Supplementary material

Ancestral hybridization yields evolutionary distinct hybrids lineages and species boundaries in crocodiles, posing unique conservation conundrums

Gualberto Pacheco-Sierra, Ella Vázquez-Domínguez, Jessica Pérez-Alquicira, Marco Suárez-Atilano, Jerónimo Domínguez-Laso

Figures S2-S5

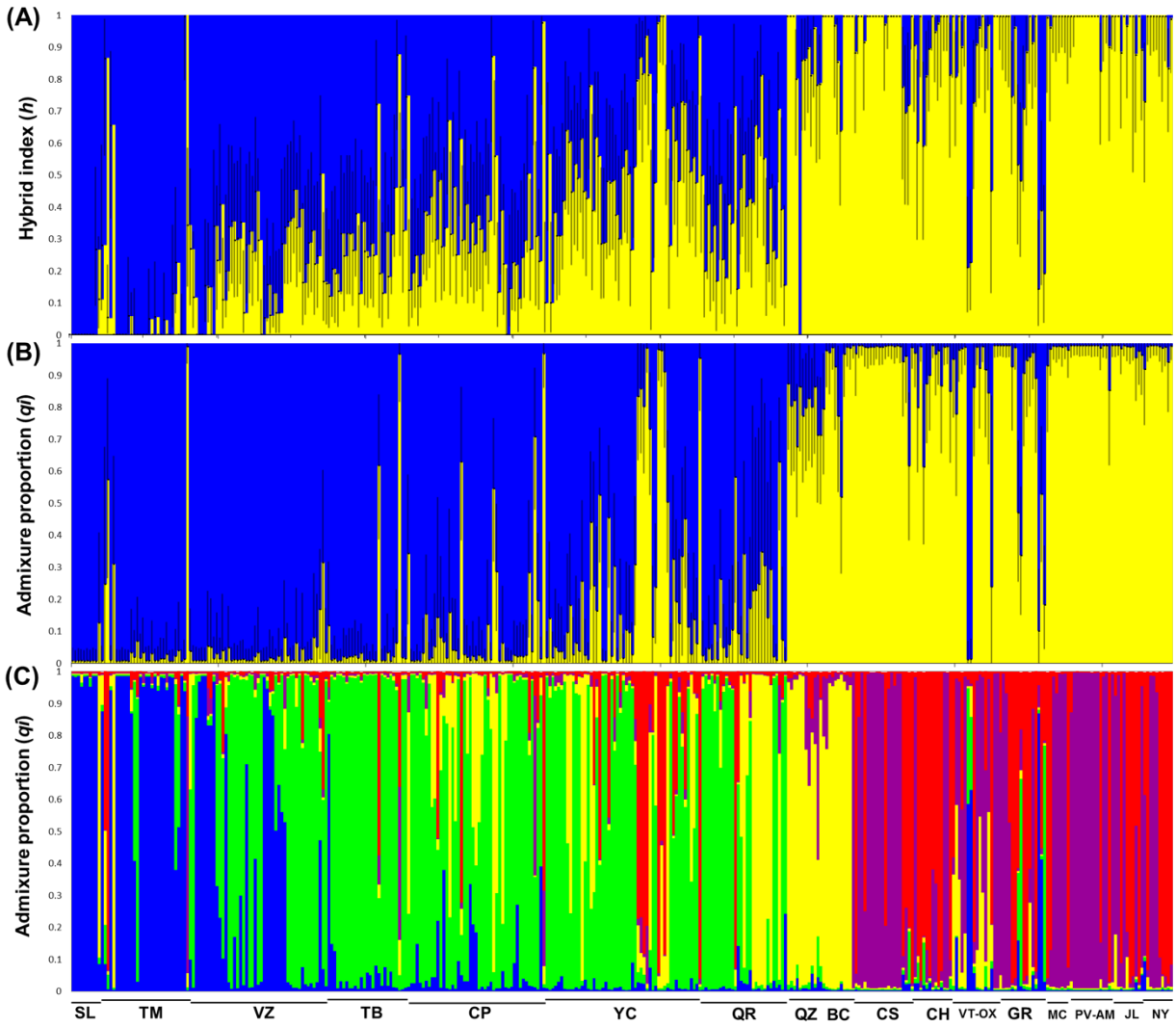

Fig. S2. Genetic structure, admixture and hybridization in *Crocodylus acutus* and *C. moreletii* from Mexico. Bar plots of (**A**) Maximum likelihood estimates of hybrid indexes (Buerkle, 2005), obtained with nuclear markers (microsatellites), where solid lines are 95% confidence intervals and blue and yellow bars represent the statistical proportion of the genome inherited from *C. moreletii* (1-*h*) and *C. acutus* (*h*), respectively. Admixture proportions obtained with STRUCTURE, with (**B**) *K*=2 and (**C**) *K*=5; in the latter the different colors indicate ancestry for *C. acutus* from Caribbean islands (yellow*), C. acutus* from Pacific (group 1; purple), *C. acutus* from Pacific (group 2; red), *C. moreletii* ancestry (blue) and hybrids (green). Samples are ordered following the geographic cline from northeast to southeast along the Gulf of Mexico and Caribbean, following then along the Pacific from southwest to northwest (see Figure 1).

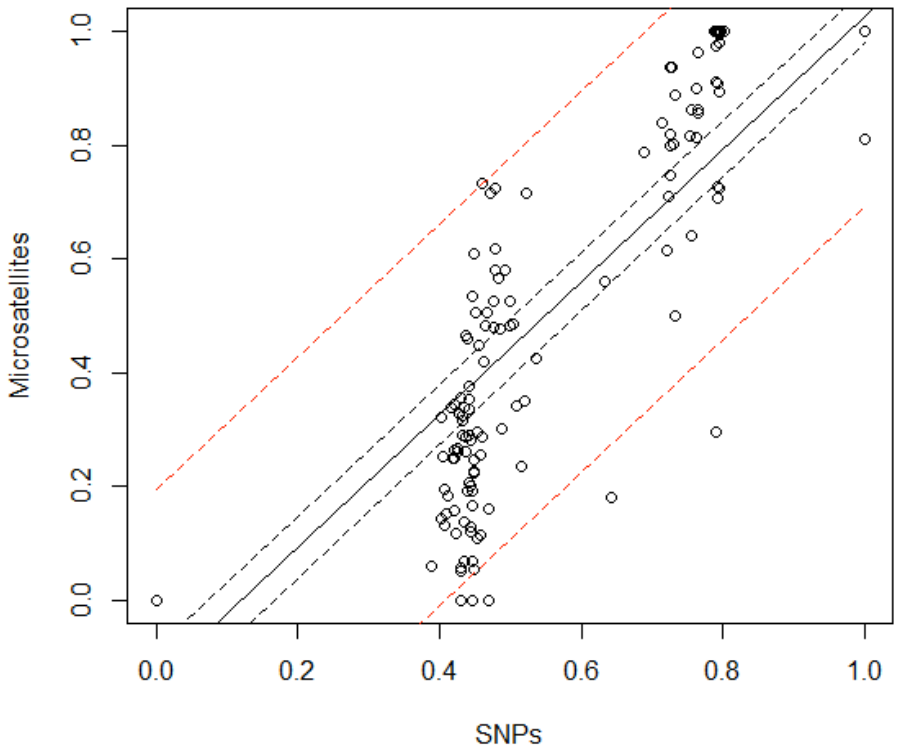

Fig. S3. Congruence between hybridization metrics. Regression analysis between the hybrid indices estimated based on microsatellites and on SNPs loci (R^2=0.79, $F_{1,170}$=659, P<0.05) for *Crocodylus acutus* and *C. moreletii* from Mexico. Confidence and prediction intervals are shown as black and red dashed lines, respectively.

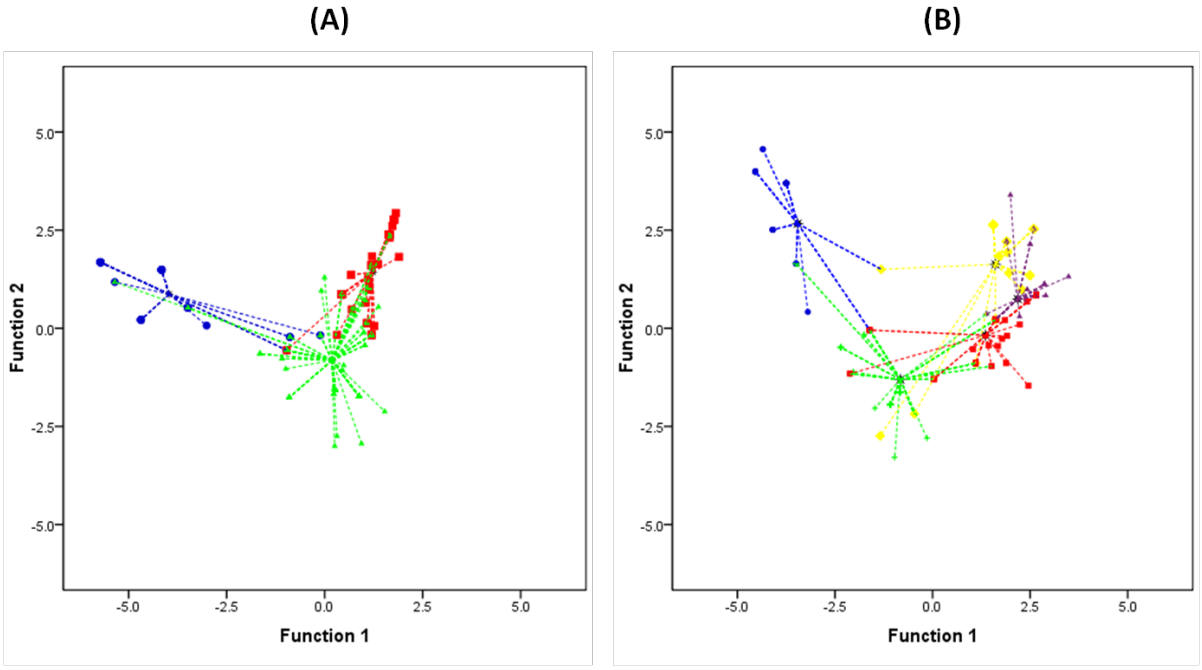

Fig. S4. Canonical discriminant analysis based on 123 mtDNA polymorphic sites for *Crocodylus acutus* and *C. moreletii*. (**A**) Dot colors are based on the statistical proportion of the hybrid index: non-admixed *C. moreletii* (blue), non-admixed *C. acutus* (red) and admixed (green). (**B**) Dot colors are based on the admixture proportions (*qi*) from the STRUCTURE results (*K*=5): *C. acutus* ancestry (Caribbean islands: yellow, Pacific group 1: purple, Pacific group 2: red), *C. moreletii* ancestry (blue) and hybrids (green).

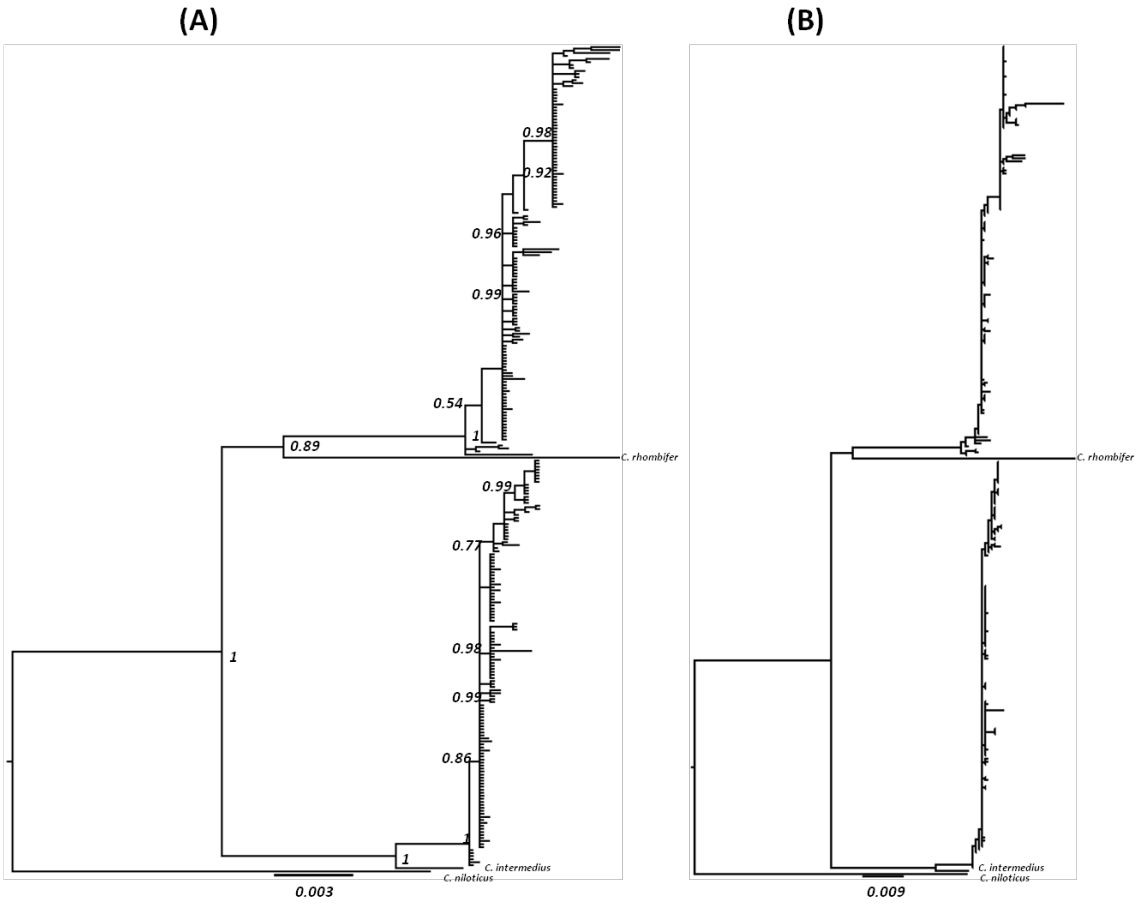

Fig. S5. Phylogenetic relationships among *Crocodylus* species. (**A**) Bayesian and (**B**) Maximum likelihood phylogenetic trees based on mtDNA sequences for *Crocodylus acutus* (bottom clade) and *C. moreletii* (upper clade) from Mexico. Sister species *C. intermedius* and *C. rhombifer* were included, whereas *C. niloticus* was used as outgroup. The scale bar represents substitutions per site.