

Table S1: Absolute frequencies of haplotype distribution in each sampled locality and GenBank accession numbers of COI haplotypes for *Ruditapes decussatus*. Populations are labelled as in Table 1. Asterisks (*) identify samples with sequences were taken from the GenBank database: Cordero et al. (2014). The template (§) identifies samples with sequences taken from the GenBank database: Keskin & Atar (2013). Due to the loss of haplotype B4 along with its informative polymorphisms (Cordero et al. 2014) (see the methods section for more details), the Aegean individuals previously attributed to the haplotype B4 by Cordero et al. (2014) fall within the haplotype B1 in the present study. Note that in order to analyse the same COI fragment obtained in this study, we used just a portion of the sequences whose GenBank accession numbers are reported in this table. See the main text (Statistical analysis in the Materials and Methods section) for more details. The localities are labelled as in Table I.

	OL	PA	PQ	TR	ST	CA	MU	SP	SG	LO	DN	TH	TL	EBR*	MME*	MG	VEN*	SFX*	HAL*	IZM*	MAR [§]	RF	FOR*	MLF*	MUG*	LUL*	GMO*	Tot	GB #
A1*	27	19	20	31	24	19	28	15	19	16	22	18	5	19	28	18	22	27	8	3		7	28	17	27	33	26	527	JX051518
A2*	1	1		1	3	1				2				1	2		5		4									21	JX051519
A3*																								4				4	JX051520
A4*								1					1		2		1					1	1					7	JX051521
A5*	2				1		1											3										7	JX051522
A6*																										2	2	JX051523	
A7*				1						1		1		2														5	JX051524
A8*																						1	2					3	JX051525
A9*											1															1	2	JX051526	
A10*																										1	1	JX051527	
A11*																										1	1	JX051528	
A12*																										1	1	JX051529	
A13*																								1			1	JX051530	
A15*																							1					1	JX051532
A16*								2	1			2			1													6	JX051533
A17*																		1										1	JX051534
A18*				3	1			1		1	1	2				1	1											11	JX051535
A19*																	1											1	JX051536
A20*																	1											1	JX051537
A21*																	1											1	JX051538
A22	5																											5	KU557025
A23	1																											1	KU557026
A24	1										1	1																3	KU557027
A25	1																											1	KU557028
A26	1							1																				2	KU557029
A27	3		2							1						1												7	KU557030
A28	1		1																									2	KU557031
A29	1																											1	KU557032
A30		1																										1	KU557033
A31		1																										1	KU557034
A32			1							1																		2	KU557035
A33										1																		1	KU557036
A34						1																						1	KU557037
A35																1												1	KU557038
A36																						1						1	KU557039
A37																						1						1	KU557040
A38																						1						1	KU557041
A39												1																1	KU557042
A40												1																1	KU557043
A41				1																								1	KU557044
A42					1																							1	KX981455
B1*																			7	19								26	JX051539
B2*				1															13	1								15	JX051540
B3*																				3								3	JX051541
B5*																				2								2	JX051543
B6*																			1									1	JX051544
B7*																				1								1	JX051545
B8*																				1								1	JX051546
C1 [§]																					23							23	KC311418
Tot	44	22	24	38	30	21	29	20	20	23	25	26	6	22	33	21	32	31	33	30	23	12	32	17	32	33	32	711	

Table S2: Pairwise Φ_{ST} values between *Ruditapes decussatus* populations. Significance was assessed by a permutation test with 10,000 replicates. The Φ_{ST} values that were significant after correction for multiple testing ($p < 0.0001$ alpha-level after Bonferroni correction) are reported in bold.

Asterisks (*) identify samples with sequences from the GenBank database: Cordero et al. (2014). The template (§) identifies samples with sequences from the GenBank database: Keskin & Atar (2013). The localities are labelled as in Table I.

	OL	RF	TH	TR	MU	SP	SG	DN	GMO*	MUG*	LUL*	MLF*	FOR*	MME*	EBR*	PA	PQ	CA	LO	MG	ST	TL	MAR [§]	IZM*	HAL*	SFX*	VEN*
OL	0.00000																										
RF	0.04941	0.00000																									
TH	0.05183	0.00479	0.00000																								
TR	0.05685	0.01700	0.00199	0.00000																							
MU	0.06267	0.06402	0.02445	0.01286	0.00000																						
SP	0.05380	0.01123	-0.03258	0.01318	0.05256	0.00000																					
SG	0.04500	0.02091	-0.02263	0.00182	0.01211	-0.02595	0.00000																				
DN	0.05588	0.03342	0.00273	-0.00489	0.00339	0.02797	0.00193	0.00000																			
GMO*	0.06526	0.03316	0.02364	0.01429	0.00620	0.03883	0.00431	-0.00333	0.00000																		
MUG*	0.08023	0.06067	0.04035	0.03384	0.06003	0.06122	0.04027	0.04321	0.04185	0.00000																	
LUL*	0.07587	0.09320	0.03221	0.01701	0.00453	0.06834	0.02625	0.01120	0.01105	0.07940	0.00000																
MLF*	0.04276	0.02831	0.00003	-0.00759	-0.01995	0.02295	-0.00843	-0.01648	-0.01393	0.04055	0.00000	0.00000															
FOR*	0.06818	0.01338	0.02375	0.01901	0.01042	0.04200	0.01090	0.00812	0.01263	0.05006	0.01629	-0.00982	0.00000														
MME	0.05569	0.01595	-0.00029	0.00867	0.01088	0.00009	-0.01770	0.00789	0.01384	0.04194	0.01582	-0.00988	0.00605	0.00000													
EBR*	0.05368	0.03462	0.00965	-0.00046	0.03436	0.03850	0.01677	0.01737	0.01656	0.05511	0.05640	0.01578	0.02564	0.00432	0.00000												
PA	0.02623	0.01633	0.00420	-0.01133	0.00888	0.01945	0.00012	-0.00903	0.00661	0.03634	0.01811	-0.01299	0.01100	-0.00305	0.00098	0.00000											
PQ	-0.00507	0.04920	0.04353	0.03844	0.08918	0.05858	0.05424	0.06386	0.06212	0.09195	0.11360	0.06204	0.07318	0.05014	0.05933	0.02748	0.00000										
CA	0.04732	0.02936	0.01117	-0.00335	0.00711	0.03062	0.00134	-0.00042	0.00193	0.04387	0.02243	-0.01047	0.00697	-0.01289	-0.00036	-0.01437	0.05279	0.00000									
LO	0.01113	0.01832	0.01124	-0.00419	0.03007	0.02696	0.01378	0.01135	0.02355	0.04771	0.04164	0.00535	0.02908	0.00595	-0.00834	-0.01433	-0.01746	-0.00336	0.00000								
MG	-0.01054	0.02052	-0.00264	0.00649	0.04156	0.00225	-0.00099	0.01763	0.02936	0.05554	0.05727	0.01556	0.03623	0.01843	0.03126	-0.00561	-0.02168	0.02296	-0.01761	0.00000							
ST	0.05365	0.03905	0.02277	-0.00582	0.01791	0.04072	0.01840	0.01103	0.02256	0.05328	0.03738	0.00600	0.02850	-0.00321	0.00443	-0.01161	0.05149	-0.01418	-0.00756	0.03036	0.00000						
TL	0.00297	-0.07832	-0.05434	-0.03423	0.14271	-0.04528	0.00703	0.02420	-0.00141	0.04957	0.34132	0.19176	-0.00808	-0.05770	0.03188	-0.01706	0.02472	0.03965	-0.02301	-0.01683	0.00971	0.00000					
MAR [§]	0.82267	0.90127	0.84232	0.84934	0.98731	0.88104	0.95476	0.96010	0.93263	0.94705	1.00000	1.00000	0.95431	0.92330	0.95891	0.93122	0.91711	0.97071	0.89843	0.90645	0.93199	0.98004	0.000				
IZM*	0.82752	0.79279	0.80297	0.81868	0.86172	0.80323	0.82945	0.84362	0.84959	0.85544	0.87309	0.83478	0.85775	0.84857	0.83808	0.82798	0.83049	0.83857	0.82065	0.81586	0.84466	0.78629	0.894	0.0000			
HAL*	0.57433	0.47085	0.51021	0.53471	0.57254	0.49506	0.51903	0.54468	0.56786	0.57541	0.59167	0.51572	0.57716	0.56895	0.53485	0.52375	0.53584	0.53142	0.52155	0.50971	0.55587	0.43149	0.699	0.1563	0.000		
SFX*	0.06185	0.05485	0.03325	0.02553	-0.00264	0.05479	0.02673	0.02636	0.02677	0.06545	0.05342	0.01917	0.03399	0.02941	0.04215	0.02379	0.08338	0.02693	0.03822	0.04594	0.02185	0.04786	0.955	0.8562	0.573	0.000	
VEN*	0.06362	0.03477	0.03436	0.01223	0.04960	0.04617	0.03430	0.03371	0.04274	0.06560	0.06011	0.02546	0.04519	0.00534	0.01746	0.00529	0.05288	0.00436	0.00058	0.04228	-0.00970	-0.01641	0.890	0.8380	0.560	0.057	0.000

Table S3: Pairwise Φ_{ST} values between Bayesian groups (R1, R2, R3, R4, and R5). Significance was assessed by a permutation test with 10,000 replicates. The Φ_{ST} values that were significant after correction for multiple testing ($p < 0.0001$ alpha-level after Bonferroni correction) are reported in bold.

	R1	R2	R3	R4	R5
R1	0.0000				
R2	0.2283	0.0000			
R3	0.9940	0.5591	0.0000		
R4	0.9988	0.6359	0.9623	0.0000	
R5	0.9923	0.8334	0.9229	0.9583	0.0000