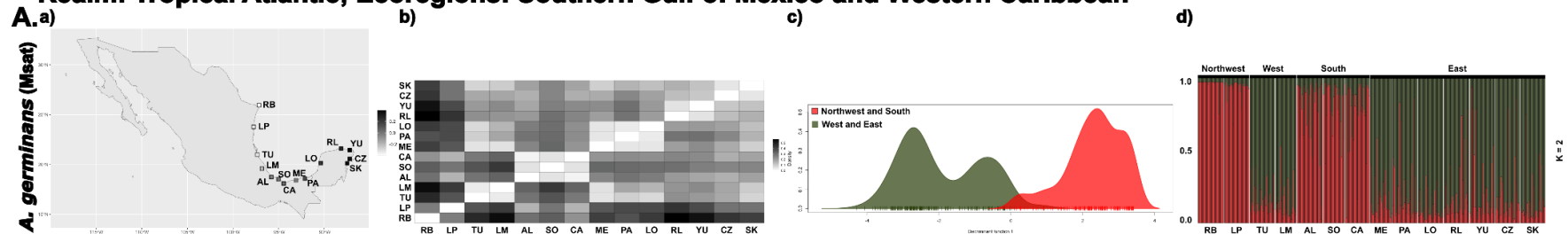
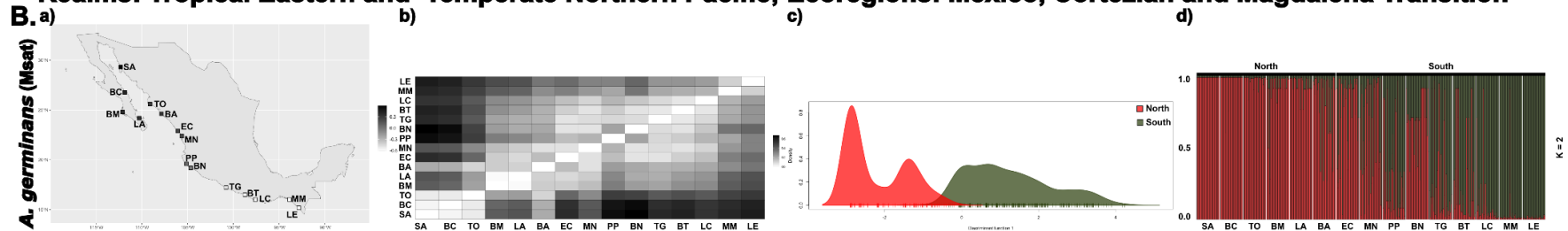


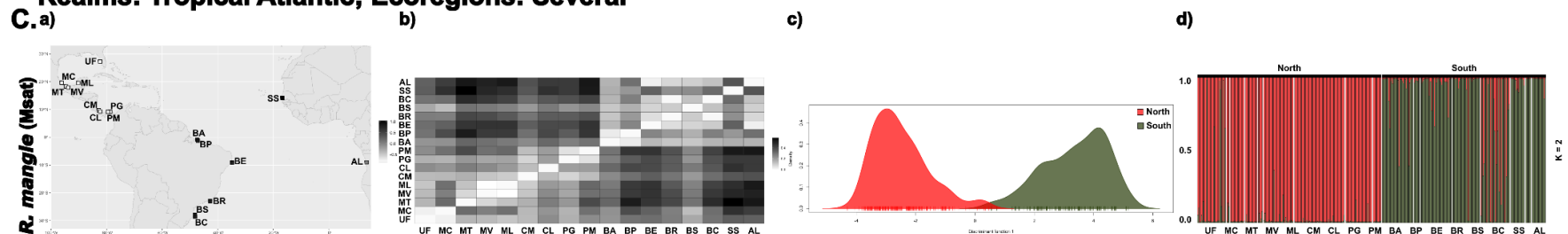
Realm: Tropical Atlantic; Ecoregions: Southern Gulf of Mexico and Western Caribbean



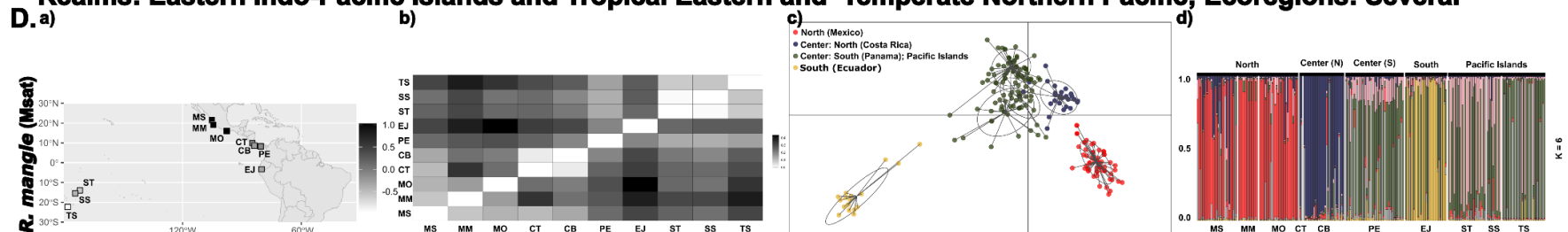
Realms: Tropical Eastern and Temperate Northern Pacific; Ecoregions: Mexico, Cortezian and Magdalena Transition



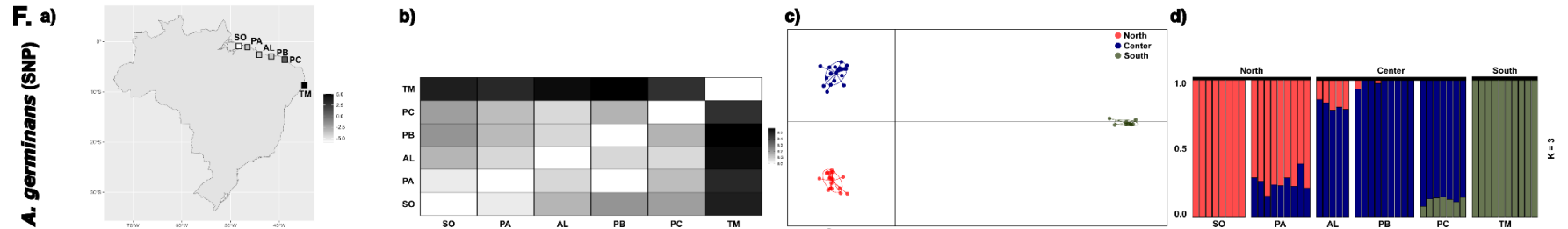
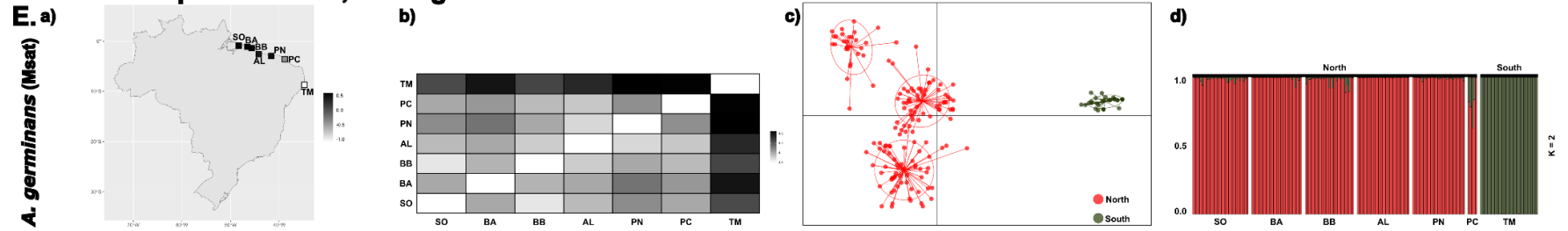
Realms: Tropical Atlantic; Ecoregions: Several



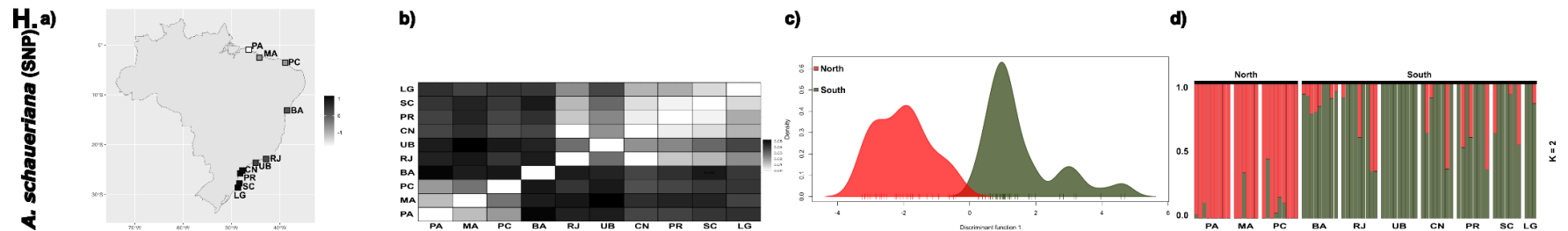
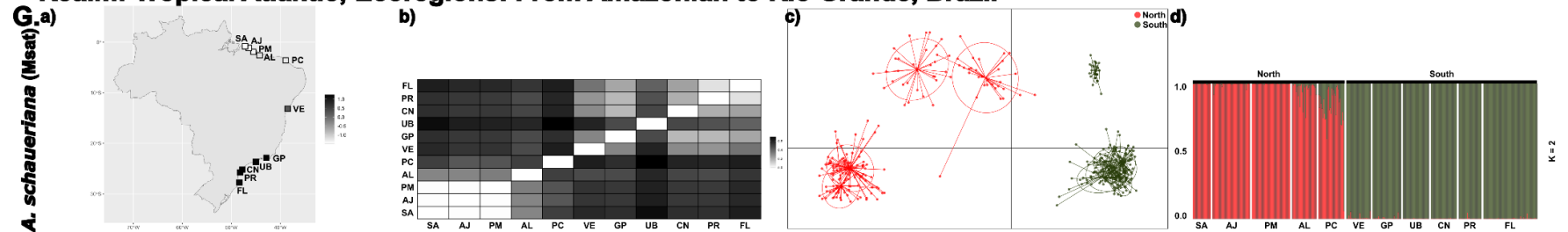
Realms: Eastern Indo-Pacific Islands and Tropical Eastern and Temperate Northern Pacific; Ecoregions: Several



Realm: Tropical Atlantic; Ecoregions: Amazonian and Northeastern Brazil

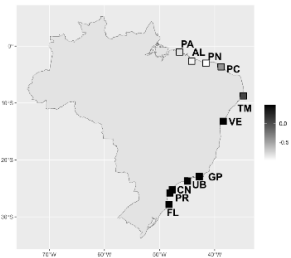


Realm: Tropical Atlantic; Ecoregions: From Amazonian to Rio Grande, Brazil

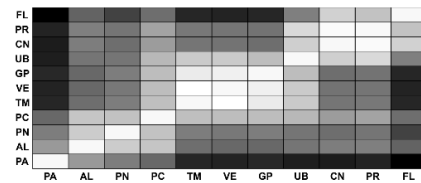


I. a)

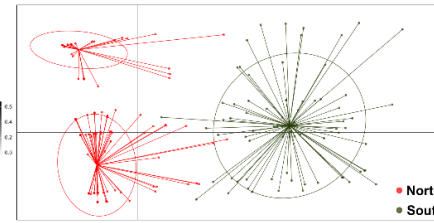
R. mangle (Msat)



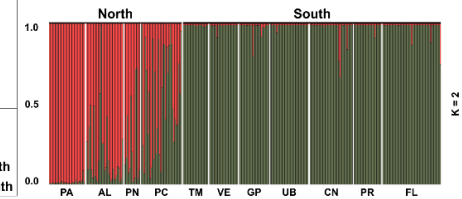
b)



c)

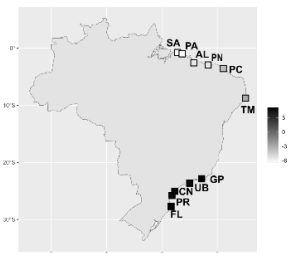


d)

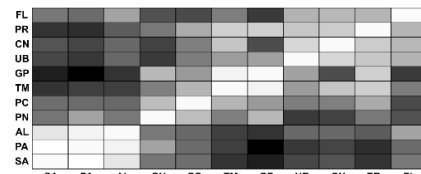


J. a)

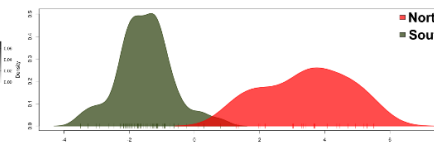
R. mangle (SNP)



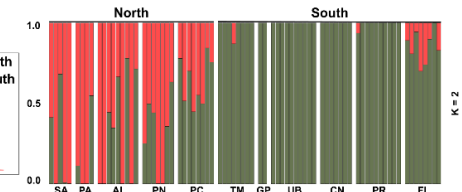
b)



c)



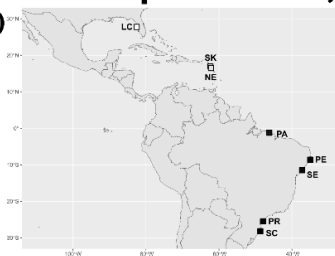
d)



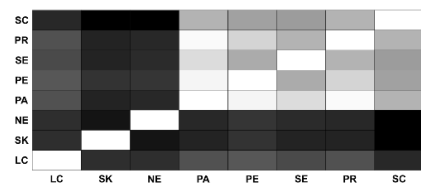
Realm: Tropical Atlantic; Ecoregions: From Amazonian to Rio Grande of Brazil, Floridian and Eastern Caribbean

K. a)

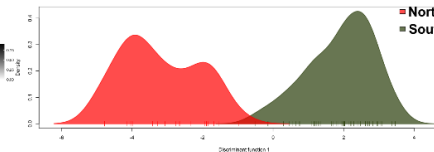
L. racemosa (Msat)



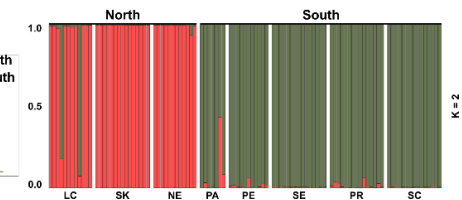
b)



c)



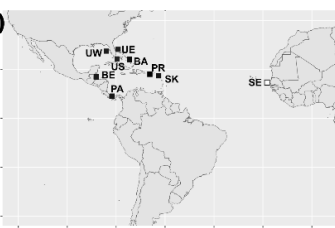
d)



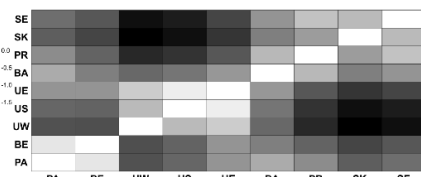
Realm: Tropical Atlantic; Ecoregions: Floridian, Bahamian, Eastern, Southern and Southwestern Caribbean and Sahelian

L. a)

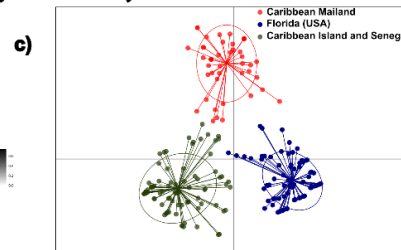
R. mangle (Msat)



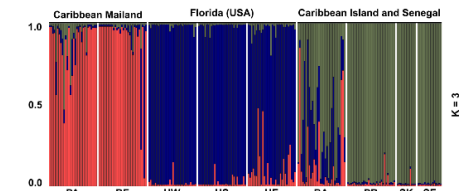
b)



c)

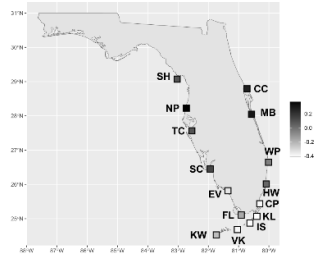


d)

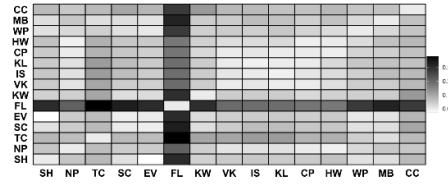


Realm: Tropical Atlantic; Ecoregion: Floridian

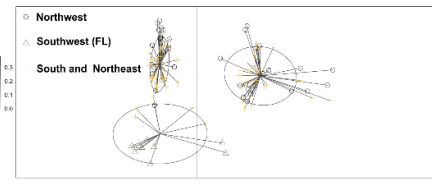
M.a)
A. germinans (Msat)



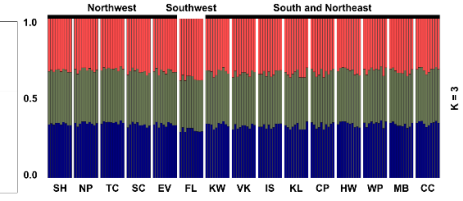
b)



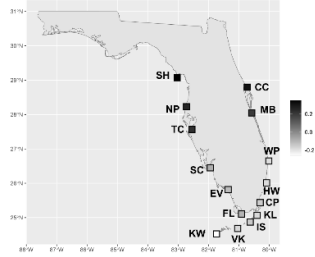
c)



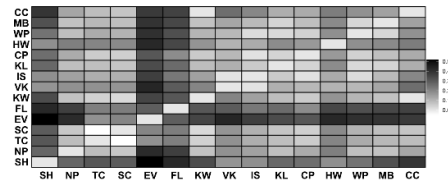
d)



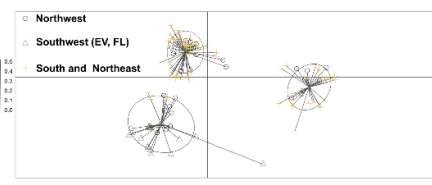
N.a)
R. mangle (Msat)



b)



c)

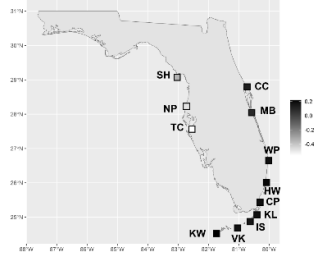


d)

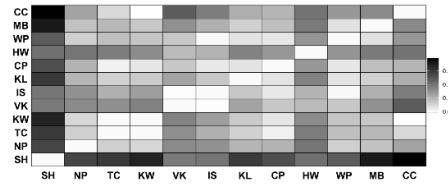


K = 2 data from Hodel et al., 2016

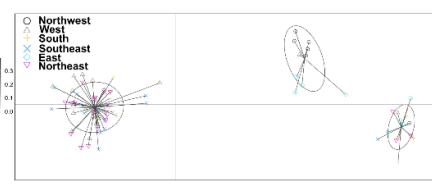
O.a)
R. mangle (Msat)



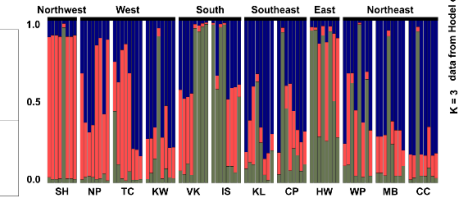
b)



c)

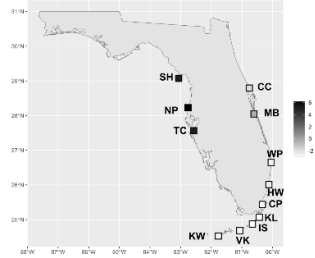


d)

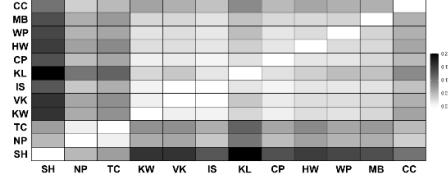


K = 3 data from Hodel et al., 2017

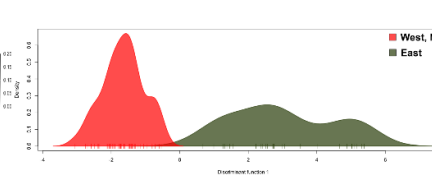
P.a)
R. mangle (SNP)



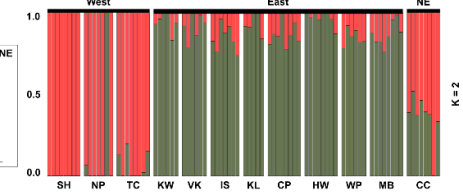
b)



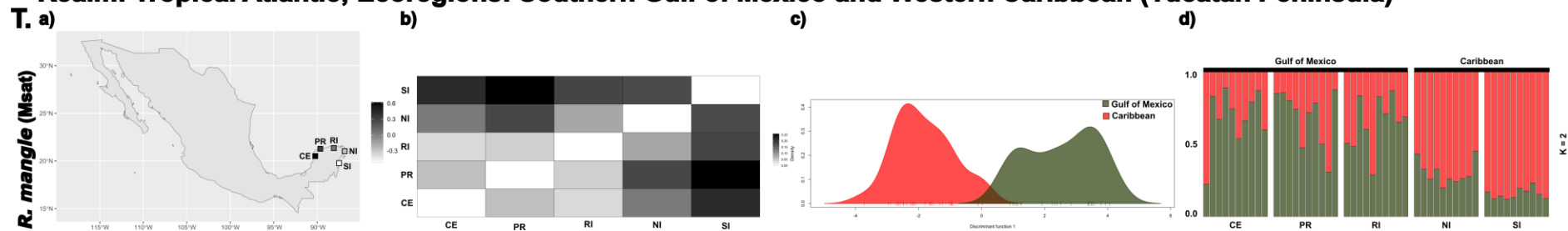
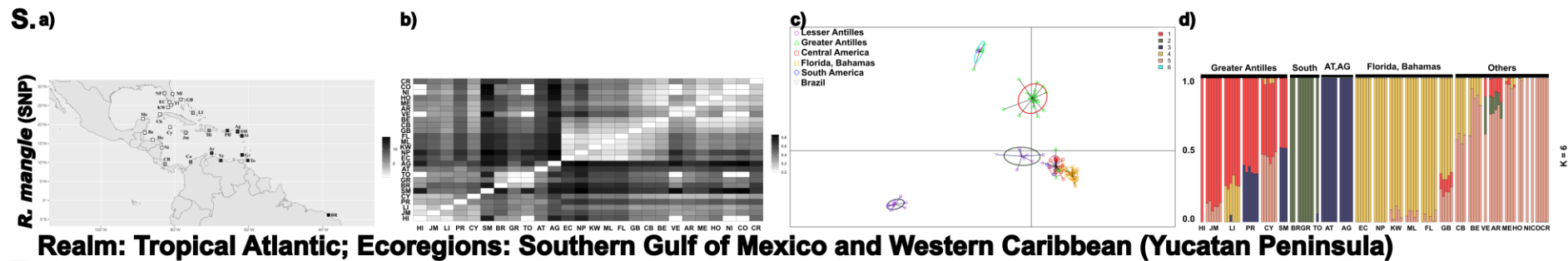
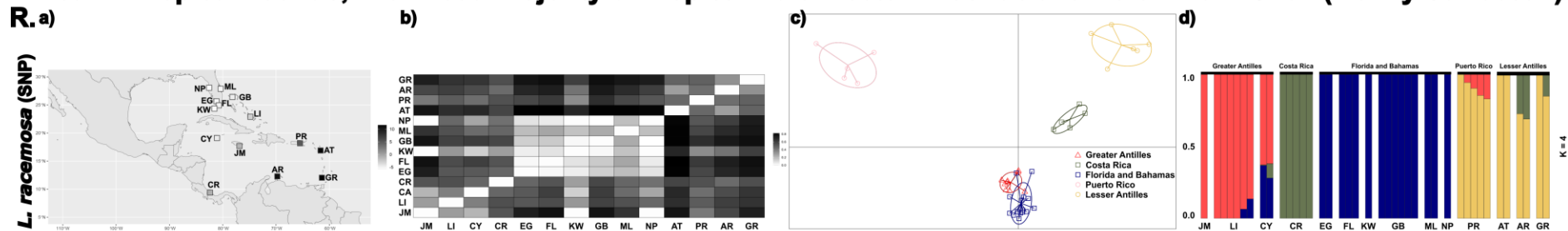
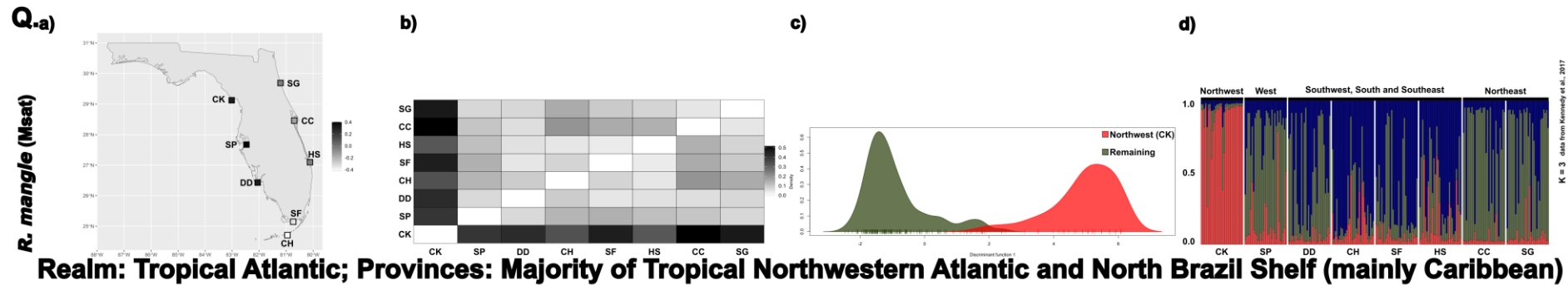
c)



d)



K = 2



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

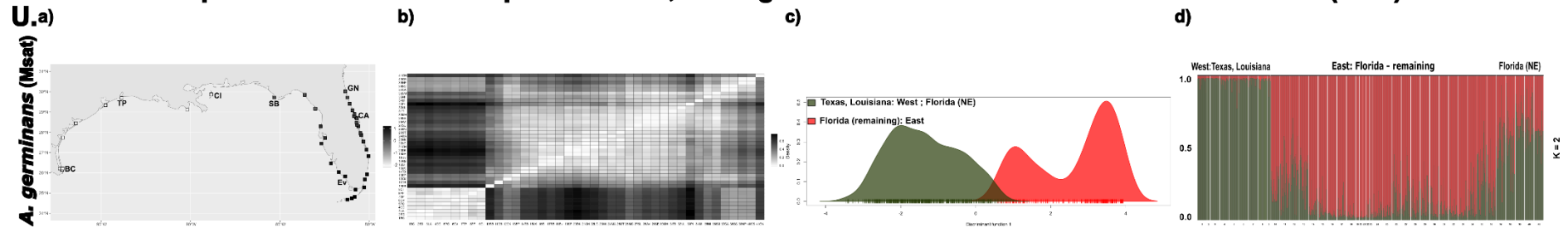


Figure S1. Population genetic structure of all (re)analyzed datasets (From A to U). For each dataset, the following are reported: Realms, Ecoregions or Provinces (according to Spalding et al., 2007), species and genetic marker (the origin of the data is informed, if the information coincide). From right 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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