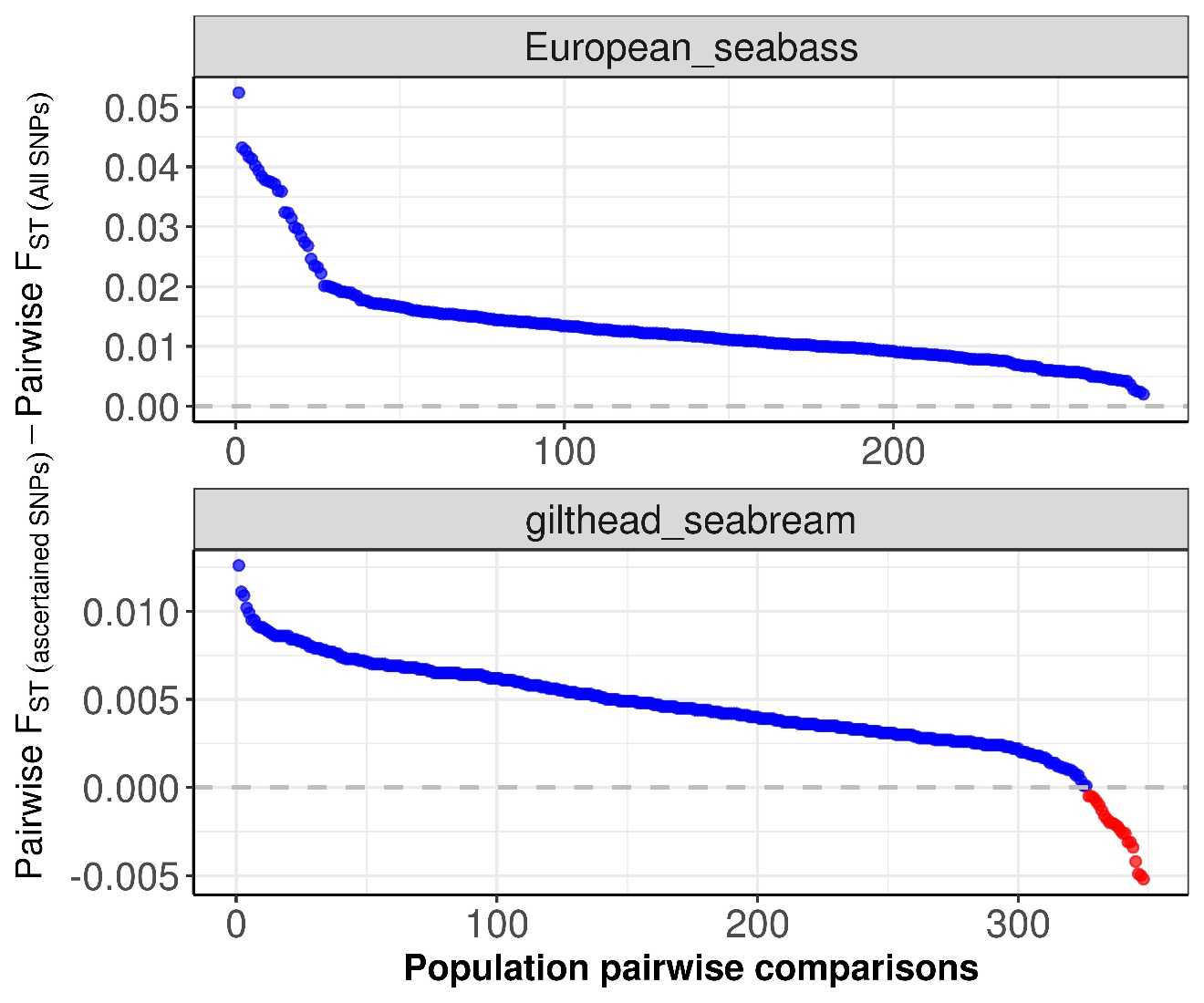
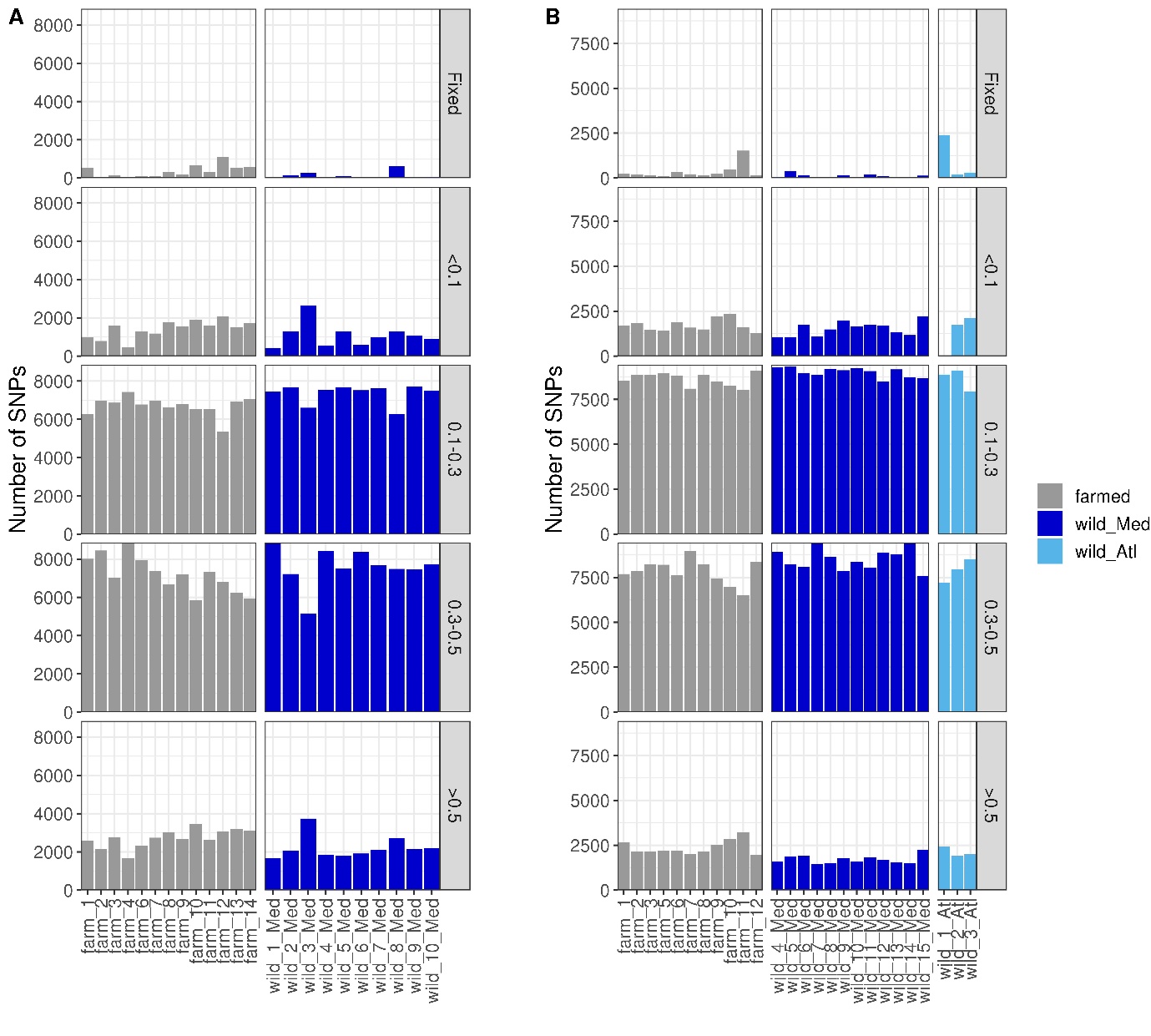


**Figure S1. Density plots showing the distribution of the inter-marker distances of the markers on the combined-species SNP array.**



**Figure S2. Higher pairwise FST values were obtained for populations from both species when using a panel that only contained genotype data at the genomic positions of the array markers (‘ascertained’ dataset) compared to the full SNP panel (‘non-ascertained’ dataset).**



**Figure S3. Allele frequency of the SNPs typed with the combined species SNP array across different farmed and wild (A) European seabass and (B) gilthead seabream populations.** Panels are stratified by allele frequency as indicated in the labels along the y-axes on the right side. Populations are coloured coded according to their known origin, as shown in the legend at the right.