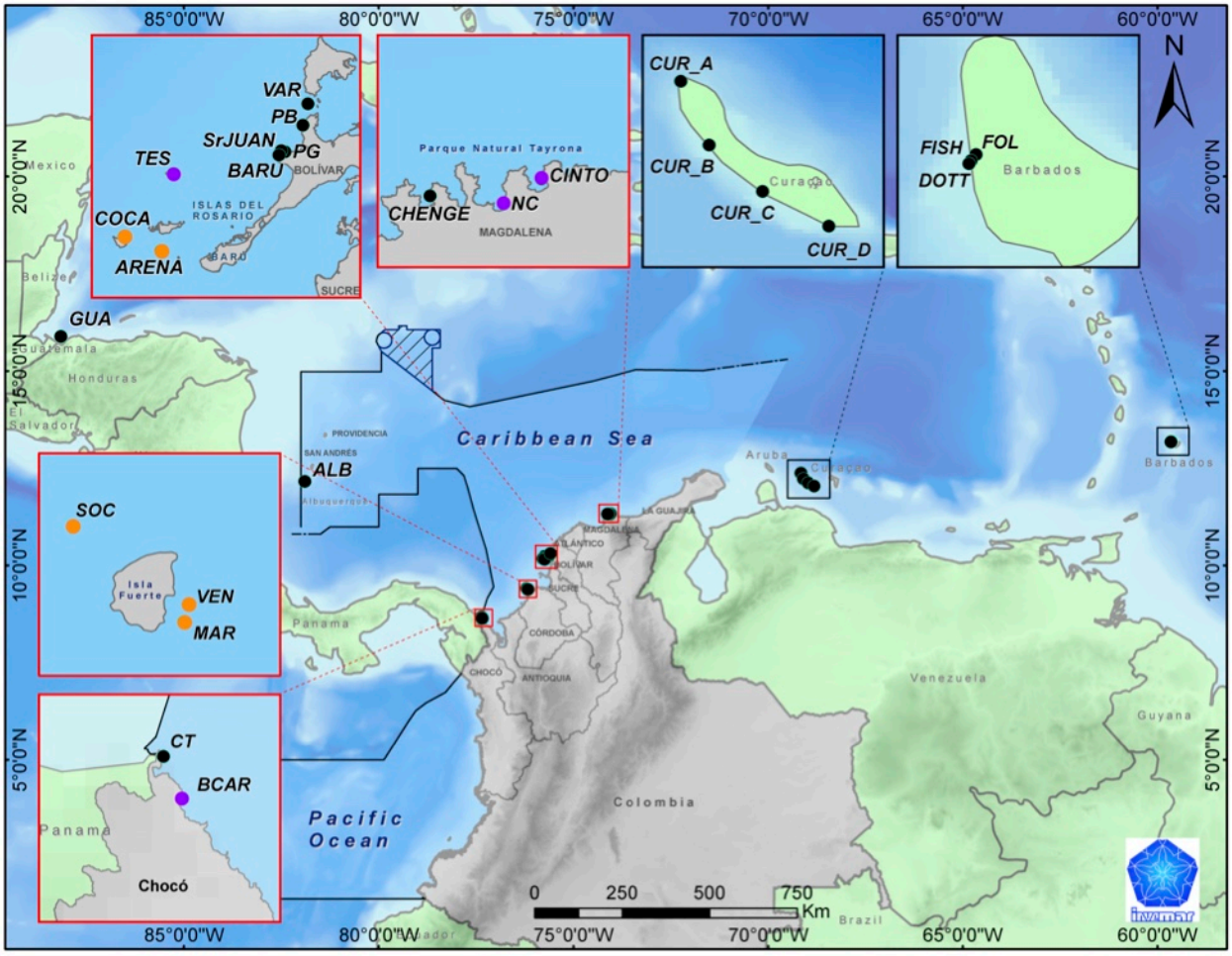
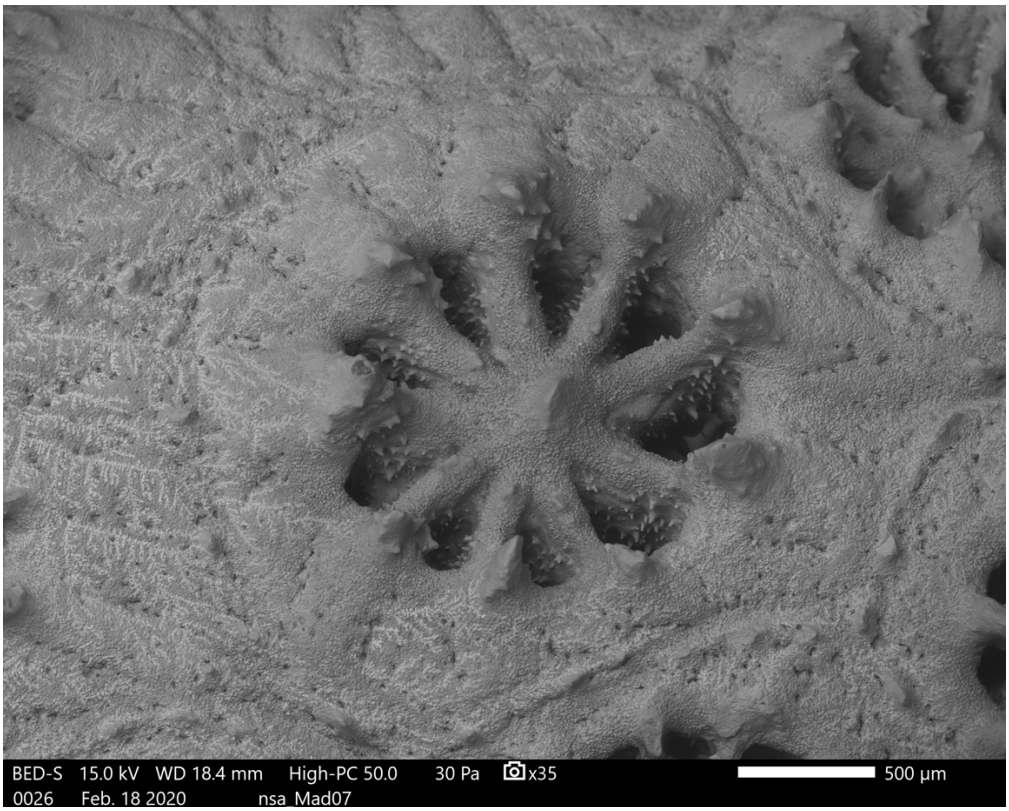
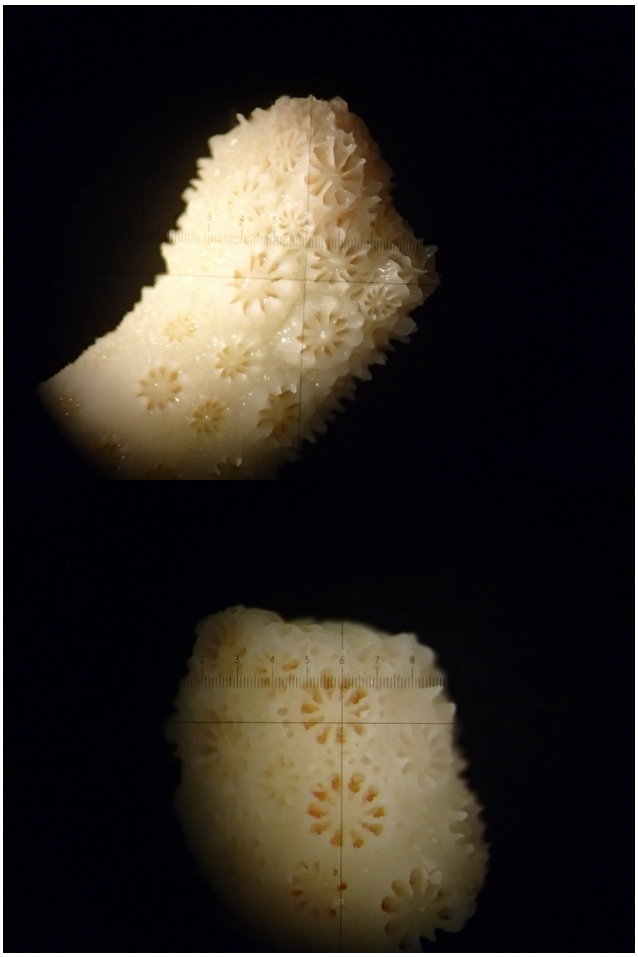


Supplementary Figure 1a. Sampling localities of M. auretenra in the Caribbean Sea. Red squares show a close up of the samples from Colombia. Black squares show a close up of the samples in Curacao and Barbados. Localities with less than 10 samples are represented in purple dots. Orange localities are grouped in areas below of 2.5km2 of distance: Isla Rosario (COCA and ARENA grouped) and Isla Fuerte (SOC, VEN and VEN grouped).



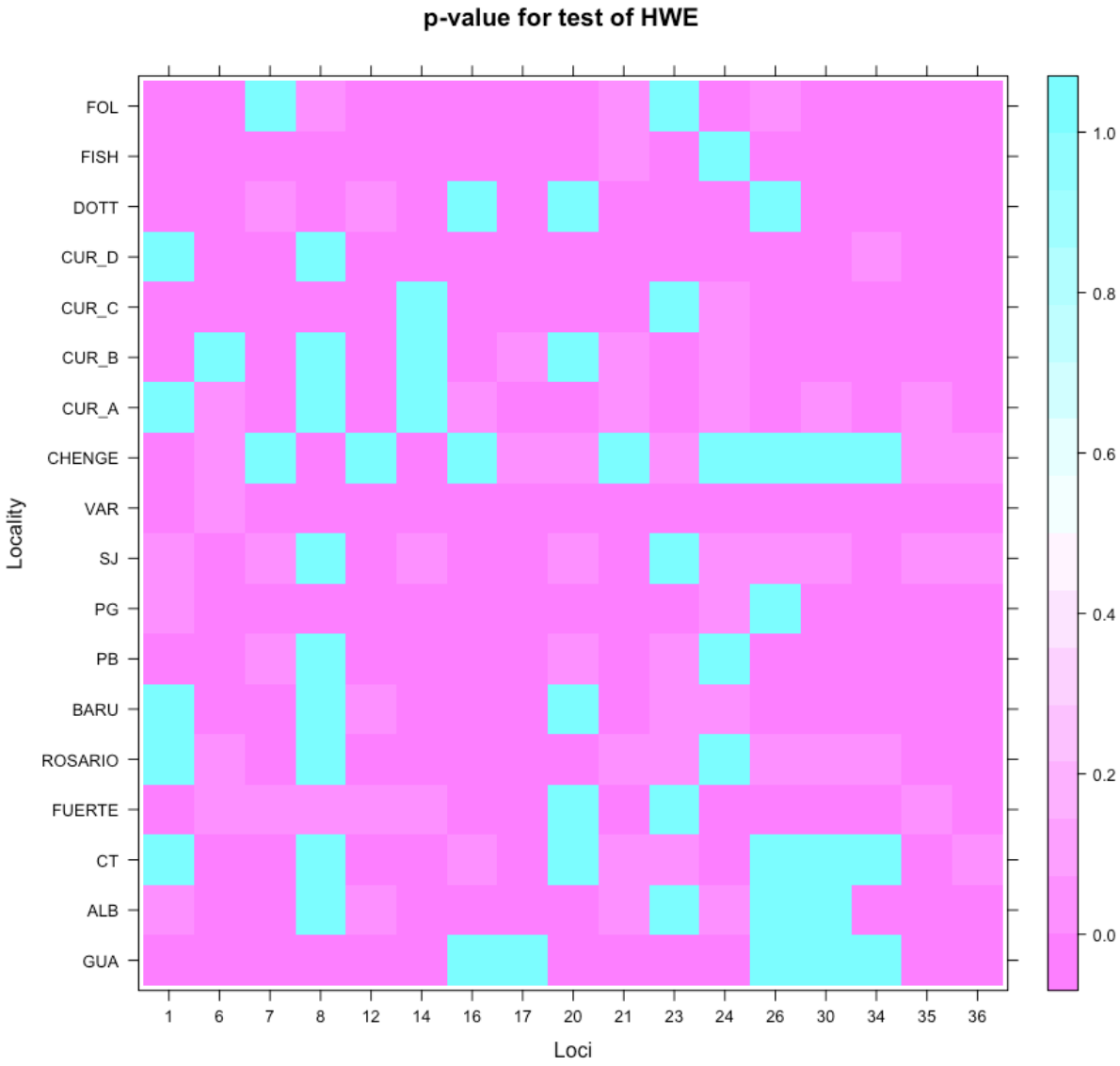
Supplementary Figure 2a. Samples of Madracis auretenra from Curacao under electron microscopy-SEM (Zeiss Supra 40VP FE-SEM).



Supplementary Figure 2b. detail of calyxes in sample of *Madracis auretenra* from Curacao under stereoscope-Zeiss Stemi 305. The scales are presented in millimeters.

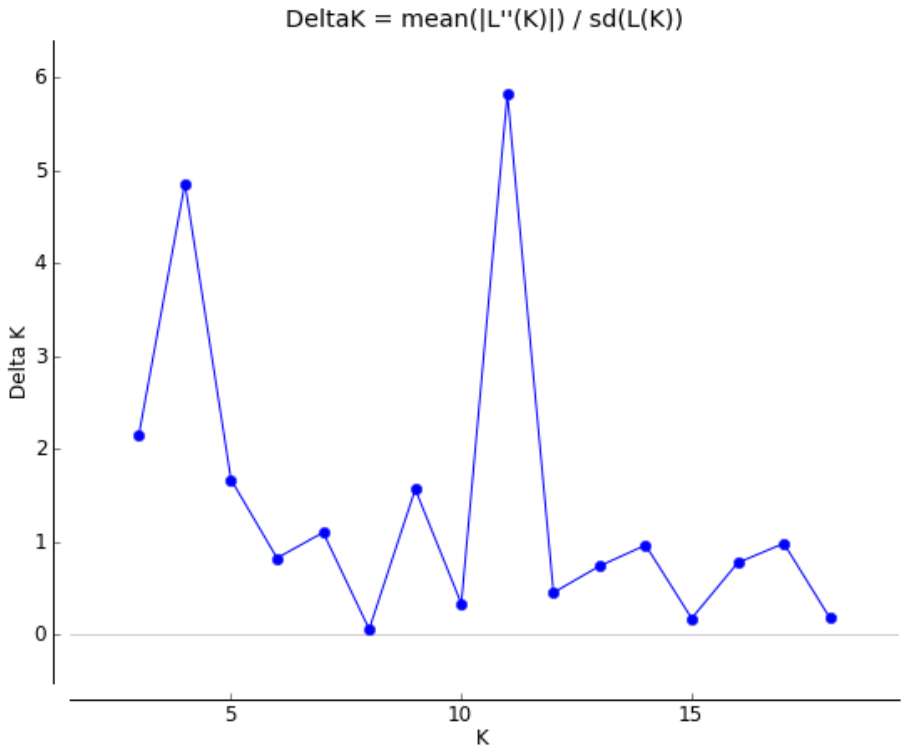
Supplementary Figure 2c.

Thirteen samples (6, 3, 2 and 2 samples from Colombia, Curacao, Barbados and Guatemala, respectively) were amplified using COX1, primers LCO1 490 5' - GGTCAACAAATCATAAAGATATTGG and HCO2 198 5' - TAAACTTCAGGGTGACCAAAAAATCA (Folmer et al., 1994) and 28s, primers 28S.F63sq 5'-AATAAGCGGAGGAAAAGAAAC and 28S.R635sq 5'-GGTCCGTGTTTCAAGACGG (Stolarski et al., 2011). The reactions were carried out in 10µl, with 1µl of DNA diluted at 20µM in Buffer AE (QIAGEN DNeasy Blood & Tissue kit), 5µL MyTaq Red Mix de Bioline, 0,2µL of each primer, 3,6µL of molecular grade. The PCR conditions for COX1 were 95°C for 1 min, then 35 cycles of 30 s at 95°C, 30 s at 40°C, and 90 s at 72° C, followed by 10 min at 72°C; and PCR conditions for 28s were 95°C for 5 min, then 30 cycles of 30 s at 94°C, 60 s at 54°C, 90 s at 72°C, followed by 5 min at 72°C. the samples were sent to the Core Genomics Facility at the University of Sheffield, previously cleaned using the ExoProStar 1 step Kit from Fisher-Scientific. the amplification of the samples was matched with sequences of *M. auretenra* (95,43 - 99.85% similarity) in NCBI database.

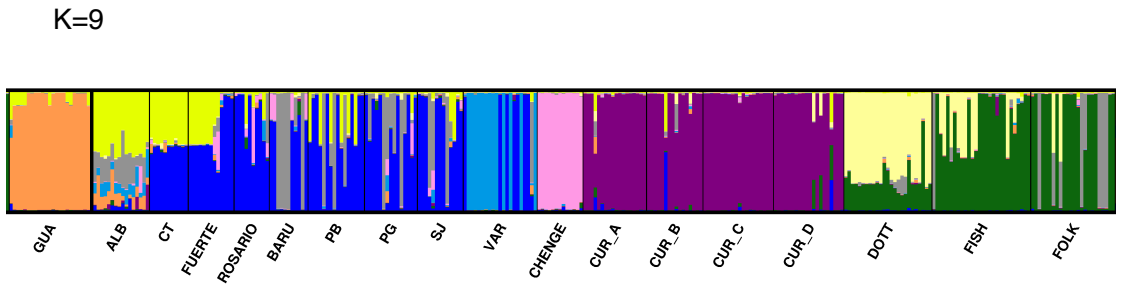


Supplementary Figure 2d. Probability of deviation from Hardy Weinberg Equilibrium (HWE) deviation for each locality. Localities with $p<0.05$ are in pink and localities with $p>0.05$ are in blue colours.

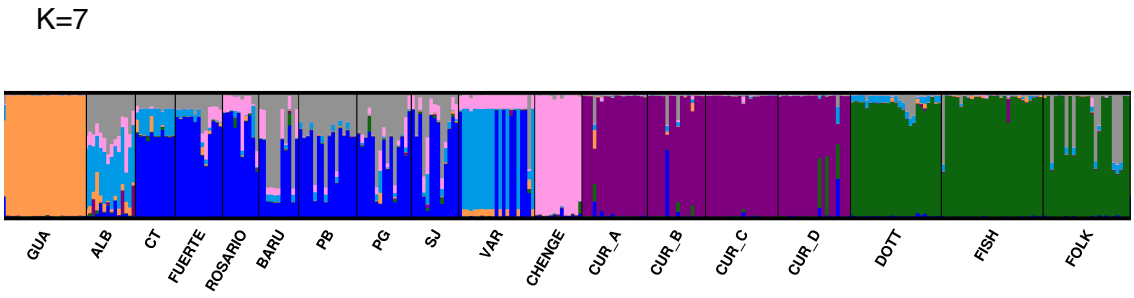
Supplementary Figure 3a. DeltaK. Values obtained using STRUCTURE HARVESTER, after a 20 runs per K in Structure.



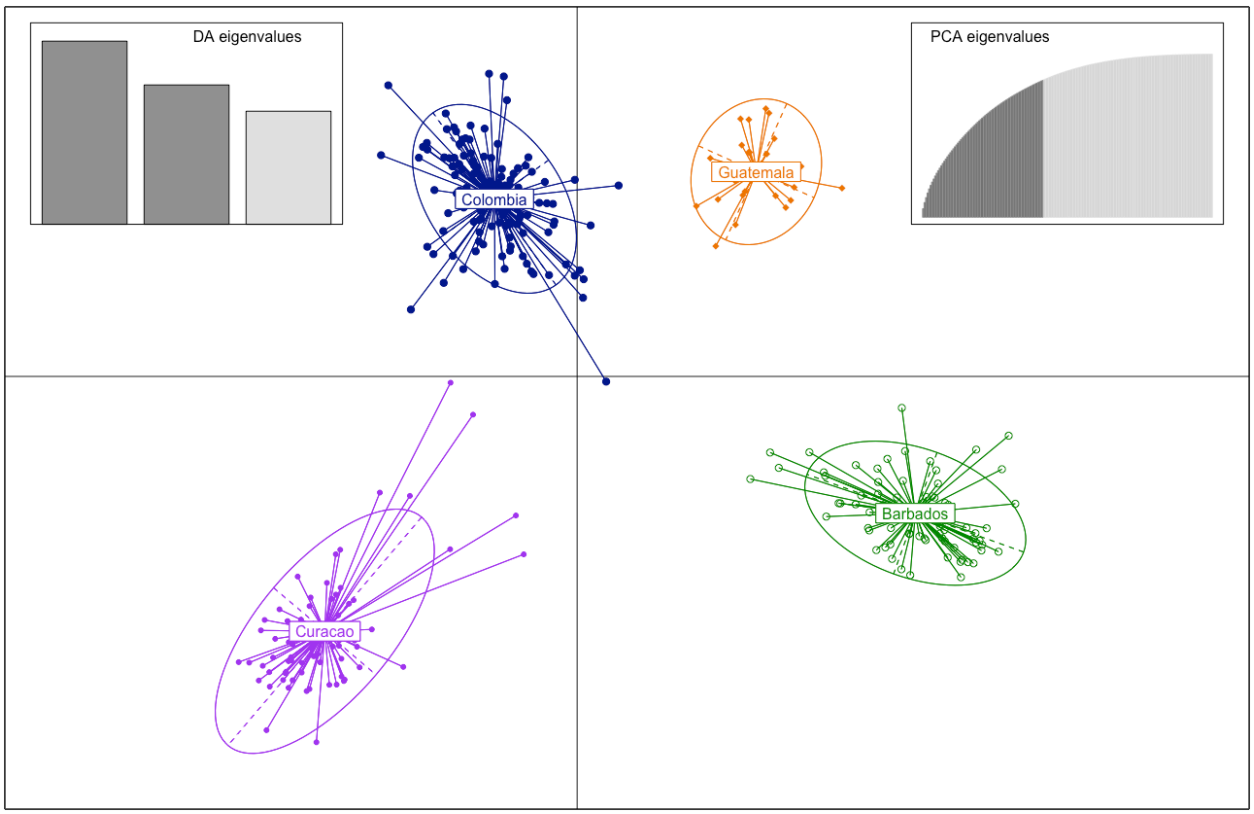
Supplementary Figure 3b. Individual genotype assignment for *M. auretenra* to clusters (K) as inferred by STRUCTURE for all studied sites with K= 9



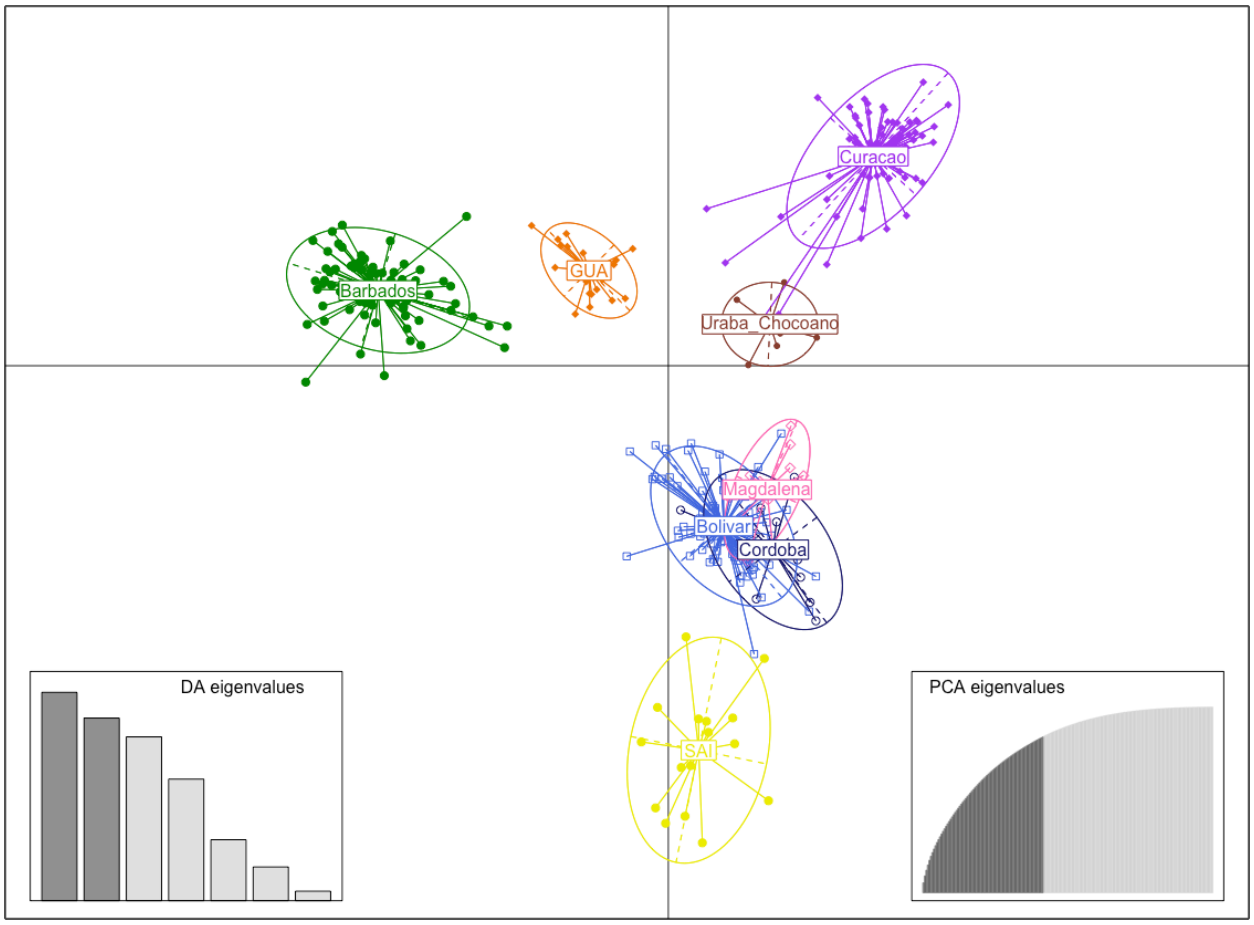
Supplementary Figure 3c. Individual genotype assignment for *M. auretenra* to clusters (K) as inferred by STRUCTURE for all studied sites with K= 7



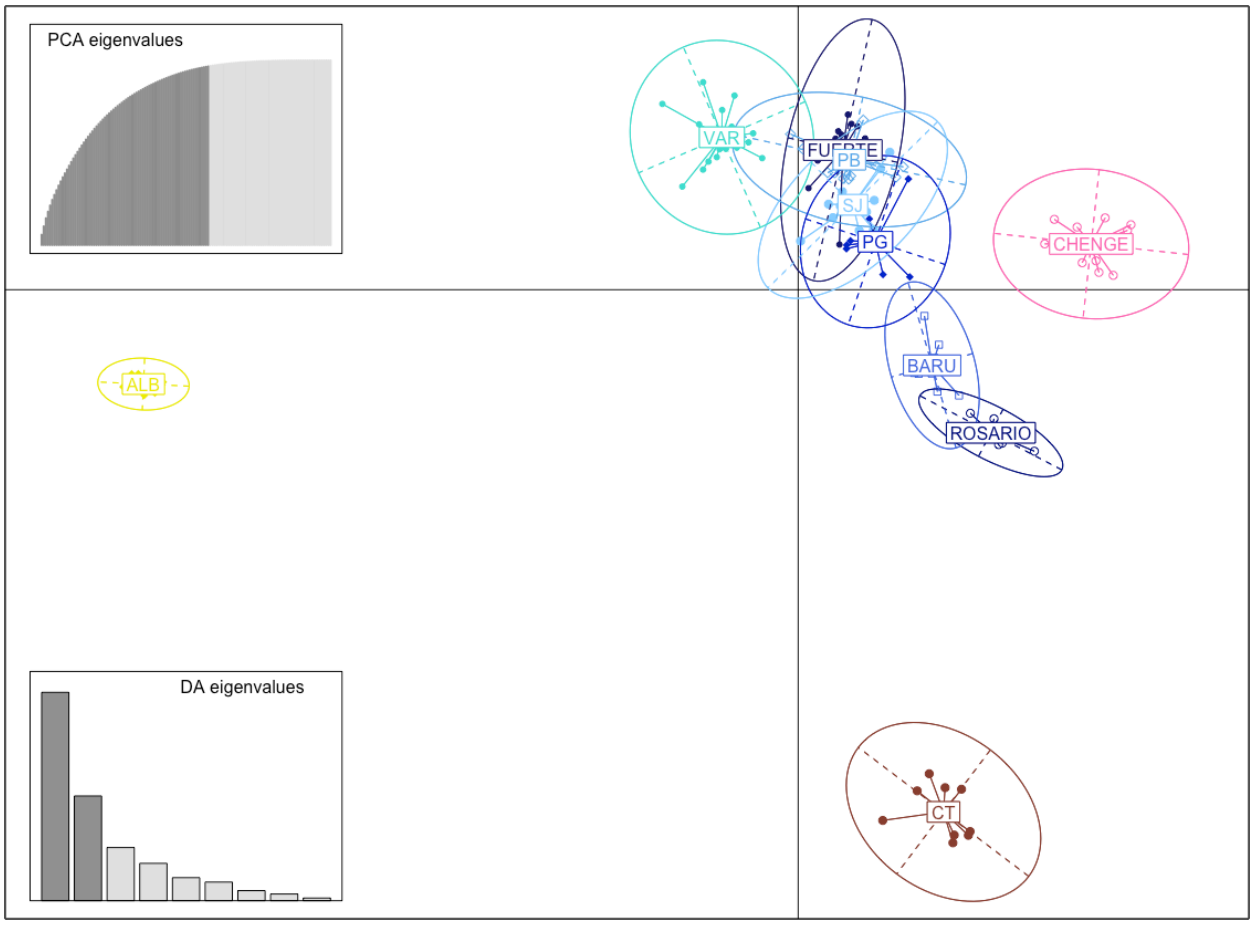
Supplementary Figure 4a. DAPC using the first two principal components by Country



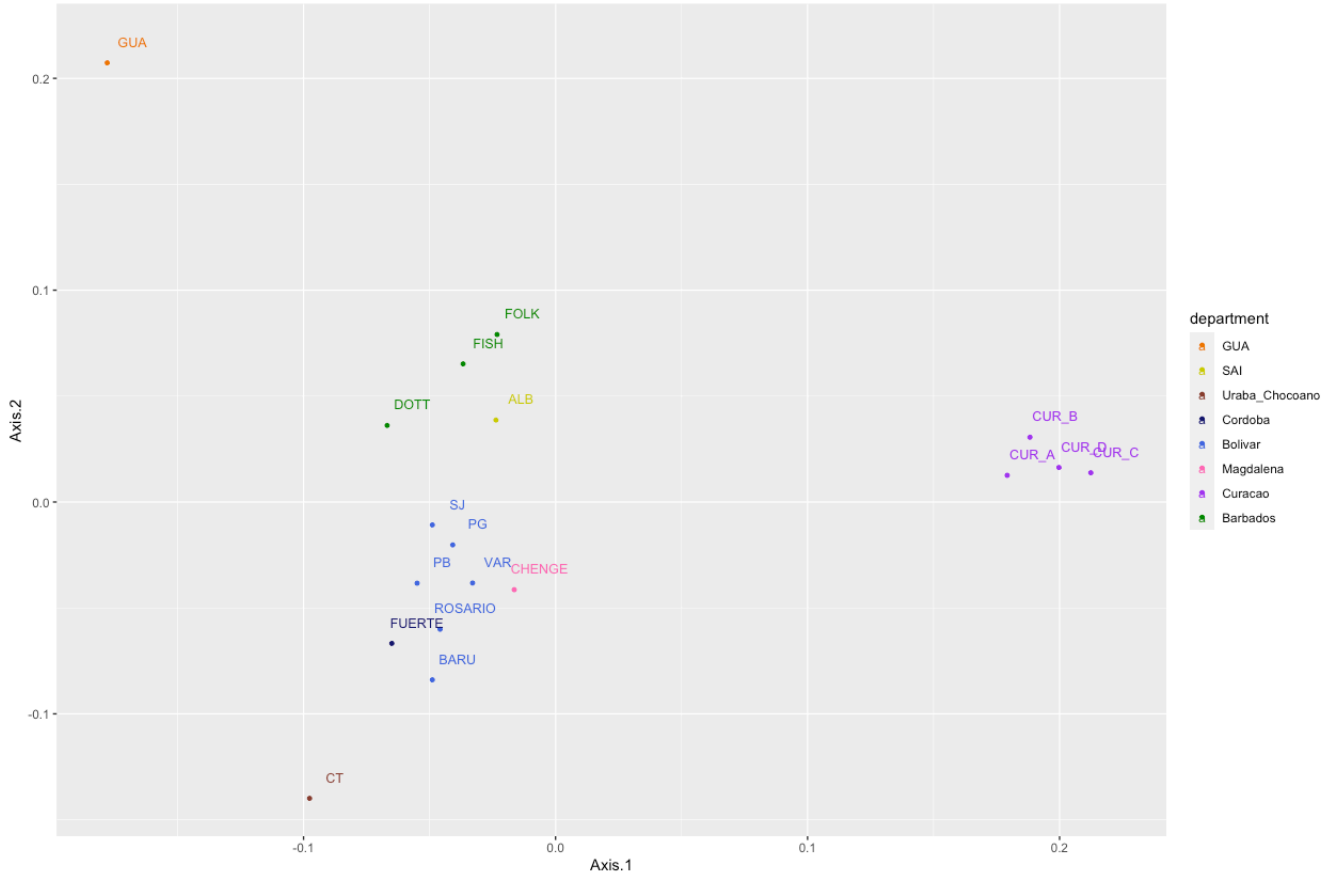
Supplementary Figure 4b. DAPC using the first two principal components by Department.



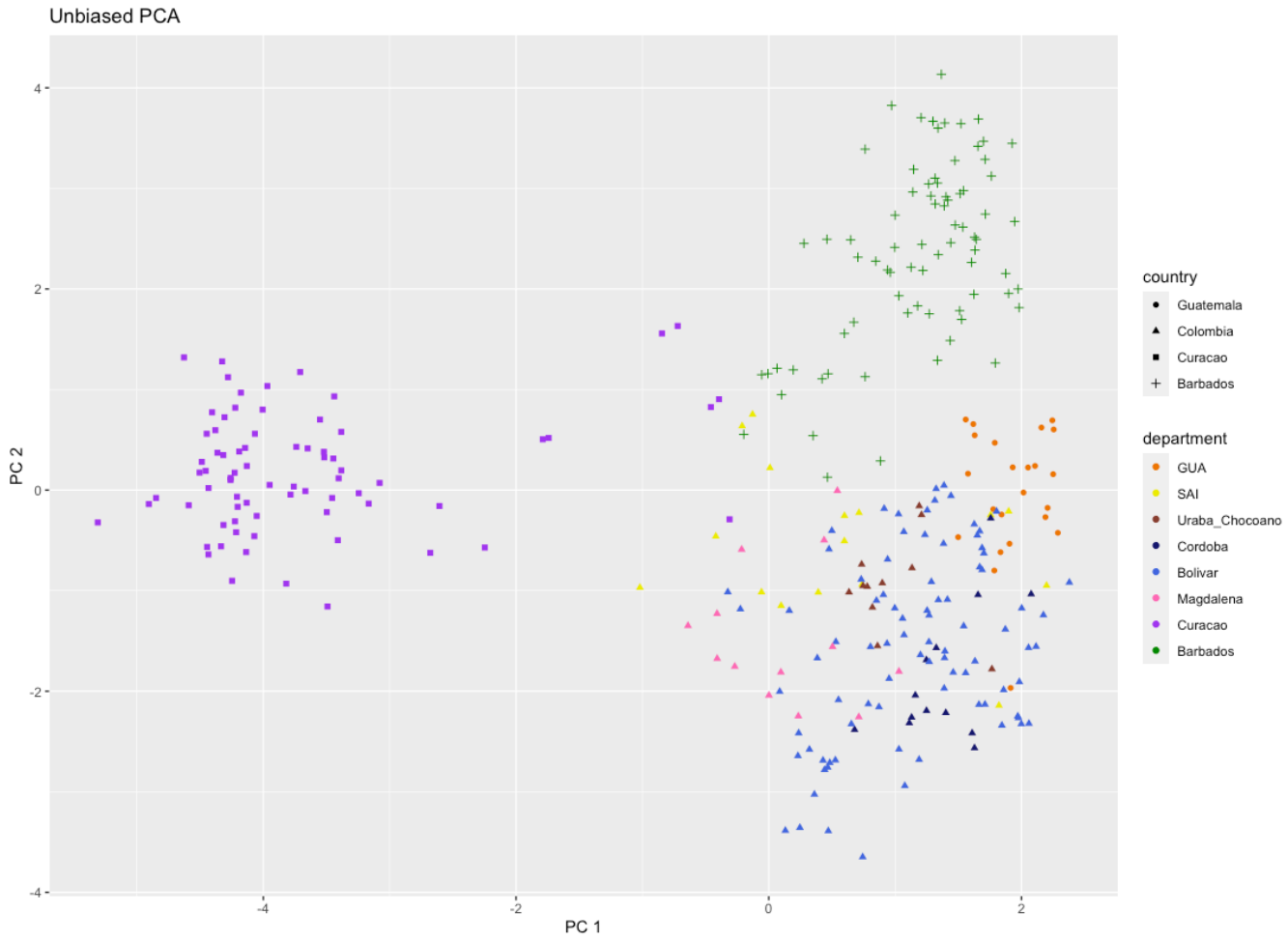
Supplementary Figure 4c. DAPC using the first two principal components in Colombia.



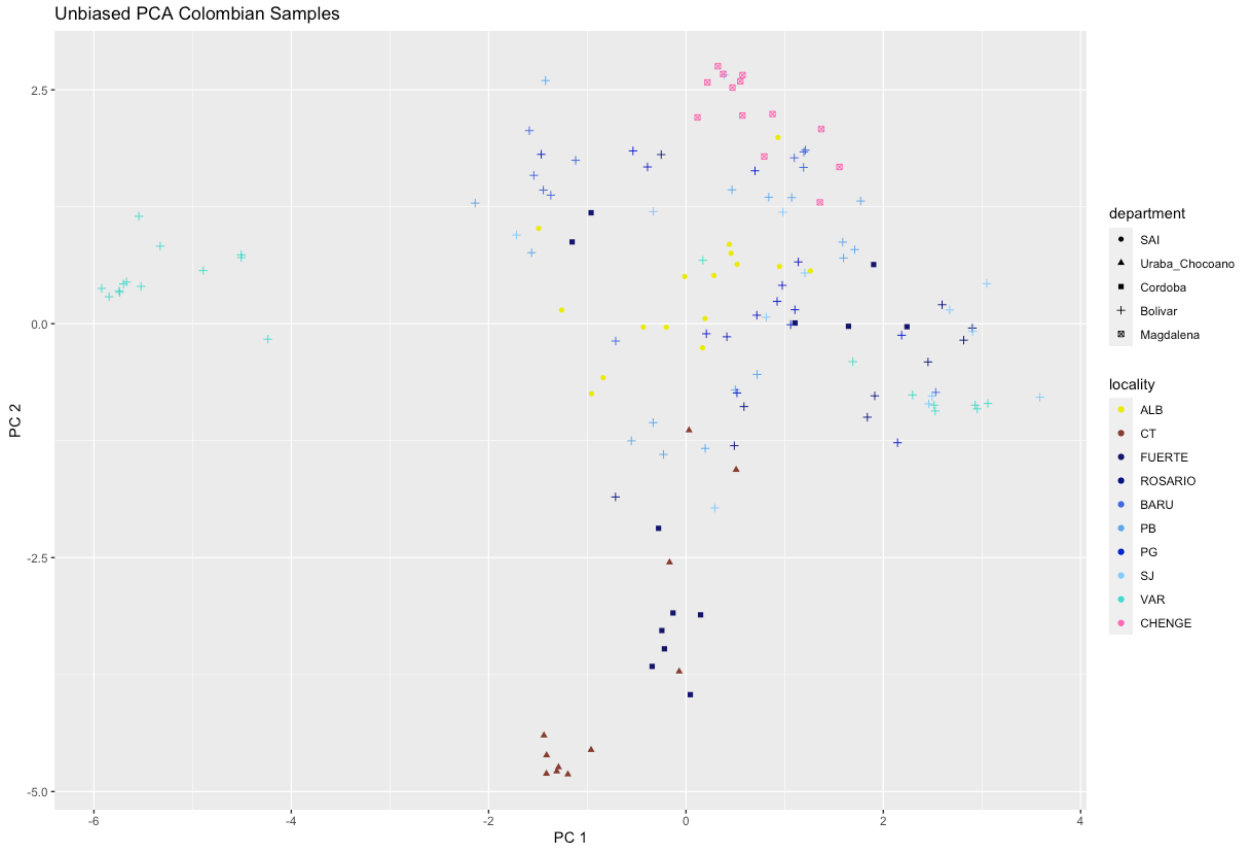
Supplementary Figure 5a. PCoA (Principal Coordinate Analysis) using the first two principal components by Department



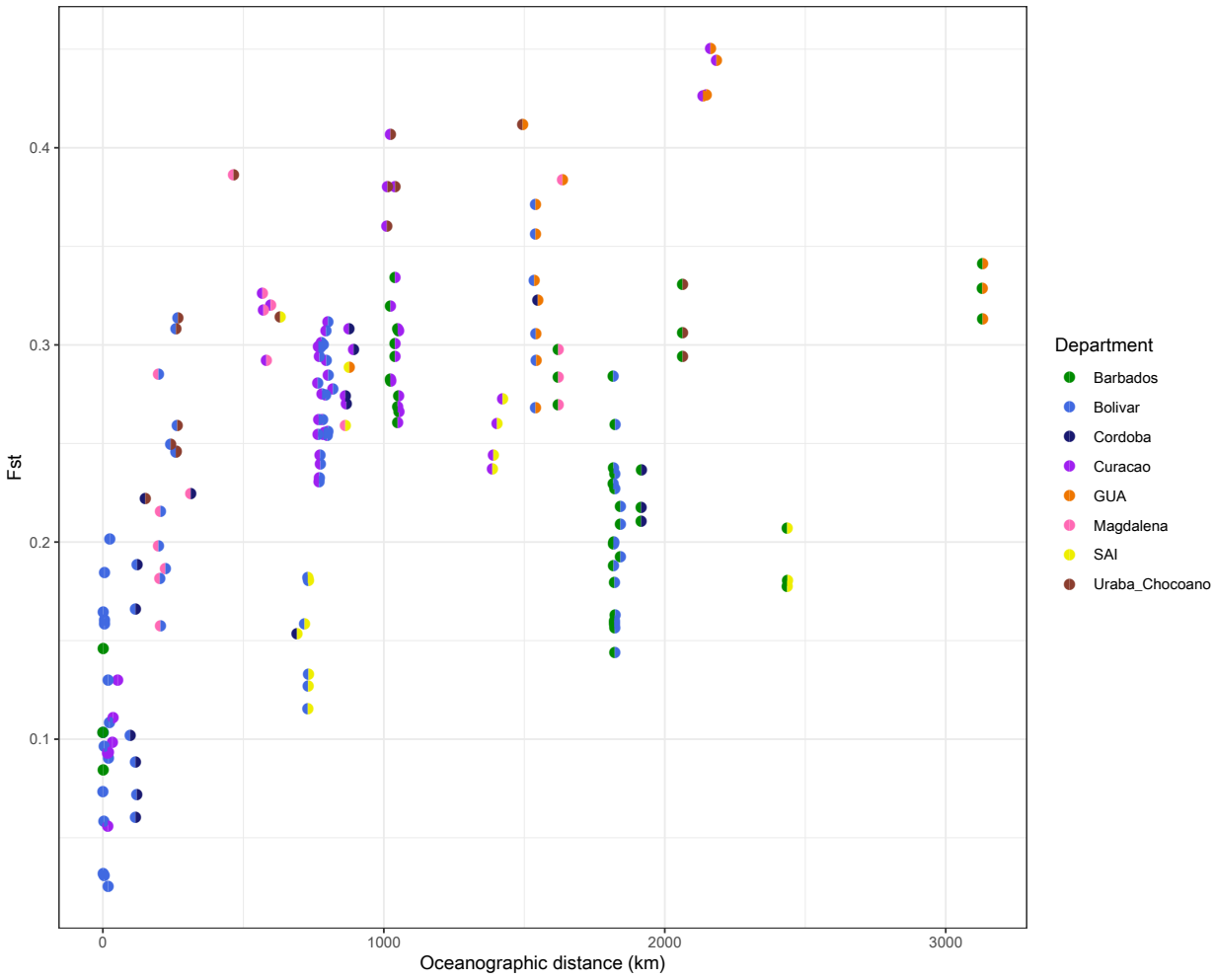
Supplementary Figure 5b. PCA by department



Supplementary Figure 5c. PCA by localities in Colombia



Supplementary Figure 6a. Genetic isolation by distance using pairwise calculations Fst and oceanographic distance.



Supplementary Figure 7a. Population assignment showing the percentage of the population per locality