

Table S2. Mixture analysis of fisheries samples performed in ONCOR without FASH and FSSH samples. Samples collected from the supposed mixed fisheries were tested against three spawning components, NSSH, ISSH and NSAH genetic clusters. No individuals from mixed fisheries were assigned to NSAH by this approach, which is therefore not reported. Area refers to the number reported in Fig. 6 and numbers in Table 1.

Area	Reporting group	Estimate	95% CI
10-11	ISSH	1.000	1.000 - 1.000
	NSSH	0.000	0.000 - 0.000
12	ISSH	0.000	0.000 - 0.000
	NSSH	1.000	1.000 - 1.000
13	ISSH	0.024	0.000 - 0.071
	NSSH	0.976	0.905 - 1.000
14	ISSH	0.163	0.070 - 0.280
	NSSH	0.837	0.698 - 0.930
15	ISSH	0.000	0.000 - 0.000
	NSSH	1.000	1.000 - 1.000
16	ISSH	0.105	0.026 - 0.211
	NSSH	0.895	0.790 - 0.974
17	ISSH	0.010	0.000 - 0.040
	NSSH	0.990	0.960 - 1.000

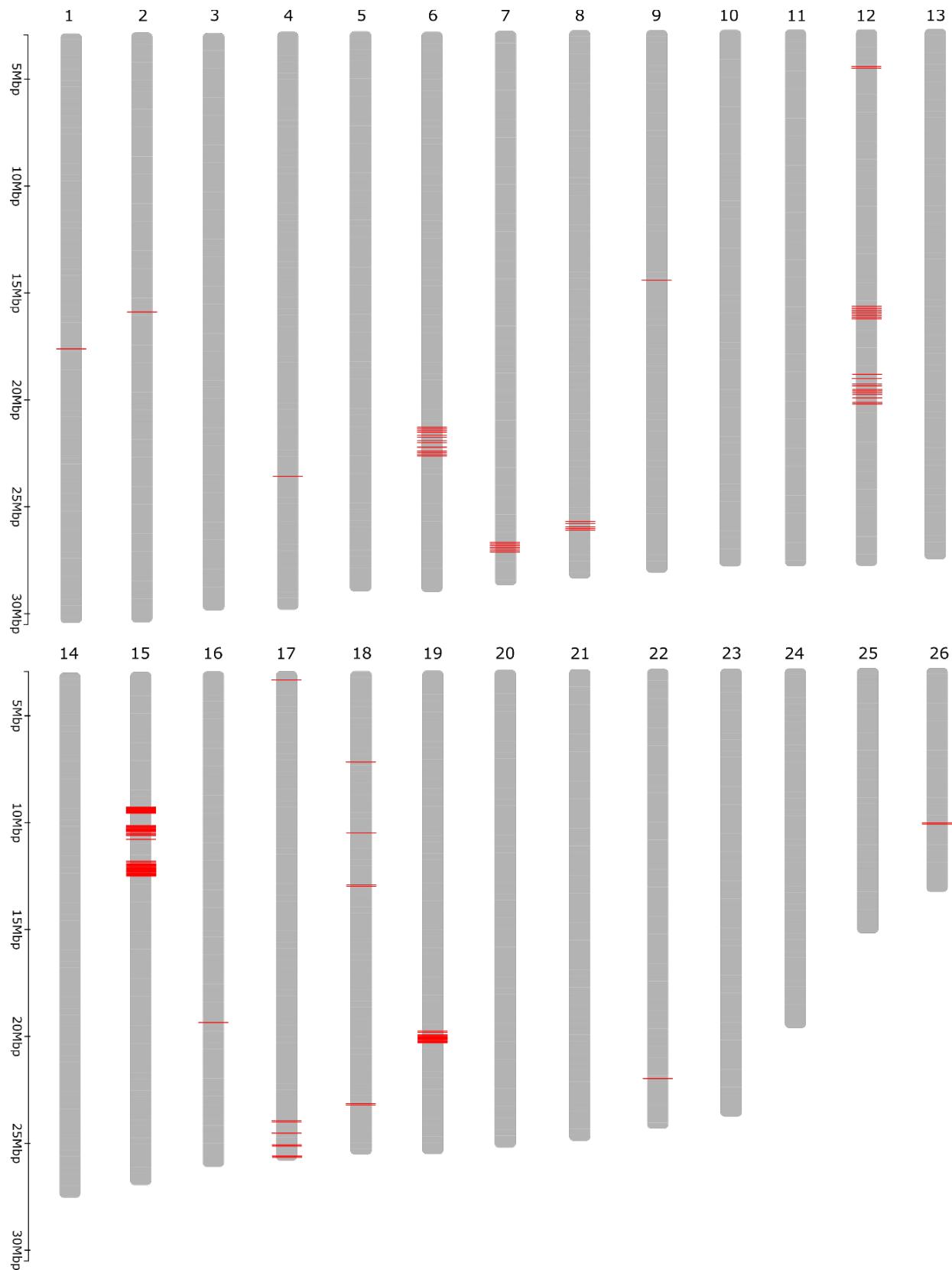


Figure S1. Chromosomal position of the 120 outliers SNPs used during the present study.

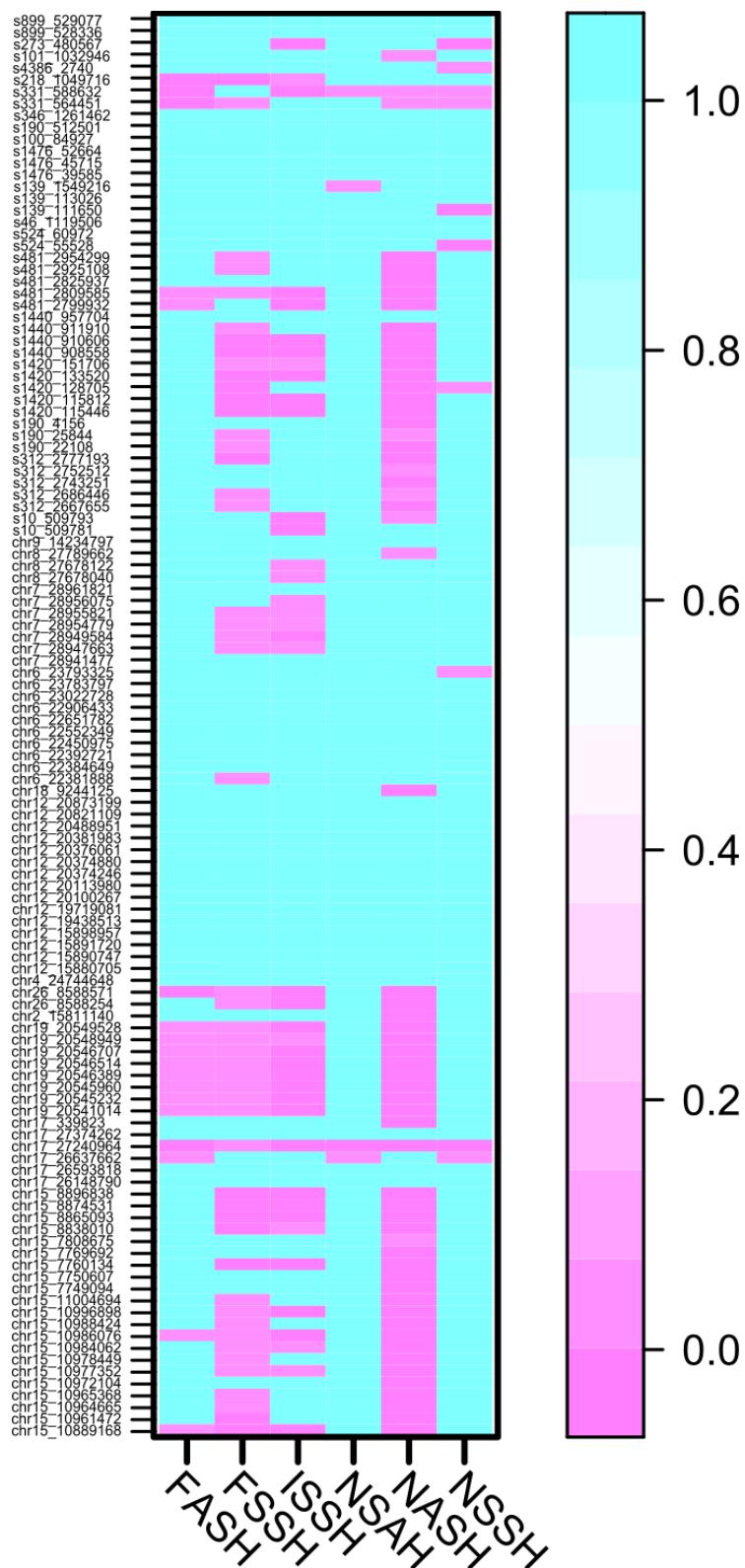


Figure S2. Hardy-Weinberg equilibrium for spawning samples (vertical) and SNPs loci (horizontal). Pink colour indicates significant deviations ($p<0.05$) from HWE.

Figure S3a–g. The index of pairwise association between SNPs calculated as \bar{r}_d for all spawning samples and for each sample was relatively high since all SNPs were selected due to their potential association with spawning characteristics and salinity preferences. a) all spawning samples, b) FASH, c) FSSH, d) ISSH, e) NSSH, f) NSAH and g) NASH.

