**Appendix S4**



**Fig.S4.7:** At centre are plots of sample-wise frequency of cluster membership assigned to individuals by the *snapclust* function of the R package *adegenet*, using the maximum value of genetic clusters (*K*)at which resultant clusters remained informatively aligned to spatial sampling. At right are plots of the modified Akaike Information Criteria (AICc) for *snapclust* models corresponding to all possible values of *K*, in which the optimal value of *K* is denoted via various metrics: the sharpest pre-plateau decline in *snapclust* AICc (red plus); alignment of maximum *snapclust* clusters to spatial sampling (red line) and; visual identification of DAPC clusters (blue cross). The species and sampling scales covered are denoted at left, as **a**)full range lobsters, *Homarus gammarus*, **b**)Atlantic lobsters, **c**)Mediterranean lobsters, and **d**)full range crawfish, *Palinurus elephas*.