

## **Supplementary Material**

### **Drivers of population structure of the bottlenose dolphin (*Tursiops truncatus*) in the Eastern Mediterranean Sea**

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**Table S1.** List of accession numbers used in the comparison with Atlantic mtDNA haplotypes, and corresponding source references.

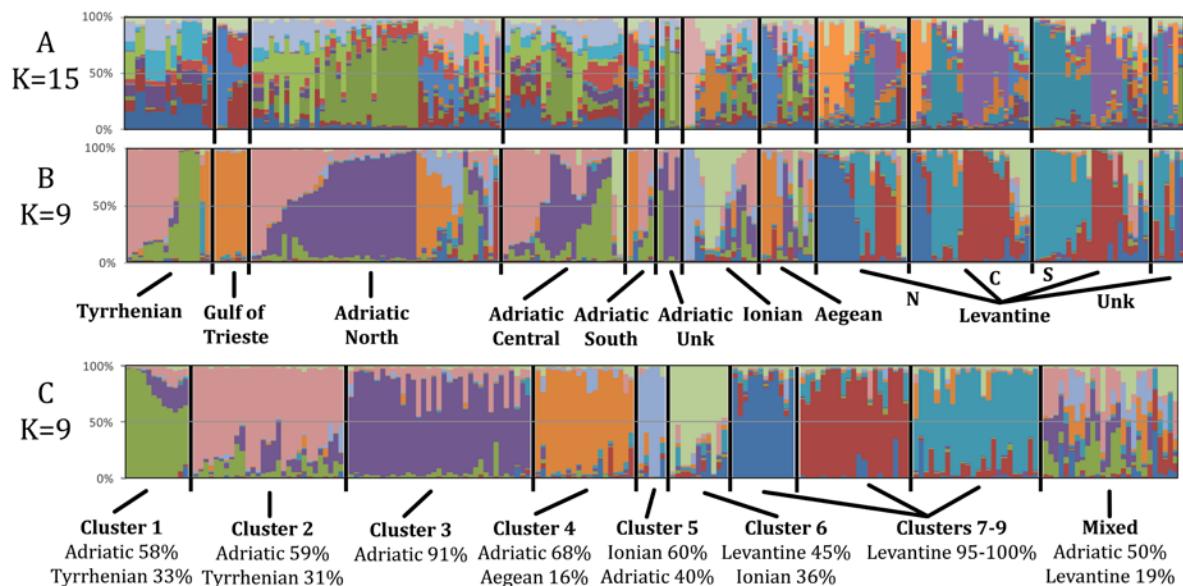
<b>Genebank Accession Number</b>	<b>Reference</b>
AF268357	Parsons <i>et al.</i> 2002
AY963588-AY963626	Natoli <i>et al.</i> 2005
DQ073641-DQ073673	Quérouil <i>et al.</i> 2007
DQ073675-DQ073728	
DQ525357-DQ525388	
FJ68001- FJ68019	Quérouil <i>et al.</i> 2009a
GQ241419	Quérouil <i>et al.</i> 2009b
HQ634245-HQ634252	Mirimin <i>et al.</i> 2011
HQ634254-HQ634258	
KF650783-KF650837	Louis <i>et al.</i> 2014

Table S2. Pairwise Fst values between: A- the five Mediterranean basins compared in this study; B- within the Adriatic subdivided into sub-regions along its North/South and East/West directions.

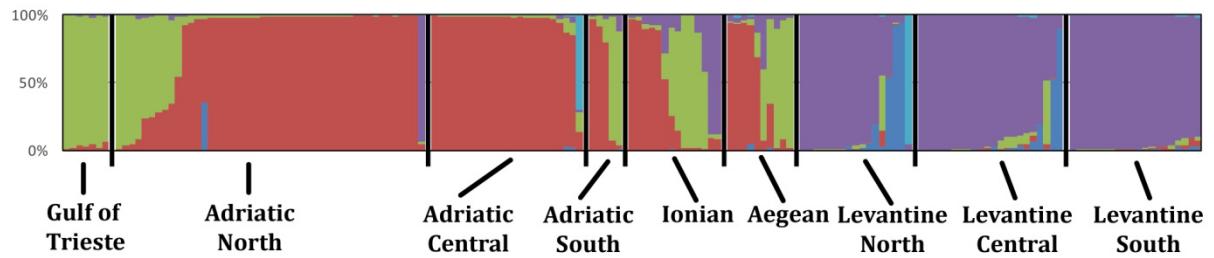
A- Mediterranean				
	Adriatic	Ionian	Aegean	Tyrrhenian
<b>Adriatic</b>				
<b>Ionian</b>	0.034** (0.000)			
<b>Aegean</b>	0.002 (0.389)	0.031* (0.039)		
<b>Tyrrhenian</b>	0.062** (0.000)	0.073** (0.000)	0.036 (0.051)	
<b>Levantine</b>	0.081** (0.000)	0.067** (0.000)	0.037* (0.006)	0.146** (0.000)

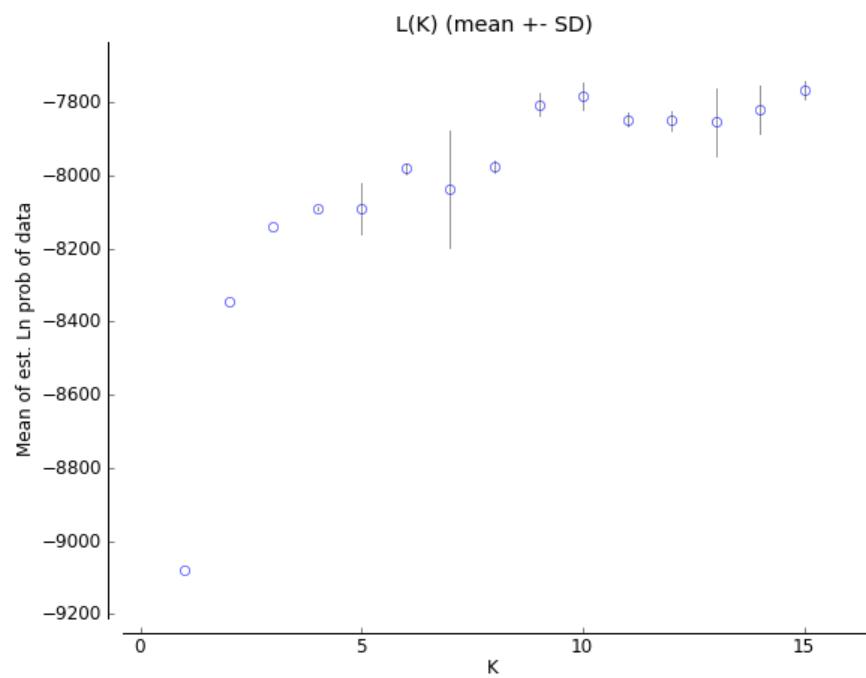
B- Adriatic				
	Gulf of Trieste	Adriatic North	Adriatic East	
<b>Gulf of Trieste</b>				
<b>Adriatic North</b>	0.050* (0.008)			
<b>Adriatic Central-South</b>	0.052* (0.005)	0.000 (0.047)		
<b>Adriatic West</b>			0.024** (0.000)	



**Figure S1.** Individual ancestry plots using Bayesian clustering method implemented in the software STRUCTURE (Pritchard *et al.*, 2000), for all Mediterranean *Tursiops truncatus*. **A** - for K=15 with individuals ordered by sampling basin; **B** - for K=9 with individuals ordered by sampling basin; **C** - for K=9 with individuals ordered by cluster assignment. The proportions of the two most represented basins in each cluster, are included below. Unk identifies individuals sampled in a given basin, but whose exact location is unknown.

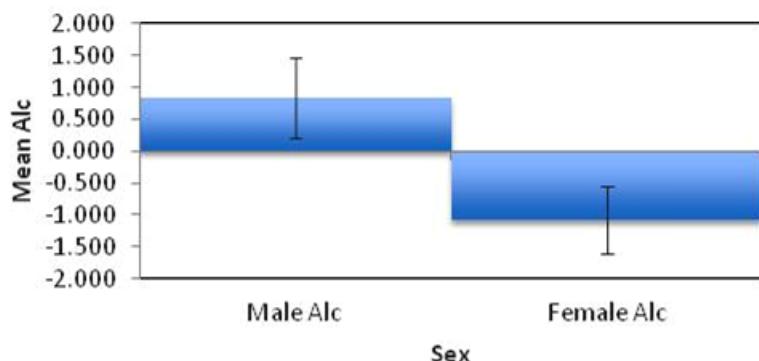


**Figure S2.** Individual ancestry plots using Bayesian clustering method as implemented in the software TESS (Durand *et al.*, 2011), to investigate local structure within the Eastern Mediterranean Sea (K=5).

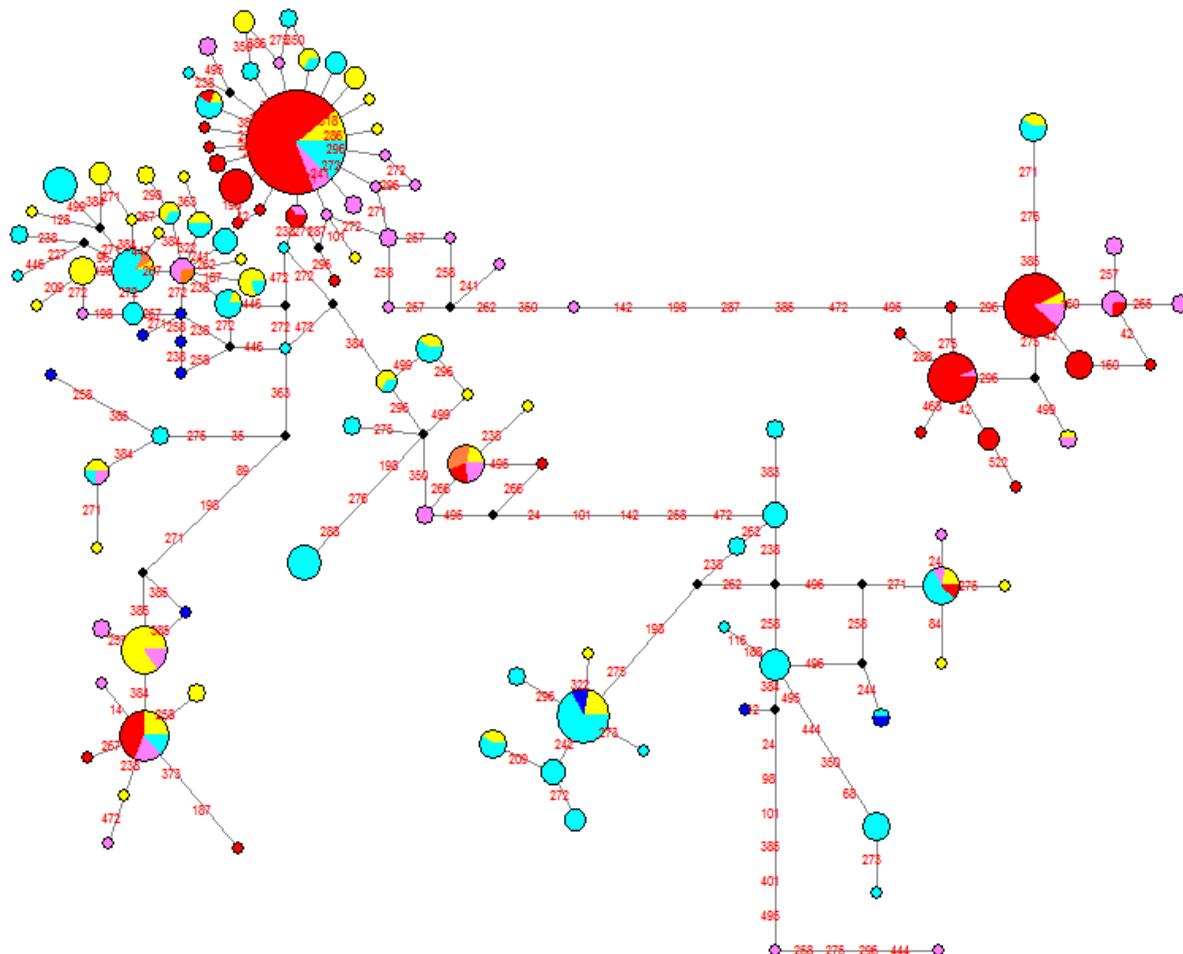


**Figure S3.** Likelihood plot for all STRUCTURE (Pritchard *et al.*, 2000) runs for K = 1-15. Plot drawn using STRUCTURE-HARVESTER (Earl & vonHoldt, 2012).

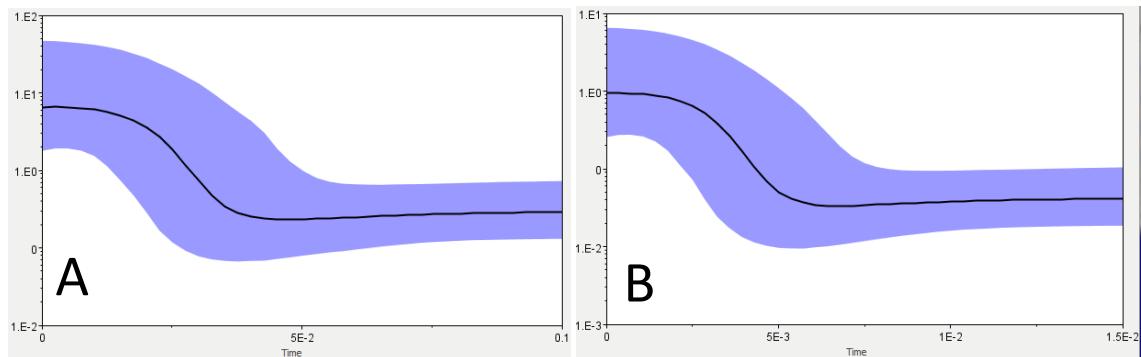
### Male vs Female Mean Assignment Bias



**Figure S4.** Mean AIC for male and female *Tursiops truncatus* in the Mediterranean sea, calculated based on microsatellite data using GenAIEx (Peakall & Smouse, 2006). Negative values indicate high frequency of migrants, while positive values indicate low frequency of migrants.



**Figure S5.** Medium joining network of all *Tursiops truncatus* mtDNA haplotypes produced in this study, together with mtDNA sequences from North Atlantic samples used in previous studies (Table S1). Dark Blue - Western North Atlantic Pelagic ecotype (as defined in Hoelzel et al 1998), data from previous studies; Light Blue - North Atlantic Pelagic (from Azores and Madeira), data previous studies; Yellow - Atlantic "coastal" European, data from previous studies; Pink - Mediterranean, data from previous studies; Red - Mediterranean "coastal", data from this study; Orange - Mediterranean Ionian sea "pelagic", data from this study. Numbers in red refer to single mutational steps.



**Figure S6.** Bayesian skyline plot constructed using all mtDNA sequence obtained from Mediterranean *Tursiops truncatus* in this study, using the software BEAST (Drummond *et al.*, 2012). A fixed mutation rate was used, calculated using a date for the opening of the Bosphorus strait of 10 kya, as described in (Moura *et al.*, 2013). **A** - using the mutation rate calculated for the whole mitogenome; **B** - using the mutation rate calculated for D-Loop region only. See main text for more details.

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