Table S1. Distribution of extended D-loop (738 bp) haplotype frequencies in Atlantic green turtle (*Chelonia mydas*) nesting populations, including novel data for three sites, showed in bold. For rookery abbreviations see Table 3 in the manuscript or Table S9.

Extended D-loop	CEFL	SEFL	DRT	EBCMX	CUB	CR	CI	AV	SUR	FG	RA	FN	TRI	ASC	GB	STP
CM-A1.1	315	23	0	1	7		1									
CM-A1.2	19	12	8	1	12		2									
CM-A1.4	1				1											
CM-A1.5					1											
CM-A1.6					2											
CM-A2.1	8	4														
CM-A3.1	171	115	39	147	73	343	37	5	1							
CM-A3.2					2	2										
CM-A3.5						2										
CM-A3.6						3										
CM-A3.8					4											
CM-A3.9					7											
CM-A5.1	2		17			33	4	48	55	16						
CM-A5.2					1			14								
CM-A6.1									2					7		9
CM-A8.1	1									1	27	14	55	212	287	52
CM-A8.3											1		12	3	1	
CM-A9.1											2		19	10		
CM-A10.1											2			9		
CM-A11.1													1			
CM-A12.1											3					
CM-A13.1	10	2			11		2									
CM-A13.2					1											
CM-A16.1	3	1			1		1									
CM-A17.1		2			2		2									
CM-A18.1			1	21	1											
CM-A18.2	1	1		3	4		1									

Extended D-loop	CEFL	SEFL	DRT	EBCMX	CUB	CR	CI	AV	SUR	FG	RA	FN	TRI	ASC	GB	STP
CM-A20.1						2										
CM-A21.1						3										
CM-A22.1							2			1						
CM-A23.1													6			
CM-A24.1													1	6		
CM-A25.1											1	2				
CM-A26.1			1													
CM-A27.1					17		3									
CM-A27.2					1											
CM-A28.1	3	2	1		7											
CM-A32.1											1		5	2		
CM-A34.1							1									
CM-A36.1																20
CM-A37.1																2
CM-A39.1														6		
CM-A40.1																11
CM-A42.1														4	1	
CM-A45.1														7		
CM-A48.2					12											
CM-48.3					19											
CM-A53.1		3														
CM-A56.1					2											
CM-A57.1					1											
CM-A69.1														1		
CM-A75.1																2
CM-A78.1							1									
sample size	534	165	67	173	189	388	57	67	58	18	37	16	99	267	289	96

Table S2. Distribution of combined D-loop (738 bp) and mitochondrial short tandem repeat (mtSTR, ~200 bp) haplotype frequencies in 12 Atlantic green turtle (*Chelonia mydas*) nesting populations, including novel data for three sites, showed in bold. For rookery abbreviations see Table 3 in the manuscript or Table S9.

D-loop	mtSTR	CEFL	SEFL	DRT	CI	CR	**FG**	TRI	RA	FN	ASC	**GB**	**STP**
CM-A1.1	5-8-4-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A1.1	6-7-4-4	41	3	0	0	0	0	0	0	0	0	0	0
CM-A1.1	6-8-4-4	265	18	0	0	0	0	0	0	0	0	0	0
CM-A1.1	7-7-4-4	7	2	0	1	0	0	0	0	0	0	0	0
CM-A1.1	8-7-4-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A1.2	6-8-4-4	0	1	8	1	0	0	0	0	0	0	0	0
CM-A1.2	7-7-4-4	19	2	0	0	0	0	0	0	0	0	0	0
CM-A1.2	7-8-4-4	0	8	0	0	0	0	0	0	0	0	0	0
CM-A1.2	8-10-4-4	0	1	0	1	0	0	0	0	0	0	0	0
CM-A1.3	7-7-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A1.4	7-8-4-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A2.1	7-7-4-4	8	4	0	0	0	0	0	0	0	0	0	0
CM-A3.1	5-8-4-4	8	12	1	0	6	0	0	0	0	0	0	0
CM-A3.1	5-9-4-4	15	19	1	2	6	0	0	0	0	0	0	0
CM-A3.1	5-9-5-4	0	0	0	0	1	0	0	0	0	0	0	0
CM-A3.1	6-7-4-4	2	0	0	0	5	0	0	0	0	0	0	0
CM-A3.1	6-7-4-5	0	0	0	0	0	0	0	0	0	0	0	0
CM-A3.1	6-8-4-4	67	9	0	19	262	0	0	0	0	0	0	0
CM-A3.1	6-8-4-5	6	3	0	0	0	0	0	0	0	0	0	0
CM-A3.1	6-8-5-4	0	1	0	0	2	0	0	0	0	0	0	0
CM-A3.1	6-9-4-4	2	0	0	0	8	0	0	0	0	0	0	0
CM-A3.1	6-13-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A3.1	7-7-4-4	9	1	36	1	8	0	0	0	0	0	0	0
CM-A3.1	7-7-4-5	36	52	0	0	1	0	0	0	0	0	0	0
CM-A3.1	7-8-4-4	16	4	1	13	42	0	0	0	0	0	0	0
CM-A3.1	7-8-4-5	9	14	0	0	0	0	0	0	0	0	0	0
CM-A3.1	7-8-4-6	0	0	0	2	0	0	0	0	0	0	0	0
CM-A3.1	7-8-5-4	0	0	0	0	1	0	0	0	0	0	0	0
CM-A3.1	7-9-4-5	1	0	0	0	0	0	0	0	0	0	0	0
CM-A3.1	7-10-4-4	0	0	0	0	1	0	0	0	0	0	0	0
CM-A3.1	7-12-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A3.4	7-8-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A3.5	6-8-4-4	0	0	0	0	1	0	0	0	0	0	0	0
CM-A3.5	7-8-4-4	0	0	0	0	1	0	0	0	0	0	0	0
CM-A3.6	6-8-4-4	0	0	0	0	3	0	0	0	0	0	0	0
CM-A5.1	5-13-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A5.1	6-8-4-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A5.1	6-12-4-4	0	0	0	1	12	2	0	0	0	0	0	0
CM-A5.1	6-13-3-5	0	0	0	0	0	0	0	0	0	0	0	0
CM-A5.1	6-13-4-4	0	0	0	1	17	2	0	0	0	0	0	0
CM-A5.1	6-14-4-4	0	0	0	0	1	0	0	0	0	0	0	0
CM-A5.1	7-11-4-4	0	0	17	0	0	0	0	0	0	0	0	0

D-loop	mtSTR	CEFL	SEFL	DRT	CI	CR	FG	TRI	RA	FN	ASC	GB	STP
CM-A5.1	7-12-4-4	0	0	0	2	1	6	0	0	0	0	0	0
CM-A5.1	7-13-4-4	0	0	0	0	0	1	0	0	0	0	0	0
CM-A5.1	7-15-0-4	0	0	0	0	1	0	0	0	0	0	0	0
CM-A5.1	7-17-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A5.1	8-10-4-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A5.1	8-11-4-4	0	0	0	0	1	0	0	0	0	0	0	0
CM-A5.3	7-12-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	5-13-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	6-8-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	6-12-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	6-13-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	6-16-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	7-7-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	7-11-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A6.1	7-11-5-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	7-12-4-4	0	0	0	0	0	0	0	0	0	5	0	6
CM-A6.1	7-14-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A6.1	7-16-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	5-13-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A8.1	5-14-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A8.1	6-8-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	6-12-4-4	0	0	0	0	0	0	2	0	0	5	0	0
CM-A8.1	6-13-4-4	0	0	0	0	0	0	6	0	0	9	0	0
CM-A8.1	6-14-4-4	0	0	0	0	0	0	0	0	0	3	0	0
CM-A8.1	6-15-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	6-16-4-4	0	0	0	0	0	0	0	1	0	0	0	0
CM-A8.1	6-17-4-4	0	0	0	0	0	0	0	0	0	3	0	0
CM-A8.1	7-7-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	7-8-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	7-11-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	7-11-4-4	0	0	0	0	0	0	9	5	1	13	5	1
CM-A8.1	7-11-4-5	0	0	0	0	0	0	0	0	2	0	1	0
CM-A8.1	7-11-5-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A8.1	7-12-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	7-12-4-2	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	7-12-4-4	1	0	0	0	0	0	22	12	2	85	276	27
CM-A8.1	7-12-4-5	0	0	0	0	0	0	0	0	2	0	0	0
CM-A8.1	7-12-5-4	0	0	0	0	0	0	0	0	1	0	0	0
CM-A8.1	7-13-4-4	0	0	0	0	0	0	1	3	0	14	4	0
CM-A8.1	7-14-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	7-14-4-4	0	0	0	0	0	0	1	1	0	1	0	0
CM-A8.1	7-15-4-4	0	0	0	0	0	0	1	1	1	2	0	0

D-loop	mtSTR	CEFL	SEFL	DRT	CI	CR	**FG**	TRI	RA	FN	ASC	**GB**	**STP**
CM-A8.1	7-16-3-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	7-16-3-5	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	7-16-4-4	0	0	0	0	0	1	5	1	2	6	0	6
CM-A8.1	7-17-4-4	0	0	0	0	0	0	3	0	0	0	0	0
CM-A8.1	8-9-4-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A8.1	8-10-4-4	0	0	0	0	0	0	3	0	0	1	0	0
CM-A8.1	8-11-4-4	0	0	0	0	0	0	0	0	0	7	0	0
CM-A8.1	8-12-4-4	0	0	0	0	0	0	0	0	1	5	0	0
CM-A8.1	8-13-4-4	0	0	0	0	0	0	0	2	0	1	0	0
CM-A8.1	8-14-3-3	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.1	8-14-4-4	0	0	0	0	0	0	0	1	0	5	0	0
CM-A8.1	8-15-4-4	0	0	0	0	0	0	1	0	0	1	0	0
CM-A8.1	8-16-4-4	0	0	0	0	0	0	0	0	2	0	0	0
CM-A8.1	9-14-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.2	7-11-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.2	7-12-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A8.3	7-11-4-4	0	0	0	0	0	0	3	1	0	2	0	0
CM-A8.3	7-11-5-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A8.3	7-12-4-4	0	0	0	0	0	0	7	0	0	1	1	0
CM-A8.3	7-16-4-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A9.1	6-12-4-4	0	0	0	0	0	0	3	0	0	0	0	0
CM-A9.1	6-13-4-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A9.1	7-11-4-4	0	0	0	0	0	0	3	0	0	3	0	0
CM-A9.1	7-12-4-4	0	0	0	0	0	0	11	1	0	5	0	0
CM-A9.1	7-13-4-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A9.1	8-11-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A9.1	8-12-4-4	0	0	0	0	0	0	0	1	0	0	0	0
CM-A10.1	6-13-4-5	0	0	0	0	0	0	0	0	0	0	0	0
CM-A10.1	7-12-4-4	0	0	0	0	0	0	0	2	0	2	0	0
CM-A10.1	7-13-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A10.1	7-17-4-4	0	0	0	0	0	0	0	0	0	1	0	0
CM-A10.1	8-11-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A10.1	8-12-4-4	0	0	0	0	0	0	0	0	0	1	0	0
CM-A11.1	7-17-4-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A12.1	7-12-4-4	0	0	0	0	0	0	0	3	0	0	0	0
CM-A13.1	5-7-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	5-7-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	5-7-7-4	0	2	0	2	0	0	0	0	0	0	0	0
CM-A13.1	5-8-5-5	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	5-8-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	5-9-5-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	5-10-6-4	0	1	0	0	0	0	0	0	0	0	0	0

D-loop	mtSTR	CEFL	SEFL	DRT	CI	CR	**FG**	TRI	RA	FN	ASC	**GB**	**STP**
CM-A13.1	6-7-5-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-7-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-8-5-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-8-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-8-7-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-8-8-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-8-9-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-9-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-9-7-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-9-8-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-10-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	6-11-5-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-7-7-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-8-5-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-8-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-8-7-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-8-8-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-9-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-10-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-11-5-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	7-11-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	8-6-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	8-7-7-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A13.1	8-9-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A14.1	7-8-7-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A14.1	7-8-8-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A16.1	5-7-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A16.1	5-8-6-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A16.1	5-10-6-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A16.1	5-12-6-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A16.1	5-11-6-5	0	0	0	1	0	0	0	0	0	0	0	0
CM-A16.2	5-8-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A17.1	5-8-5-4	0	1	0	0	0	0	0	0	0	0	0	0
CM-A17.1	7-10-7-4	0	1	0	2	0	0	0	0	0	0	0	0
CM-A18.1	7-7-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A18.2	7-6-5-4	0	0	0	1	0	0	0	0	0	0	0	0
CM-A18.2	7-7-4-4	1	1	1	0	0	0	0	0	0	0	0	0
CM-A20.1	7-13-4-4	0	0	0	0	2	0	0	0	0	0	0	0
CM-A21.1	6-13-4-4	0	0	0	0	3	0	0	0	0	0	0	0
CM-A21.1	7-11-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A22.1	5-8-4-5	0	0	0	2	0	0	0	0	0	0	0	0
CM-A22.1	5-8-4-6	0	0	0	0	0	1	0	0	0	0	0	0

D-loop	mtSTR	CEFL	SEFL	DRT	CI	CR	**FG**	TRI	RA	FN	ASC	**GB**	**STP**
CM-A22.1	7-7-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A23.1	7-12-4-4	0	0	0	0	0	0	6	0	0	0	0	0
CM-A24.1	7-12-4-4	0	0	0	0	0	0	0	0	0	6	0	0
CM-A24.1	7-13-4-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A25.1	7-12-4-4	0	0	0	0	0	0	0	1	2	0	0	0
CM-A26.1	6-8-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A26.1	7-8-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A26.1	7-9-4-4	0	0	1	0	0	0	0	0	0	0	0	0
CM-A27.1	5-8-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A27.1	5-9-4-4	0	0	0	3	0	0	0	0	0	0	0	0
CM-A27.1	5-9-8-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A28.1	5-8-5-4	2	2	1	0	0	0	0	0	0	0	0	0
CM-A28.1	6-8-4-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A30.1	7-8-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A32.1	6-12-4-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A32.1	6-13-4-4	0	0	0	0	0	0	0	1	0	0	0	0
CM-A32.1	7-10-4-4	0	0	0	0	0	0	1	0	0	0	0	0
CM-A32.1	7-11-4-4	0	0	0	0	0	0	2	0	0	0	0	0
CM-A32.1	7-12-4-4	0	0	0	0	0	0	1	0	0	1	0	0
CM-A32.1	8-12-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A34.1	7-7+6-6-4*	0	0	0	1	0	0	0	0	0	0	0	0
CM-A35.1	6-18-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A35.1	7-16-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A35.1	7-17-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A36.1	7-11-4-4	0	0	0	0	0	0	0	0	0	0	0	6
CM-A36.1	7-12-4-4	0	0	0	0	0	0	0	0	0	0	0	11
CM-A36.1	7-13-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A37.1	7-11-5-4	0	0	0	0	0	0	0	0	0	0	0	2
CM-A39.1	7-12-4-4	0	0	0	0	0	0	0	0	0	2	0	0
CM-A39.1	8-12-4-4	0	0	0	0	0	0	0	0	0	3	0	0
CM-A40.1	7-12-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A40.1	7-13-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A40.1	7-14-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A40.1	7-14-4-5	0	0	0	0	0	0	0	0	0	0	0	1
CM-A40.1	7-15-4-4	0	0	0	0	0	0	0	0	0	0	0	4
CM-A40.1	8-15-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A42.1	6-17-4-4	0	0	0	0	0	0	0	0	0	1	0	0
CM-A42.1	7-12-4-4	0	0	0	0	0	0	0	0	0	2	1	0
CM-A42.1	8-12-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A44.1	8-13-4-2	0	0	0	0	0	0	0	0	0	0	0	0
CM-A45.1	5-12-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A45.1	5-13-4-4	0	0	0	0	0	0	0	0	0	1	0	0

D-loop	mtSTR	CEFL	SEFL	DRT	CI	CR	**FG**	TRI	RA	FN	ASC	**GB**	**STP**
CM-A45.1	5-14-4-4	0	0	0	0	0	0	0	0	0	1	0	0
CM-A45.1	5-15-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A46.1	7-12-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A47.1	7-7-5-5	0	0	0	0	0	0	0	0	0	0	0	0
CM-A48.3	6-7-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A53.1	5-8-4-4	1	0	0	0	0	0	0	0	0	0	0	0
CM-A53.1	6-8-4-4	2	0	0	0	0	0	0	0	0	0	0	0
CM-A60.1	6-8-8-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A62.1	6-8-8-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A68.1	5-6-6-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A69.1	7-12-4-4	0	0	0	0	0	0	0	0	0	1	0	0
CM-A75.1	6-12-4-4	0	0	0	0	0	0	0	0	0	0	0	1
CM-A75.1	7-13-4-4	0	0	0	0	0	0	0	0	0	0	0	0
CM-A78.1	8-7-4-4	0	0	0	1	0	0	0	0	0	0	0	0
sample size		527	162	67	57	386	13	99	37	16	199	288	74

*This sample presents a (T) insertion in STR 2 that divides this STR in two fragments (see Barbanti et al. 2019)

Table S3. Distribution of all mtSTR (mitochondrial short tandem repeat) haplotype frequencies in 12 Atlantic green turtle (*Chelonia mydas*) nesting populations, including novel data for three sites, showed in bold. For rookery abbreviations see Table 3 in the manuscript or Table S9.

mtSTR code	CEFL	SEFL	DRT	CI	CR	FG	RA	FN	TRI	ASC	GB	STP
5-7-7-4		2		2								
5-8-4-4	10	12	1		6							
5-8-4-5				2								
5-8-4-6						1						
5-8-5-4	2	3	1									
5-8-6-4	1											
5-9-4-4	15	19	1	5	6							
5-9-5-4					1							
5-10-6-4	1	1										
5-11-6-5				1								
5-12-6-4	1											
5-13-4-4										1		1
5-14-4-4										1		1
6-7-4-4	43	3			5							
6-8-4-4	336	28	8	20	266							
6-8-4-5	6	3										
6-8-5-4		1			2							
6-9-4-4	2				8							
6-12-4-4				1	12	2			6	6		1
6-13-3-5						1						
6-13-4-4				1	20	3	1		7	9		
6-14-4-4					1					3		
6-16-4-4							1					
6-17-4-4										4		
7-6-5-4				1								
7-7-4-4	44	10	37	2	8							
7-7-4-5	36	52			1							
7-8-4-4	17	12	1	13	43							
7-8-4-5	9	14										
7-8-4-6				2								
7-8-5-4					1							
7-9-4-4			1									
7-9-4-5	1											
7-10-4-4					1				1			
7-10-7-4		1		2								
7-11-4-4			17				6	1	17	18	5	8
7-11-4-5								2			1	
7-11-5-4									1			3
7-12-4-4	1			2	1	7	19	4	47	112	278	45
7-12-4-5								2				
7-12-5-4								1				
7-13-4-4					2	1	3		3	14	4	2
7-14-4-4							1		1	1		1
7-14-4-5												1
7-15-0-4					1							
7-15-4-4							1	1	1	2		4
7-16-4-4						2	1	2	6	6		6
7-17-4-4									4	1		
7-7+6-6-4*				1								
8-7-4-4	1			1								
8-9-4-4										1		
8-10-4-4	1	1		1					3	1		

mtSTR code	CEFL	SEFL	DRT	CI	CR	**FG**	RA	FN	TRI	ASC	**GB**	**STP**
8-11-4-4					1					7		
8-12-4-4							1	1		9		
8-13-4-4							2			1		
8-14-4-4							1			5		
8-15-4-4									1	1		1
8-16-4-4								2				
Sample size	527	162	67	57	386	17	37	16	99	202	288	74

*This sample presents a (T) insertion in STR 2 that divides this STR in two fragments (see Barbanti et al. 2019)

Table S4. Pairwise exact test P-values (above diagonal) and respective pairwise F_{ST} values (using only haplotype frequency, below diagonal) among 30 Atlantic green turtle (*Chelonia mydas*) foraging aggregations, based on 486 bp sequences of the D-loop in the control region of the mtDNA. The study site is in bold, and abbreviations follow those in Table 2 in the manuscript. Non-significant values, after false discovery rate (FDR) correction, are marked in bold (for a p < 0.05, FDR = 0.0075; Narum, 2006).

Foraging grounds	NC	EcFL	SFL	BB	SJB	SRI	LA	TX	BHM	PR	COL	MT	BRB	ALF	RA	FN	ALG	BA	ES	SFI	UB	PAR	AI	CB	URU	BuA	ST	CV	CAN	**MAU**
NC		0.001	0.342	0.450	0.263	0.146	0.000	0.000	0.000	0.002	0.000	0.000	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
EcFL	0.065		0.009	0.002	0.003	0.001	0.000	0.000	0.199	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
SFL	0.000	0.039		0.368	0.826	0.022	0.000	0.000	0.001	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
BB	-0.001	0.055	0.000		0.444	0.148	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
SJB	0.002	0.041	-0.003	-0.001		0.021	0.000	0.000	0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
SRI	0.011	0.143	0.031	0.010	0.028		0.122	0.031	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
LA	0.083	0.261	0.116	0.085	0.111	0.014		0.757	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
TX	0.108	0.285	0.144	0.109	0.137	0.028	-0.003		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
BHM	0.045	0.004	0.022	0.042	0.028	0.113	0.218	0.245		0.051	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
PR	0.038	0.036	0.023	0.046	0.031	0.109	0.216	0.248	0.009		0.105	0.000	0.017	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
COL	0.080	0.134	0.076	0.105	0.087	0.161	0.264	0.294	0.075	0.015		0.019	0.429	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	**0.000**
MT	0.199	0.341	0.212	0.237	0.224	0.264	0.329	0.349	0.256	0.162	0.058		0.003	0.000	0.000	0.043	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.173	0.164	**0.000**
BRB	0.055	0.131	0.066	0.089	0.074	0.127	0.219	0.252	0.081	0.029	-0.002	0.075		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.008	**0.000**
ALF	0.193	0.305	0.218	0.242	0.224	0.271	0.338	0.367	0.252	0.176	0.095	0.088	0.054		0.398	0.004	0.000	0.132	0.016	0.000	0.000	0.000	0.009	0.007	0.000	0.005	0.001	0.005	0.212	**0.000**
RA	0.230	0.359	0.258	0.280	0.263	0.304	0.363	0.388	0.299	0.222	0.134	0.097	0.088	-0.001		0.010	0.000	0.584	0.224	0.001	0.000	0.001	0.074	0.050	0.000	0.049	0.002	0.011	0.275	**0.000**
FN	0.262	0.393	0.284	0.307	0.290	0.333	0.383	0.403	0.323	0.237	0.126	0.030	0.110	0.035	0.030		0.000	0.109	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.726	0.931	**0.000**
ALG	0.382	0.532	0.411	0.423	0.398	0.476	0.498	0.495	0.429	0.397	0.336	0.301	0.253	0.078	0.060	0.152		0.007	0.002	0.387	0.825	0.510	0.063	0.102	0.188	0.165	0.023	0.000	0.004	**0.000**
BA	0.271	0.431	0.300	0.324	0.305	0.350	0.406	0.424	0.349	0.268	0.169	0.098	0.124	0.012	-0.006	0.016	0.059		0.824	0.035	0.003	0.020	0.294	0.197	0.000	0.196	0.008	0.077	0.434	**0.000**
ES	0.302	0.436	0.331	0.349	0.330	0.379	0.420	0.435	0.364	0.296	0.203	0.133	0.151	0.020	0.003	0.034	0.040	-0.010		0.015	0.001	0.004	0.259	0.156	0.000	0.207	0.004	0.010	0.279	**0.000**
SFI	0.364	0.503	0.394	0.407	0.384	0.449	0.475	0.477	0.413	0.373	0.299	0.250	0.225	0.057	0.040	0.112	-0.001	0.031	0.019		0.198	0.965	0.334	0.409	0.006	0.624	0.019	0.000	0.018	**0.000**
UB	0.376	0.529	0.405	0.418	0.392	0.472	0.495	0.493	0.425	0.393	0.336	0.310	0.249	0.081	0.066	0.162	-0.005	0.070	0.050	0.003		0.230	0.043	0.068	0.386	0.095	0.025	0.000	0.004	**0.000**
PAR	0.371	0.499	0.401	0.413	0.390	0.450	0.477	0.479	0.416	0.378	0.305	0.259	0.231	0.061	0.043	0.121	-0.002	0.036	0.023	-0.004	0.002		0.230	0.299	0.005	0.491	0.018	0.000	0.014	**0.000**
AI	0.307	0.450	0.338	0.356	0.335	0.387	0.428	0.442	0.374	0.313	0.230	0.181	0.166	0.027	0.011	0.069	0.012	0.002	0.002	0.000	0.017	0.002		0.987	0.001	0.965	0.021	0.001	0.084	**0.000**
CB	0.307	0.453	0.338	0.356	0.336	0.387	0.429	0.443	0.378	0.316	0.236	0.190	0.170	0.031	0.016	0.076	0.009	0.007	0.005	-0.001	0.013	0.001	-0.008		0.001	0.940	0.050	0.000	0.057	**0.000**
URU	0.436	0.580	0.463	0.470	0.441	0.531	0.541	0.526	0.464	0.457	0.413	0.388	0.320	0.129	0.111	0.223	0.003	0.120	0.087	0.021	-0.001	0.017	0.045	0.039		0.004	0.006	0.000	0.000	**0.000**
BuA	0.322	0.472	0.352	0.370	0.349	0.406	0.445	0.455	0.388	0.330	0.249	0.199	0.182	0.035	0.016	0.079	0.006	0.008	0.004	-0.004	0.011	-0.002	-0.008	-0.008	0.037		0.024	0.000	0.058	**0.000**
ST	0.317	0.485	0.350	0.368	0.347	0.403	0.448	0.459	0.397	0.342	0.280	0.268	0.201	0.074	0.066	0.153	0.036	0.073	0.066	0.039	0.034	0.036	0.037	0.026	0.049	0.037		0.000	0.005	**0.000**
CV	0.278	0.433	0.298	0.323	0.304	0.359	0.413	0.427	0.337	0.248	0.130	0.015	0.122	0.054	0.050	-0.009	0.203	0.033	0.054	0.151	0.217	0.160	0.100	0.110	0.289	0.113	0.202		0.864	**0.000**
CAN	0.268	0.442	0.293	0.320	0.300	0.359	0.422	0.437	0.336	0.243	0.123	0.028	0.101	0.013	0.008	-0.027	0.135	-0.009	0.004	0.084	0.149	0.092	0.041	0.050	0.222	0.052	0.144	-0.032		**0.000**
MAU	**0.610**	**0.757**	**0.620**	**0.614**	**0.569**	**0.728**	**0.694**	**0.632**	**0.560**	**0.633**	**0.639**	**0.627**	**0.538**	**0.292**	**0.281**	**0.407**	**0.076**	**0.335**	**0.223**	**0.107**	**0.071**	**0.092**	**0.173**	**0.167**	**0.036**	**0.166**	**0.192**	**0.530**	**0.495**	

Table S5. Pairwise exact test P-values (above diagonal) and respective pairwise ϕ_{ST} values (below diagonal) among 30 Atlantic green turtle (*Chelonia mydas*) foraging aggregations, based on 486 bp sequences of the D-loop in the control region of the mtDNA. The study site is in bold, and abbreviations follow those in Table 2 in the manuscript. Non-significant values, after false discovery rate (FDR) correction, are marked in bold (for a $p < 0.05$, FDR = 0.0075; Narum, 2006).

Foraging grounds	NC	EcFL	SFL	BB	SJB	SRI	LA	TX	BHM	PR	COL	MT	BRB	ALF	RA	FN	ALG	BA	ES	SFI	UB	PAR	AI	CB	URU	BuA	ST	CV	CAN	MAU
NC		0.019	0.328	0.050	0.030	0.115	0.000	0.000	0.100	0.007	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
EcFL	0.035		0.038	0.015	0.007	0.006	0.000	0.000	0.049	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SFL	0.001	0.020		0.416	0.507	0.280	0.000	0.000	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BB	0.013	0.027	-0.001		0.781	0.697	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SJB	0.012	0.028	-0.001	-0.003		0.555	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
SRI	0.015	0.056	0.003	-0.007	-0.003		0.163	0.104	0.014	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
LA	0.058	0.146	0.048	0.036	0.039	0.008		0.886	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
TX	0.073	0.160	0.060	0.045	0.047	0.011	-0.003		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
BHM	0.007	0.018	0.012	0.027	0.028	0.039	0.084	0.101		0.002	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
PR	0.043	0.100	0.073	0.115	0.116	0.107	0.178	0.231	0.035		0.019	0.000	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
COL	0.219	0.317	0.276	0.360	0.357	0.309	0.435	0.512	0.221	0.060		0.005	0.634	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000
MT	0.541	0.643	0.587	0.664	0.653	0.632	0.724	0.764	0.532	0.347	0.132		0.003	0.050	0.006	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.078	0.226	0.000
BRB	0.227	0.324	0.286	0.364	0.364	0.311	0.422	0.505	0.241	0.079	-0.012	0.128		0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000
ALF	0.552	0.632	0.595	0.653	0.649	0.624	0.689	0.742	0.550	0.395	0.198	0.032	0.165		0.192	0.000	0.000	0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.006	0.162	0.000
RA	0.643	0.731	0.676	0.730	0.717	0.729	0.776	0.802	0.610	0.486	0.299	0.067	0.258	0.005		0.010	0.000	0.070	0.009	0.001	0.001	0.000	0.011	0.003	0.000	0.010	0.002	0.016	0.298	0.000
FN	0.689	0.768	0.716	0.763	0.751	0.768	0.805	0.825	0.649	0.543	0.366	0.066	0.333	0.054	0.030		0.000	0.109	0.011	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.695	0.993	0.000
ALG	0.768	0.859	0.784	0.823	0.799	0.867	0.874	0.862	0.684	0.634	0.515	0.267	0.449	0.087	0.047	0.106		0.017	0.003	0.573	0.521	0.677	0.307	0.518	0.061	0.318	0.010	0.000	0.003	0.001
BA	0.722	0.833	0.746	0.802	0.780	0.844	0.866	0.859	0.668	0.556	0.390	0.134	0.346	0.060	0.022	0.015	0.043		0.931	0.069	0.004	0.038	0.231	0.113	0.000	0.220	0.001	0.035	0.284	0.000
ES	0.754	0.834	0.772	0.810	0.790	0.839	0.853	0.852	0.682	0.623	0.484	0.176	0.431	0.073	0.026	0.024	0.036	-0.011		0.016	0.000	0.003	0.119	0.039	0.000	0.125	0.000	0.006	0.218	0.000
SFI	0.769	0.846	0.785	0.819	0.798	0.850	0.861	0.856	0.689	0.646	0.523	0.246	0.462	0.084	0.039	0.081	-0.002	0.019	0.018		0.120	0.925	0.899	0.935	0.002	0.900	0.007	0.000	0.012	0.000
UB	0.749	0.846	0.768	0.811	0.787	0.854	0.865	0.855	0.671	0.608	0.481	0.252	0.413	0.075	0.044	0.119	-0.002	0.065	0.054	0.006		0.091	0.073	0.123	0.314	0.066	0.016	0.000	0.003	0.011
PAR	0.786	0.852	0.801	0.828	0.810	0.855	0.862	0.858	0.705	0.680	0.562	0.278	0.504	0.101	0.049	0.095	-0.003	0.025	0.024	-0.003	0.007		0.618	0.793	0.002	0.764	0.004	0.006	0.006	0.000
AI	0.744	0.835	0.764	0.807	0.786	0.841	0.857	0.854	0.675	0.605	0.467	0.203	0.409	0.069	0.028	0.060	0.001	0.004	0.007	-0.005	0.011	-0.002		0.917	0.001	0.982	0.005	0.000	0.036	0.000
CB	0.741	0.833	0.762	0.806	0.785	0.840	0.857	0.855	0.675	0.599	0.462	0.212	0.404	0.075	0.037	0.073	-0.002	0.015	0.017	-0.005	0.007	-0.004	-0.006		0.006	0.916	0.013	0.000	0.016	0.000
URU	0.799	0.879	0.811	0.842	0.817	0.886	0.887	0.871	0.701	0.682	0.587	0.363	0.515	0.126	0.091	0.183	0.009	0.119	0.095	0.024	0.001	0.020	0.035	0.024		0.002	0.007	0.000	0.000	0.097
BuA	0.744	0.841	0.764	0.810	0.787	0.849	0.864	0.858	0.675	0.599	0.461	0.204	0.403	0.071	0.031	0.062	0.000	0.006	0.008	-0.006	0.013	-0.004	-0.008	-0.007	0.036		0.004	0.000	0.031	0.000
ST	0.725	0.841	0.749	0.805	0.781	0.854	0.871	0.861	0.669	0.564	0.417	0.243	0.360	0.093	0.078	0.151	0.044	0.121	0.106	0.051	0.032	0.049	0.056	0.040	0.037	0.061		0.000	0.000	0.002
CV	0.682	0.785	0.712	0.773	0.754	0.789	0.833	0.841	0.642	0.507	0.313	0.040	0.290	0.060	0.048	-0.009	0.189	0.047	0.060	0.147	0.200	0.164	0.116	0.131	0.296	0.120	0.231		0.898	0.000
CAN	0.671	0.795	0.706	0.775	0.754	0.805	0.849	0.847	0.636	0.479	0.263	0.022	0.245	0.025	0.008	-0.033	0.142	0.007	0.013	0.092	0.154	0.106	0.066	0.081	0.254	0.073	0.205	-0.038		0.000
MAU	0.853	0.926	0.858	0.881	0.853	0.935	0.925	0.895	0.730	0.753	0.696	0.503	0.620	0.189	0.158	0.273	0.036	0.240	0.162	0.056	0.021	0.046	0.082	0.064	0.004	0.092	0.075	0.450	0.443	

Table S6. Pairwise exact test P-values (above diagonal) and pairwise F_{ST} values (using only haplotype frequency, below diagonal) among 12 Atlantic green turtle (*Chelonia mydas*) foraging aggregations, based on 738 bp sequences of the D-loop in the control region of the mtDNA (extended D-loop). The study site is in bold, and abbreviations follow those in Table 2 in the manuscript. Non-significant values, false discovery rate (FDR) correction, are marked in bold (for a $P < 0.05$, FDR = 0.0105; Narum, 2006).

Foraging grounds	SFL	BB	SJB	SRI	LA	TX	PR	COL	ALG	URU	STP	MAU
SFL		0.529	0.763	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
BB	-0.001		0.682	0.025	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
SJB	-0.003	-0.002		0.005	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
SRI	0.051	0.029	0.046		0.167	0.308	0.000	0.000	0.000	0.000	0.000	**0.000**
LA	0.128	0.100	0.124	0.009		0.756	0.000	0.000	0.000	0.000	0.000	**0.000**
TX	0.118	0.090	0.113	0.001	0.004		-0.000	0.000	0.000	0.000	0.000	**0.000**
PR	0.046	0.061	0.058	0.123	0.195	0.194		-0.000	0.000	0.000	0.000	**0.000**
COL	0.085	0.098	0.089	0.172	0.254	0.249	0.078		-0.000	0.000	0.000	**0.000**
ALG	0.394	0.401	0.396	0.481	0.487	0.486	0.335	0.385		0.832	0.027	**0.000**
URU	0.371	0.381	0.375	0.456	0.468	0.470	0.311	0.355	-0.008		0.050	**0.001**
STP	0.329	0.342	0.336	0.403	0.430	0.434	0.266	0.304	0.035	0.029		**0.000**
MAU	**0.605**	**0.594**	**0.590**	**0.729**	**0.683**	**0.667**	**0.575**	**0.656**	**0.062**	**0.074**	**0.192**	

Table S7. Pairwise exact test P-values (above diagonal) and pairwise φ$_{ST}$ values (below diagonal) among 12 Atlantic green turtle (*Chelonia mydas*) foraging aggregations, based on 738 bp sequences of the D-loop in the control region of the mtDNA (extended D-loop). The study site is in bold, and abbreviations follow those in Table 2 in the manuscript. Non-significant values, false discovery rate (FDR) correction, are marked in bold (for a P < 0.05, FDR = 0.0105; Narum, 2006).

Foraging grounds	SFL	BB	SJB	SRI	LA	TX	PR	COL	ALG	URU	STP	MAU
SFL		0.435	0.320	0.223	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
BB	-0.001		0.804	0.502	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
SJB	0.001	-0.003		0.530	0.000	0.000	0.000	0.000	0.000	0.000	0.000	**0.000**
SRI	0.005	-0.002	-0.003		0.158	0.640	0.000	0.000	0.000	0.000	0.000	**0.000**
LA	0.042	0.031	0.036	0.007		0.631	0.000	0.000	0.000	0.000	0.000	**0.000**
TX	0.034	0.023	0.025	-0.005	-0.002		0.000	0.000	0.000	0.000	0.000	**0.000**
PR	0.087	0.128	0.140	0.121	0.184	0.193		0.014	0.000	0.000	0.000	**0.000**
COL	0.293	0.378	0.388	0.332	0.450	0.470	0.063		0.000	0.000	0.000	**0.000**
ALG	0.778	0.821	0.825	0.889	0.883	0.878	0.610	0.504		0.305	0.001	**0.040**
URU	0.752	0.804	0.807	0.868	0.871	0.867	0.565	0.438	0.002		0.003	**0.035**
STP	0.656	0.719	0.722	0.661	0.753	0.771	0.467	0.285	0.051	0.033		**0.000**
MAU	**0.856**	**0.879**	**0.882**	**0.940**	**0.926**	**0.918**	**0.744**	**0.695**	**0.015**	**0.021**	**0.118**	

Table S8. Reassessment of the relative contributions of green turtle (*Chelonia mydas*) Atlantic rookeries to a foraging ground in the Banc d'Arguin, Mauritania through 'many-to-one' mixed stock analysis with two markers combined: the extended mitochondrial DNA control region D-loop haplotype (738 bp) and mitochondrial short tandem repeats (mtSTR, ~200 bp), including a novel haplotype combination (extended D-loop + mtSTR) in the main source population of Poilão Island, Guinea-Bissau. This haplotype combination (CM-A5.1 '7-12-4-4') has not yet been directly sampled at Poilão, but was identified in a foraging turtle in the Banc d'Arguin, that was later found nesting at Poilão.

| Rookery location | D-loop + mtSTR | | | | | |
| | population size as prior | | | no priors | | |
	mean	max	min	mean	max	min
Poilão Island, Guinea-Bissau	0.881	0.932	0.818	0.875	0.925	0.812
Cayenne, French Guiana	0.076	0.122	0.038	0.080	0.125	0.044
Ascension Island, UK	0.035	0.086	0.000	0.023	0.076	0.000
São Tomé Isl., São Tomé and Príncipe	0.001	0.004	0.000	0.012	0.053	0.000
Rocas Atoll, Brazil	0.000	0.000	0.000	0.003	0.025	0.000
Fernando de Noronha, Brazil	0.000	0.000	0.000	0.001	0.007	0.000
Trindade Island, Brazil	0.000	0.004	0.000	0.004	0.028	0.000
Central Eastern Florida, USA	0.001	0.010	0.000	0.001	0.009	0.000
South Eastern Florida, USA	0.000	0.002	0.000	0.000	0.003	0.000
Dry Tortugas National Park, FL, USA	0.000	0.000	0.000	0.000	0.004	0.000
Cayman Islands	0.000	0.000	0.000	0.000	0.004	0.000
Tortuguero, Costa Rica	0.006	0.020	0.000	0.001	0.010	0.000

Table S9. References for mitochondrial DNA haplotype frequencies for the extended D-loop (738 bp) and mitochondrial short tandem repeat (mtSTR, ~200 bp) at 16 Atlantic green turtle (*Chelonia mydas*) nesting populations.

Region	Rookery location	Short name	References: extended D-loop haplotype frequencies	References: mtSTR haplotype frequencies
Northwest Atlantic	Central Eastern Florida, USA	CEFL	Shamblin et al. 2020	Shamblin et al. 2020
	South Eastern Florida, USA	SEFL	Shamblin et al. 2020	Shamblin et al. 2020
	Dry Tortugas National Park, Florida, USA	DRT	Shamblin et al. 2020	Shamblin et al. 2020
	Campeche and Yucatán, Mexico	EBCMX	Millán-Aguilar 2009	n.a.
Caribbean Sea	Tortuguero, Costa Rica	CR	Shamblin et al. 2023	Shamblin et al. 2023
	Southwest Cuba	CUB	Azanza-Ricardo et al. 2023	n.a.
	Cayman Islands	CI	Barbanti et al. 2019	Barbanti et al. 2019
	Aves Island, Venezuela	AV	Shamblin et al. 2012	n.a.
Southwest Atlantic	Matapica and Galibi, Suriname	SUR	Shamblin et al. 2012	n.a.
	Cayenne, French Guiana	FG	This study	This study
	Rocas Atoll, Brazil	RA	Shamblin et al. 2015	Shamblin et al. 2015
	Fernando de Noronha, Brazil	FN	Shamblin et al. 2015	Shamblin et al. 2015
	Trindade Island, Brazil	TRI	Shamblin et al. 2015	Shamblin et al. 2015
	Ascension Island, UK	ASC	Ascension Island Government, Conservation and Fisheries Directorate, unpublished data	Ascension Island Government, Conservation and Fisheries Directorate, unpublished data
Eastern Atlantic	Poilão Island, Guinea-Bissau	GB	Patrício et al. 2017 and this study	Patrício et al. 2017 and this study
	São Tomé Island, São Tomé and Príncipe	STP	Hancock et al. 2019	This study

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