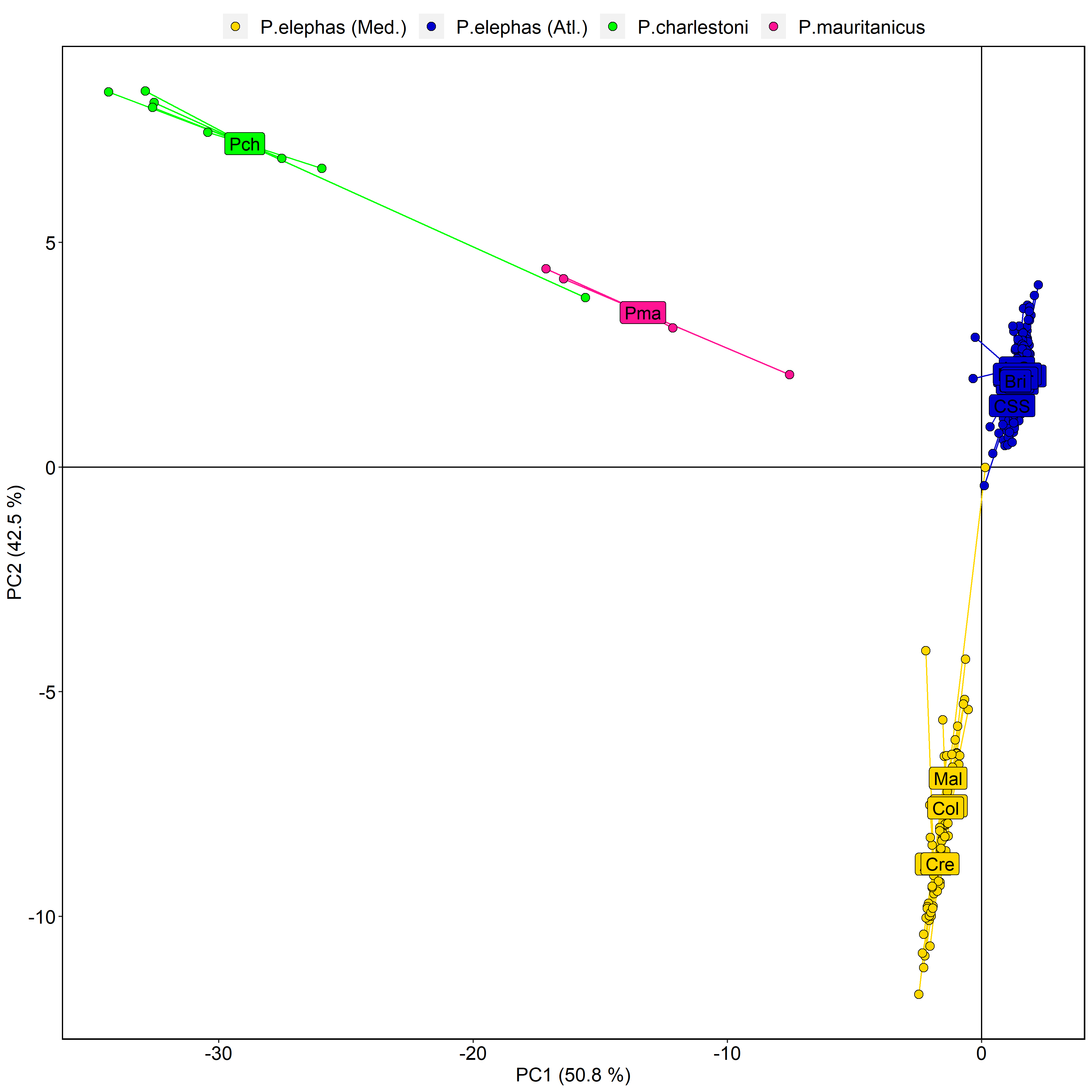
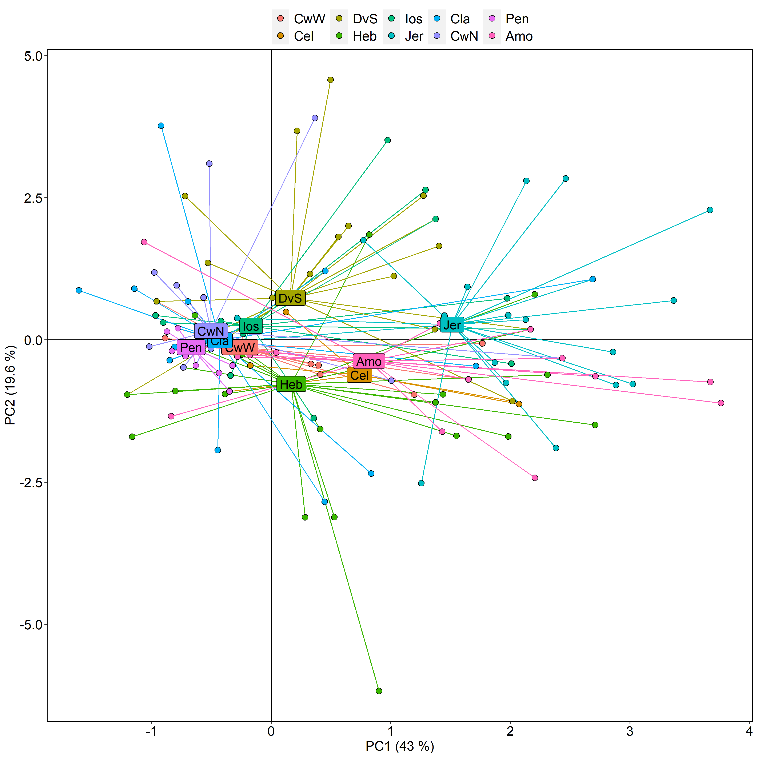
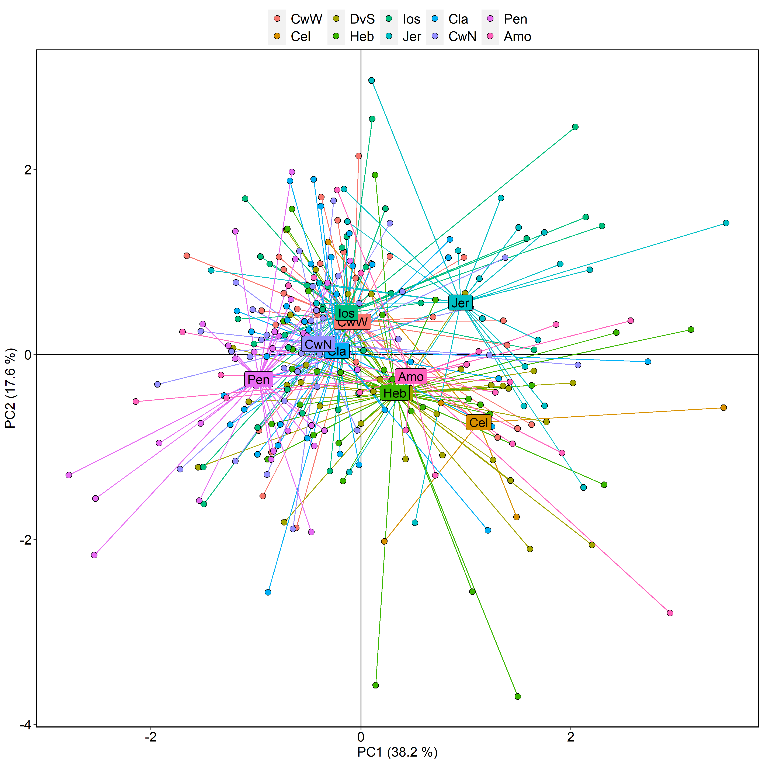
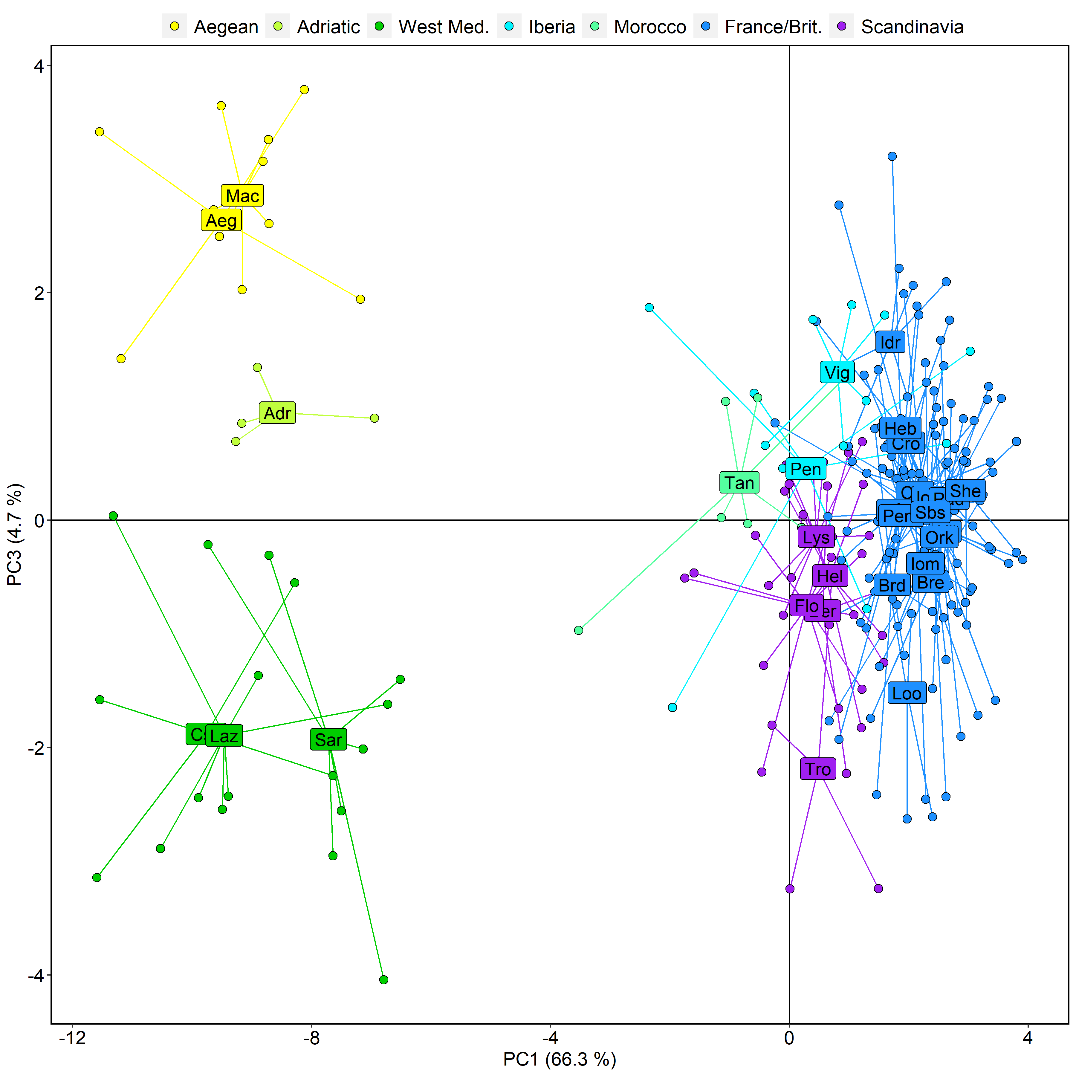
**Appendix S2**

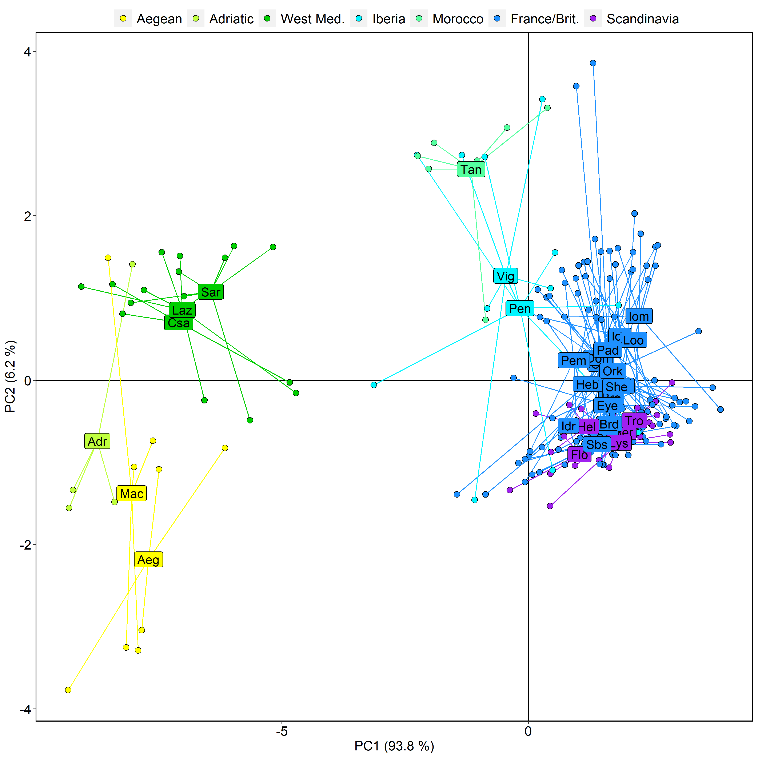
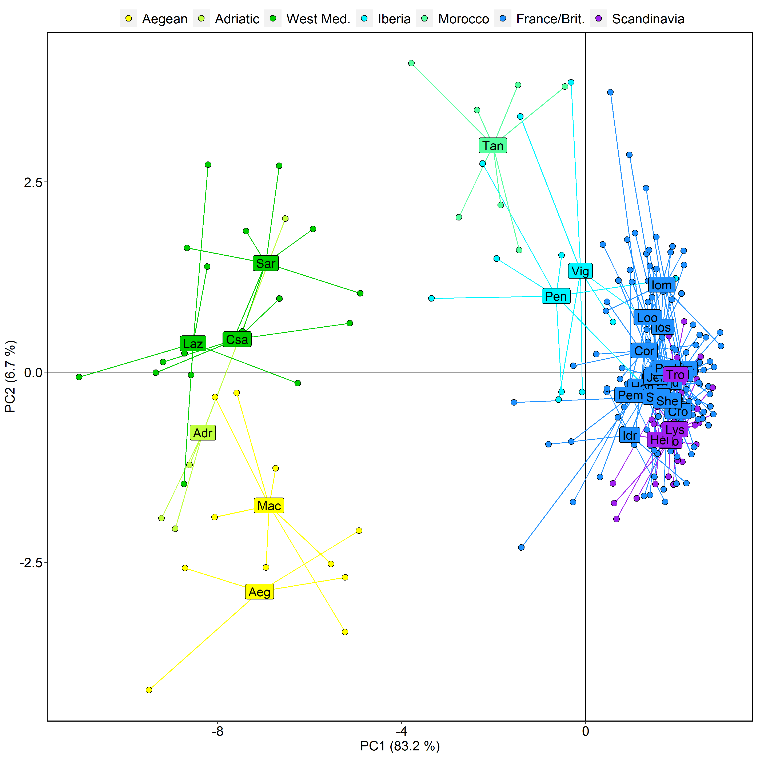


**Fig.S2.1:** A DAPC plot for 11,122 SNP loci in 376 *Palinurus sp.* individuals from 17 species/location samples. Putatively *P. elephas* samples are all distinct from clusters attributed to congenic species with overlapping ranges, *P. mauritanicus* and *P. charlestoni*, both supplied via fishers in Cape Verde. One putatively *P. charlestoni* individual clusters with *P. mauritanicus* likely representing an erroneous taxonomic designation by the sampler. Additionally, one *P. elephas* attributed to a Mediterranean stock actually groups with Atlantic individuals. This sample was putatively of Tunisian origin, but was sourced from a holding facility in France and appears not to be of Mediterranean descent. This sample and all interspecific controls were removed from the dataset ahead of downstream analysis. Note: axis labels should be LD1/2, not PC1/2.

**Fig.S2.2:** DAPC plots of 276 *P. elephas* individuals from 10 Atlantic locations using 16 outlier SNPs detected by Bayescan v2.1 (left plot) and 58 outlier SNPs detected by Outflank v0.2 (Whitlock & Lotterhos, 2015) using the gl.outflank function of the dartR package v1.1.11 in R (right plot). Note: axis labels should be LD1/2, not PC1/2.



**Fig.S2.3:** DAPC plot of 214 *H. gammarus* from 32 sites using 51 outlier SNPs detected by Bayescan. Note: axis labels should be LD1/3, not PC1/3.



**Fig.S2.4:** DAPC plots of all 214 *H. gammarus* from all sites: (left) using 87 outlier SNPs with genotype-environment associations (GEA) as identified by RDA; (right) using 30 outlier SNPs detected by both GEA-RDA and Bayescan. Note: axis labels should be LD1/2, not PC1/2.