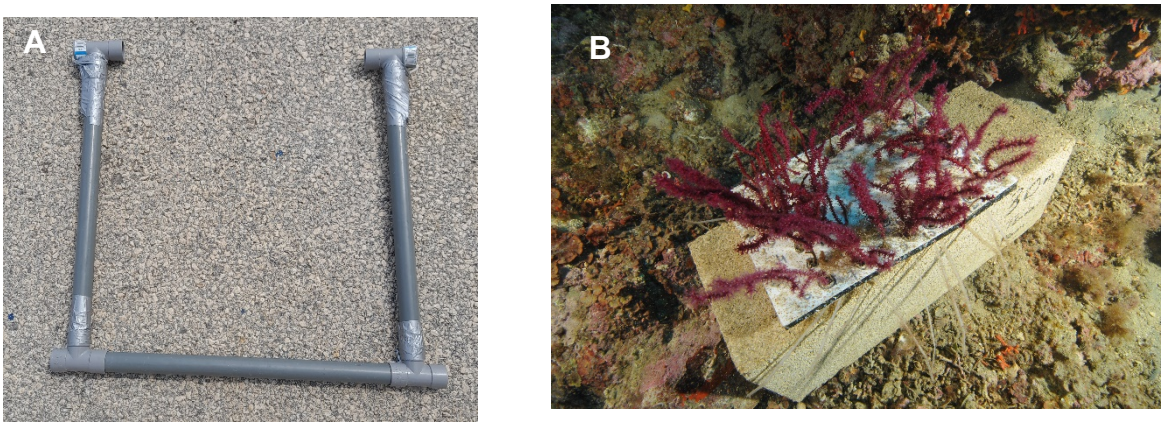

Fig. S2. (A) Open quadrat used to characterize the size structure (50x50cm), and (B) experiment design for the transplantation of *Paramuricea clavata* colonies (samples of colonies are fixed on a plastic plate and numbered)

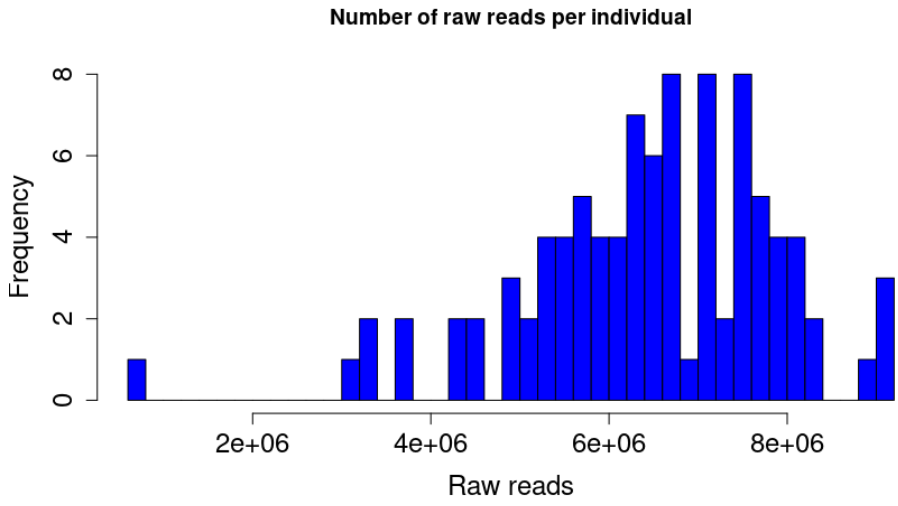

Fig. S3. Distribution of the number of raw reads per individuals obtained with RAD-sequencing

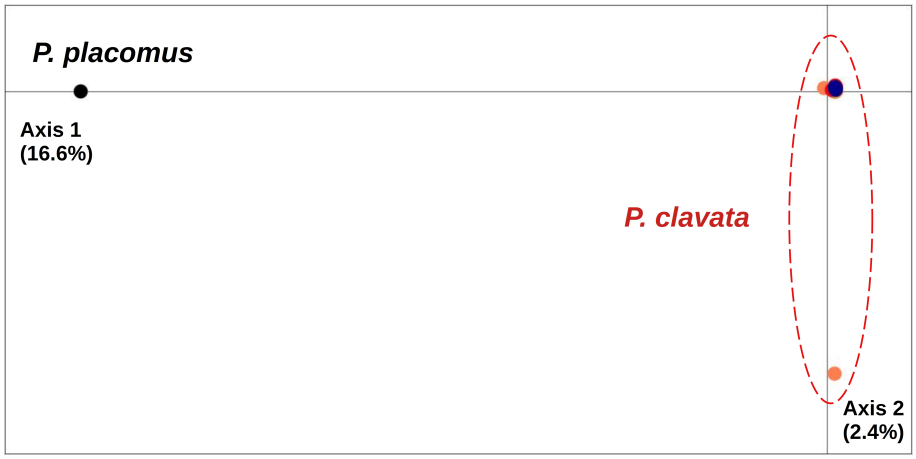

Fig. S4. Results of the preliminary PCA including *P. clavata* and *P. placomus* (one individual). The analysis is based on 45 251 SNPs

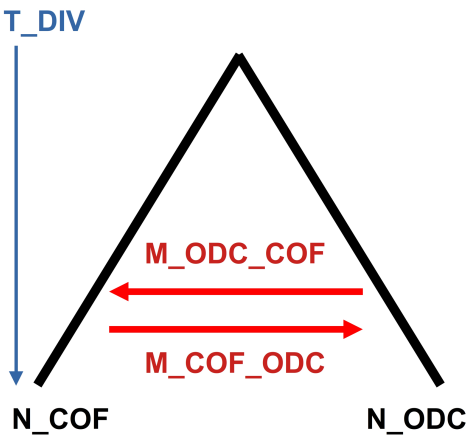

Fig. S5. Model of evolution used for demographic inferences with fastsimcoal2: this is a model of divergence with gene flow. T_DIV: time of divergence; M_ODC_COF and M_COF_ODC: gene flow (forward in time) between the two populations; N_COF and N_ODC: effective sizes of populations COF and ODC, respectively

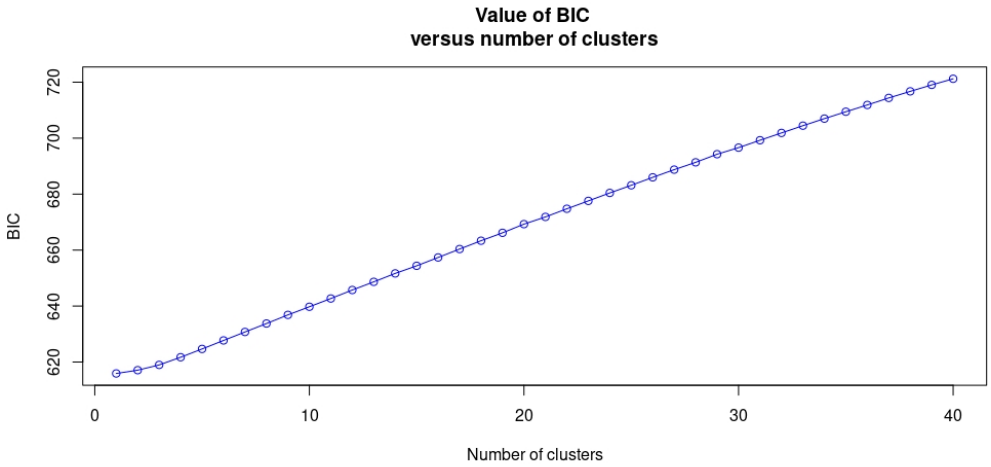

Fig. S6. Evolution of the BIC parameter according to the number of clusters for the DAPC

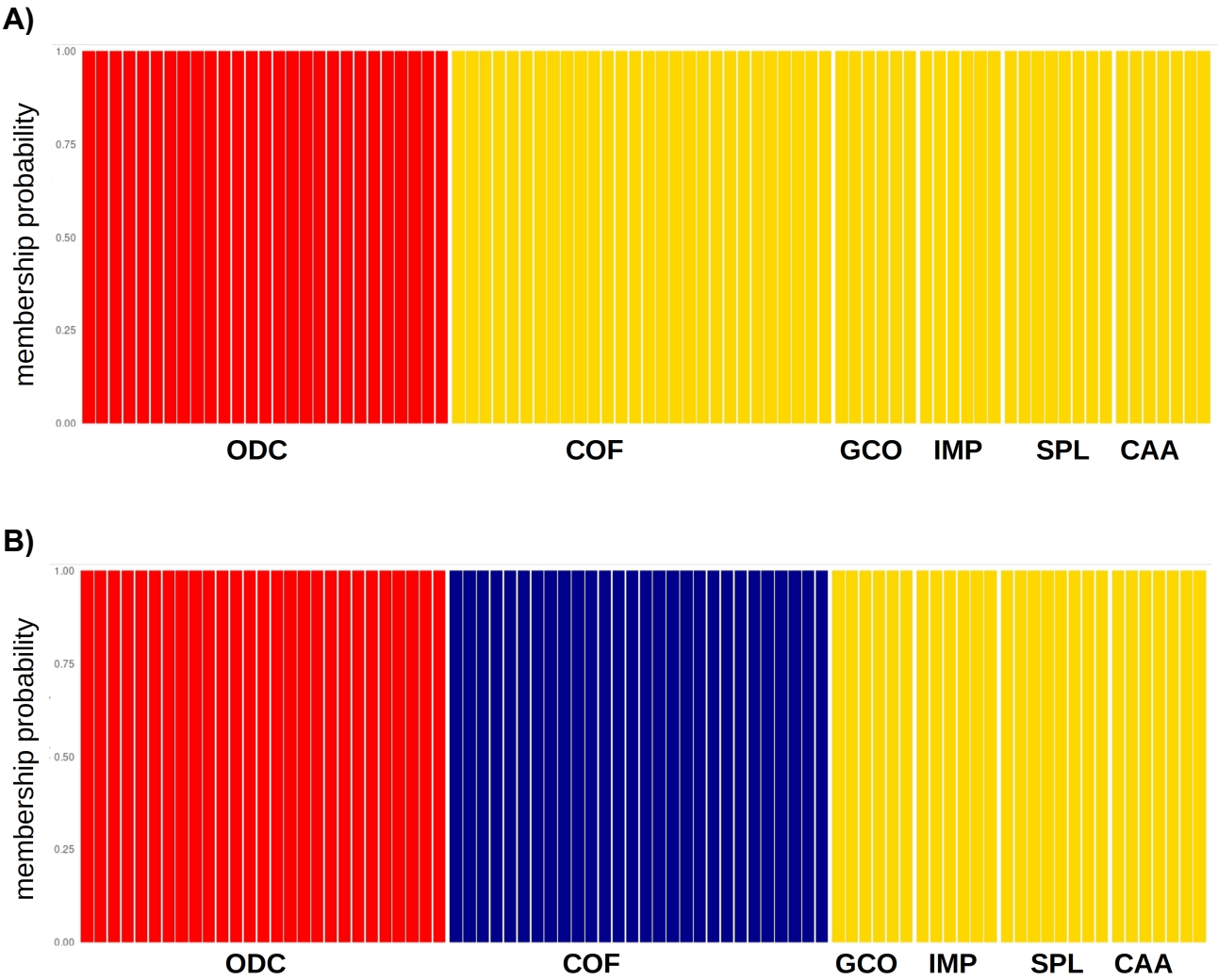

Fig. S7. Barplot presenting the results of the DPAC for (A) K = 2; and (B) K = 3 clusters. ODC: Yeux de chat; COF: Catchoff–Stn A; GCO: Grand Congloue; IMP: Impérial du large; SPL: Sec du petit langoustier; CAA: Cap d'Arme

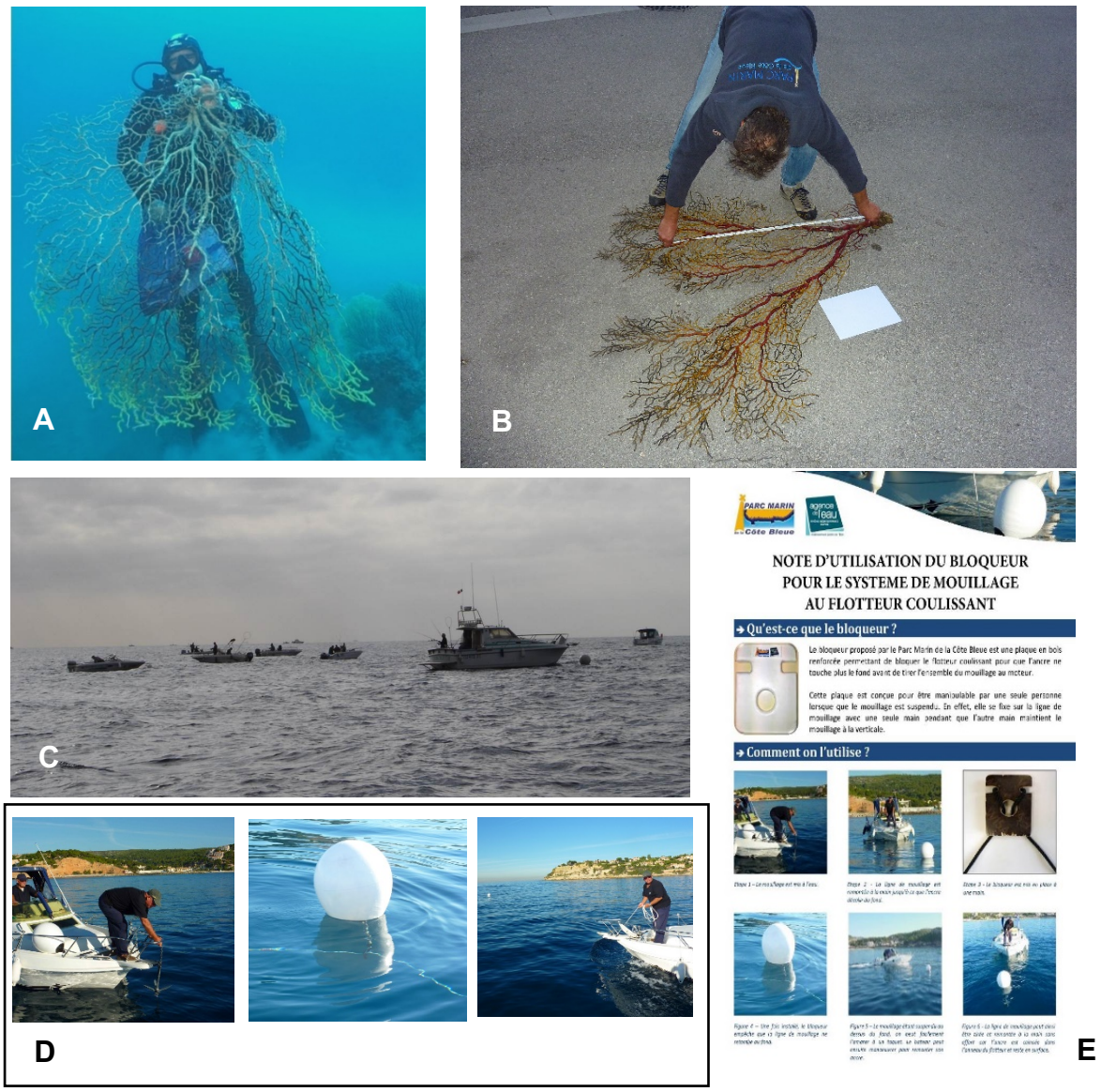

Fig. S8. Impact of anchoring on giant *Paramuricea clavata* populations: (A) Giant colony of *P. clavata* (height: 170 cm) ripped apart by an anchor belonging to a small fishing boat; (B) giant colony of *P. clavata* (height: 152 cm) brought to the Marine Park of the 'Côte Bleue' by a recreational fisherman; (C) group of fishing boats anchored on gorgonian population (15th November 2016); (D) a recreational boat moored by dropping anchor attached to a sliding buoy on the Catchoff site. The boat is attached to the buoy by means of rope or chain, which is, in turn, attached to the anchor which sits on (or is fixed to) the floor of the water body. (E) Instructions regarding using a blocker for mooring with a sliding buoy (method implemented by the Marine Park of the 'Côte Bleue' to prevent damaging the giant gorgonians). A blocker is a reinforced wooden plate which prevents the sliding buoy from moving by keeping straight the rope and the chain attaching the buoy to the boat and the anchor, respectively. The blocker can be installed in 2 steps: first, the mooring anchor with the sliding buoy is dropped until it touches the floor of the water body. Next, the mooring chain is pulled. When the anchor begins to move upwards, the blocker is installed on the rope to keep it straight and to keep the chain away from the bottom.