

Supplemental Figure S1. Phylogeographic Association of *F. grandis* haplotypes. Haplotypes from the northwest Gulf of Mexico, inferred using concatenated sequences (1088 bp) of three mtDNA segments: Control Region, ND2, and ND5, are numerically identified with an acronym at the tip of the branches, and each individual carrying a specific haplotype is geographically identified with a color-coded symbol (see inset) corresponding to its locality of capture. Tree is the ML consensus of 1,000 trees, rooted using *F. heteroclitus* as an outgroup.