The following supplement accompanies the article

Multiple management units of short-beaked common dolphins subject to fisheries bycatch off southern and southeastern Australia

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Supplement. The supplementary material (1) provides additional analyses of the microsatellite dataset of common dolphins from southern Australia (Indian Ocean MU1-MU5) in STRUCTURE, excluding MU6 of the Pacific Ocean; (2) shows the genetic autocorrelation of common dolphin MU1-MU6 as a function of distance in kilometres; (3) gives summary information on common dolphin samples used for population genetic analyses in southern and southeastern Australia, comparing previous studies with the one presented here; and (4) lists the genetic variation at 13 microsatellite loci for the 6 common dolphin MUs of southern and southeastern Australia.

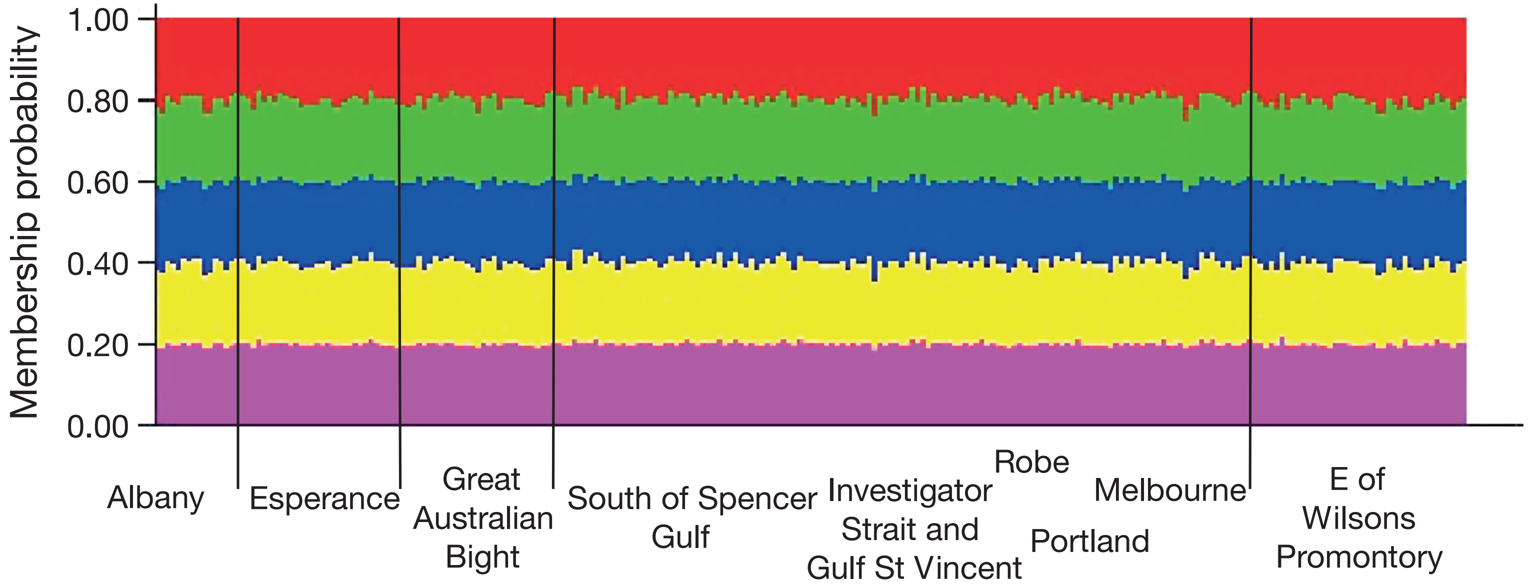

Fig. S1. Results from the analysis of samples in STRUCTURE using the same data set (common dolphin from the Indian Ocean only; n = 245) and using the same program settings as in Fig. 2b (100,000 burn-in, 1 million iterations, admixture model, correlated allele frequencies) but using no location information. The graph shows the output for $K = 5$. Each dolphin is represented by one vertical line and membership proportions of the arbitrary populations are colour coded. Sampling locations are presented along the x-axis

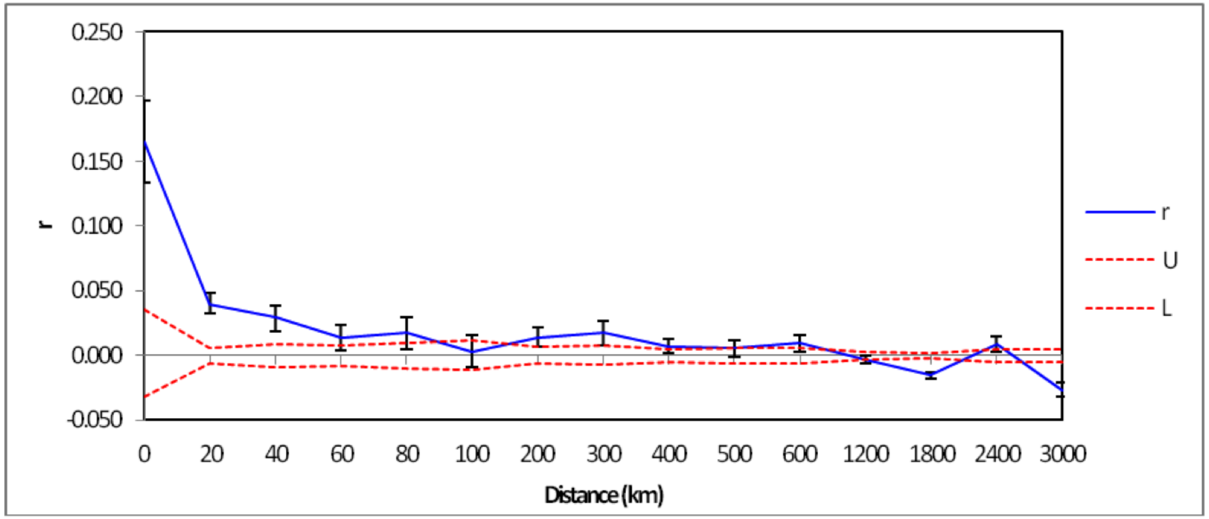

Fig. S2. Correlogram showing spatial genetic autocorrelation (r) of common dolphins from southern and southeastern Australia (MU1-6) as a function of distance in kilometres. Dotted lines represent upper (U) and lower (L) 95% confidence intervals. Error bars around the data points represent the 95% confidence intervals determined by bootstrapping

Table S1. Summary information for samples of short-beaked common dolphins used for population genetic analyses in southern and south-eastern Australia, comparing previous studies with the one presented here. For each Management Unit (MU) we list from previous studies: geographic area covered, authors, sample sizes and number of microsatellite loci used; and for this study: sample sizes and number of microsatellite loci used. Numbers in parentheses show samples that were used in previous studies, but were not available for the current analyses. ↑ = Increase in number of samples and/or microsatellite loci in the current study compared to previous ones

	PREVIOUS STUDIES				**THIS STUDY**		
Population	**Area covered**	**Authors**	**Sample size**	**Microsatellites**	**Area covered**	**Sample size**	**Microsatellites**
MU 1 (Albany, WA)					New	19 ↑	13 ↑
MU 2 (Esperance, WA)					New	33 ↑	13 ↑
MU 3 (Great Australian Bight, SA)	All	Bilgmann et al. 2008	32 (+4)	7	**Same**	32	13 ↑
MU 4 (Eyre Pen., SA - Wilsons Prom., VIC)	Partly (sub-sample) Partly (sub-sample)	Bilgmann et al. 2008 Amaral et al. 2012	16 25	7 14	Increased	143 ↑	13 ↑
MU 5 (East of Wilsons Promontory, VIC)					New	18 ↑	13 ↑
MU 6 (southeastern Australia, NSW/TAS)	Partly (TAS only) Partly (NSW only) Partly (sub-sample)	Bilgmann et al. 2008 Möller et al. 2011 Amaral et al. 2012	15 (+5) 20 (+25) 20 (+15)	7 7 14	Partly Increased (migratory animals)	63 ↑	13 ↑

Table S2. Genetic variation at 13 microsatellite loci for 6 Management Units (MUs) of common dolphins in southern and southeastern Australia. (H_O: observed heterozygosity; H_E: expected heterozygosity, F_{IS}). Loci that showed significant deviation ($p < 0.05$) from Hardy-Weinberg equilibrium prior to Bonferroni corrections are shown with an asterisk. (For location of MUs see Fig. 4)

Microsatellites		Management Unit					
		MU 1 (n = 19)	MU 2 (n = 33)	MU 3 (n = 32)	MU 4 (n = 143)	MU 5 (n = 18)	MU 6 (n = 63)
Tur142	H_O	0.79	0.55	0.53	0.59*	0.39	0.62
	H_E	0.62	0.54	0.62	0.68	0.47	0.70
	F_{IS}	–0.28	–0.02	0.15	0.13	0.17	0.08
Tur141	H_O	0.63	0.64	0.66	0.69	0.61	0.76
	H_E	0.57	0.68	0.72	0.68	0.74	0.80
	F_{IS}	–0.10	0.06	0.09	0.00	0.18	0.03
TurF10	H_O	0.79	0.85*	0.75	0.65*	0.72	0.68
	H_E	0.71	0.72	0.72	0.73	0.71	0.65
	F_{IS}	–0.12	–0.18	–0.04	0.10	–0.01	–0.13
Tur_E12	H_O	0.42	0.45	0.38	0.52	0.39	0.65
	H_E	0.55	0.44	0.38	0.50	0.38	0.62
	F_{IS}	0.24	–0.03	0.01	–0.03	–0.01	–0.06
Tur105	H_O	0.74	0.55	0.53*	0.59*	0.83	0.70
	H_E	0.59	0.58	0.67	0.62	0.71	0.78
	F_{IS}	–0.26	0.06	0.21	0.05	–0.19	0.08
Tur87	H_O	0.16	0.48	0.31	0.31	0.50	0.60
	H_E	0.15	0.43	0.28	0.31	0.56	0.63
	F_{IS}	–0.04	–0.14	–0.11	0.00	0.11	0.00
Tur80	H_O	0.84	0.94	0.72	0.74	0.78	0.84
	H_E	0.71	0.77	0.76	0.78	0.80	0.79
	F_{IS}	–0.19	–0.22	0.05	0.06	0.03	–0.09
Dd66	H_O	0.37	0.45	0.69	0.51*	0.56	0.71
	H_E	0.50	0.49	0.64	0.54	0.52	0.74
	F_{IS}	0.27	0.08	–0.08	0.05	–0.07	0.03
KW12	H_O	0.68	0.67	0.56	0.63	0.50	0.90
	H_E	0.83	0.66	0.62	0.63	0.64	0.86
	F_{IS}	0.18	0.00	0.09	–0.01	0.23	–0.05
EV1	H_O	0.79	0.79	0.75	0.80	0.89	0.92
	H_E	0.76	0.84	0.75	0.80	0.88	0.93
	F_{IS}	–0.04	–0.02	–0.01	–0.03	–0.01	–0.02
MK6	H_O	0.79	0.79	0.78	0.79*	0.83	0.79
	H_E	0.82	0.88	0.82	0.84	0.80	0.88
	F_{IS}	0.04	0.08	0.05	0.06	–0.04	0.10
MK8	H_O	0.63	0.70	0.72	0.70*	0.72	0.83
	H_E	0.66	0.69	0.64	0.72	0.55	0.83
	F_{IS}	0.05	–0.02	–0.12	–0.01	–0.32	0.01
EV37	H_O	0.63	0.48	0.25	0.48	0.78	0.79
	H_E	0.66	0.48	0.23	0.52	0.70	0.80
	F_{IS}	–0.20	0.00	–0.07	–0.04	–0.12	0.01
Mean (SD)	H_O	0.63 (0.17)	0.64 (0.16)	0.59 (0.18)	0.64 (0.14)	0.65 (0.17)	0.75 (0.10)
	H_E	0.64 (0.20)	0.63 (0.15)	0.60 (0.19)	0.61 (0.14)	0.65 (0.15)	0.77 (0.10)

LITERATURE CITED

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