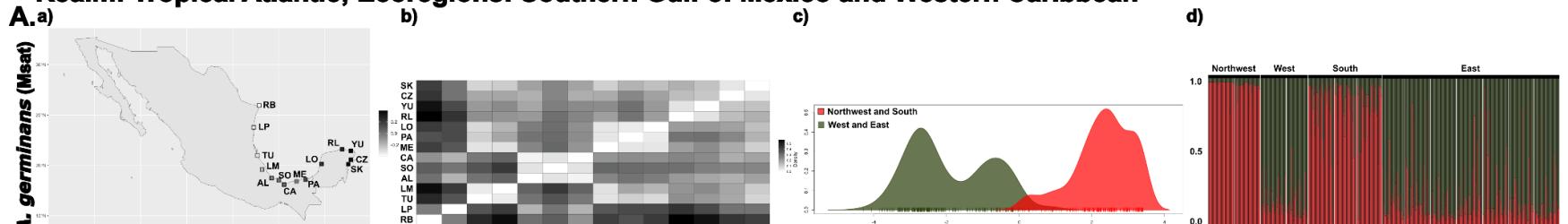
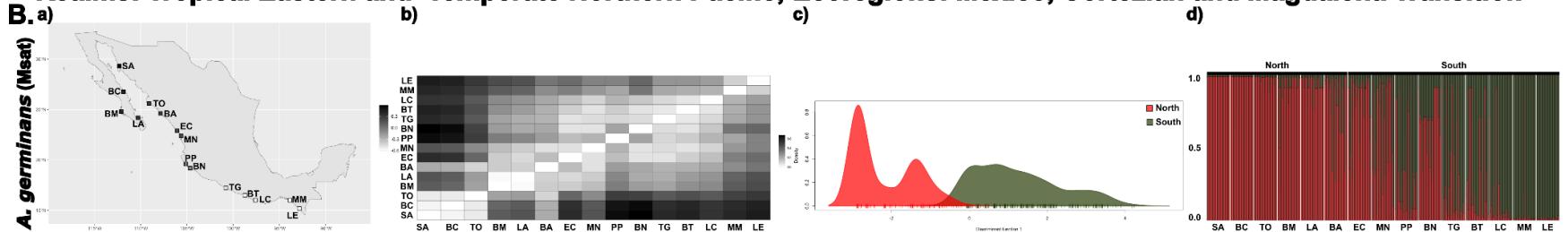


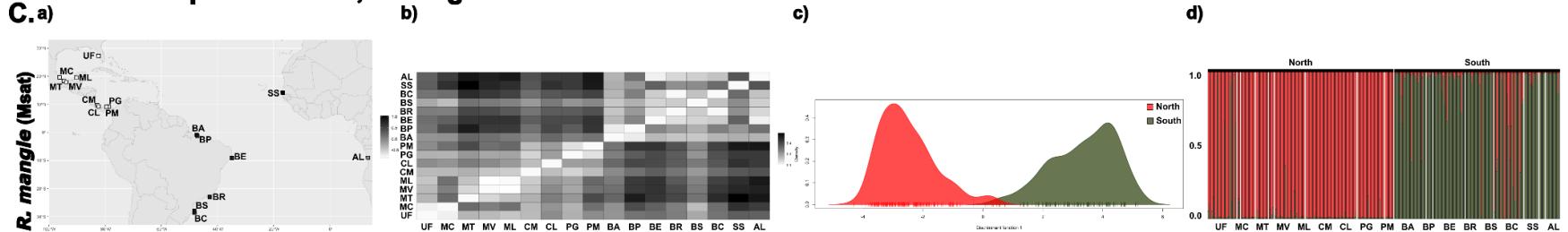
**Realm: Tropical Atlantic; Ecoregions: Southern Gulf of Mexico and Western Caribbean**



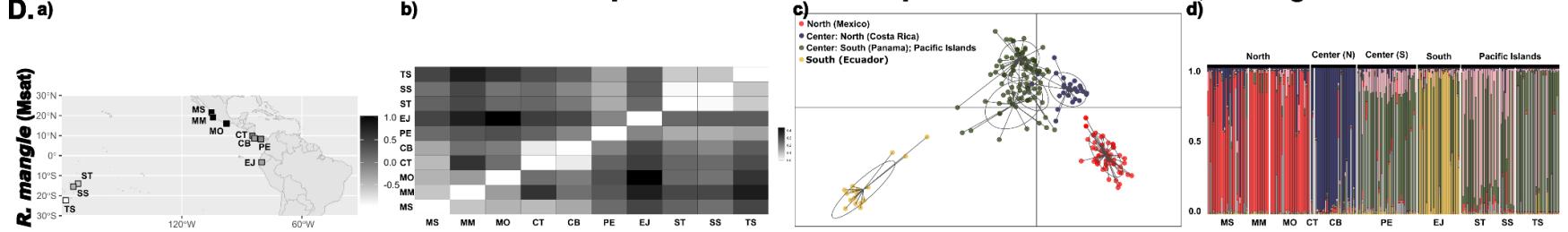
**Realms: Tropical Eastern and Temperate Northern Pacific; Ecoregions: Mexico, Cortezian and Magdalena Transition**



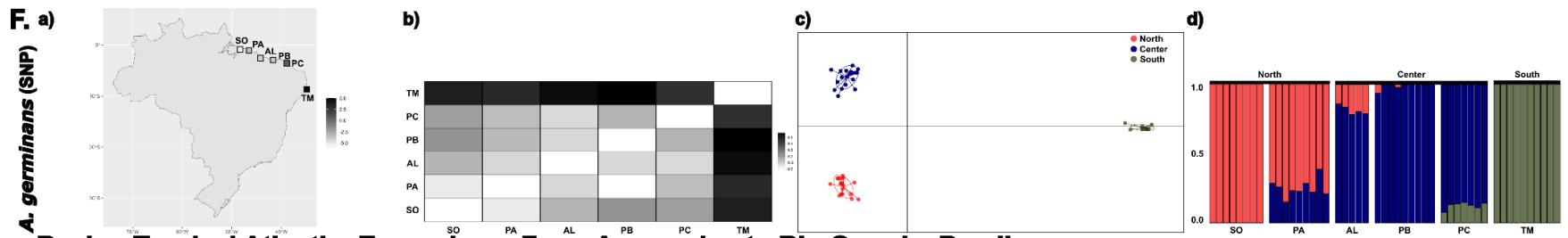
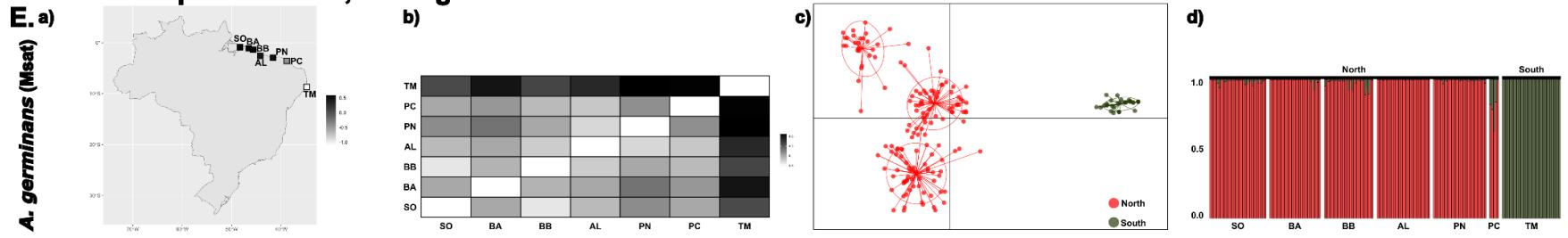
**Realms: Tropical Atlantic; Ecoregions: Several**



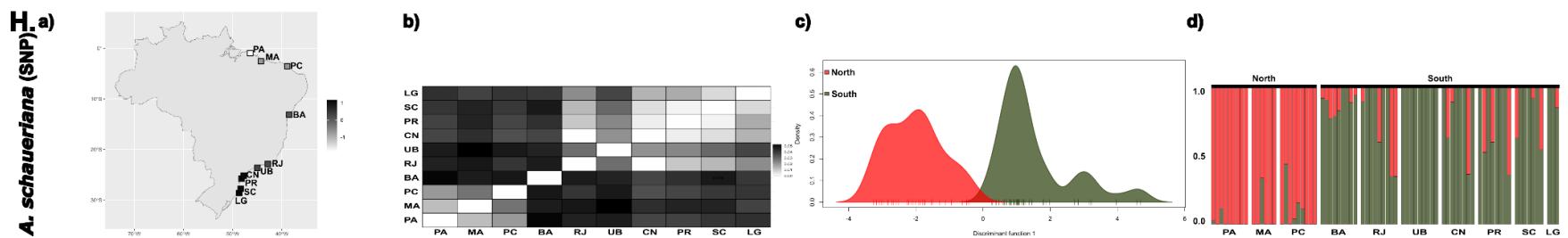
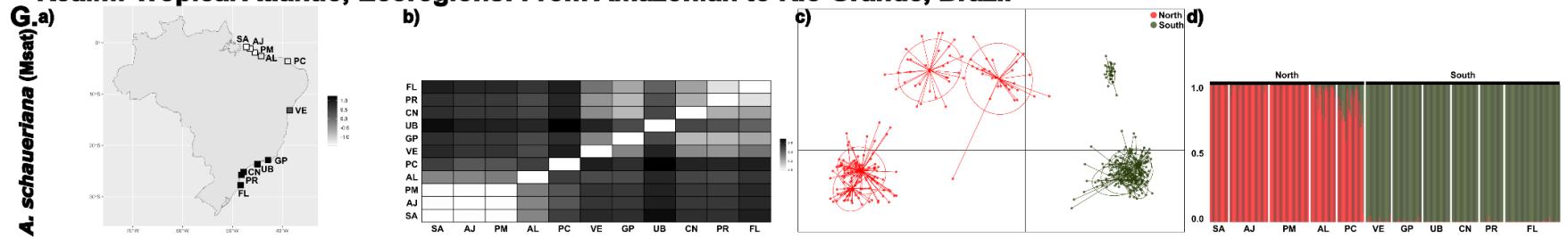
**Realms: Eastern Indo-Pacific Islands and Tropical Eastern and Temperate Northern Pacific; Ecoregions: Several**

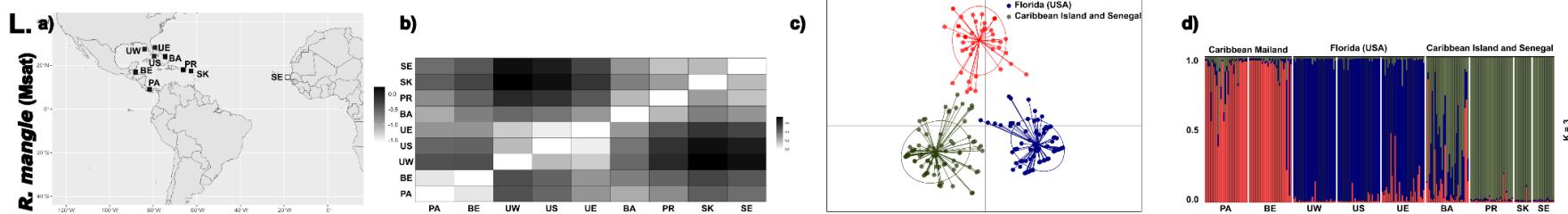
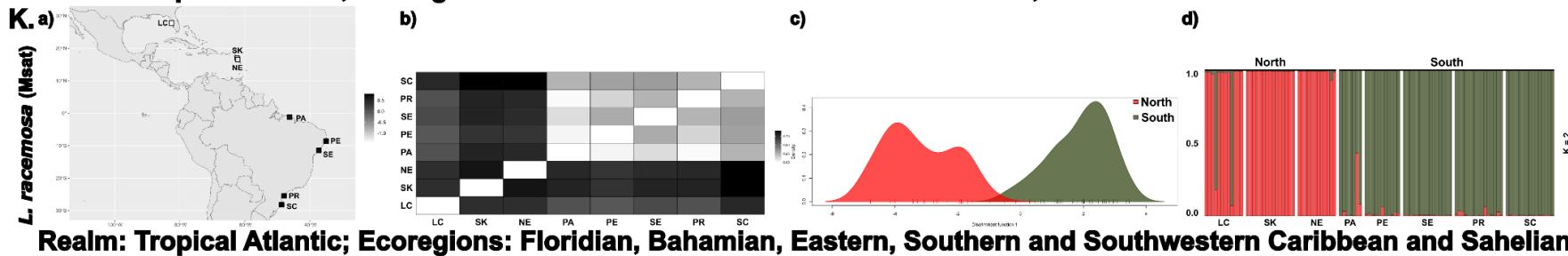
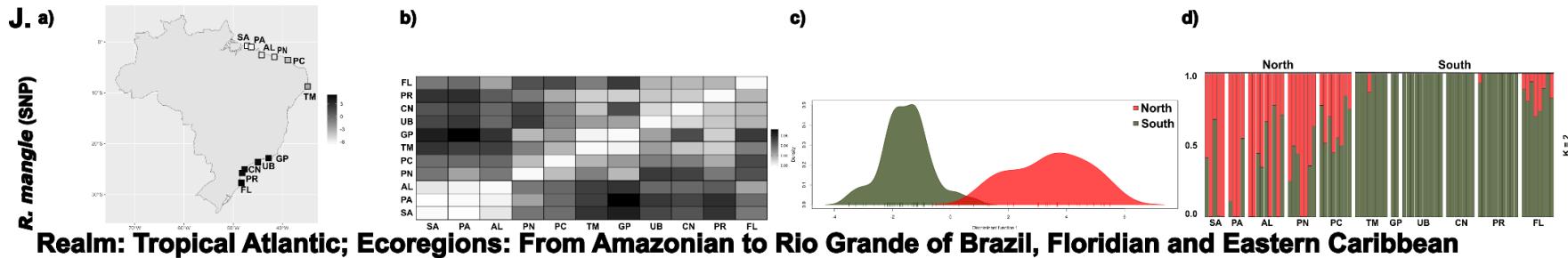
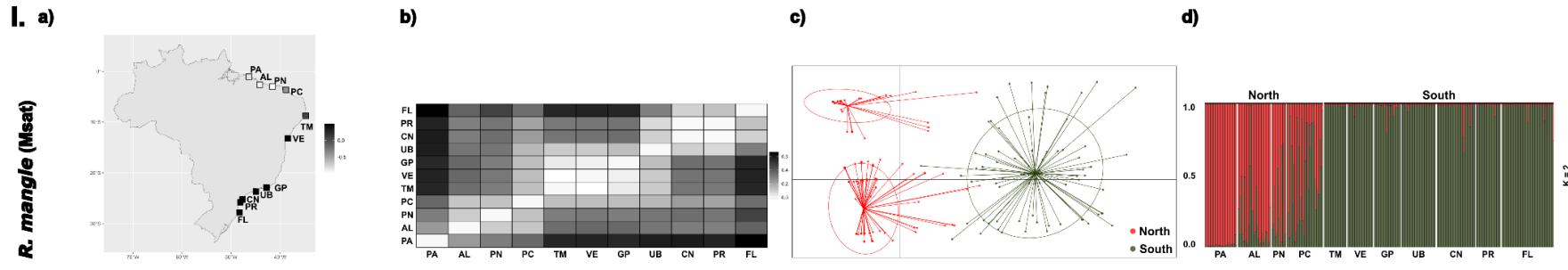


### Realm: Tropical Atlantic; Ecoregions: Amazonian and Northeastern Brazil

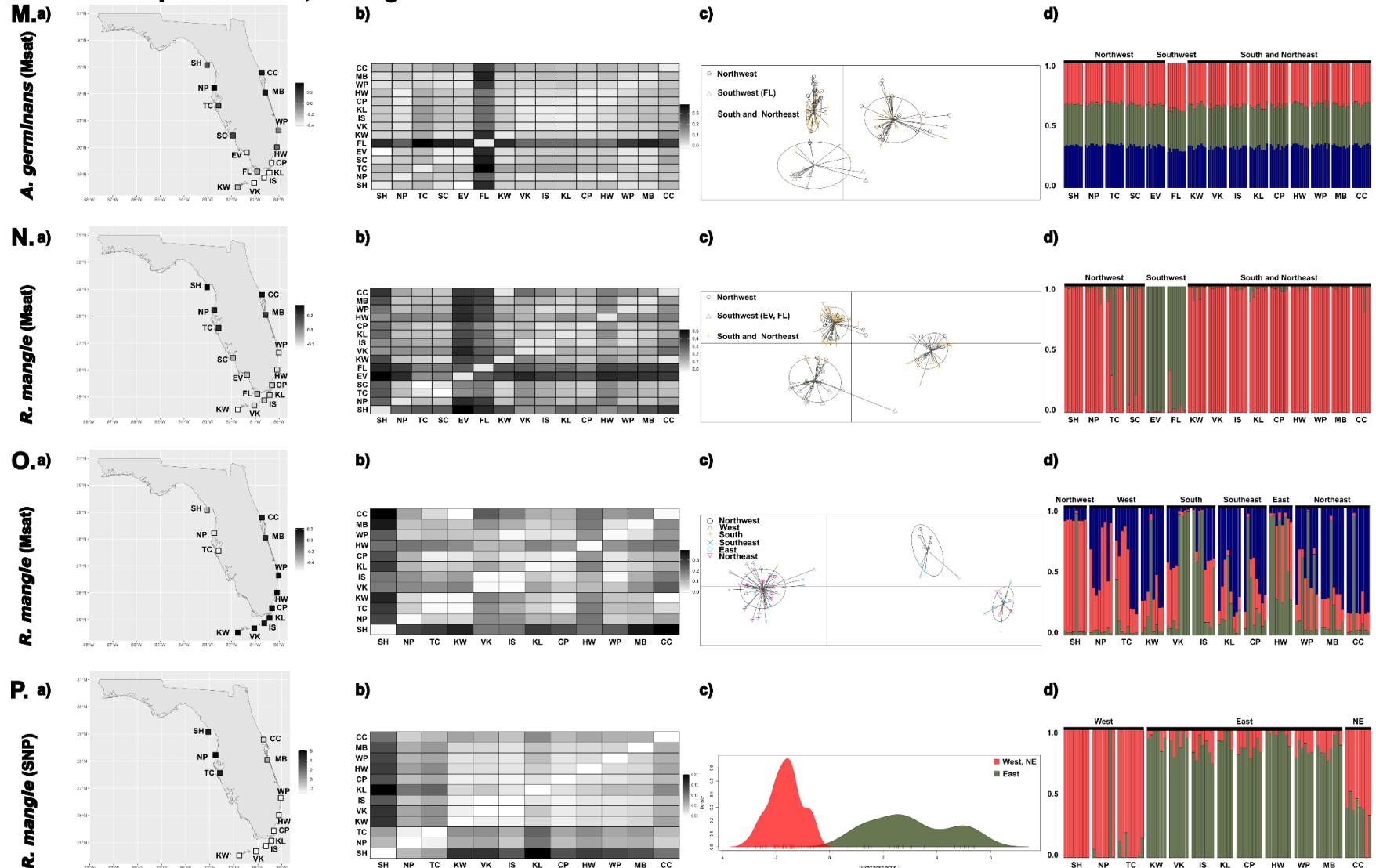


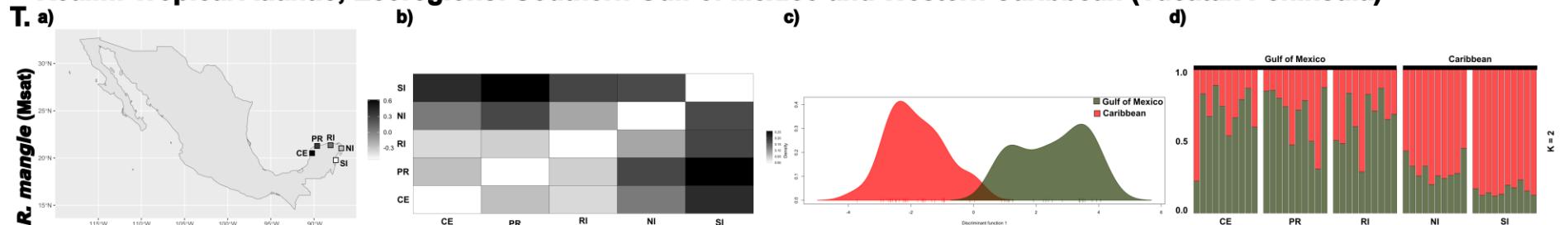
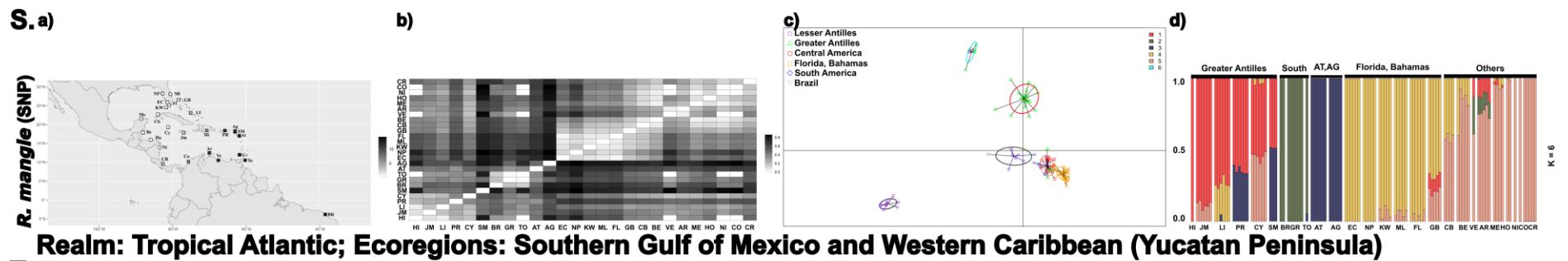
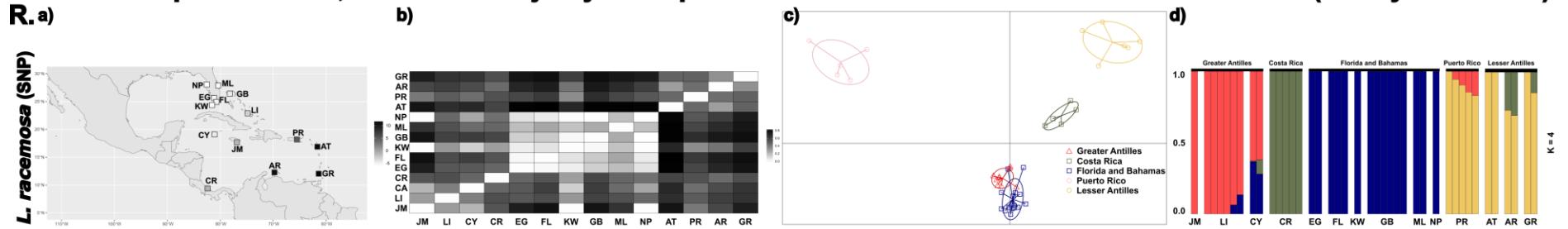
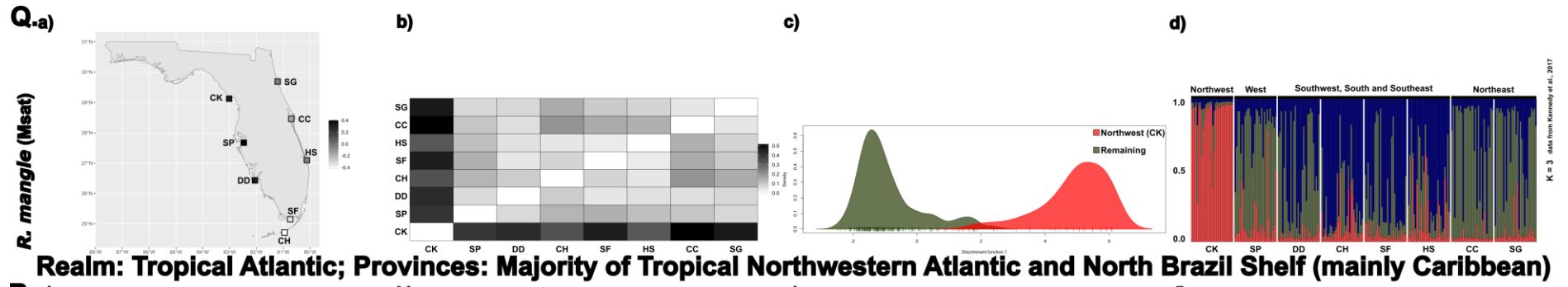
### Realm: Tropical Atlantic; Ecoregions: From Amazonian to Rio Grande, Brazil



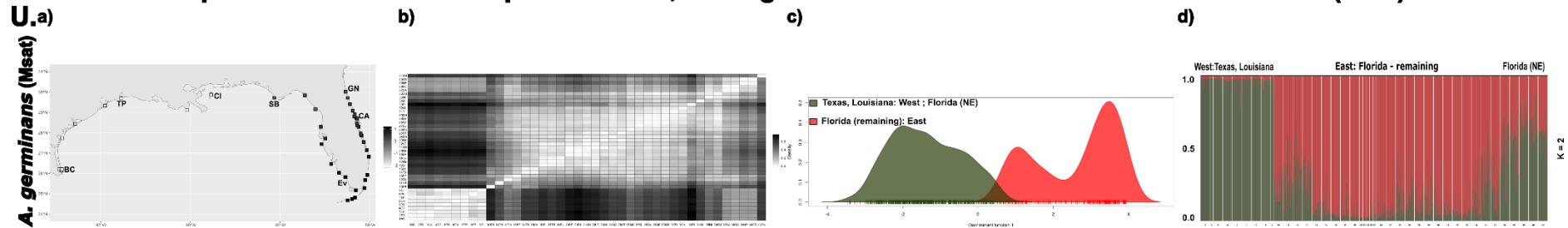


## Realm: Tropical Atlantic; Ecoregion: Floridian





**Realms: Temperate Northern and Tropical Atlantic; Ecoregions: Northern Gulf of Mexico and Floridian (USA)**



**Figure S1.** Population genetic structure of all (re)analyzed datasets (From A to U). For each dataset, the following are reported: Realms, Ecoregions or Provinces (according to Spalding et al., 2007), species and genetic marker (the origin of the data is informed, if the information coincide). From right to left, the following are shown - a) spatial PCA (sPCA), b) pairwise  $F_{ST}$ , c) Discriminant Analysis of Principal Components (DAPC) and d) methods based on genetic models (STRUCTURE for microsatellite data and ADMIXTURE for SNP data). Sampling site acronyms can be found in the original paper.

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### **Realms, ecoregions or provinces according to**

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