

Supplementary Figures

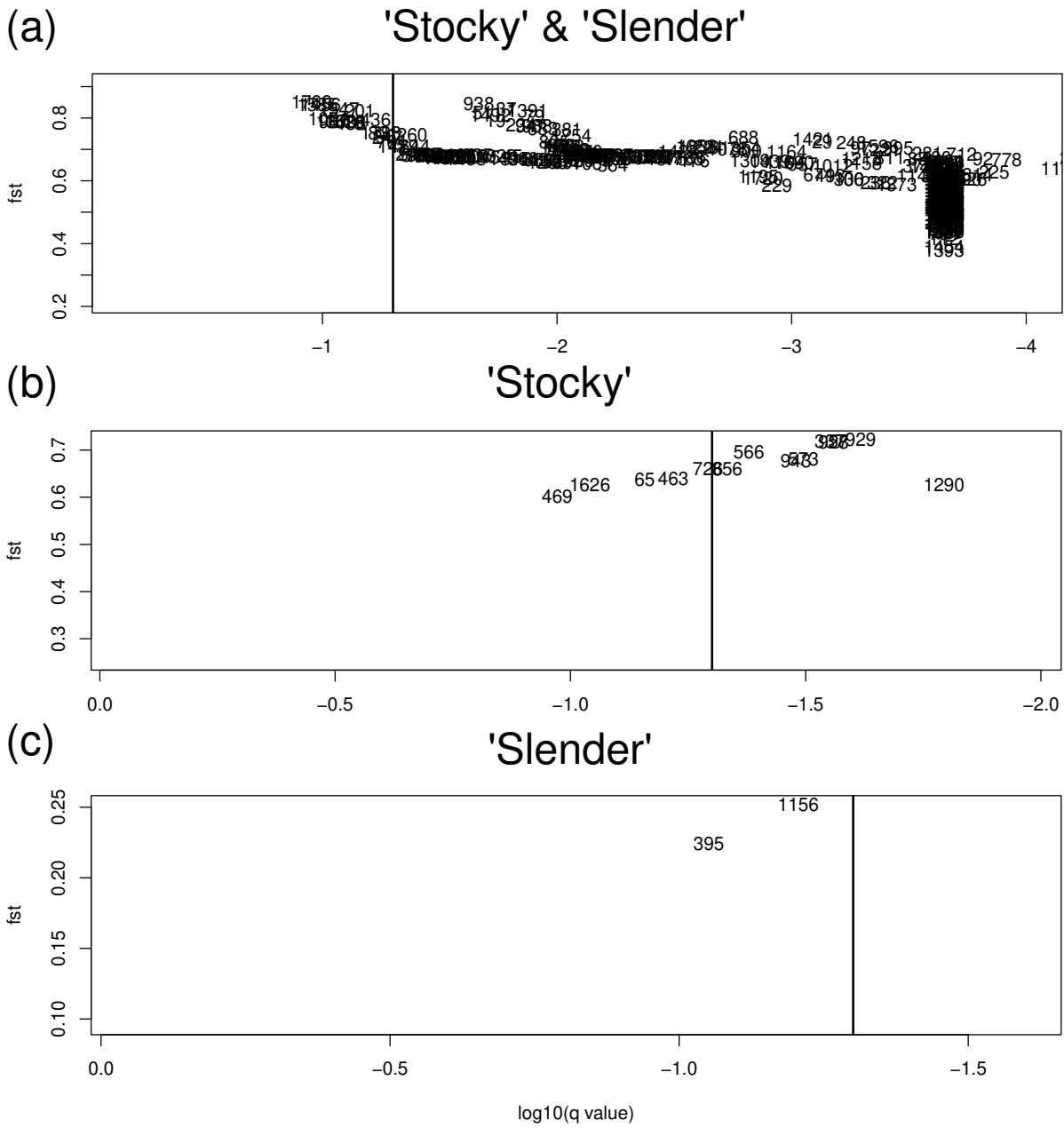
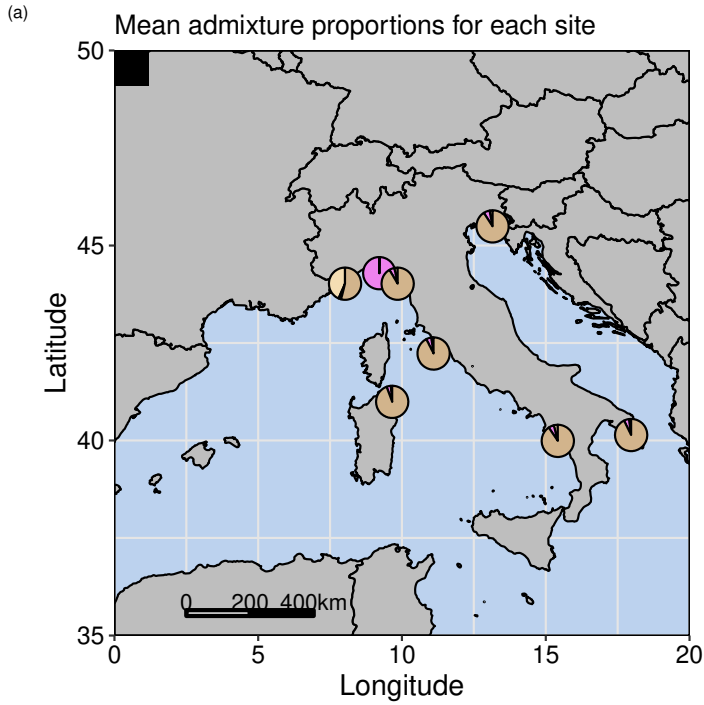


FIGURE S1 BayeScan analysis. Outlier loci detected at (a) 'Y&O', (b) 'O' and (c) 'Y' levels.



(b) Individual admixture proportions

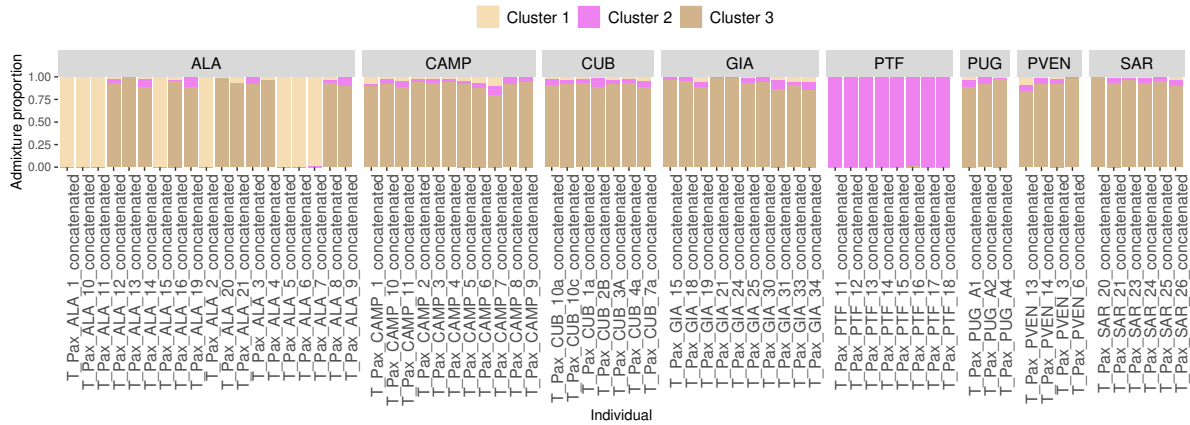


FIGURE S2 Admixture analysis in 'LEA' R package computed at the 'Y' level to detect the true number of ancestral populations (K_s). (a) Mean admixture proportions for each site are presented as pie charts and shown on the map. (b) Individual admixture proportions are shown as bar plots for each of the sampling sites. Individuals are grouped within their corresponding Slender sampling localities on the barplot.

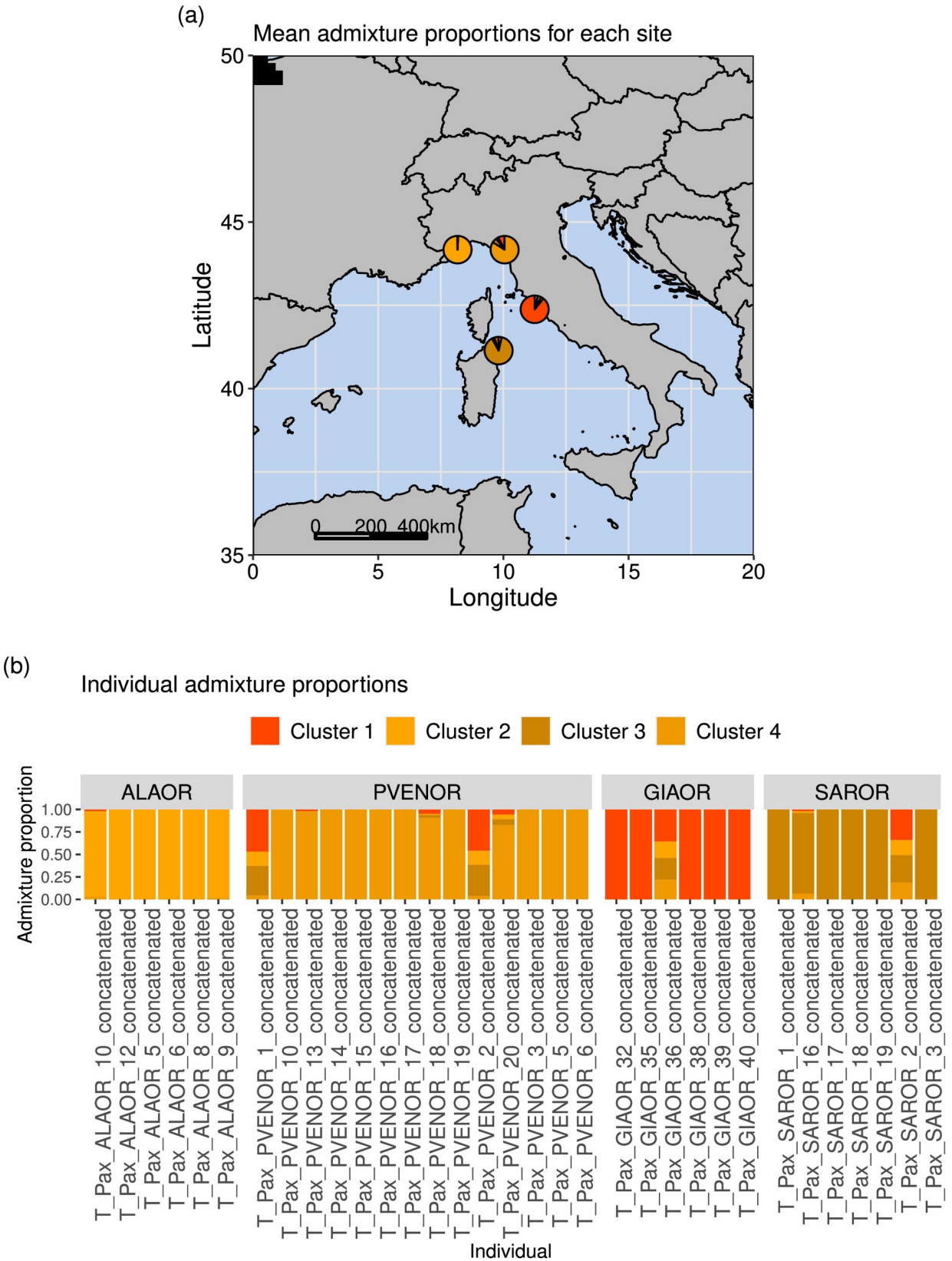


FIGURE S3 Admixture analysis in 'LEA' R package computed at the 'O' level to detect the true number of ancestral populations (K_s). (a) Mean admixture proportions for each site are presented as pie charts and shown on the map. (b) Individual admixture proportions are shown as bar plots for each of the sampling sites. Individuals are grouped within their corresponding Stocky sampling localities on the barplot. Y&OY&O

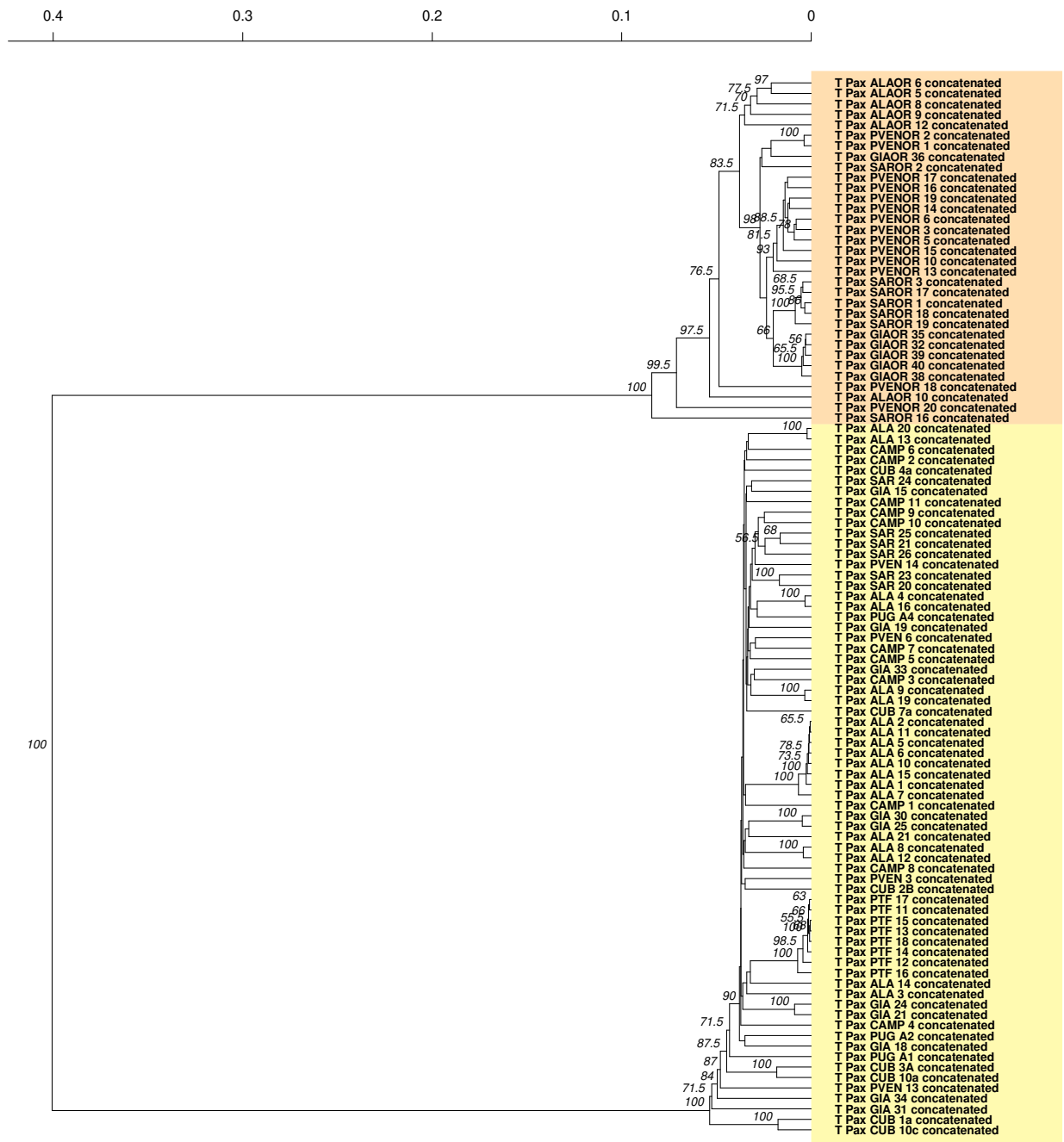


FIGURE S4 UPGMA phylogenetic tree computed at the 'Y&O' level with Prevosti's genetic distances. Individual samples are presented on the tree nodes. Bootstrap support values based on 1000 iterations are shown on tree branches with a cutoff value of $p=50$ (%). Inferior values were considered as unresolved and were thereby not presented. All individuals belonging to Slender or Stocky morphotypes are colored in yellow or orange, respectively.

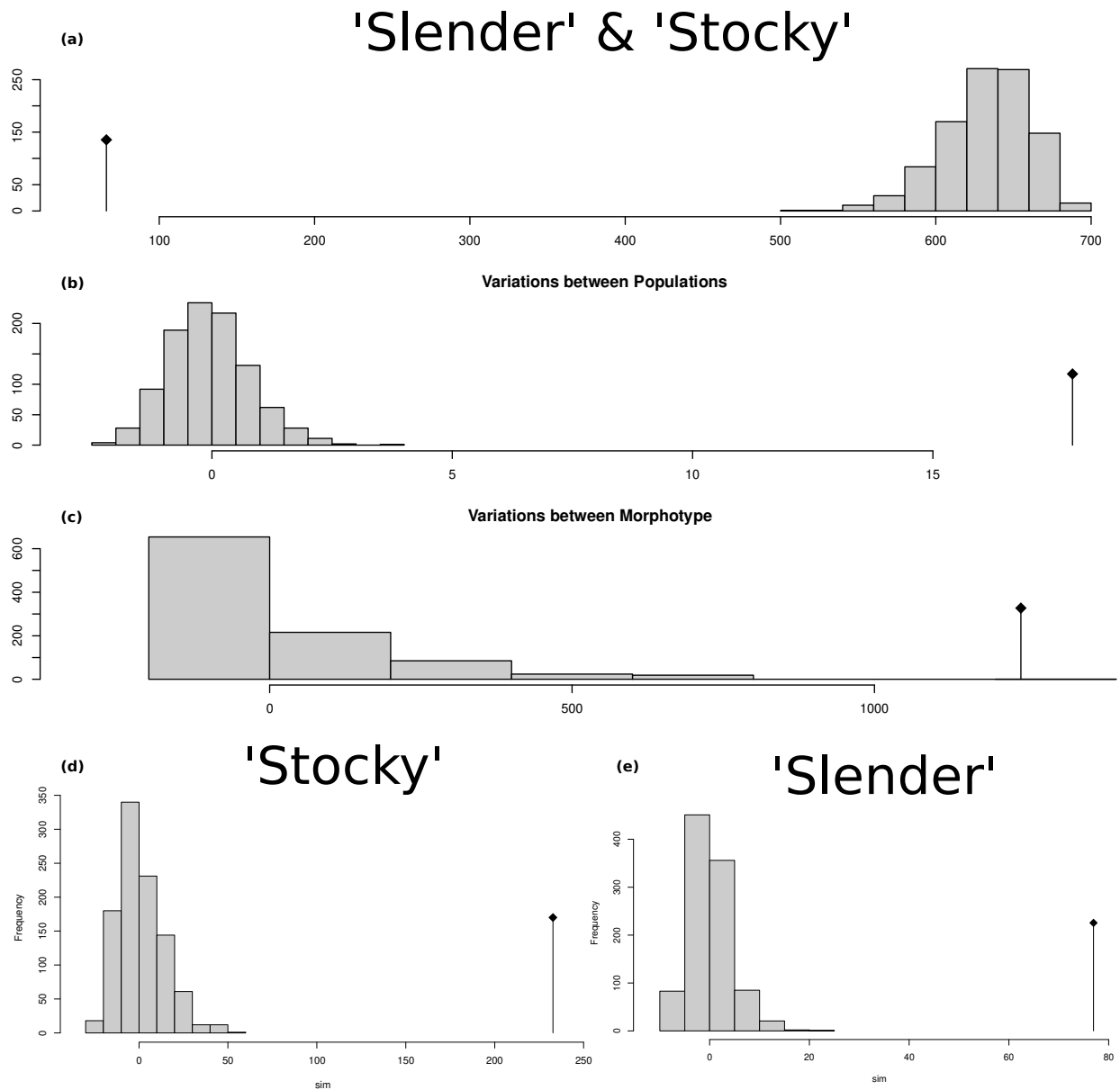


FIGURE S5 Analysis of Molecular Variance (AMOVA). Hierarchical AMOVA (based on Prevosti genetic distances) was computed at the 'Y&O' level with two factors: (1) 'Morphotype' and (2) 'Populations', to test genetic structuring at the following levels: (a) within 'Populations', (b) between 'Populations' (nested within 'Morphotype') and (c) between 'Morphotypes'. One-way AMOVA was computed at (d) 'O' and (e) 'Y' levels to test the effect of 'Populations' on overall genetic structuring, within (d) Stocky and (e) Slender levels. Histograms represent the distribution of the randomized strata, while the black line represents the observed data.

(a)



(b)

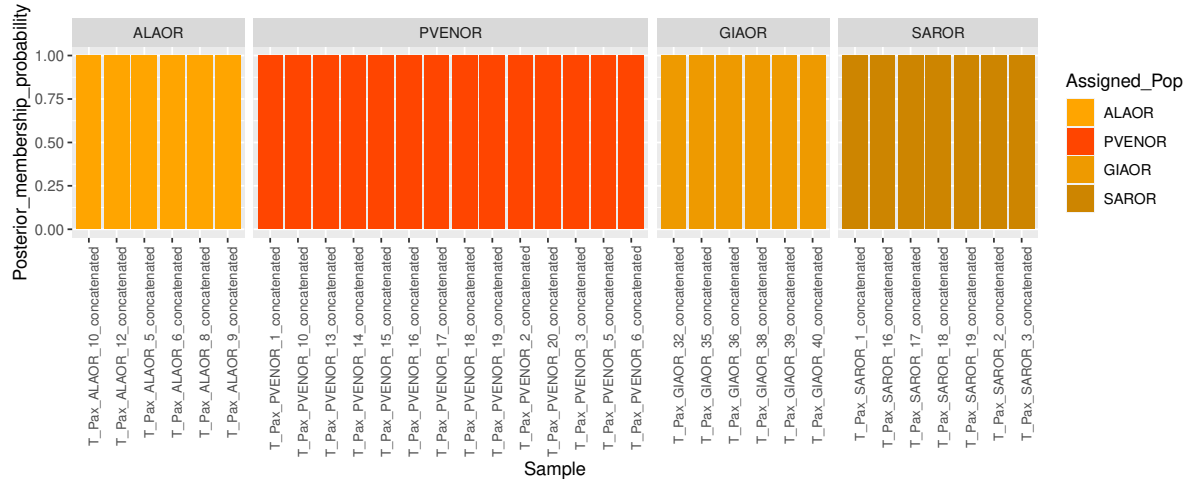


FIGURE S6 Discriminant Analysis of Principal Components (DAPC), computed at the 'O' level. (a) DAPC with localities as prior grouping information. (b) Stacked bar plots show posterior assignment probabilities of individuals to their predetermined Stocky locations and were constructed using previously calculated DAPC population membership assignments, at the 'O' level.

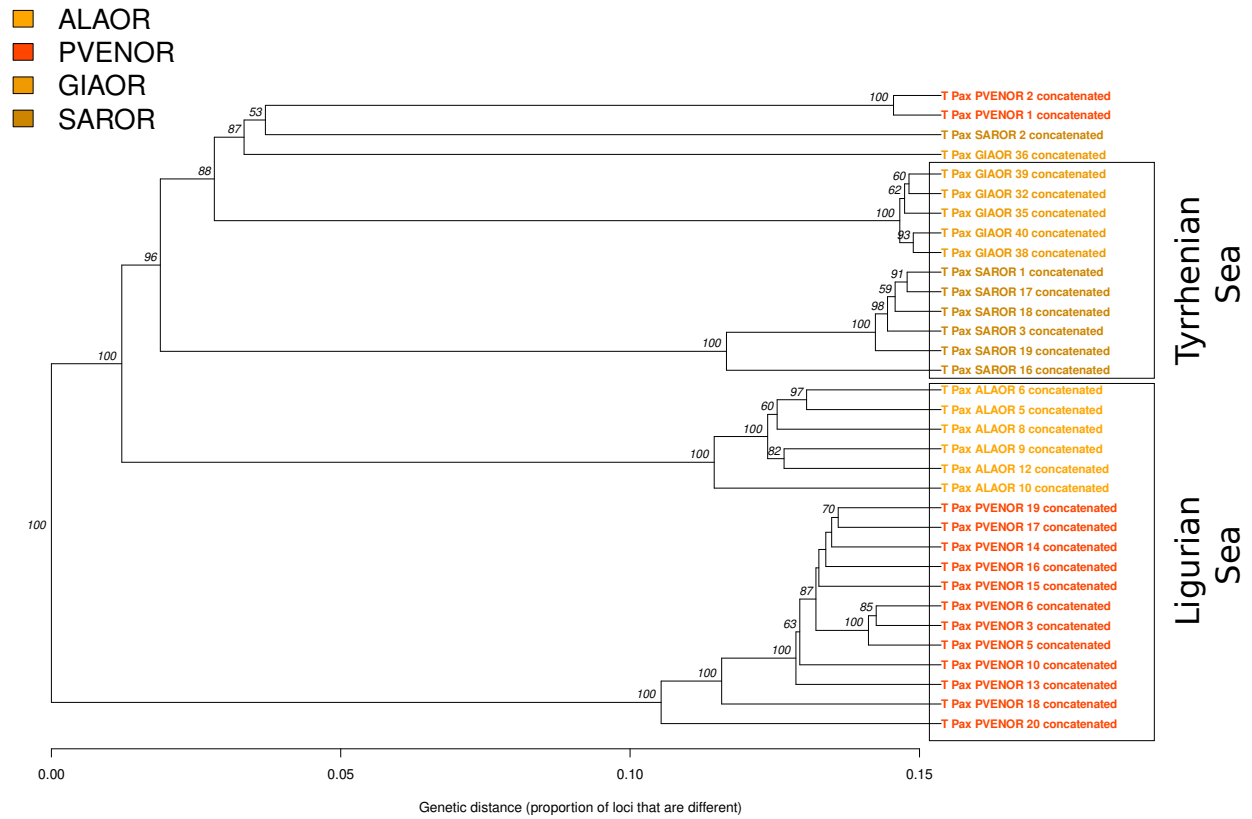


FIGURE S7 UPGMA tree computed at the ‘O’ level with Prevosti’s genetic distances. Individual samples are presented on the tree nodes. Bootstrap support values based on 1000 iterations are shown on tree branches with a cutoff value of $p=50$ (%). Inferior values were considered as unresolved and were thereby not presented. Ligurian (ALAOR + PVENOR) and Tyrrhenian (GIAOR + SAROR) sub-clusters were detected, and are emphasized with the black rectangles.

(a)



(b)

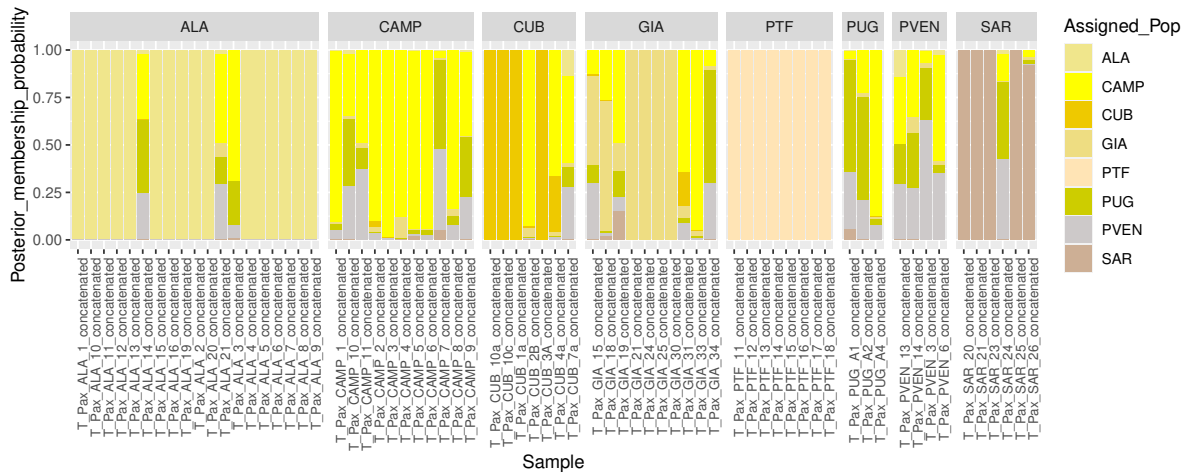


FIGURE S8 Discriminant Analysis of Principal Components (DAPC), computed at the 'Y' level. (a) DAPC with localities as prior grouping information. (b) Stacked bar plots show posterior assignment probabilities of individuals to their predetermined Slender locations and were constructed using previously calculated DAPC population membership assignments, at the 'Y' level.

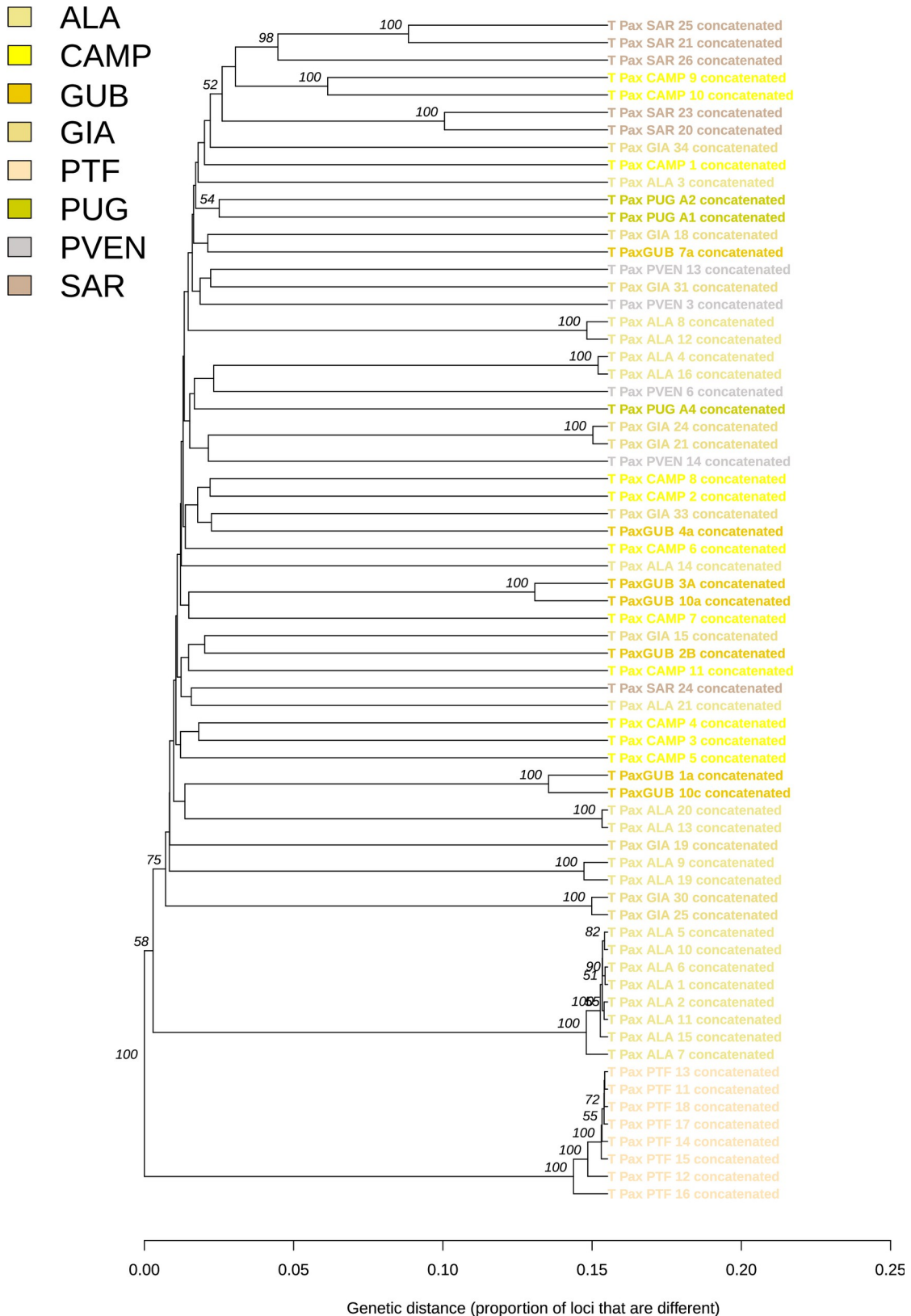


FIGURE S9 UPGMA tree computed at the 'Y' level with Prevosti's genetic distances. Individual samples are presented on the tree nodes. Bootstrap support values based on 1000 iterations are shown on tree branches with a cutoff value of $p=50$ (%). Inferior values were considered as unresolved and were thereby not presented.

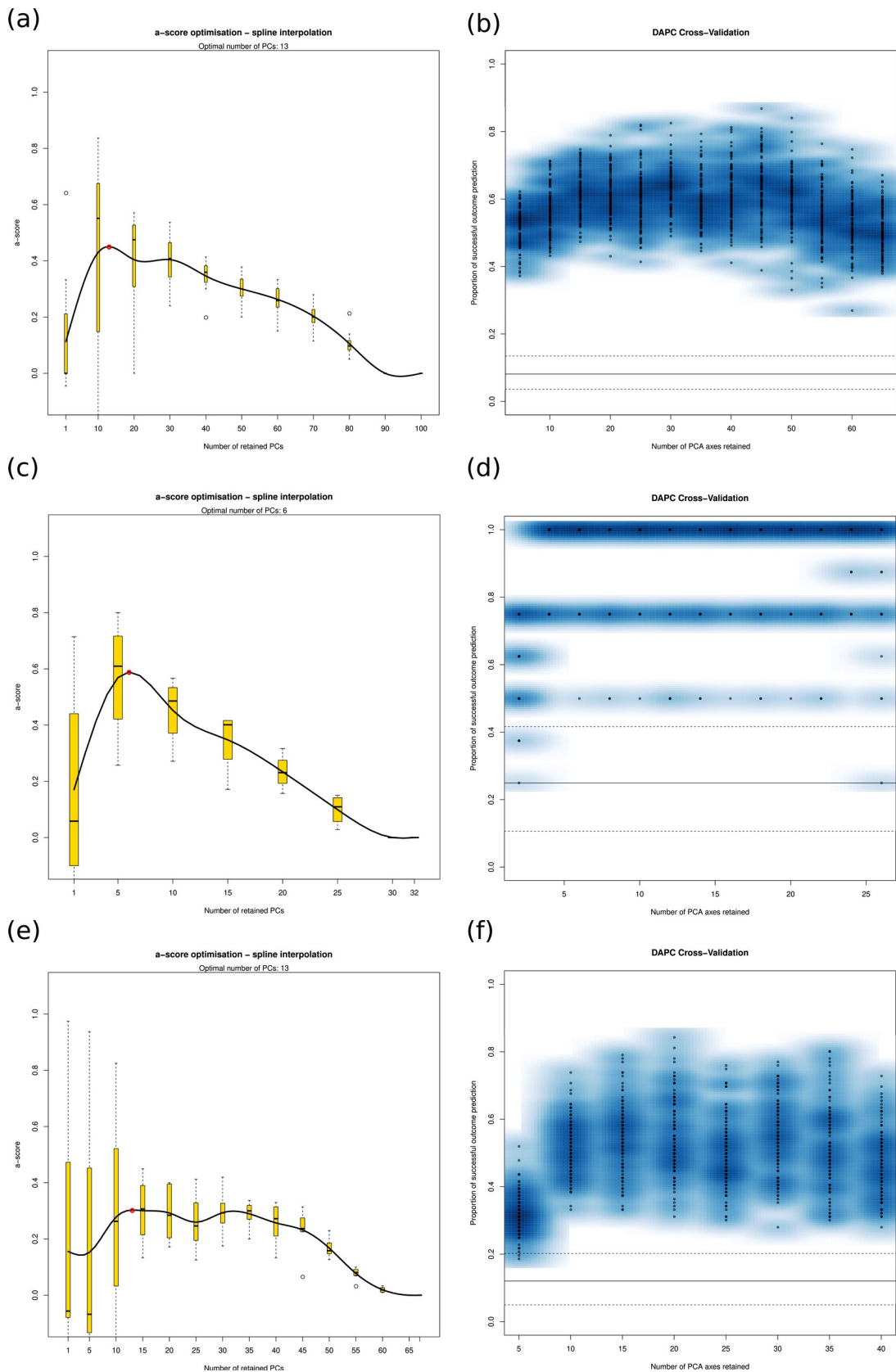


FIGURE S10 Determination of the optimal number of Principal Components (PCs) to retain for the DAPC analysis. Alpha (α) optimization (**left**) and Cross validation (**right**) scores, computed with 999 permutations for the 'Y&O' (**a-b**), 'O' (**c-d**) and 'Y' (**e-f**) levels. Total numbers of 13 ('Y&O'), 6 ('O') and 13 ('Y') PCs were retained to perform the DAPC analysis for each of the hierarchical levels, as suggested by the alpha (α) and cross-validation scores.