

1 **SUPPLEMENTARY MATERIALS FOR RESEARCH ARTICLE: Molecular Ecology**

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3 What influences the worldwide genetic structure of sperm whales (*Physeter macrocephalus*)?

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19 **Supplementary Material 1:** Summary of the variable sites that define the sperm whale mtDNA CR haplotypes found in this  
 20 study. Sequences from this study start 5 bp later than those from Mesnick *et al.* (2011), so both numbering schemes are provided  
 21 (Mes Ref and Alx Ref). Dashes indicate no information for a sequence at that site (no indels were observed among the samples  
 22 sequenced in this study). Haplotypes named with reference to identity over 394, 569 and 619 bp consensus lengths. Haplotypes  
 23 CC-HH, JJ-OO are new to this study.

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Haplotypes (bp)			Mes Ref	43	58	62	105	107	109	121	150	184	200	207	208	211	235	238	243	260	272	273	283	286	287	288	289	291	295	305	308	319	324	350	574	608	624	
394	569	619	Alx Ref	38	53	57	100	102	104	116	145	179	195	202	203	206	230	233	238	255	267	268	278	281	282	283	284	286	290	300	303	314	319	345	569	603	619	
A	.001	.001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G	
A	.001	.002		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	A	
A	.001	.003		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	G	G	
A	.002	.001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	T	A	G	
B	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G	
B	.001	.002		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	A	
B	.002	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	T	A	G	
C	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	A	G	C	A	G	C	C	G	A	A	
C	.001	.002		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	A	G	C	A	G	C	C	G	A	A	
C	.002	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	A	G	C	A	G	C	C	T	A	G	
D	.001	.001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G	
E	.001	.001		T	C	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G	
F	.NA	.NA		T	C	C	C	A	G	C	T	T	T	A	A	C	A	T	G	A	A	T	C	A	A	A	T	A	G	C	A	G	C	C	-	-	-	
G	.NA	.NA		T	C	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	T	-	-	-	
H	.001	.001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	T	C	A	G	A	T	A	G	C	A	G	C	C	G	A	G	
I	.001	.001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	T	C	G	A	G	
J	.001	.001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	A	G	C	A	G	C	C	G	A	G	
J	.002	.001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	A	G	C	A	G	C	C	T	A	G	
K	.NA	.NA		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	T	C	A	A	G	T	A	G	C	A	G	T	C	-	-	-	
L	.NA	.NA		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	A	A	A	C	C	A	A	G	T	A	G	C	A	G	C	C	-	-	-	
M	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	G	A	A	T	A	G	C	A	G	C	C	G	A	G	
N	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	A	C	C	G	A	A	
N	.001	.002		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	A	C	C	G	A	A	
N	.002	.NA		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	A	C	C	T	-	-	
O	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	G	A	A	C	C	A	A	A	T	A	G	C	A	A	T	C	G	A	G
P	.NA	.NA		T	T	T	C	A	G	C	C	T	T	A	A	T	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	-	-	-	
Q	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	G	G	C	C	A	A	A	T	A	G	C	A	A	T	C	G	A	G	
R	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	G	A	C	C	A	A	A	T	A	G	C	A	A	T	C	G	A	G	
S	.001	.001		T	T	T	T	A	G	C	C	T	T	A	A	C	A	T	G	G	G	C	C	A	A	A	T	A	G	C	A	A	T	C	G	A	G	
T	.NA	.NA		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	G	C	C	A	A	A	T	A	G	C	A	G	C	C	-	-	-	
U	.NA	.NA		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	A	C	C	-	-	-	
V	.NA	.NA		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	C	A	G	C	A	G	C	C	-	-	-	
W	.001	.NA		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	-	-	
X	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	G	T	A	G	C	A	G	C	C	G	A	G
Y	.NA	.NA		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	G	C	C	A	A	G	T	A	G	C	A	G	C	C	-	-	-	
Z	.001	.001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	A	G	C	A	G	C	C	G	A	G	
AA	.NA	.NA		T	C	C	C	A	G	C	T	T	T	A	A	C	G	T	G	A	A	C	C	A	A	A	T	A	G	T	A	G	C	C	-	-	-	
BB	.001	.001		T	T	C	C	A	G	T	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	T	A	G	

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27 **Supplementary Material 1 (Continued)**

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Haplotypes (bp)	Mes Ref	43	58	62	105	107	109	121	150	184	200	207	208	211	235	238	243	260	272	273	283	286	287	288	289	291	295	305	308	319	324	350	574	608	624
394 569 619	Aix Ref	38	53	57	100	102	104	116	145	179	195	202	203	206	230	233	238	255	267	268	278	281	282	283	284	286	290	300	303	314	319	345	569	603	619
CC .001 .001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	T	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G
DD .001 .001		T	T	T	C	A	G	C	C	C	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G
EE .001 .001		T	T	C	C	G	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G
FF .001 .001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	A	C	A	G	C	C	T	A	G
GG .001 .001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	C	G	A	A	C	C	A	A	G	T	A	G	C	A	G	C	C	G	A	G
HH .001 .001		C	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	T	C	G	A	G
II .001 .001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	T	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G
JJ .001 .001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	A	G	C	A	G	T	C	T	A	G
JJ .002 .001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	A	G	C	A	G	T	C	G	A	G
KK .001 .001		T	T	C	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	G	T	G	G	C	A	G	C	C	G	A	G
LL .001 .001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	A	C	T	A	A	G	T	A	G	C	A	G	C	C	G	A	G
MM .001 .001		T	T	T	C	A	G	C	C	T	T	A	A	C	A	T	G	A	G	C	C	A	A	G	T	A	G	C	A	G	C	C	G	A	G
NN .001 .001		T	C	C	C	A	G	C	T	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	G	C	C	G	A	G
OO .001 .001		T	T	T	C	A	A	C	C	T	T	A	A	C	A	T	G	A	A	C	C	A	A	A	T	A	G	C	A	A	C	C	G	-	-

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32 **Supplementary Material 2:** Summary of the sperm whale mtDNA CR haplotypes obtained for  
 33 samples from previous publications, with ocean and geographic region. Haplotype definitions are  
 34 listed in **Supplementary Material 1**. Haplotypes were also available from Drouot *et al.* (2004) but  
 35 were not included as they were 200 bp shorter than the haplotypes listed here. Ortega-Ortiz *et al.*  
 36 (2012) samples were confirmed as a subset of those included in Engelhaupt *et al.* (2009) so are  
 37 not included in analyses. No other attempt has been made to identify replicate samples between  
 38 studies. Abbreviations: PAC (Pacific), IO (Indian), ATL (Atlantic), NA (North Atlantic), SH  
 39 (Southern Hemisphere), GPG (Galapagos), JC (Japanese Coast), NPW (western North Pacific),  
 40 NPC (central North Pacific), NPE (eastern North Pacific), GMX (Gulf of Mexico), NSEA (North  
 41 Sea), WNAO (western North Atlantic), MED (Mediterranean), CHI/PER (Chile/Peru), GPG/ECU  
 42 (Galapagos/Ecuador), SWP (southwest Pacific), CA/OR (California/Oregon), HAW (Hawai'i),  
 43 ETP (eastern tropical Pacific), CHI (Chile), PER (Peru).

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Haplotype (394 bp)	569bp	619bp	Region	Ocean	Publication	No. of individuals	Notes
A	NA	NA	NA	ATL	Lyrholm & Gyllensten 1998	18	
A	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	12	
A	NA	NA	GPG	PAC	Lyrholm & Gyllensten 1998	15	
A	NA	NA	JC	PAC	Lyrholm & Gyllensten 1998	19	
A	NA	NA	NPW	PAC	Lyrholm & Gyllensten 1998	11	
A	NA	NA	NPC	PAC	Lyrholm & Gyllensten 1998	5	
A	NA	NA	NPE	PAC	Lyrholm & Gyllensten 1998	15	
C	NA	NA	NA	ATL	Lyrholm & Gyllensten 1998	17	
C	NA	NA	GPG	PAC	Lyrholm & Gyllensten 1998	8	
C	NA	NA	JC	PAC	Lyrholm & Gyllensten 1998	2	
C	NA	NA	NPW	PAC	Lyrholm & Gyllensten 1998	3	
C	NA	NA	NPC	PAC	Lyrholm & Gyllensten 1998	5	
C	NA	NA	NPE	PAC	Lyrholm & Gyllensten 1998	1	
B	NA	NA	NA	ATL	Lyrholm & Gyllensten 1998	9	
B	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	12	
B	NA	NA	GPG	PAC	Lyrholm & Gyllensten 1998	14	
B	NA	NA	JC	PAC	Lyrholm & Gyllensten 1998	2	
B	NA	NA	NPW	PAC	Lyrholm & Gyllensten 1998	12	
B	NA	NA	NPC	PAC	Lyrholm & Gyllensten 1998	1	
B	NA	NA	NPE	PAC	Lyrholm & Gyllensten 1998	9	
BB	NA	NA	NA	ATL	Lyrholm & Gyllensten 1998	1	
E	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	1	This is also a match to haplotype G (slightly shorter than 394 bp)
E	NA	NA	JC	PAC	Lyrholm & Gyllensten 1998	1	This is also a match to haplotype G (slightly shorter than 394 bp)
E	NA	NA	NPW	PAC	Lyrholm & Gyllensten 1998	4	This is also a match to haplotype G (slightly shorter than 394 bp)
E	NA	NA	NPE	PAC	Lyrholm & Gyllensten 1998	3	This is also a match to haplotype G (slightly shorter than 394 bp)
Q	NA	NA	JC	PAC	Lyrholm & Gyllensten 1998	1	
J	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	9	
N	NA	NA	NA	ATL	Lyrholm & Gyllensten 1998	2	
N	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	2	
N	NA	NA	JC	PAC	Lyrholm & Gyllensten 1998	4	
N	NA	NA	NPE	PAC	Lyrholm & Gyllensten 1998	1	
O	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	2	
H	NA	NA	GPG	PAC	Lyrholm & Gyllensten 1998	1	
H	NA	NA	NPW	PAC	Lyrholm & Gyllensten 1998	1	
M	NA	NA	NPW	PAC	Lyrholm & Gyllensten 1998	1	
K	NA	NA	NPW	PAC	Lyrholm & Gyllensten 1998	2	
D	NA	NA	NPE	PAC	Lyrholm & Gyllensten 1998	2	

45 **Supplementary Material 2 (Continued)**

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Haplotype (394 bp)	569bp	619bp	Region	Ocean	Publication	No. of individuals	Notes
R	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	1	
S	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	1	
II	NA	NA	SH	IO/PAC	Lyrholm & Gyllensten 1998	1	
A	NA	NA	GMX	ATL	Engelhaupt <i>et al.</i> 2009	4	
A	NA	NA	NSEA	ATL	Engelhaupt <i>et al.</i> 2009	8	
A	NA	NA	WNAO	ATL	Engelhaupt <i>et al.</i> 2009	36	
B	NA	NA	GMX	ATL	Engelhaupt <i>et al.</i> 2009	23	
B	NA	NA	NSEA	ATL	Engelhaupt <i>et al.</i> 2009	2	
B	NA	NA	WNAO	ATL	Engelhaupt <i>et al.</i> 2009	8	
C	NA	NA	MED	ATL	Engelhaupt <i>et al.</i> 2009	38	
C	NA	NA	GMX	ATL	Engelhaupt <i>et al.</i> 2009	11	
C	NA	NA	NSEA	ATL	Engelhaupt <i>et al.</i> 2009	8	
C	NA	NA	WNAO	ATL	Engelhaupt <i>et al.</i> 2009	37	
X	NA	NA	GMX	ATL	Engelhaupt <i>et al.</i> 2009	105	
X	NA	NA	WNAO	ATL	Engelhaupt <i>et al.</i> 2009	1	
Y	NA	NA	GMX	ATL	Engelhaupt <i>et al.</i> 2009	10	
N	NA	NA	WNAO	ATL	Engelhaupt <i>et al.</i> 2009	1	
BB	NA	NA	WNAO	ATL	Engelhaupt <i>et al.</i> 2009	1	
A	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
C	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
Z	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
J	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
C	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
J	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
A	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
I	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
C	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	19	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	5	
A	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
C	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	7	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	8	
C	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
A	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
O	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
E	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
E	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	2	
E	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
D	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
B	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	6	
A	NA	NA	CHI/PER	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	9	
C	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	4	
G	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	1	
N	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	3	
M	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	4	
A	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	17	
H	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	3	
B	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	13	

47

48 **Supplementary Material 2 (Continued)**

49

Haplotype (394 bp)	569bp	619bp	Region	Ocean	Publication	No. of individuals	Notes
C	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	1	
F	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	3	
A	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	1	
B	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	2	
C	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	17	
C	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	2	
A	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	2	
D	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	3	
A	NA	NA	GPG/ECU	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	4	
A	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	1	
C	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	2	
O	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	2	
C	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	1	
M	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	1	
B	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	2	
G	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	2	
D	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	1	
G	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	1	
I	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	5	
B	NA	NA	SWP	PAC	Rendell <i>et al.</i> 2012	1	
A	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	15	
A	NA	NA	HAW	PAC	Mesnick <i>et al.</i> 2011	15	
A	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	38	
AA	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	2	
B	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	10	
B	NA	NA	HAW	PAC	Mesnick <i>et al.</i> 2011	6	
B	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	39	
C	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	6	
C	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	10	
D	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	3	
E	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	11	
E	NA	NA	HAW	PAC	Mesnick <i>et al.</i> 2011	1	
E	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	2	
F	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	1	
F	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	4	
G	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	1	
H	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	2	
H	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	3	
I	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	1	
J	NA	NA	HAW	PAC	Mesnick <i>et al.</i> 2011	6	
J	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	11	
L	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	1	
M	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	1	
N	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	1	
N	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	1	
O	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	1	
P	NA	NA	CA/OR	PAC	Mesnick <i>et al.</i> 2011	1	
P	NA	NA	ETP	PAC	Mesnick <i>et al.</i> 2011	1	
B	NA	NA	CHI/PER	PAC	Whitehead <i>et al.</i> 1998	2	
A	NA	NA	CHI/PER	PAC	Whitehead <i>et al.</i> 1998	1	
B	NA	NA	CHI/PER	PAC	Whitehead <i>et al.</i> 1998	6	
A	NA	NA	CHI	PAC	Whitehead <i>et al.</i> 1998	1	
C	NA	NA	CHI	PAC	Whitehead <i>et al.</i> 1998	1	
B	NA	NA	CHI	PAC	Whitehead <i>et al.</i> 1998	2	
E	NA	NA	CHI	PAC	Whitehead <i>et al.</i> 1998	1	
I	NA	NA	CHI	PAC	Whitehead <i>et al.</i> 1998	1	
A	NA	NA	PER	PAC	Whitehead <i>et al.</i> 1998	1	

50

51 **Supplementary Material 2 (Continued)**

52

Haplotype (394 bp)	569bp	619bp	Region	Ocean	Publication	No. of individuals	Notes
N	NA	NA	PER	PAC	Whitehead <i>et al.</i> 1998	2	
O	NA	NA	PER	PAC	Whitehead <i>et al.</i> 1998	1	
A	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	3	
B	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	1	
J	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	1	
A	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	3	
C	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	1	
B	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	13	
D	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	1	
A	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	2	
A	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	1	
C	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	17	
B	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	2	
A	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	2	
A	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	9	
C	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	4	
J	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	1	
T	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	3	
S	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	4	
B	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	6	
E	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	1	
I	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	2	
A	NA	NA	GPG/ECU	PAC	Whitehead <i>et al.</i> 1998	4	
A	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	1	
C	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	2	
U	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	1	
A	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	4	
O	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	5	
J	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	1	
A	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	2	
C	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	1	
S	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	1	
A	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	1	
B	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	2	
J	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	2	
E	NA	NA	SWP	PAC	Whitehead <i>et al.</i> 1998	1	
A	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	3	
C	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	1	
B	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	12	
A	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	1	
C	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	17	
B	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	2	
A	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	8	
C	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	3	
N	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	1	
O	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	3	
J	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	1	
J	NA	NA	GPG/ECU	PAC	Richard <i>et al.</i> 1996	3	

53

54

55

56 **Supplementary Material 3:** PCR reaction conditions, dye-labels, repeat unit, size range, and  
 57 reference for the 13 microsatellite loci used in this study. \* Not explicitly stated  
 58

<b>Locus</b>	<b>MgCl<sub>2</sub> [mM]</b>	<b>Polymerase [U]</b>	<b>Anneal temp</b>	<b>Dye label</b>	<b>Repeat unit</b>	<b>Size range</b>	<b>Reference</b>
<b>EV1</b>	3.63	0.125	50°C	NED	2	118 – 142	(Valsecchi & Amos 1996)
<b>EV5</b>	1.36	0.25	59°C	FAM	2	148 – 174	(Valsecchi & Amos 1996)
<b>EV14</b>	2.27	0.125	50°C	VIC	2	121 - 155	(Valsecchi & Amos 1996)
<b>EV37</b>	3.18	0.25	56°C	NED	2	177 - 250	(Valsecchi & Amos 1996)
<b>EV94</b>	2.27	0.25	50°C	FAM	2	193 - 225	(Valsecchi & Amos 1996)
<b>GATA417</b>	2.27	0.125	50°C	FAM	4	172 - 202	(Palsbøll <i>et al.</i> 1997)
<b>GT23</b>	2.27	0.125	50°C	VIC	2	75 - 99	(Bérubé <i>et al.</i> 2000)
<b>GT575</b>	1.36	0.125	50°C	FAM	2	131 - 137	(Bérubé <i>et al.</i> 2000)
<b>rw4-10</b>	2.72	0.125	50°C	VIC	2	177 - 213	(Waldick <i>et al.</i> 1999)
<b>SW13</b>	1.81	0.25	57°C	VIC	2	134 - 176	(Richard <i>et al.</i> 1996b)
<b>464/465</b>	2.27	0.125	50°C	FAM	2	141 - 145	(Schlötterer <i>et al.</i> 1991)
<b>SW19</b>	1.36	0.25	56°C	NED	2	89 - 167	(Richard <i>et al.</i> 1996b)
<b>FCB1</b>	1.36	0.25	53°C	FAM	2*	107 - 145	(Buchanan <i>et al.</i> 1996)

59  
60



61 **Supplementary Material 4:** R code for comparing microsatellite heterozygosity/allelic richness  
 62 levels between different geographic partitions. Code courtesy of Rebecca Hamner (Hamner  
 63 2014).

```

64
65 data <- read.table("Data.txt", header=T)
66 #Data format in "Data.txt" is as follows for 3 populations (tab
67 #separated):
68 # Pop_1 Pop_2 Pop_3
69 # L1_ho L1_ho L1_ho
70 # L2_ho L2_ho L2_ho
71 # L3_ho L3_ho L3_ho
72 # Population names in row one, then observed heterozygosities/allelic
73 # richness in the rows below this
74 # Separate row for each microsatellite locus
75 # If additional populations, code below can be expanded
76
77 attach(data)
78 data
79
80 #test for equal variances
81 var.test(data$Pop_1, data$Pop_2)
82 var.test(data$Pop_2, data$Pop_3)
83 var.test(data$Pop_1, data$Pop_3)
84
85 #test for normality of differences between pairs
86 shapiro.test(data$Pop_1-data$Pop_2)
87 shapiro.test(data$Pop_2-data$Pop_3)
88 shapiro.test(data$Pop_1-data$Pop_3)
89
90 #t-test (if variances equal and differences between pairs are normal)
91 t.test(data$Pop_1, data$Pop_2, alternative = c("two.sided"), paired = TRUE,
92 var.equal=T)
93 t.test(data$Pop_2, data$Pop_3, alternative = c("two.sided"), paired = TRUE,
94 var.equal=T)
95 t.test(data$Pop_1, data$Pop_3, alternative = c("two.sided"), paired = TRUE,
96 var.equal=T)
97
98 #Wilcoxon signed rank test (if differences between pairs are NOT
99 # normal)
100 wilcox.test(data$Pop_1, data$Pop_2, alternative = c("two.sided"), paired =
101 TRUE)
102
103
```

104 **Supplementary Material 5:** Social groups used in genetic analyses, separated by headers  
 105 indicating region and ocean. Within region, groups ordered by group type (♀ females present; ♂  
 106 only males sampled; ? unknown). Number of sampled individuals indicated by *n* (QC). For  
 107 groups contributed by the current study, *n* (QC) also represents the number of individuals that  
 108 were included in microsatellite analyses. Number of females/males in each group was determined  
 109 using genetic data. Number of individuals with mtDNA data shown in *n*(mtDNA). ‘--’ indicates  
 110 missing data. The AMOVA column indicates which hierarchical AMOVA analyses at the  
 111 worldwide scale social groups with 5+ sampled individuals were included in (mtDNA,  
 112 microsatellite: usat, or Both). Regions were included in Pacific/Indian Ocean AMOVA only  
 113 when multiple groups were available with 5+ individuals sampled. References: [1] This study; [2]  
 114 (Richard *et al.* 1996a); [3] (Engelhaupt 2004); [4] (Ortega-Ortiz et al. 2012). Social groups  
 115 obtained from other publications used in mtDNA analyses only.  
 116

Group type	Group name	Estimated group size	<i>n</i> (QC)	<i>n</i> (F)	<i>n</i> (M)	<i>n</i> (mtDNA)	AMOVA (mtDNA, usat, both)	Ref
<b>PACIFIC</b>								
<b>Gulf of California</b>								
♀	GCA002	27	7	7	0	7	Both	[1]
♀	GCA003	8-11	45	38	5	45	Both	[1]
♀	GCA005	4	8	6	2	8	Both	[1]
♀	GCA007	3	3	3	0	3		[1]
♀	GCA010	--	4	3	1	4		[1]
♀	GCA011	--	4	3	1	4		[1]
♀	GCA012	--	2	2	0	2		[1]
♀	GCA017	--	2	1	1	2		[1]
♀	GCA019	--	13	11	1	13	Both	[1]
♀	GCA020	20+	2	2	0	2		[1]
♀	GCA023	18	2	1	1	2		[1]
♀	GCA024	60	5	4	1	5	Both	[1]
♀	GCA026	30	3	2	0	3		[1]
♀	GCA029	--	4	3	1	4		[1]
♀	GCA030	--	3	2	1	3		[1]
♂	GCA009	--	2	0	1	2		[1]
<b>Galapagos/Ecuador</b>								
♀	RIC_Ecu_A	28.5	18	12	6	17	mtDNA	[2]
♀	RIC_Ecu_B	24.3	20	16	4	20	mtDNA	[2]
♀	RIC_Ecu_C	--	18	16	2	18	mtDNA	[2]
♂	GPG001	9	3	0	3	3		[1]
♂	GPG012	9-14	2	0	2	2		[1]
♂	GPG015	12	3	0	3	3		[1]
♂	GPG016	5	2	0	2	2		[1]
♂	GPG022	6	3	0	3	3		[1]
<b>‘Pacific Crossing’</b>								
♀	PX003	50-75	35	20	12	34	Both	[1]
♂	PX001	2-3	2	0	2	2		[1]
<b>Kiribati</b>								
♀	KR02001	18-23	11	9	1	11	Both	[1]
<b>Papua New Guinea</b>								
♀	PNG002	18	2	2	0	1		[1]
♀	PNG006	15-18	10	10	0	10	Both	[1]
♀	PNG007	50	8	8	0	8	Both	[1]
♀	PNG010	22-23	16	12	1	16	Both	[1]
♀	PNG011	5-25	4	3	1	4		[1]
♀	PNG012	18	4	4	0	3		[1]
♀	PNG013	10	4	3	1	4		[1]
♀	PNG014	18-20	7	7	0	7	Both	[1]
♀	PNG018	30	4	4	0	4		[1]
♂	PNG008	4-5	4	0	4	4		[1]

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## 119 Supplementary Material 5 (Continued)

Group type	Group name	Estimated size	<i>n</i> (QC)	<i>n</i> (F)	<i>n</i> (M)	<i>n</i> (mtDNA)	AMOVA (mtDNA, usat, both)	Ref
<b>INDIAN</b>								
<b>Southwestern Australia</b>						21		
?	AUS001	11-13	3	0	0	3		[1]
♀	AUS005	17-20	2	1	0	2		[1]
♀	S_AUS008	18	8	8	0	8	Both	[1]
♂	S_AUS006	9	2	0	1	2		[1]
♂	S_AUS007	2-3	4	0	3	4		[1]
<b>Cocos Island</b>								
♀	COC001	11	6	6	0	6	Both	[1]
♀	COC002	11-20	11	11	0	11	Both	[1]
<b>Sri Lanka</b>								
♀	SRI002	--	25	20	1	21	Both	[1]
♀	SRI004	--	2	2	0	2		[1]
♀	SRI005	--	13	10	0	13	Both	[1]
♀	SRI006	--	10	9	1	2	usat	[1]
♀	SRI009	13	2	1	1	--		[1]
♂	SRI003	8	3	0	3	3		[1]
<b>Maldives/Chagos Archipelago</b>								
?	MAL002	5	4	0	0	4		[1]
♀	MAL008	16	9	5	2	9	Both	[1]
♀	MAL012	14	6	4	0	5	Both	[1]
♂	MAL013	7	3	0	2	3		[1]
♂	CHG004	1-13	6	0	6	6	Both	[1]
<b>Aldabras</b>								
♀	ALD001	9	3	3	0	3		[1]
♀	ALD003	13	9	3	2	9	Both	[1]
<b>Seychelles</b>								
?	SEY003	3-23	7	0	0	7	Both	[1]
♀	SEY004	23-30	7	2	0	7	Both	[1]
♀	SEY002	14-20	15	15	0	15	Both	[1]
<b>ATLANTIC</b>								
<b>Mediterranean</b>								
♂	N_MED015	2	2	0	2	--		[1]
<b>Canary Islands</b>								
♀	CNI005	12-15	5	4	1	4	usat	[1]
♀	CNI007	4-5	2	1	1	1		[1]
♀	CNI009	12-15	5	5	0	2	usat	[1]
♀	CNI012	6-11	2	1	1	2		[1]
♀	CNI014	7-10	2	1	1	1		[1]
♂	CNI002	8-13	2	0	2	1		[1]
♂	CNI010	15-18	2	0	2	--		[1]
♂	CNI013	3	2	0	1	2		[1]
<b>Central Atlantic</b>								
♀	C_ATL006	10-20	3	2	0	2		[1]
<b>Gulf of Mexico</b>								
♀	G0	6	3	2	1	3		[3, 4]
♀	G1	6	5	4	1	5	mtDNA	[3, 4]
♀	G2	--	3	3	0	3		[3, 4]
♀	G3	7	7	7	0	7	mtDNA	[3, 4]
♀	G4	4	4	3	1	4		[3, 4]
♀	G5	7	5	4	1	5	mtDNA	[3, 4]
♀	G10	11	5	4	1	5	mtDNA	[3, 4]
♀	G11	9	4	3	1	4		[3, 4]
♀	G13	12	3	2	1	3		[3, 4]
♀	G14	15	6	5	1	6	mtDNA	[3, 4]
♀	G15	25	4	4	0	4		[3, 4]
♀	G16	22	4	4	0	4		[3, 4]
♀	G17	22	3	3	0	3		[3, 4]
♀	G18	10	8	7	1	8	mtDNA	[3, 4]
♀	G19	8	2	2	0	2		[3]
♀	G20	18	5	1	4	5	mtDNA	[3]

120 **Supplementary Material 5 (Continued)**

121

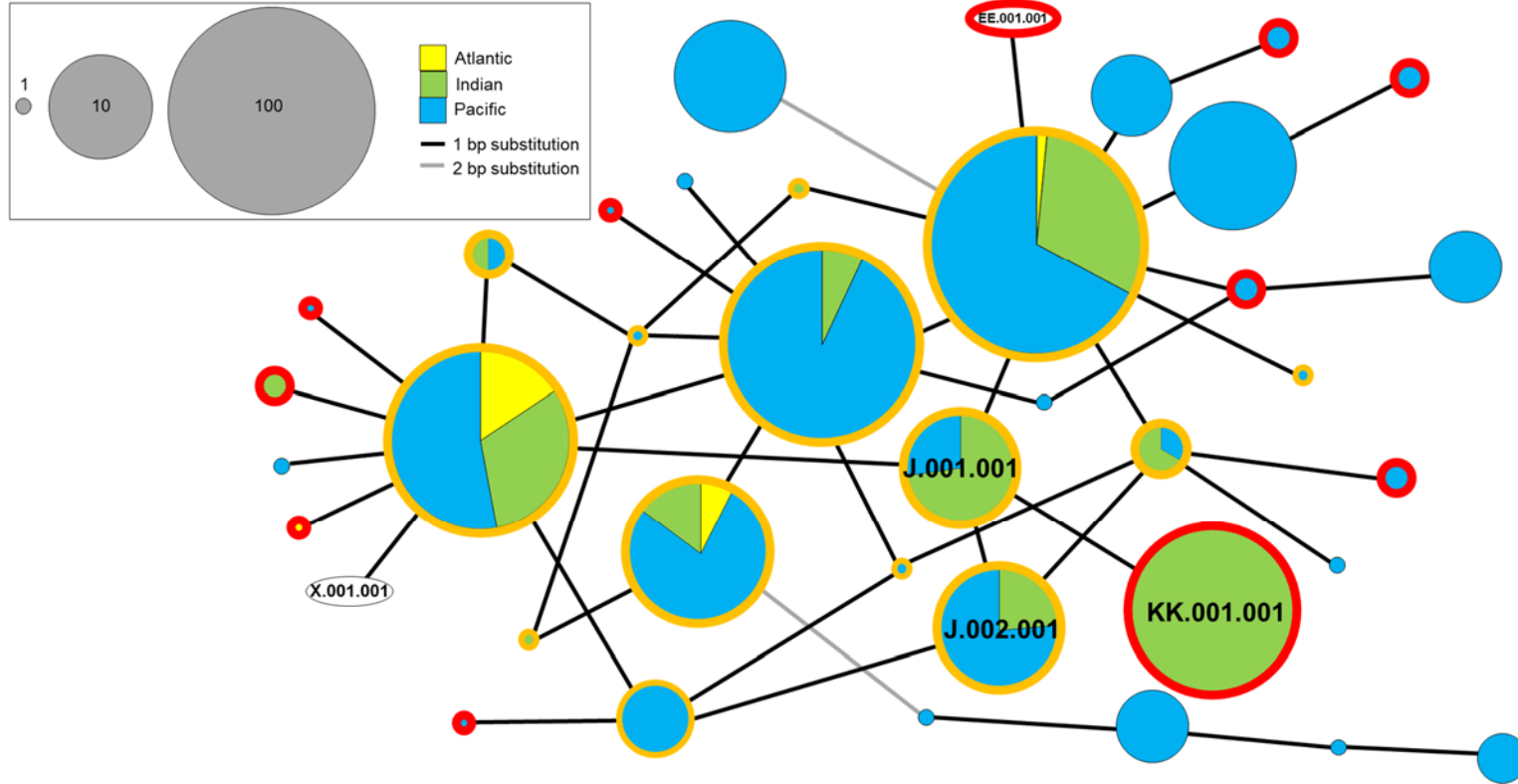
Group type	Group name	Estimated size	<i>n</i> (QC)	<i>n</i> (F)	<i>n</i> (M)	<i>n</i> (mtDNA)	AMOVA (mtDNA, usat, both)	Ref
<b>Gulf of Mexico</b>								
♀	G21	8	2	2	0	2		[3]
♀	G22	9	7	7	0	7	mtDNA	[3]
♀	G23	7	2	1	1	2		[3]
♀	G24	15	2	2	0	2		[3]
♂	G6	2	2	0	2	2		[3, 4]
♂	G7	3	3	0	3	3		[3, 4]
♂	G8	6	3	0	3	3		[3, 4]
♂	G9	6	2	0	2	2		[3, 4]
♂	G12	12	2	0	2	2		[3, 4]

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128  
129 **Supplementary Material 6:** 619 bp mtDNA CR analyses of diversity and differentiation.  
130 (a) Maximum parsimony network based on 619 bp haplotype length dataset. Sequences of this length were not available for the  
131 following 394 bp haplotypes: F, G, K, L, P, T, W, U, V, X, Y, AA, EE, and OO. Haplotypes are colored by ocean. Size of  
132 haplotype pie is proportional on a log scale to the total number of individuals with the haplotype. Lines represent substitutions  
133 (one or two between haplotypes as defined by the key). New haplotypes over 394 bp characterized in this study are outlined in  
134 red, variants of 394 bp haplotypes split over the longer 619 bp fragment are outlined in light orange.  
135  
136 (b) Number of individuals in the ‘full’ and ‘kin-restricted’ *Odyssey* dataset successfully sequenced for 619 bp mtDNA CR,  
137 number of haplotypes ( $k$ ), haplotype diversity ( $h$ ) and nucleotide diversity (in %,  $\pi$ ). Data were not used from previous studies as  
138 haplotypes from these studies were defined over the shorter 394 bp length. In comparison with the 394 bp analyses conducted in  
139 this paper, the following regions were too limited in samples to include: western North Atlantic, Gulf of Mexico, Mediterranean,  
140 and Hawaii. “=” in the ‘restricted’ columns indicates the values are the same as the ‘full’ dataset.  
141

142 **Supplementary Material 6 (Continued) (a)**



143

144

145 **Supplementary Material 6 (Continued) (b)**

146

147

<b>(b)</b> <b>Ocean/Region</b>	<b>'Full' dataset</b>				<b>'Restricted' dataset</b>			
	<b>n</b>	<b>k</b>	<b>h</b>	<b><math>\pi</math> (%)</b>	<b>n</b>	<b>k</b>	<b>h</b>	<b><math>\pi</math> (%)<sup>48</sup></b>
Atlantic	13	4	0.615	0.192	=	=	=	=
<i>Canary Islands</i>	7	3	0.667	0.215	=	=	=	=
Indian	144	12	0.796	0.286	141	=	0.800	0.285
<i>Aldabras</i>	12	4	0.773	0.258	=	=	=	=
<i>Cocos Island</i>	18	3	0.451	0.146	=	=	=	=
<i>Maldives/ Chagos Archipelago</i>	29	4	0.591	0.200	28	=	0.601	0.204
<i>Seychelles</i>	26	7	0.745	0.328	=	=	=	=
<i>Sri Lanka</i>	37	2	0.315	0.0511	35	=	0.329	0.0534
<i>Southwestern Australia</i>	20	5	0.790	0.191	=	=	=	=
Pacific	243	23	0.807	0.257	237	=	0.808	0.256
<i>Gulf of California</i>	117	12	0.798	0.269	112	=	0.799	0.266
<i>Galapagos</i>	20	5	0.742	0.195	=	=	=	=
<i>Kiribati</i>	11	4	0.746	0.355	=	=	=	=
<i>Papua New Guinea</i>	59	9	0.760	0.219	58	=	0.764	0.221
<i>Pacific Crossing</i>	36	8	0.679	0.200	=	=	=	=
TOTAL	400	28	0.843	0.286	391	=	0.842	0.285

- 149 **Supplementary Material 7: Diversity results by microsatellite locus and for the ‘kin-restricted’**  
 150 **dataset**
- 151 (a) Microsatellite diversity and sex-identification for *Odyssey* dataset. Values for the ‘full’ dataset  
 152 are given, with ‘restricted’ dataset values given in parentheses. As for the full dataset, no  
 153 significant differences in heterozygosity were detected between oceans, or between regions  
 154 within oceans for the restricted dataset.
- 155
- 156 (b) Locus by locus observed and expected heterozygosity results for the 13 microsatellite loci  
 157 used in this study for both the ‘full’ and ‘restricted’ datasets.
- 158
- 159 (c) Microsatellite differentiation indices for ‘full’ and ‘restricted’ datasets.
- 160
- 161 (d) Pairwise microsatellite regional comparisons for ‘restricted’ dataset.  $F_{ST}$  above diagonal of  
 162 matrix,  $G''_{ST}$  underneath diagonal. Significant values italicized and shown in bold, with \* <0.05,  
 163 \*\* <0.001. Within-ocean comparisons are shown shaded in gray. Abbreviations: Gulf of  
 164 California (GCA), Galapagos (GPG), ‘Pacific Crossing’ (PX), Kiribati (KR), Papua New Guinea  
 165 (PNG), SW Australia (SWAUS), Cocos Island (COC), Sri Lanka (SRI), Maldives/Chagos  
 166 Archipelago (MAL), Seychelles (SEY), Aldabras (ALD), Mediterranean (MED), Canary Island  
 167 (CNI).
- 168
- 169 (e) Results for the sex-specific  $F_{ST}$  comparison by marker for the ‘restricted’ dataset. Regional  
 170 analyses were limited to areas with more than two identified females and males: the Canary  
 171 Islands, Aldabras, southwestern Australia, Maldives/Chagos Archipelago, Seychelles, Sri Lanka,  
 172 Gulf of California, Kiribati, Papua New Guinea, and the Pacific Crossing. Due to limited sample  
 173 sizes, a within-ocean regional analysis was not conducted for the Atlantic. Statistically significant  
 174 values are bolded and italicized, with \* significant at  $p < 0.05$ , \*\* significant at  $p < 0.001$ .
- 175

(a)	Microsatellites				Sex	
	No of individuals	Allelic richness	Mean proportion of individuals typed for loci	Mean observed heterozygosity	No. of individuals	Sex ratio (F: M)
Atlantic	41 (39)	8.817 (8.731)	0.9681 (0.9665)	0.6685 (0.6694)	36 (34)	1.12 (1.00)
<i>Canary Islands</i>	25 (24)	5.155 (5.213)	0.9754 (0.9744)	0.6897 (0.6993)	24 (23)	1.70 (1.56)
<i>Mediterranean</i>	9 (=)	4.597 (=)	0.9573 (=)	0.6307 (=)	9 (=)	0.13 (=)
Indian	175 (171)	8.838 (8.722)	0.9178 (0.9163)	0.6863 (0.6841)	132 (128)	3.40 (3.41)
<i>Aldabras</i>	12 (=)	5.147 (=)	0.9487 (=)	0.6774(=)	8 (=)	3.00 (=)
<i>Cocos Island</i>	18 (=)	5.243 (=)	0.9359 (=)	0.7121 (=)	18 (=)	F only (=)
<i>Maldives/Chagos Archipelago</i>	34 (33)	5.315 (5.285)	0.9367 (0.9347)	0.7002 (0.6926)	24 (23)	0.60 (0.64)
<i>Seychelles</i>	31 (=)	5.317 (=)	0.8859 (=)	0.6973 (=)	19 (=)	8.50 (=)
<i>Sri Lanka</i>	56 (53)	5.073 (5.058)	0.9272 (0.9245)	0.6709 (0.6678)	48 (45)	7.00 (6.50)
<i>Southwestern Australia</i>	21 (=)	5.148(=)	0.8791 (=)	0.6968 (=)	13 (=)	2.25 (=)
Pacific	260 (254)	8.870 (8.767)	0.8970 (0.8958)	0.6944 (0.6935)	247 (241)	2.68 (2.60)
<i>Galapagos</i>	23 (=)	5.089 (=)	0.8361 (=)	0.6770 (=)	23 (=)	M only (=)
<i>Gulf of California</i>	122 (117)	5.203 (5.217)	0.8909 (0.8889)	0.7022 (0.7018)	116 (111)	4.80 (4.55)
<i>Kiribati</i>	13 (=)	5.328 (=)	0.9112 (=)	0.6836 (=)	12 (=)	5.00 (=)
<i>"Pacific crossing"</i>	37 (=)	5.101 (=)	0.9023 (=)	0.7040 (=)	34 (=)	1 (=)
<i>Papua New Guinea</i>	65 (64)	5.104 (5.103)	0.9243 (0.9231)	0.6867 (0.6853)	62 (61)	6.75 (6.63)
<b>Total</b>	476 (464)	13.07 (13.03)	0.9108 (0.9093)	0.6896 (0.6884)	415 (403)	2.64 (2.57)



177 **Supplementary Material 7 (Continued) (b)**

178

"All" Dataset	EV1					EV5				EV94				GT23				GT575				rw4-10				464/465			
	n	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp
Total	541	12	520	0.6	0.641	11	528	0.71	0.707	17	533	0.818	0.804	12	522	0.508	0.497	4	486	0.609	0.61	14	460	0.72	0.768	3	403	0.529	0.54
Atlantic	41	9	41	0.585	0.65	9	40	0.75	0.744	12	41	0.902	0.823	6	38	0.368	0.404	4	41	0.732	0.636	5	40	0.65	0.744	3	39	0.462	0.553
"Atlantic crossing"	1	2	1	1	1	2	1	1	1	2	1	1	1	1	1	0	0	1	1	0	0	1	1	0	0	1	1	0	0
Bahamas	3	3	3	0.667	0.6	3	3	1	0.733	3	3	0.667	0.6	4	3	1	0.8	2	3	1	0.6	3	3	0.667	0.6	2	2	0.5	0.5
Central Atlantic	3	3	3	0.667	0.733	2	3	0.333	0.333	3	3	1	0.733	2	3	0.333	0.333	2	3	0.667	0.533	2	3	0.333	0.333	2	3	0.333	0.333
Canary Islands	25	8	25	0.48	0.618	8	24	0.792	0.772	10	25	0.92	0.838	3	23	0.261	0.305	4	25	0.76	0.672	5	24	0.75	0.734	2	24	0.5	0.507
Eastern Mediterranean	1	2	1	1	1	1	1	0	0	2	1	1	1	1	1	0	0	1	1	0	0	2	1	1	1	2	1	1	1
Central Mediterranean	3	3	3	1	0.733	4	3	0.667	0.867	4	3	1	0.867	2	2	0.5	0.5	3	3	1	0.733	3	3	1	0.733	2	3	0.333	0.6
Northern Mediterranean	5	4	5	0.6	0.533	4	5	0.8	0.711	7	5	0.8	0.933	3	5	0.6	0.511	3	5	0.6	0.689	3	5	0.2	0.511	2	5	0.4	0.533
Indian	175	11	168	0.571	0.605	11	171	0.655	0.657	13	175	0.846	0.805	7	171	0.515	0.487	4	153	0.516	0.589	12	151	0.762	0.76	3	124	0.532	0.533
Aldabras	12	6	12	0.5	0.554	5	11	0.545	0.472	6	12	1	0.772	3	11	0.455	0.385	3	12	0.417	0.638	5	12	0.583	0.75	3	11	0.455	0.558
Southwestern Australia	21	5	21	0.524	0.585	7	20	0.75	0.774	8	21	0.905	0.819	5	21	0.762	0.581	3	17	0.471	0.392	6	14	0.857	0.783	3	9	0.556	0.542
Cocos Island	18	5	18	0.5	0.47	8	18	0.611	0.706	9	18	0.778	0.783	3	17	0.647	0.528	4	17	0.412	0.586	7	16	0.813	0.748	3	12	0.583	0.583
"Indian crossing"	1	2	1	1	1	2	1	1	1	2	1	1	1	2	1	1	1	0	0	0	0	2	1	1	1	2	1	1	1
Maldives/Chagos Archipelago	34	10	32	0.688	0.673	8	34	0.735	0.684	10	34	0.794	0.827	5	34	0.5	0.525	4	30	0.7	0.636	10	33	0.727	0.774	3	25	0.52	0.611
Mauritius	2	1	2	0	0	2	1	1	1	3	2	0.5	0.833	1	2	0	0	3	2	0.5	0.833	3	2	1	0.833	1	1	0	0
Seychelles	31	8	29	0.448	0.538	6	31	0.613	0.641	10	31	0.839	0.795	4	30	0.467	0.49	4	23	0.522	0.622	7	24	0.792	0.776	3	22	0.636	0.542
Sri Lanka	56	9	53	0.642	0.669	7	55	0.618	0.611	10	56	0.857	0.804	5	55	0.436	0.451	4	52	0.481	0.541	9	49	0.755	0.755	3	43	0.488	0.475
Pacific	325	12	311	0.617	0.658	9	317	0.735	0.723	15	317	0.792	0.8	9	313	0.521	0.513	4	292	0.64	0.617	13	269	0.706	0.774	3	240	0.538	0.54
Gulf of California	122	12	117	0.65	0.672	9	121	0.727	0.728	12	122	0.836	0.806	4	119	0.462	0.446	4	111	0.649	0.603	10	93	0.72	0.769	3	88	0.534	0.54
Galapagos	23	9	23	0.739	0.733	6	23	0.652	0.596	9	23	0.696	0.795	5	23	0.565	0.542	4	16	0.5	0.694	7	12	1	0.833	2	7	0.571	0.44
Kiribati	13	8	13	0.692	0.757	7	13	0.538	0.76	5	12	0.75	0.743	4	12	0.333	0.605	4	12	0.667	0.667	6	11	0.636	0.727	3	8	0.75	0.592
New Zealand	62	9	55	0.545	0.581	8	59	0.797	0.715	13	59	0.797	0.832	8	59	0.695	0.61	4	60	0.683	0.63	9	60	0.7	0.799	3	60	0.55	0.549
Oregon	2	2	2	0.5	0.5	4	2	1	1	4	2	1	1	2	2	0.5	0.5	2	2	1	0.667	3	2	1	0.833	2	2	0.5	0.5
Papua New Guinea	65	9	63	0.587	0.677	7	63	0.73	0.744	9	63	0.762	0.746	5	61	0.557	0.527	4	59	0.61	0.63	6	59	0.61	0.739	3	48	0.542	0.504
"Pacific crossing"	37	8	37	0.568	0.578	8	35	0.771	0.732	10	35	0.771	0.828	5	36	0.417	0.512	4	31	0.645	0.561	8	31	0.742	0.781	3	26	0.423	0.548
Samoa	1	2	1	1	1	2	1	1	1	1	1	0	0	1	1	0	0	1	1	0	0	2	1	1	1	2	1	1	1

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181 **Supplementary Material 7 (Continued) (b)**

182

	GATA417				SW13				EV37				EV14				FCB1				SW19			
	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp
"All" Dataset	7	437	0.508	0.532	14	522	0.826	0.836	32	502	0.855	0.905	14	481	0.688	0.717	16	517	0.793	0.836	32	506	0.879	0.921
Atlantic	3	41	0.39	0.401	10	41	0.78	0.835	17	39	0.795	0.885	11	40	0.7	0.734	10	38	0.684	0.817	17	37	0.892	0.929
"Atlantic crossing"	1	1	0	0	2	1	1	1	2	1	1	1	2	1	1	1	2	1	1	1	1	1	0	0
Bahamas	1	3	0	0	4	3	1	0.867	2	2	0.5	0.5	2	3	0.333	0.333	4	3	0.333	0.867	4	2	1	1
Central Atlantic	2	3	0.333	0.333	3	3	0.667	0.6	5	3	1	0.933	3	2	1	0.833	4	3	0.667	0.8	5	3	1	0.933
Canary Islands	3	25	0.44	0.448	8	25	0.68	0.829	16	24	0.833	0.898	9	25	0.8	0.733	9	24	0.833	0.803	16	24	0.917	0.934
Eastern Mediterranean	1	1	0	0	2	1	1	1	2	1	1	1	2	1	1	1	0	0	0	0	0	0	0	0
Central Mediterranean	2	3	0.333	0.333	3	3	1	0.733	2	3	0.333	0.333	4	3	0.667	0.8	4	3	0.667	0.867	4	2	1	1
Northern Mediterranean	3	5	0.6	0.6	5	5	1	0.844	6	5	0.8	0.844	2	5	0.2	0.556	2	4	0	0.429	5	5	0.8	0.756
Indian	5	152	0.572	0.578	12	167	0.814	0.843	24	162	0.833	0.907	12	161	0.702	0.734	14	167	0.743	0.825	27	166	0.861	0.921
Aldabras	4	10	0.8	0.726	9	11	0.818	0.9	10	10	0.9	0.921	8	12	0.667	0.659	8	12	0.75	0.786	11	12	0.917	0.92
Southwestern Australia	3	15	0.667	0.632	9	20	0.6	0.629	15	21	0.762	0.931	6	20	0.55	0.662	8	20	0.75	0.851	14	21	0.905	0.935
Cocos Island	3	15	0.6	0.508	9	18	0.889	0.881	13	17	0.941	0.914	8	18	0.944	0.833	8	17	0.706	0.824	12	18	0.833	0.905
"Indian crossing"	2	1	1	1	2	1	1	1	2	1	1	1	2	1	1	1	2	1	1	1	2	1	1	1
Maldives/Chagos Archipelago	3	32	0.5	0.555	9	33	0.818	0.811	18	30	0.933	0.888	9	31	0.613	0.756	12	32	0.75	0.831	14	34	0.824	0.913
Mauritius	2	2	0.5	0.5	3	2	0.5	0.833	2	2	0	0.667	2	1	1	1	2	2	0.5	0.5	2	2	0	0.667
Seychelles	3	24	0.583	0.542	10	31	0.871	0.874	16	29	0.897	0.926	10	29	0.724	0.728	12	28	0.75	0.855	15	26	0.923	0.919
Sri Lanka	4	53	0.528	0.594	10	51	0.843	0.849	19	52	0.75	0.895	10	49	0.714	0.713	11	55	0.745	0.814	19	52	0.865	0.917
Pacific	7	244	0.488	0.519	14	314	0.838	0.832	29	301	0.874	0.905	14	280	0.679	0.703	16	312	0.833	0.842	29	303	0.888	0.919
Gulf of California	3	77	0.429	0.515	14	117	0.855	0.826	24	116	0.888	0.909	12	102	0.647	0.69	14	116	0.845	0.855	26	114	0.886	0.918
Galapagos	3	12	0.333	0.366	9	22	0.773	0.813	16	23	0.826	0.916	8	22	0.545	0.648	7	23	0.696	0.807	13	21	0.905	0.904
Kiribati	3	12	0.25	0.62	10	13	0.923	0.886	10	13	0.923	0.898	6	10	0.9	0.8	8	13	0.692	0.803	11	12	0.833	0.902
New Zealand	6	57	0.649	0.554	11	61	0.77	0.849	20	54	0.87	0.9	10	52	0.731	0.714	13	57	0.86	0.844	20	54	0.926	0.935
Oregon	2	2	1	0.667	3	2	1	0.833	4	2	1	1	1	1	0	0	2	2	0.5	0.5	4	2	1	1
Papua New Guinea	4	54	0.481	0.463	9	63	0.81	0.82	19	61	0.82	0.898	11	60	0.717	0.706	12	64	0.844	0.842	18	63	0.857	0.919
"Pacific crossing"	3	29	0.483	0.56	12	35	0.943	0.846	17	32	0.938	0.891	9	33	0.667	0.7	12	37	0.892	0.822	17	37	0.892	0.908
Samoa	1	1	0	0	2	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0

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185 **Supplementary Material 7 (Continued) (b)**

186

"Restricted" Dataset	Locus			EV1				EV5				EV94				GT23				GT575				rw4-10				464/465			
	Measures	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp		
Total	526	12	505	0.594	0.637	11	513	0.702	0.706	17	518	0.822	0.805	12	508	0.504	0.497	4	471	0.609	0.611	14	445	0.719	0.769	3	388	0.528	0.54		
Atlantic	39	9	39	0.564	0.647	9	38	0.737	0.748	12	39	0.897	0.827	6	36	0.389	0.422	4	39	0.769	0.641	5	38	0.632	0.747	3	37	0.459	0.554		
<i>"Atlantic crossing"</i>	As for "all" dataset																														
<i>Bahamas</i>	As for "all" dataset																														
<i>Central Atlantic</i>	2	2	2	0.5	0.5	1	2	0	0	2	2	1	0.667	2	2	0.5	0.5	2	2	1	0.667	1	2	0	0	1	2	0	0		
<i>Canary Islands</i>	24	8	24	0.458	0.616	8	23	0.783	0.781	10	24	0.917	0.841	3	22	0.273	0.317	4	24	0.792	0.675	5	23	0.739	0.739	2	23	0.522	0.51		
<i>Eastern Mediterranean</i>	As for "all" dataset																														
<i>Central Mediterranean</i>	As for "all" dataset																														
<i>Northern Mediterranean</i>	As for "all" dataset																														
Indian	171	11	164	0.567	0.592	11	167	0.647	0.655	13	171	0.854	0.804	7	167	0.503	0.483	4	149	0.51	0.59	12	147	0.762	0.758	3	120	0.542	0.535		
<i>Aldabras</i>	As for "all" dataset																														
<i>Southwestern Australia</i>	As for "all" dataset																														
<i>Cocos Island</i>	As for "all" dataset																														
<i>"Indian crossing"</i>	As for "all" dataset																														
<i>Maldives/Chagos Archipelago</i>	33	10	31	0.677	0.655	8	33	0.727	0.675	10	33	0.818	0.828	5	33	0.485	0.523	4	29	0.69	0.639	10	32	0.719	0.774	3	24	0.5	0.614		
<i>Mauritius</i>	As for "all" dataset																														
<i>Seychelles</i>	As for "all" dataset																														
<i>Sri Lanka</i>	53	9	50	0.64	0.649	7	52	0.596	0.61	10	53	0.868	0.797	5	52	0.404	0.436	4	49	0.469	0.541	9	46	0.761	0.752	3	40	0.525	0.477		
Pacific	316	12	302	0.613	0.658	9	308	0.727	0.721	15	308	0.795	0.801	9	305	0.518	0.513	4	283	0.64	0.617	13	260	0.708	0.776	3	231	0.532	0.538		
<i>Gulf of California</i>	117	12	112	0.634	0.669	9	116	0.716	0.722	12	117	0.829	0.804	4	115	0.461	0.447	4	106	0.651	0.603	10	88	0.727	0.777	3	83	0.518	0.537		
<i>Galapagos</i>	As for "all" dataset																														
<i>Kiribati</i>	As for "all" dataset																														
<i>New Zealand</i>	59	9	52	0.538	0.584	8	56	0.786	0.719	13	56	0.839	0.84	8	56	0.696	0.614	4	57	0.667	0.631	9	57	0.702	0.798	3	57	0.561	0.553		
<i>Oregon</i>	As for "all" dataset																														
<i>Papua New Guinea</i>	64	9	62	0.597	0.683	7	62	0.726	0.742	9	62	0.758	0.745	5	60	0.55	0.525	4	58	0.621	0.633	6	58	0.603	0.734	3	47	0.532	0.503		
<i>"Pacific crossing"</i>	As for "all" dataset																														
<i>Samoa</i>	As for "all" dataset																														

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189 **Supplementary Material 7 (Continued) (b)**

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	GATA417				SW13				EV37				EV14				FCB1				SW19			
"Restricted" Dataset	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp	k	N	HObs	HExp
Total	7	423	0.504	0.529	14	507	0.826	0.838	32	487	0.856	0.906	14	469	0.682	0.716	16	502	0.795	0.837	32	491	0.882	0.922
Atlantic	3	39	0.385	0.399	10	39	0.795	0.844	16	37	0.811	0.889	11	38	0.684	0.728	10	36	0.694	0.826	17	35	0.886	0.929
<i>"Atlantic crossing"</i>																								
<i>Bahamas</i>																								
<i>Central Atlantic</i>	2	2	0.5	0.5	3	2	1	0.833	4	2	1	1	2	1	1	1	3	2	0.5	0.833	4	2	1	1
<i>Canary Islands</i>	3	24	0.417	0.435	8	24	0.667	0.836	16	23	0.87	0.909	9	24	0.792	0.733	9	23	0.87	0.812	16	23	0.913	0.934
<i>Eastern Mediterranean</i>																								
<i>Central Mediterranean</i>																								
<i>Northern Mediterranean</i>																								
Indian	5	148	0.561	0.576	12	163	0.81	0.844	24	158	0.835	0.908	12	158	0.696	0.73	14	163	0.742	0.824	27	162	0.864	0.922
<i>Aldabras</i>																								
<i>Southwestern Australia</i>																								
<i>Cocos Island</i>																								
<i>"Indian crossing"</i>																								
<i>Maldives/Chagos Archipelago</i>	3	31	0.484	0.554	9	32	0.813	0.814	17	29	0.931	0.881	9	30	0.6	0.749	11	31	0.742	0.831	14	33	0.818	0.91
<i>Mauritius</i>																								
<i>Seychelles</i>																								
<i>Sri Lanka</i>	4	50	0.5	0.589	10	48	0.833	0.845	19	49	0.755	0.902	10	47	0.702	0.706	11	52	0.75	0.809	19	49	0.878	0.921
Pacific	7	236	0.487	0.515	14	305	0.839	0.834	29	292	0.873	0.904	14	273	0.674	0.704	16	303	0.835	0.843	29	294	0.891	0.92
<i>Gulf of California</i>	3	73	0.438	0.501	14	112	0.857	0.829	24	111	0.892	0.908	12	99	0.646	0.693	14	111	0.856	0.857	26	109	0.899	0.919
<i>Galapagos</i>																								
<i>Kiribati</i>																								
<i>New Zealand</i>	6	54	0.63	0.552	11	58	0.776	0.854	20	51	0.863	0.902	9	49	0.714	0.715	13	54	0.852	0.842	20	51	0.922	0.935
<i>Oregon</i>																								
<i>Papua New Guinea</i>	4	53	0.491	0.469	9	62	0.806	0.821	19	60	0.817	0.897	11	59	0.712	0.706	12	63	0.841	0.844	18	62	0.855	0.918
<i>"Pacific crossing"</i>																								
<i>Samoa</i>																								

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192 **Supplementary Material 7 (Continued) (c)**

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Comparison	Dataset	F <sub>ST</sub>	p-value	G'' <sub>ST</sub>	p-value
AMOVA among regions (worldwide)	FULL	0.0048	1.07E-07	0.027	0
	RESTRICTED	0.0048	2.42E-06	0.027	0
AMOVA among oceans	FULL	0.0032	3.0E-06	0.015	0.001
	RESTRICTED	0.0032	6.2E-05	0.015	0.002
Pairwise PAC-IO	FULL	0.0026	0.0043	0.009	0.005
	RESTRICTED	0.0027	0.0094	0.009	0.008
Pairwise PAC-ATL	FULL	0.0043	0.0003	0.015	<0.001
	RESTRICTED	0.0040	<0.0001	0.014	0.003
Pairwise IO-ATL	FULL	0.0065	0.0001	0.023	0.000
	RESTRICTED	0.0063	0.0009	0.022	0.001
AMOVA among Pacific regions	FULL	0.0014	0.0117	0.012	0.091
	RESTRICTED	0.0014	0.0121	0.012	0.092
AMOVA among Indian regions	FULL	0.0051	0.0009	0.018	0.034
	RESTRICTED	0.0021	0.0393	0.004	0.326
AMOVA among Atlantic regions	FULL	0.0161	0.0180	0.052	0.042
	RESTRICTED	0.0144	0.0252	0.048	0.057

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(d)	GCA	GPG	PX	KR	PNG	SWAUS	COC	SRI	MAL	SEY	ALD	MED	CNI
GCA	--	0.0000	0.0000	<b>0.0085*</b>	<b>0.0009*</b>	0.0088	0.0103	<b>0.0041*</b>	0.0026	0.0000	0.0114	<b>0.0181*</b>	0.0018
GPG	0.0000	--	0.0000	<b>0.0123*</b>	<b>0.0018*</b>	0.0078	<b>0.0164*</b>	<b>0.0052*</b>	0.0039	0.0000	0.011	<b>0.0166*</b>	0.0088
PX	0.0000	0.0000	--	0.0039	<b>0.0044*</b>	0.0018	0.0046	<b>0.0043*</b>	0.0000	0.0000	0.0016	<b>0.0202**</b>	0.001
KR	<b>0.0308*</b>	<b>0.0515*</b>	0.0135	--	<b>0.0049*</b>	<b>0.0201*</b>	0.0000	<b>0.0145**</b>	0.0025	0.0062	0.0152	<b>0.0181*</b>	0.0001
PNG	<b>0.0030*</b>	<b>0.0046*</b>	<b>0.0149*</b>	<b>0.0169*</b>	--	<b>0.0116*</b>	<b>0.0101*</b>	<b>0.0069**</b>	<b>0.0054*</b>	<b>0.0028*</b>	<b>0.0156*</b>	<b>0.0218**</b>	<b>0.0027*</b>
SWAUS	0.0282	0.0308	0.0038	<b>0.0691*</b>	<b>0.0387*</b>	--	0.0179	<b>0.0097*</b>	0.0141	0.0078	0.0086	<b>0.0232*</b>	<b>0.0177*</b>
COC	0.0325	<b>0.0522*</b>	0.0132	0.0000	<b>0.0317*</b>	0.0539	--	<b>0.0064*</b>	0.003	0.0000	0.0072	<b>0.0231*</b>	0.0048
SRI	<b>0.0141*</b>	<b>0.0216*</b>	<b>0.0136*</b>	<b>0.0523**</b>	<b>0.0229**</b>	<b>0.0270*</b>	<b>0.0200*</b>	--	<b>0.0086*</b>	0.0000	0.0009	<b>0.0252**</b>	<b>0.0066*</b>
MAL	0.0093	0.0246	0.0000	0.0084	<b>0.0192*</b>	0.0532	0.0095	<b>0.0314*</b>	--	0.0000	0.0031	<b>0.0189*</b>	0.001
SEY	0.0000	0.0000	0.0000	0.0223	<b>0.0084*</b>	0.023	0.0000	0.0000	0.0000	--	0.0000	<b>0.0144*</b>	0.0026
ALD	0.0416	0.0461	0.0064	0.0559	<b>0.0565*</b>	0.0254	0.0239	0.0036	0.0134	0.0000	--	<b>0.0268*</b>	0.0148
MED	<b>0.0617*</b>	<b>0.0604*</b>	<b>0.0696**</b>	<b>0.0675*</b>	<b>0.0731**</b>	<b>0.0781*</b>	<b>0.0763*</b>	<b>0.0796**</b>	<b>0.0656*</b>	<b>0.0489*</b>	<b>0.0860*</b>	--	<b>0.0144*</b>
CNI	0.0065	0.0307	0.0035	0.0003	<b>0.0096*</b>	<b>0.0588*</b>	0.0151	<b>0.0220*</b>	0.0038	0.0091	0.0525	<b>0.0481*</b>	--

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198 **Supplementary Material 7 (Continued) (e)**

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		<b>394 bp mtDNA CR</b>				<b>Microsatellites</b>						
		n	F <sub>ST</sub> (females)	F <sub>ST</sub> (males)	p - value	n	F <sub>ST</sub> (females)	F <sub>ST</sub> (males)	p -value	var. assignment (females)	var. assignment (males)	p - value
<b>Pacific</b>	By region	F: 172 M: 43	0.1113	0.0346	0.0697	F: 174 M: 44	0.0002	0.0091	0.8185	13.53	15.57	0.2832
	<b>Indian</b> By region	F: 67 M: 26	0.4705	0.2988	0.2152	F: 80 M: 28	0.0061	0.0049	0.4408	8.801	6.384	0.7720
<b>Worldwide</b>	By region	F: 248 M: 73	0.2643	0.1288	<b>0.0194*</b>	F: 268 M: 81	0.0066	0.0015	0.1730	11.73	12.45	0.2472
	By ocean	F: 268 M: 99	0.1205	0.0695	0.1028	F: 290 M: 113	0.0074	0.0000	<b>0.0150*</b>	14.88	14.94	0.4339

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202 **Supplementary Material 8:** Population expansion tests for mtDNA (Fu's Fs, mismatch distribution fit as assessed through SSD  
 203 and Raggedness r values, as well as the inferred expansion timing in years before present, and 95% CI). Estimates that  
 204 significantly ( $\alpha = 0.02$  for Fu's Fs,  $\alpha = 0.05$  for all other tests) support a population expansion are highlighted in green, with  
 205 non-significant but supportive estimates highlighted in yellow. Estimates supportive of a bottleneck are shown in orange, with  
 206 significantly supportive estimates shown in red.

	Fu's Fs	P-value	SSD	P-value	r	P-value	Tau	Expansion (yrs. ago)
<b>Worldwide</b>	-25.36	0.00	0.00	0.01	0.06	0.00	1.63	78,321 (72,296 – 97,889)
<b>Pacific</b>	-21.51	0.00	0.00	0.01	0.07	0.00	1.39	66,850 (60,825 – 87,334)
GCA	-2.72	0.15	0.00	0.23	0.05	0.36	1.50	72,296 (55,24 – 98,876)
GPG/ECU	-5.91	0.04	0.01	0.02	0.08	0.01	1.30	62,416 (48,487 – 81,791)
PX	-2.91	0.04	0.00	0.80	0.03	0.93	1.49	71,718 (0 – 160,787)
HAW	-0.28	0.40	0.03	0.05	0.19	0.03	0.97	46,703 (19,568 – 86,129)
KR	0.36	0.58	0.20	0.01	0.15	0.85	0.41	19,568 (0 – 53,740)
PNG	-2.03	0.16	0.01	0.15	0.06	0.32	1.31	63,090 (32,485 – 94,322)
<b>Indian</b>	0.38	0.62	0.05	0.03	0.20	0.00	1.97	94,901 (37,112 – 150,424)
ALD	1.45	0.81	0.29	0.03	1.10	0.00	2.23	107,480 (19,761 – 178,330)
AUS	-0.58	0.34	0.03	0.07	0.15	0.07	1.43	69,019 (30,220 – 124,542)
COC	0.89	0.69	0.17	0.14	0.71	0.08	2.86	137,796 (0 – 1,198,140)
MAL	0.93	0.71	0.22	0.06	0.79	0.01	2.40	115,481 (0 – 240,120)
SEY	-0.21	0.49	0.04	0.16	0.11	0.30	2.35	127,530 (0 – 251,060)
SRI	0.33	0.50	0.02	0.38	0.19	0.63	3.25	156,642 (0 – 552,776)
<b>Atlantic</b>	0.20	0.59	0.00	0.15	0.05	0.40	1.40	67,235 (55,234 – 86,707)
MED	NA	NA	NA	NA	NA	NA	NA	NA
CNI	1.44	0.80	0.26	0.05	0.96	0.00	2.32	111,625 (0 – 221,901)
GMX	0.30	0.59	0.01	0.60	0.11	0.69	2.09	100,733 (0 – 222,528)
WNAO	-0.29	0.48	0.07	0.10	0.24	0.06	1.81	87,334 (0 – 206,526)

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213 **Supplementary Material 9:** Significance of comparisons of haplotype and nucleotide diversity values at various geographic  
214 levels. Significant comparisons for oceanic level given to left of table. Arrow points to ocean with highest genetic diversity for a  
215 given comparison ( $h$ : haplotype diversity,  $\pi$ : nucleotide diversity). Within-ocean comparisons are listed in table format by each  
216 ocean, with nucleotide diversity above the diagonal, haplotype diversity below the diagonal. Regions colored by within-ocean  
217 diversity level with dark green = highest haplotype/nucleotide diversity through yellow and red to brown-red = lowest  
218 haplotype/nucleotide diversity. Significance of differences in diversity between within-ocean regions should be interpreted with  
219 caution, as the effect of social groups has not been taken into account in these analyses.  
220



221 **Supplementary Material 9 (Continued)**

	$h$	$\pi$ (%)	GCA	GPG	PX	HAW	KR	PNG
<b>Pacific</b> $h = 0.779$ $\pi$ (%) = 0.388			0.368	0.355	0.301	0.197	0.381	0.299
	<i>Gulf of California (GCA)</i>	0.788				0.033		
	<i>Galapagos/Ecuador (GPG/ECU)</i>	0.743				0.036		
	<i>Pacific Crossing (PX)</i>	0.679	0.023					
	<i>Hawai'i (HAW)</i>	0.643	0.010	0.045				
	<i>Kiribati (KR)</i>	0.718						
<i>Papua New Guinea (PNG)</i>	0.720							
<b>Indian</b> $h = 0.788$ $\pi$ (%) = 0.431			SWAUS	COC	SRI	MAL/CHG	SEY	ALD
			0.307	0.230	0.132	0.303	0.413	0.364
	<i>Southwestern Australia (SWAUS)</i>	0.791			0.003			
	<i>Cocos Island (COC)</i>	0.451	0.001				0.005	
	<i>Sri Lanka (SRI)</i>	0.382	<0.001			0.003	<0.001	0.001
	<i>Maldives/Chagos Archipelago (MAL/CHG)</i>	0.570	0.007		<0.001		0.041	
<i>Seychelles (SEY)</i>	0.716			0.004	<0.001	0.003		
<i>Aldabras (ALD)</i>	0.712			0.007	0.008			
<b>Atlantic</b> $h = 0.746$ $\pi$ (%) = 0.336			MED	CNI	WNAO	GMX		
			0	0.333	0.273	0.216		
	<i>Mediterranean (MED)</i>	0		<0.001	<0.001	<0.001		
	<i>Canary Islands (CNI)</i>	0.648	<0.001					
	<i>Western North Atlantic (WNAO)</i>	0.616	<0.001					
<i>Gulf of Mexico (GMX)</i>	0.506	<0.001	0.048	0.006				

$h$   
 $p = 0.017$   
 $\pi$   
 $p = 0.030$

$\pi$   
 $p = 0.014$

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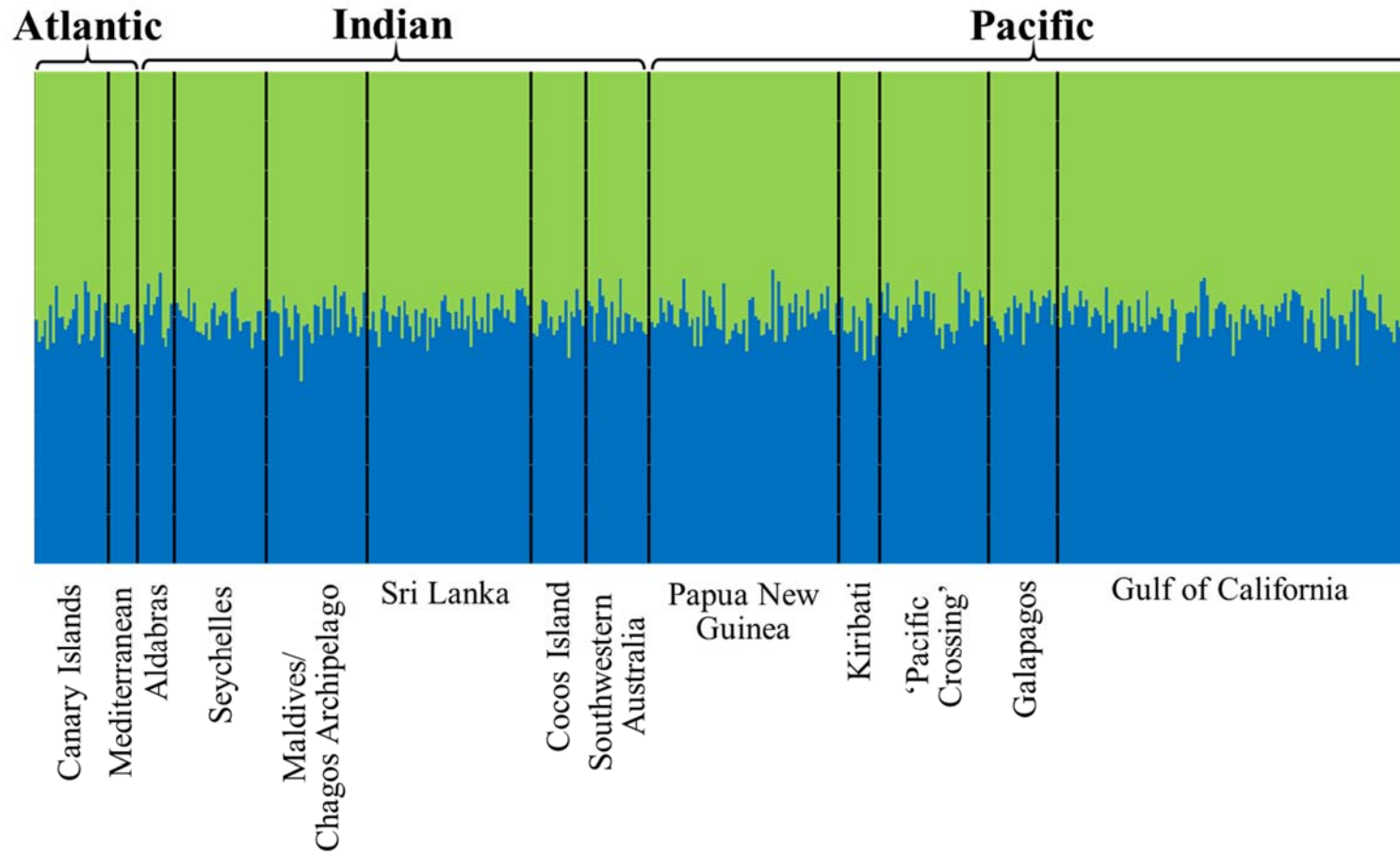
225 **Supplementary Material 10:** Summary of circumequatorial regional differentiation of mtDNA ( $F_{ST}$  and  $\Phi_{ST}$ ) and  
 226 microsatellites ( $F_{ST}$  and  $G''_{ST}$ ) for sperm whales. For each region, sample size and the number of significant pairwise  
 227 comparisons to other regions for mtDNA CR ( $F_{ST}$  and  $\Phi_{ST}$ ) and microsatellites (exact test) is given. Average fixation index  
 228 values over all pairwise comparisons are also presented. Regions with the largest number of significant pairwise  
 229 comparisons/largest average fixation index values are shaded in darkest gray through to white for the regions with fewer  
 230 numbers of significant comparisons/smaller average fixation index values. These analyses are provided for comparative purposes  
 231 with previous publications, however significance of genetic differentiation between within-ocean regions should be interpreted  
 232 with caution, as the effect of social group has not been taken into account in these analyses. Average fixation index values and  
 233 number of significant pairwise comparisons were calculated from regional pairwise comparisons for mtDNA and microsatellites  
 234 (listed in Supplementary Material 12).  
 235

Geographic area	mtDNA CR					Microsatellites				
	<i>n</i>	Total no. of sig. pairwise $F_{ST}$ comparisons	Total no. of sig. pairwise $\Phi_{ST}$ comparisons	Average pairwise $F_{ST}$	Average pairwise $\Phi_{ST}$	<i>n</i>	Total no. of sig. pairwise comparisons	Average pairwise $F_{ST}$	Average pairwise $G''_{ST}$	
<b>Pacific</b>	Gulf of California	122	14/15	13/15	0.1807	0.2010	122	5/12	0.0055	0.0186
	Galapagos*	285	12/15	12/15	0.1391	0.1581	23	4/12	0.0069	0.0267
	‘Pacific Crossing’	36	14/15	13/15	0.2089	0.2892	37	3/12	0.0034	0.0113
	Hawai’i	28	14/15	11/15	0.2224	0.2630	--	--	--	--
	Kiribati	13	15/15	11/15	0.2493	0.2353	13	5/12	0.0088	0.0322
	Papua New Guinea	63	11/15	11/15	0.1511	0.1850	65	12/12	0.0074	0.0251
<b>Indian</b>	Southwestern Australia	21	11/15	10/15	0.1609	0.2161	21	6/12	0.0124	0.0406
	Cocos Island	18	14/15	11/15	0.2781	0.2738	18	4/12	0.0088	0.0280
	Sri Lanka	42	15/15	15/15	0.4778	0.6142	56	10/12	0.0077	0.0260
	Maldives/Chagos Archipelago	33	14/15	14/15	0.2485	0.2909	34	3/12	0.0052	0.0198
	Seychelles	31	14/15	13/15	0.2713	0.2680	31	2/12	0.0029	0.0095
	Aldabras	12	10/15	12/15	0.1866	0.2343	12	2/12	0.0098	0.0346
<b>Atlantic</b>	Mediterranean	40	15/15	15/15	0.5961	0.5952	9	12/12	0.0203	0.0687
	Canary Islands	14	13/15	12/15	0.2413	0.2746	25	4/12	0.0069	0.0230
	Western North Atlantic	87	13/15	12/15	0.1847	0.1927	--	--	--	--
	Gulf of Mexico	153	15/15	15/15	0.4280	0.5566	--	--	--	--

236 \* Includes Ecuador for mtDNA dataset

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238 **Supplementary Material 11:** Structure plot ( $K = 2$ ) based on 13 microsatellites for the *Odyssey* samples where explicit spatial  
 239 coordinates were available.  
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243 **Supplementary Material 12:** Pairwise comparisons of differentiation for mtDNA and microsatellites

244 (a) Pairwise mtDNA CR oceanic comparisons, with sample sizes given by '*n*'.  $F_{ST}$  above diagonal of matrix,  $\Phi_{ST}$  underneath  
245 diagonal. Significant values italicized and shown in bold, with \* <0.05, \*\* <0.001.

246  
247 (b) Pairwise microsatellite oceanic regional comparisons for 'full' dataset, with sample sizes given by '*n*'.  $F_{ST}$  above diagonal of  
248 matrix,  $G''_{ST}$  underneath diagonal. Significant values italicized and shown in bold, with \* <0.05, \*\* <0.001.

249  
250 (c) Pairwise mtDNA CR regional comparisons, with sample sizes given by '*n*'.  $F_{ST}$  above diagonal of matrix,  $\Phi_{ST}$  underneath  
251 diagonal. Significant values italicized and shown in bold, with \* <0.05, \*\* <0.001. Within-ocean comparisons are shown shaded  
252 in gray. Abbreviations: Gulf of California (GCA), Galapagos/Ecuador (GPG/ECU), 'Pacific Crossing' (PX), Hawai'i (HAW),  
253 Kiribati (KR), Papua New Guinea (PNG), SW Australia (SWAUS), Cocos Island (COC), Sri Lanka (SRI), Maldives/Chagos  
254 Archipelago (MAL), Seychelles (SEY), Aldabras (ALD), Mediterranean (MED), Canary Island (CNI), Western North Atlantic  
255 (WNAO), Gulf of Mexico (GMX).

256  
257 (d) Pairwise microsatellite regional comparisons for 'full' dataset, with sample sizes given by '*n*'.  $F_{ST}$  above diagonal of matrix,  
258  $G''_{ST}$  underneath diagonal. Significant values italicized and shown in bold, with \* <0.05, \*\* <0.001. Within-ocean comparisons  
259 are shown shaded in gray. Abbreviations: Gulf of California (GCA), Galapagos (GPG), 'Pacific Crossing' (PX), Kiribati (KR),  
260 Papua New Guinea (PNG), SW Australia (SWAUS), Cocos Island (COC), Sri Lanka (SRI), Maldives/Chagos Archipelago  
261 (MAL), Seychelles (SEY), Aldabras (ALD), Mediterranean (MED), Canary Island (CNI).

262

(a)	<i>n</i>	Pacific	Indian	Atlantic
Pacific	1025	--	<b><i>0.0957**</i></b>	<b><i>0.1008**</i></b>
Indian	159	<b><i>0.1256**</i></b>	--	<b><i>0.1490**</i></b>
Atlantic	362	<b><i>0.2268**</i></b>	<b><i>0.2445**</i></b>	--

(b)	<i>n</i>	Pacific	Indian	Atlantic
Pacific	326	--	<b><i>0.0027**</i></b>	<b><i>0.0035*</i></b>
Indian	175	<b><i>0.009*</i></b>	--	<b><i>0.0065**</i></b>
Atlantic	41	<b><i>0.012*</i></b>	<b><i>0.023**</i></b>	--

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(c)

n	Pacific						Indian						Atlantic			
	GCA	GPG/ECU	PX	HAW	KR	PNG	SWAUS	COC	SRI	MAL	SEY	ALD	MED	CNI	WNAO	GMX
GCA 122	--	<b>0.0506**</b>	<b>0.1061**</b>	<b>0.0484*</b>	<b>0.1298**</b>	<b>0.0673**</b>	0.0331	<b>0.1850**</b>	<b>0.3642**</b>	<b>0.1737**</b>	<b>0.2106**</b>	<b>0.1524**</b>	<b>0.4874**</b>	<b>0.2222**</b>	<b>0.1594**</b>	<b>0.3199**</b>
GPG/ECU 285	<b>0.0584**</b>	--	<b>0.0999**</b>	<b>0.0806*</b>	<b>0.0749*</b>	0.0031	0.0205	<b>0.1510**</b>	<b>0.3801**</b>	<b>0.1488**</b>	<b>0.2037**</b>	0.0513	<b>0.3414**</b>	<b>0.1245*</b>	<b>0.0359*</b>	<b>0.3208**</b>
PX 36	<b>0.0453*</b>	<b>0.1597**</b>	--	<b>0.0517*</b>	<b>0.2785**</b>	<b>0.0577**</b>	<b>0.0783*</b>	0.0547	<b>0.4713**</b>	<b>0.0955*</b>	<b>0.2459**</b>	<b>0.1338*</b>	<b>0.6534**</b>	<b>0.2405**</b>	<b>0.1431**</b>	<b>0.4227**</b>
HAW 28	0.0226	<b>0.0881*</b>	0.0314	--	<b>0.2639**</b>	<b>0.0655*</b>	0.0592	<b>0.1015*</b>	<b>0.4771**</b>	<b>0.1239*</b>	<b>0.2639**</b>	<b>0.1801*</b>	<b>0.7217**</b>	<b>0.3013**</b>	<b>0.1725**</b>	<b>0.4247**</b>
KR 13	<b>0.1798**</b>	0.0498	<b>0.3270**</b>	<b>0.2894**</b>	--	<b>0.1246*</b>	<b>0.1177*</b>	<b>0.4117**</b>	<b>0.4914**</b>	<b>0.3520**</b>	<b>0.2128**</b>	<b>0.1147*</b>	<b>0.5402**</b>	<b>0.1123*</b>	<b>0.1327*</b>	<b>0.3826**</b>
PNG 63	<b>0.0307*</b>	0.0061	<b>0.1161**</b>	0.0441	<b>0.1052*</b>	--	0.0299	<b>0.1130*</b>	<b>0.4330**</b>	<b>0.1192**</b>	<b>0.2265**</b>	0.0377	<b>0.4533**</b>	<b>0.1423*</b>	0.0216	<b>0.3723**</b>
SWAUS 21	<b>0.0678*</b>	0.0154	<b>0.1806**</b>	<b>0.1608*</b>	<b>0.1130*</b>	0.0431	--	<b>0.1074*</b>	<b>0.4384**</b>	<b>0.1481*</b>	<b>0.0950*</b>	<b>0.0913*</b>	<b>0.6374**</b>	<b>0.0924*</b>	<b>0.0998*</b>	<b>0.3647**</b>
COC 18	0.0328	<b>0.1028*</b>	0.0456	0.0497	<b>0.3017**</b>	<b>0.0873*</b>	0.0699	--	<b>0.5901**</b>	<b>0.1050*</b>	<b>0.2875**</b>	<b>0.2224*</b>	<b>0.8413**</b>	<b>0.3105**</b>	<b>0.1878**</b>	<b>0.5030**</b>
SRI 42	<b>0.5464**</b>	<b>0.5127**</b>	<b>0.6374**</b>	<b>0.6583**</b>	<b>0.6450**</b>	<b>0.5795**</b>	<b>0.6814**</b>	<b>0.7074**</b>	--	<b>0.3675**</b>	<b>0.4328**</b>	<b>0.3761**</b>	<b>0.8051**</b>	<b>0.5197**</b>	<b>0.4804**</b>	<b>0.5404**</b>
MAL 33	<b>0.1632**</b>	<b>0.2032**</b>	<b>0.1670**</b>	<b>0.1142*</b>	<b>0.3092**</b>	<b>0.1747**</b>	<b>0.2650**</b>	<b>0.1891*</b>	<b>0.3856**</b>	--	<b>0.3156**</b>	0.0931	<b>0.7185**</b>	<b>0.3122**</b>	<b>0.1887**</b>	<b>0.4660**</b>
SEY 31	<b>0.2466**</b>	<b>0.1482**</b>	<b>0.3290**</b>	<b>0.3123**</b>	<b>0.1365*</b>	<b>0.2019**</b>	0.0594	<b>0.2181*</b>	<b>0.6264**</b>	<b>0.3456**</b>	--	<b>0.2161**</b>	<b>0.6082**</b>	0.0717	<b>0.2628**</b>	<b>0.4162**</b>
ALD 12	<b>0.1822**</b>	<b>0.1093*</b>	<b>0.2705**</b>	<b>0.2092*</b>	0.0834	<b>0.1147*</b>	<b>0.1934*</b>	<b>0.2808**</b>	<b>0.4020**</b>	0.0857	<b>0.2104*</b>	--	<b>0.6133**</b>	0.0866	0.0159	<b>0.4144**</b>
MED 40	<b>0.5148**</b>	<b>0.3440**</b>	<b>0.7393**</b>	<b>0.7957**</b>	<b>0.4577**</b>	<b>0.5183**</b>	<b>0.6749**</b>	<b>0.8416**</b>	<b>0.8523**</b>	<b>0.7062**</b>	<b>0.4845**</b>	<b>0.6122**</b>	--	<b>0.5412**</b>	<b>0.3502**</b>	<b>0.6289**</b>
CNI 14	<b>0.2439**</b>	<b>0.1037*</b>	<b>0.3781**</b>	<b>0.3775**</b>	0.0551	<b>0.1842*</b>	0.0692	<b>0.3095*</b>	<b>0.6926**</b>	<b>0.3818**</b>	0.0000	<b>0.1853*</b>	<b>0.5418**</b>	--	<b>0.1091*</b>	<b>0.4335**</b>
WNAO 87	<b>0.1173**</b>	<b>0.0176*</b>	<b>0.2441**</b>	<b>0.1487*</b>	0.0346	0.0289	<b>0.0847*</b>	<b>0.2073**</b>	<b>0.5592**</b>	<b>0.2297**</b>	<b>0.1803**</b>	0.0628	<b>0.3785**</b>	<b>0.1234*</b>	--	<b>0.4105**</b>
GMX 153	<b>0.5637**</b>	<b>0.4521**</b>	<b>0.6674**</b>	<b>0.6435**</b>	<b>0.4415**</b>	<b>0.5404**</b>	<b>0.5623**</b>	<b>0.6633**</b>	<b>0.7273**</b>	<b>0.6434**</b>	<b>0.5201**</b>	<b>0.5124**</b>	<b>0.4664**</b>	<b>0.4724**</b>	<b>0.4731**</b>	--

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n	Pacific Ocean					Indian						Atlantic	
	GCA	GPG	PX	KR	PNG	SWAUS	COC	SRI	MAL	SEY	ALD	MED	CNI
GCA 122	--	0.0000	0.0000	<b>0.0080*</b>	<b>0.0009*</b>	<b>0.0085*</b>	0.0103	<b>0.0041*</b>	0.0023	0.0000	0.0107	<b>0.0184*</b>	0.0022
GPG 23	0.0000	--	0.0000	0.0123	<b>0.0016*</b>	0.0078	<b>0.0164*</b>	<b>0.0046*</b>	0.0041	0.0000	0.011	<b>0.0166*</b>	0.0088
PX 37	0.0000	0.0000	--	0.0039	<b>0.0044*</b>	0.0018	0.0046	<b>0.0035*</b>	0.0000	0.0000	0.0016	<b>0.0202*</b>	0.0008
KR 13	<b>0.0288*</b>	0.0515	0.0135	--	<b>0.0055*</b>	<b>0.0201*</b>	0.0000	<b>0.0143**</b>	0.0017	0.0062	0.0152	<b>0.0181*</b>	0.0004
PNG 65	<b>0.0029*</b>	<b>0.0037*</b>	<b>0.0147*</b>	<b>0.0191*</b>	--	<b>0.0110*</b>	<b>0.0098*</b>	<b>0.0075**</b>	<b>0.0056*</b>	<b>0.0026*</b>	<b>0.0157*</b>	<b>0.0213**</b>	<b>0.0033*</b>
SWAUS 21	<b>0.0269*</b>	0.0308	0.0038	<b>0.0691*</b>	<b>0.0368*</b>	--	0.0179	<b>0.0088*</b>	0.0138	0.0078	0.0086	<b>0.0232*</b>	<b>0.0190*</b>
COC 18	0.0327	<b>0.0522*</b>	0.0132	0.0000	<b>0.0307*</b>	0.0539	--	<b>0.0071*</b>	0.0027	0.0000	0.0072	<b>0.0231*</b>	0.0068
SRI 56	<b>0.0143*</b>	<b>0.0202*</b>	<b>0.0112*</b>	<b>0.0524**</b>	<b>0.0252**</b>	<b>0.0246*</b>	<b>0.0229*</b>	--	<b>0.0078*</b>	0.0000	0.0015	<b>0.0260**</b>	<b>0.0070*</b>
MAL 34	0.0082	0.0256	0.0000	0.0052	<b>0.0201*</b>	0.0525	0.0086	<b>0.0292**</b>	--	0.0000	0.0046	<b>0.0196*</b>	0.0003
SEY 31	0.0000	0.0000	0.0000	0.0223	<b>0.008*</b>	0.0230	0.0000	0.0002	0.0000	--	0.0000	<b>0.0144*</b>	0.0033
ALD 12	0.0389	0.0461	0.0064	0.0559	<b>0.0568*</b>	0.0254	0.0239	0.0059	0.0186	0.0000	--	<b>0.0268*</b>	0.0144
MED 9	<b>0.0626*</b>	<b>0.0604*</b>	<b>0.0696*</b>	<b>0.0675*</b>	<b>0.0712**</b>	<b>0.0781*</b>	<b>0.0763*</b>	<b>0.0827**</b>	<b>0.0682*</b>	<b>0.0489*</b>	<b>0.0860*</b>	--	<b>0.0161*</b>
CNI 25	0.0079	0.0299	0.0030	0.0011	<b>0.0116*</b>	<b>0.0622*</b>	0.0213	<b>0.0234*</b>	0.0015	0.0112	0.0508	<b>0.0524*</b>	--

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268 **Supplementary Material References:**

- 269 Bérubé M, Jørgensen H, McEwing R, Palsbøll PJ (2000) Polymorphic di-nucleotide  
270 microsatellite loci isolated from the humpback whale, *Megaptera novaeangliae*.  
271 *Molecular Ecology* **9**, 2181-2183.
- 272 Buchanan FC, Friesen MK, Littlejohn RP, Clayton JW (1996) Microsatellites from the beluga  
273 whale *Delphinapterus leucas*. *Molecular Ecology* **5**, 571-575.
- 274 Drouot V, Bérubé M, Gannier A, *et al.* (2004) A note on genetic isolation of Mediterranean  
275 sperm whales (*Physeter macrocephalus*) suggested by mitochondrial DNA. *Journal of*  
276 *Cetacean Research and Management* **6**, 29-32.
- 277 Engelhaupt D, Hoelzel AR, Nicholson C, *et al.* (2009) Female philopatry in coastal basins and  
278 male dispersion across the North Atlantic in a highly mobile marine species, the sperm  
279 whale (*Physeter macrocephalus*). *Molecular Ecology* **18**, 4193-4205.
- 280 Engelhaupt DT (2004) *Phylogeography, kinship and molecular ecology of sperm whales*  
281 (*Physeter macrocephalus*) PhD, University of Durham.
- 282 Hamner RM (2014) *All in a DNA's work: conservation genetics and monitoring of the New*  
283 *Zealand endemic Maui's and Hector's dolphins*. PhD dissertation, Oregon State  
284 University.
- 285 Lyrholm T, Gyllensten U (1998) Global matrilineal population structure in sperm whales as  
286 indicated by mitochondrial DNA sequences. *Proceedings of the Royal Society -*  
287 *Biological Sciences (Series B)* **265**, 1679-1684.
- 288 Mesnick SL, Taylor BL, Archer FI, *et al.* (2011) Sperm whale population structure in the eastern  
289 and central North Pacific inferred by the use of single-nucleotide polymorphisms,  
290 microsatellites and mitochondrial DNA. *Molecular Ecology Resources* **11**, 278-298.
- 291 Ortega-Ortiz JG, Engelhaupt D, Winsor M, Mate BR, Hoelzel AR (2012) Kinship of long-term  
292 associates in the highly social sperm whale. *Molecular Ecology* **21**, 732-744.
- 293 Palsbøll PJ, Bérubé M, Larsen AH, Jørgensen H (1997) Primers for the amplification of tri-and  
294 tetramer microsatellite loci in baleen whales. *Molecular Ecology* **6**, 893-895.
- 295 Rendell L, Mesnick S, Dalebout M, Burtenshaw J, Whitehead H (2012) Can genetic differences  
296 explain vocal dialect variation in sperm whales, *Physeter macrocephalus*? *Behavior*  
297 *Genetics* **42**, 332-343.
- 298 Richard KR, Dillon MC, Whitehead H, Wright JM (1996a) Patterns of kinship in groups of free-  
299 living sperm whales (*Physeter macrocephalus*) revealed by multiple molecular genetic  
300 analyses. *Proceedings of the National Academy of Science, United States of America* **93**,  
301 8792-8795.
- 302 Richard KR, Whitehead H, Wright JM (1996b) Polymorphic microsatellites from sperm whales  
303 and their use in the genetic identification of individuals from naturally sloughed pieces of  
304 skin. *Molecular Ecology* **5**, 313-315.
- 305 Schlötterer C, Amos B, Tautz D (1991) Conservation of polymorphic simple sequence loci in  
306 cetacean species. *Nature* **354**, 63-65.
- 307 Valsecchi E, Amos W (1996) Microsatellite markers for the study of cetacean populations.  
308 *Molecular Ecology* **5**, 151-156.
- 309 Waldick RC, Brown MW, White BN (1999) Characterization and isolation of microsatellite loci  
310 from the endangered North Atlantic right whale. *Molecular Ecology* **8**, 1763.

- 311 Whitehead H, Dillon M, Dufault S, Weilgart L, Wright J (1998) Non-geographically based  
312 population structure of South Pacific sperm whales: dialects, fluke-markings and genetics.  
313 *Journal of Animal Ecology* **67**, 253-262.  
314  
315