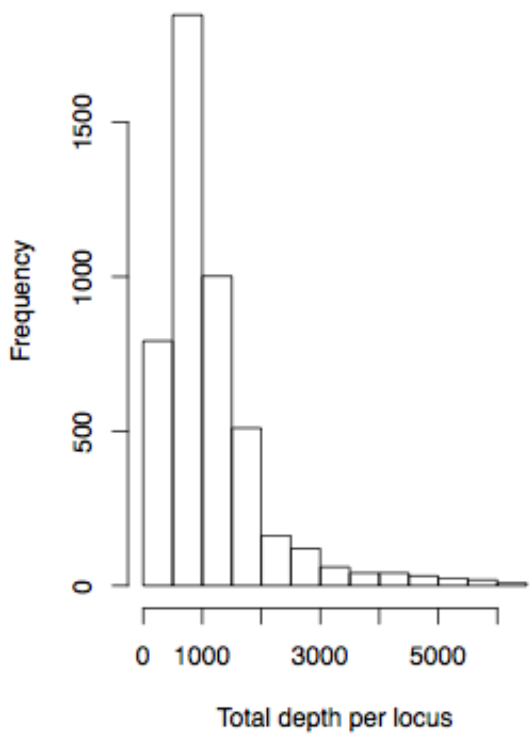
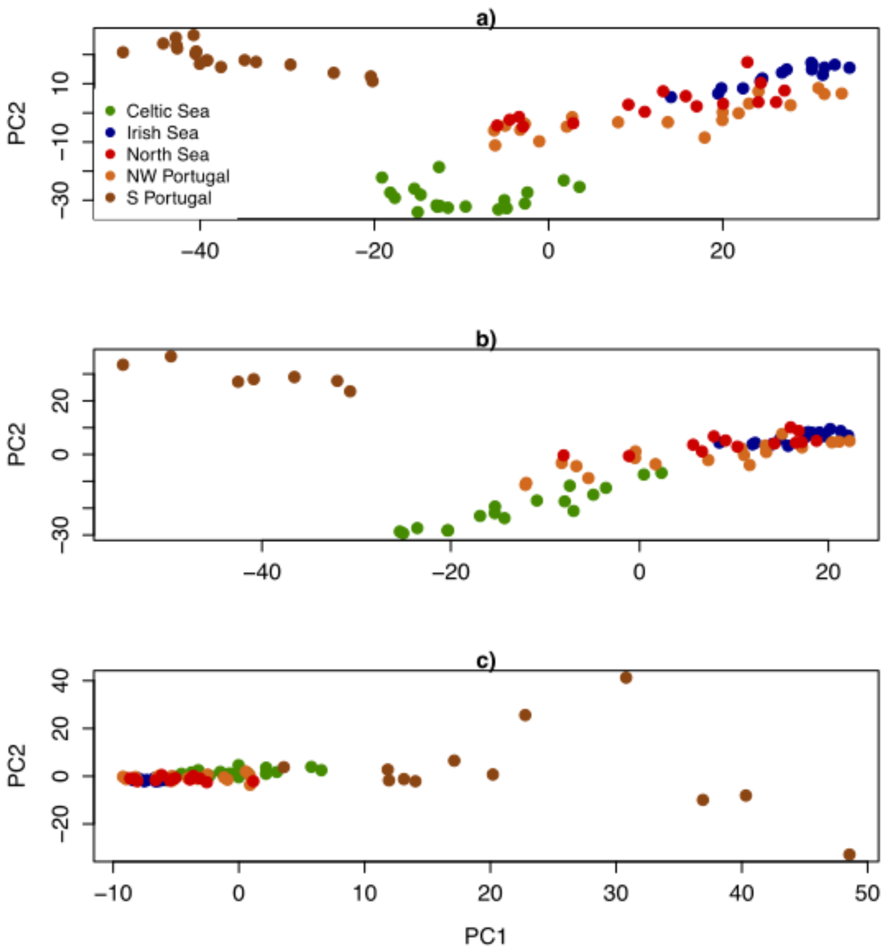
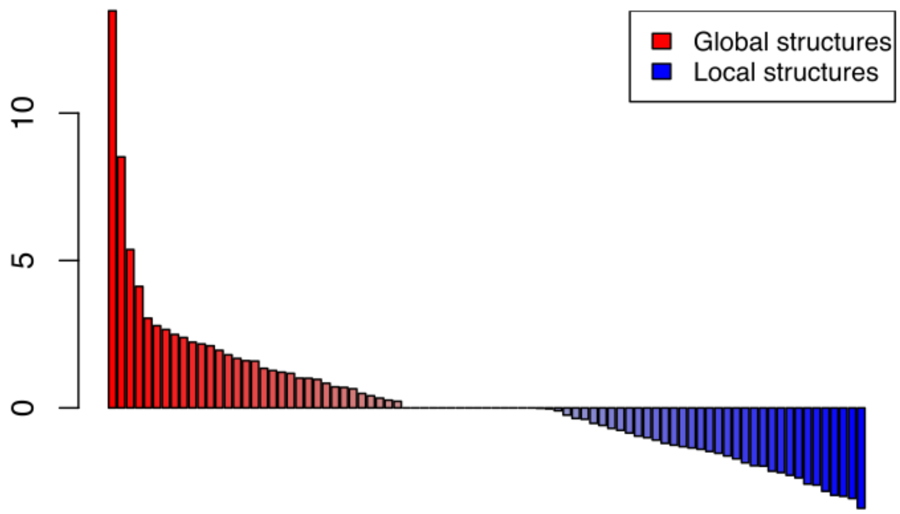
Supplemental Figure 1 – Read depth per locus for the set of 4 656 SNP loci filtered with vcftool, for the 88 individuals of *Scyliorhinus canicula* sampled.



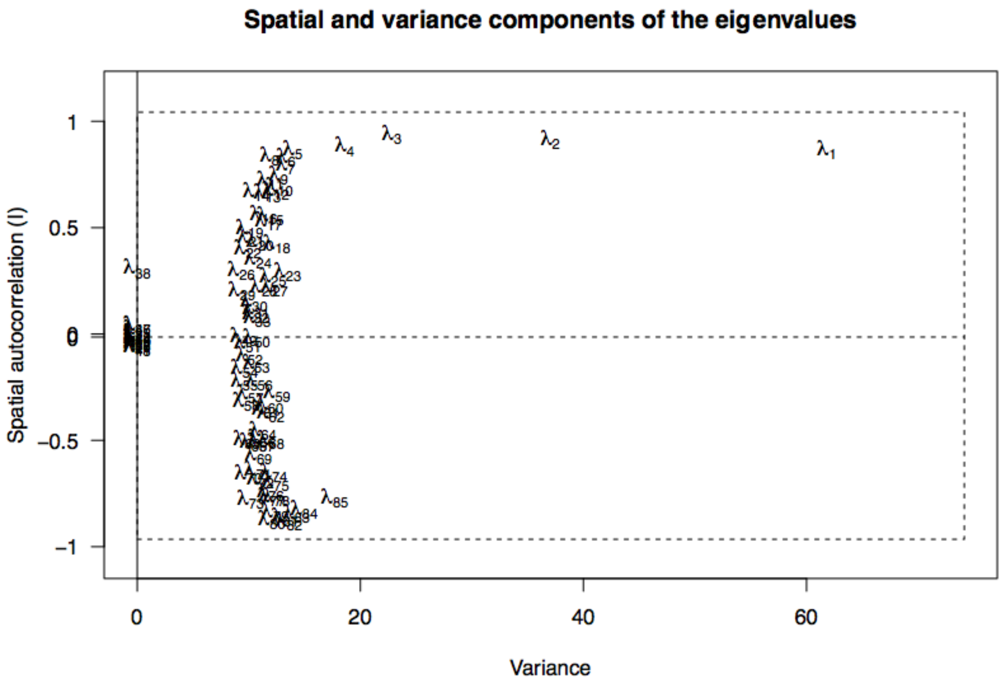
Supplemental Figure 2 – Principal Component Analysis of multilocus SNP genotypes of the lesser spotted dogfish *S. canicula*, considering a) 4 656 SNP loci and 88 individuals (filtered dataset obtained from vcftools; PC1 6.3%, PC2 3.3%); b) 2 674 SNP loci and 71 individuals, considering 20% missing data at the locus and individual levels (PC1 7.3%, PC2 4.3%); c) 1 243 SNP loci and 79 individuals, considering 5% missing data at the locus and individual levels (PC1 12.2%, PC2 4.6%). Legend on top graph is the same for all graphs.



Supplemental Figure 3 – Eigenvalues of the Spatial Principal Component Analysis based on 2674 SNPs and 71 individuals of the lesser spotted dogfish *S. canicula*, along the northeastern Atlantic coast. See Methods and Results for details.



Supplemental Figure 4 – Spatial and variance components of the eigenvalues from the Spatial Principal Component Analysis based on 2674 SNPs and 71 individuals of the lesser spotted dogfish *S. canicula*, along the northeastern Atlantic coast.



Supplemental Figure 5 - Plot of cross-validation error values, based on 5 replicate runs per K value, and a) 5% and b) 10% of masked data in the test set, using 2674 SNP loci. The most likely K corresponds to the lowest value where the first plateau of error value is reached, and corresponds to K=3 in the graphs.