

Supplementary Figures

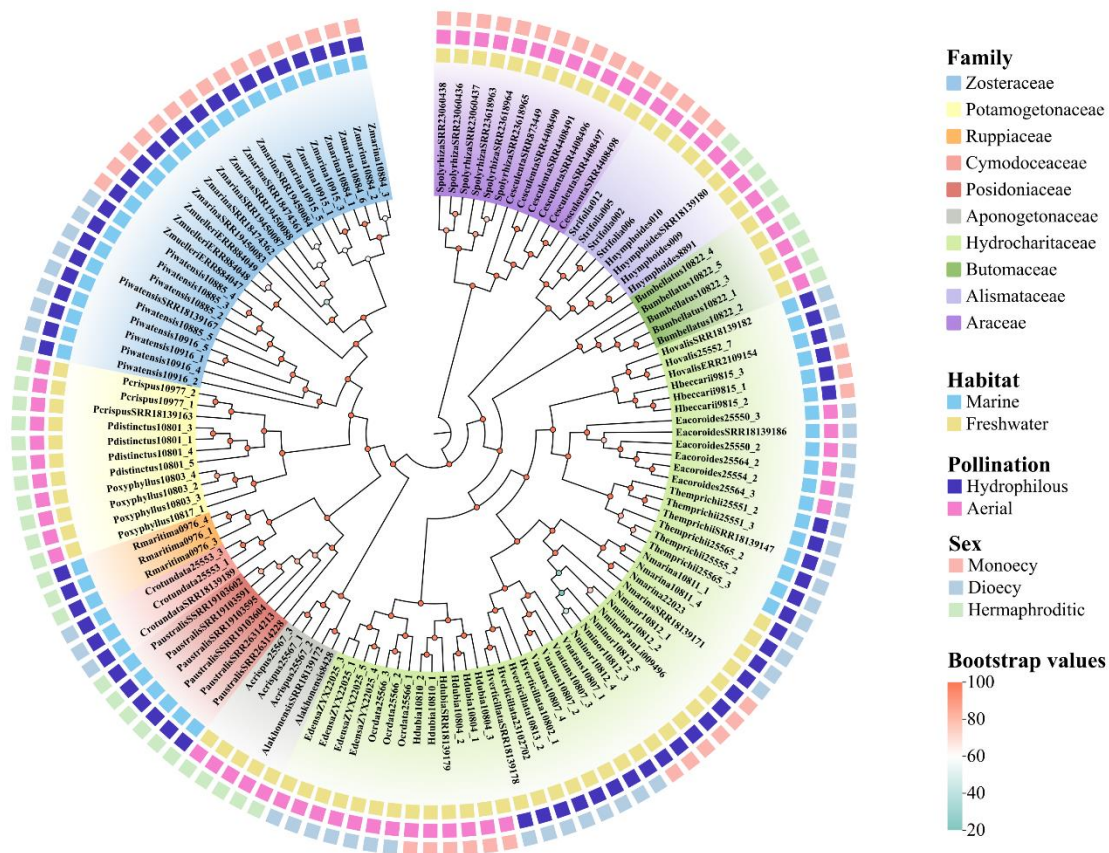


Fig. S1 The ML tree based on 127 individuals. Dots in the nodes of phylogenetic tree represent the bootstrap supporting scores and the colored squares from the inner to the outer layers represent the family, habitat, pollination, and sexual system for each species, respectively.

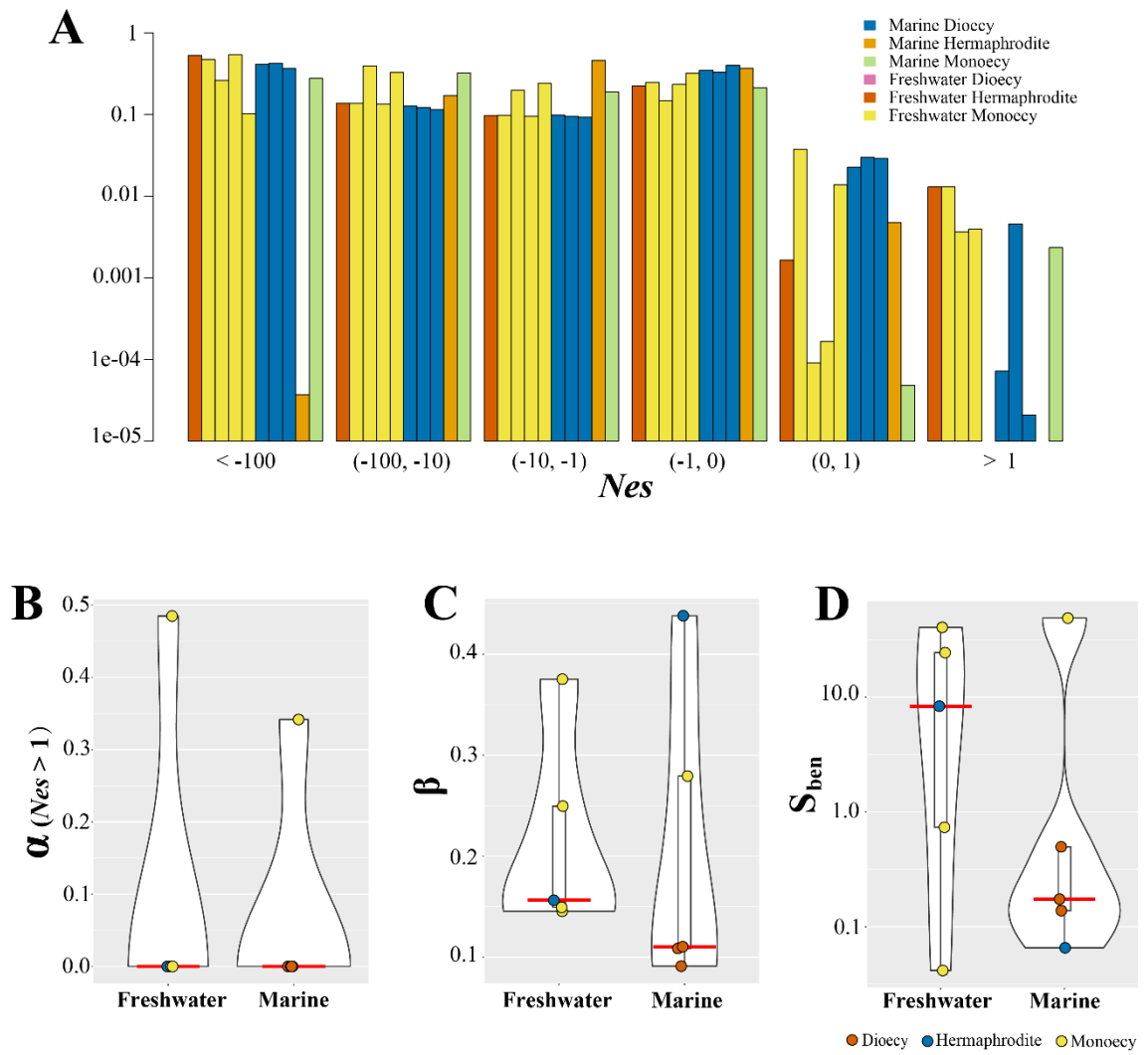


Fig. S2 The distributions of fitness effects of new mutations (DFE) for seagrasses based on sexual system and living environment. (A) Histograms for the proportions of mutations under various selective strength from $N_e s < -100$ to $N_e s > 1$; (B) The violin plots for proportions of fixed adaptive mutations (α), (C) the shape parameter (β), and (D) the selective strength for beneficial mutations.

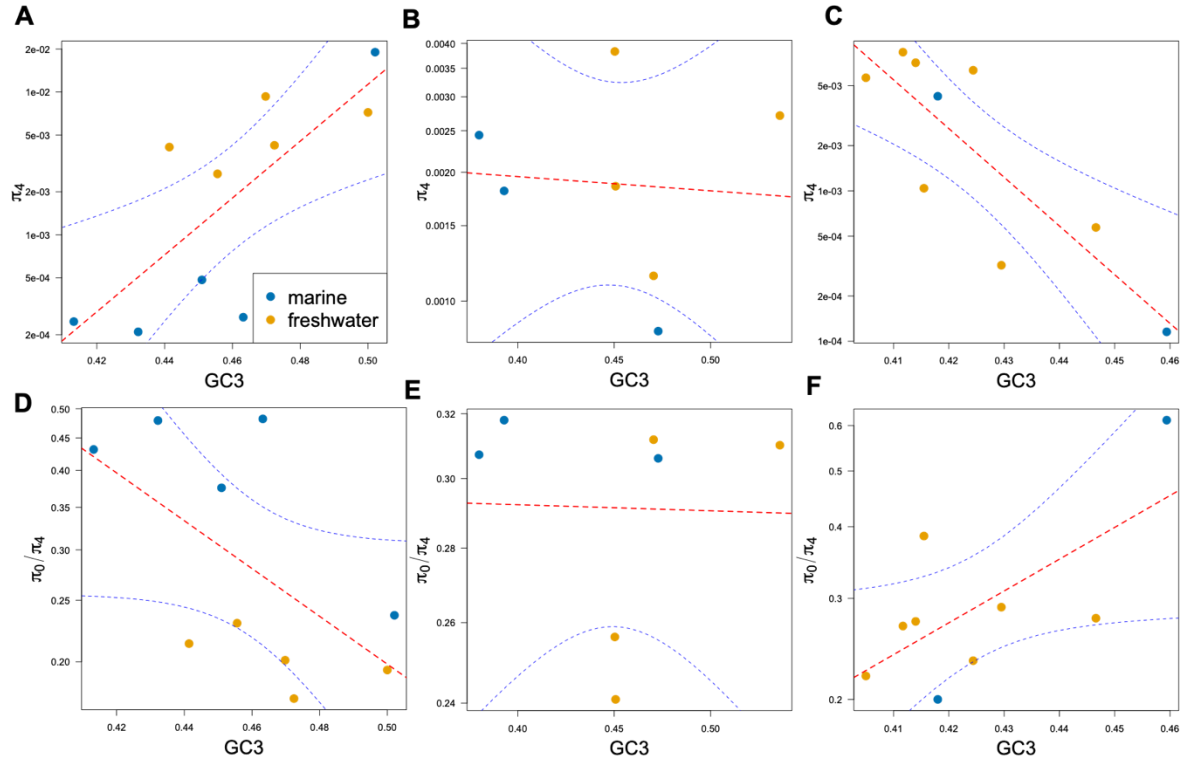


Fig. S3 The correlation between π_4 or π_0/π_4 and GC3 content. Dots in (A) and (D) represent dioecious species, (B) and (E) for monoecious species and (C) and (F) for hermaphroditic species. Blue dots show marine species and orange dots show freshwater species. Red lines represent the linear predicted curve and the blue lines are 95% confident intervals.