The following supplement accompanies the article

Candidate gene variation in gilthead sea bream reveals complex spatiotemporal selection patterns between marine and lagoon habitats

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Supplement 1

Table S1: *Sparus aurata*. List of forward (*F*) and reverse (*R*) primers for each microsatellite locus and long range (LR) amplicons used in this study.

Locus	Primers (5' -> 3')		Primer source
Microsatellites :			
Prl	*F*	GAAGAGTTTGCTTCCATTGG	Astola et al. 2003
	R	CATCCATCCAATTAAGATGG	
GH	*F*	CCTTAAATCAGTTCAGCCG	Almuly et al. 2005
	R	GGTTCAAGTTCTGGTGACTAG	
F7b	*F*	ATCGTTTTCTAGGGCGTGTG	Coscia et al. 2012
	R	CGTTTCCTCACTGCTGGTG	
B13b	*F*	CCTCCTGACCAGTCCTGCTTT	Coscia et al. 2012
	R	ACCCCTGCATTCCAGCTTC	
F6	*F*	CTGCTCACTGTTGACTGAATAC	Coscia et al. 2012
	R	GATGACTGCCTCCCTCTTATC	
Hd33F	*F*	TGAGTCTACAAAGCCAGAACCA	Coscia et al. 2012
	R	AATAAAGCTCTGCCTGTGCC	
Saimbb25	*F*	AAACAACTTCGGTCCGTCAC	Coscia et al. 2012
	R	CTGCACCTTATCCTCTTGCAC	
SauE82	*F*	ATTGGGTGGCAGTTTAGTAGG	Coscia et al. 2012
	R	CACTGCGATGAGTGACCC	
Ad10F	*F*	TGGAGGAACAGTGCAGTCAG	Coscia et al. 2012
	R	GGAATGGAAGTGCCTGATGT	
Cld29T	*F*	GTCGGATTTTCGCATGTTGT	Coscia et al. 2012
	R	CTGCAGGGAGGAAACAAGAC	
Dd16T	*F*	CACATTTAGGGCACCATATCC	Franch et al. 2006
	R	GGGAATCTCTCTGTCTGTCTGG	
SauI47	*F*	ACAGTACCCCACTGTCTCC	Franch et al. 2006
	R	CCATATCATTACACTGTGGC	
Dt23	*F*	CACACAACACACGATTACAGCA	Franch et al. 2006
	R	CCAAAAACAGCGATTTGTCC	
Bld04F	*F*	TCCGTGACTCTGTCTCACCA	Franch et al. 2006
	R	TCTTTGTCCGCATGTTTCAC	
Fd92H	*F*	AGGCATTTTGTCAATGAGGG	Franch et al. 2006
	R	CTGGGTTGGAGAGCTCAGAT	

Locus	**Primers (5' -> 3')**		**Primer source**
Cld35H	*F*	TGGGGTTTAGCTGTCAATCC	Franch et al. 2006
	R	GCGGCTATGCCTACAACTTC	
C67b	*F*	GCCCTGGTTATCATCTGTCGTT	Franch et al. 2006
	R	GCTCGTGTGTTGTTTGCTGTCT	
Bld10T	*F*	TCTCCACCACCTGCAGTTTT	Franch et al. 2006
	R	ACCGCCATCTTTGCTCTTTA	
Ct27	*F*	TTCAGATGAGAGTGGCATTAGG	Franch et al. 2006
	R	GGACGCTCTGGCTGTTCT	
172EP	*F*	GAGGGCATGTTGGAGGAAC	Franch et al. 2006
	R	GCACTCCATGTGGCTTCAG	
P20	*F*	AGAGCTCACTGTGACGATCAG	Franch et al. 2006
	R	CAGGATCCCATCCTTACACA	
C77b	*F*	CGATGGAACTACCCACCTC	Franch et al. 2006
	R	GCGACCATGAACCTGAAA	
Bd14H	*F*	TGCAGTGTCAAGGAAAACCA	Franch et al. 2006
	R	GCCATTATCAATCACTAACATGC	
LR amplicons:			
GH LR-PCR	*F*	CCAGAACCTGAACCAGACATGGACAG	This study
	R	GGCCTCTGGAGAGAGTCTACATTTTGC	
Prl LR-PCR	*F*	AGTCCTGCCGAATGAGTCCT	This study
	R	TGCTGCAGTTTGTCATCAGAC	

Table S2: *Sparus aurata*. Summary of post filtering and post reference assembly steps for each of the 24 individuals used in haplotype reconstruction (MA: Mauguio; TH: Thau).

Individuals	**Total No. of filtered reads**	**No. of *GH* reads**	**No. of *Prl* reads**	**Total No. of reads assembled**	**Assembled reads (%)**	**Reads assembled to *GH* (%)**	**Reads assembled to *Prl* (%)**
MA06	351,692	154,670	122,062	276,732	0.787	0.559	0.441
MA07	733,944	411,042	54,658	465,700	0.635	0.883	0.117
MA08	1,126,596	273,643	697,557	971,200	0.862	0.282	0.718
MA11	147,324	37,402	77,126	114,528	0.777	0.327	0.673
MA17	276,848	43,073	140,692	183,765	0.664	0.234	0.766
MA21	341,150	128,041	177,998	306,039	0.897	0.418	0.582
MA23	1,085,134	263,211	637,535	900,746	0.830	0.292	0.708
MA24	834,982	409,035	286,631	695,666	0.833	0.588	0.412
MA25	915,826	360,150	449,655	809,805	0.884	0.445	0.555
MA26	891,528	312,411	455,736	768,147	0.862	0.407	0.593
MA29	770,688	560,646	155,264	715,910	0.929	0.783	0.217
MA30	483,688	196,429	228,772	425,201	0.879	0.462	0.538
TH02	690,296	370,701	378,152	748,853	1.085	0.495	0.505
TH03	689,486	400,725	147,886	548,611	0.796	0.730	0.270
TH15	619,086	331,192	147,904	479,096	0.774	0.691	0.309
TH16	300,202	62,918	119,355	182,273	0.607	0.345	0.655
TH17	650,072	73,099	436,884	509,983	0.785	0.143	0.857
TH40	334,664	39,769	186,153	225,922	0.675	0.176	0.824
TH77	275,758	60,224	46,073	106,297	0.385	0.567	0.433
TH82	354,740	38,944	104,048	142,992	0.403	0.272	0.728
TH83	411,414	31,630	40,761	72,391	0.176	0.437	0.563
TH11	824,338	212,042	344,854	556,896	0.676	0.381	0.619
TH28	806,196	196,129	270,495	466,624	0.579	0.420	0.580
TH72	492,264	100,003	47,525	147,528	0.300	0.678	0.322
Sum/ *Mean*	**14,407,916**	**5,067,129**	**5,753,776**	**10,820,905**	***0.712***	***0.459***	***0.541***

Figure S1: *Sparus aurata*. Estimates of recruitment date of autumn (= migrating) individuals in each lagoon (box plots), together with sampling dates of spring (= entering) individuals (red circles). Estimates of recruitment events for autumn individuals were back-calculated from otolithometry data (Isnard et al. 2015). Adapted from Isnard et al. (2015).

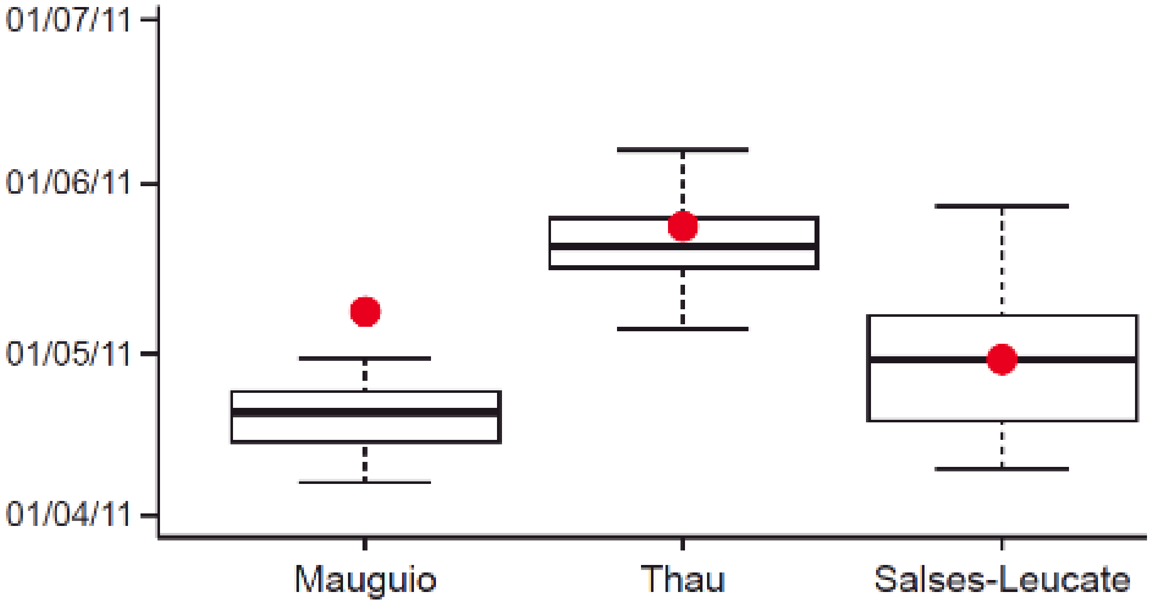

Figure S2: *Sparus aurata*. Results of Beaumont and Nichols' (1996) neutrality test using LOSITAN (Antao et al. 2008), based on comparisons among (A) entering (spring), and (B) migrating (autumn) samples, respectively. The test based on all samples is not provided because it reported a similar result as the one obtained for spring samples (see Fig. 2). Dots indicate markers, and only labels of outlier loci are reported. The grey area illustrates the 'neutral' envelop obtained with a null F_{ST} distribution generated with 100,000 simulated loci. Outlier loci falling in the red area were considered as candidate for diversifying selection. The locus falling in the yellow area (*Dd16T*) in panel B was not considered as a candidate for balancing selection due to the panmictic regime of the sea bream population studied (i.e. false positive). This locus exactly lies on the limit of the neutral envelop (p-value: 0.0503). He: expected heterozygosity. F_{ST}/He: "F_{ST} conditional on heterozygosity", a feature of the Beaumont and Nichols (1996) model.