Table S1 Summary of genetic variation based on 16 microsatellite loci in the Heaviside's dolphin

Locus	Primer sequence	Repeat motif	T_a (°C)	Size range (bp)	N_a	H_O	H_E	n	PI	PIsib	Pooled after amplification for loading	Reference
SCA22	F: GTT TGA GGA GAA GAC ATA C R: CCC TGA CCA CAG AAG TTG	$(CT)_7TTCT(CA)_{36}$	55	130–146	Null allele	-	-	395	-	-	1a	1
SCO11	F: ACC GCC TCT GTC TGT TTC TC R: AAG TCA CTC GGA GGA GTC CA	$(CTAT)_6CTAA$	55	171–227	9	0.8405	0.6158	395	0.2107	0.4927	1b	2
SCA17	F: TCC TGA GAC CTT GAG TTC R: ATT CAT TTC CAG AGC ATC	$(CA)_{18}$	55	184–192	26	0.8379	0.7961	395	0.0656	0.3682	2a	1
SCA37	F: TGT GTC CTA TTT CTA TTG R: ACA TTC TAC GGA GTC TTC	$(CA)_{22}$	55	227–231	13	0.8329	0.7932	395	0.0655	0.3686	2b	1
SCO28	F: AAA CCA TTC CAT TTT GAG GTA A R: CCC TAG TAT AAG AAC ATG GGA AGA	$(GATA)_5$	55	134–146	6	0.7038	0.4881	395	0.3575	0.5917	3a	2
SCA9	F: GTC TTC TTC ATC GGC TGT R: CTG AAA AGA GGG CTA AGG	$(CA)_{23}$	55	192–222	11	0.8784	0.7694	395	0.0875	0.3860	3b	1
SCA27	F: TGC CAG GAA AAT AAG GAG R: GCG TGG AGA GGG TAT ATG	$(CA)_{21}$	55	184–194	17	0.9949	0.7631	395	0.0855	0.3886	4a	1

Locus	Primer sequence	Repeat motif	T_a (℃)	Size range (bp)	N_a	H_O	H_E	n	PI	$PIsib$	Pooled after amplification for loading	Reference
SCA39	F: TGA GAT GCT TCT TAC CTA R: TAT TAC CTT ATG GGC TTG	$(CA)_{20}$	55	209−215	11	0.9594	0.7169	395	0.1221	0.4206	4b	1
EV14	F: TAA ACA TCA AAG CAG ACC CC R: CCA GAG CCA AGG TCA AGA G	$(GT)_n$	55	127−151	13	0.8481	0.8143	395	0.0507	0.3494	5a	3
Ttr11	F: CTT TCA ACC TGG CCT TTC TG R: GTT TGG CCA CTA CAA GGG AGT GAA	$(CA)_{21}$	55	193−223	10	0.9595	0.8070	395	0.0539	0.3532	5b	4
Ttr63	F: CAG CTT ACA GCC AAA TGA GAG R: GTT TCT CCA TGG CTG AGT CAT CA	$(CA)_{34}$	55	83−151	16	0.8633	0.8419	395	0.0381	0.3344	6a	4
EV37	F: AGC TTG ATT TGG AAG TCA TGA R: TAG TAG AGC CGT GAT AAA GTG C	$(AC)_n$	55	176−186	9	0.8329	0.6598	395	0.1505	0.4463	6b	3
SCA54	F: GTC AGG AGG TTG GGA GTA R: ACA AGA GAA TCA GAA AAT CA	$(CA)_{20}$	55	197−201	3	0.7386	0.5183	394	0.3019	0.5646	7a	1
Dde66	F: AAC ATT GCC AGT GCC TTA GAA R: GTG GAA CAG ACG CGC ATA T	$(GT)_{19}$	55	346−362	8	0.9721	0.6479	394	0.1813	0.4692	7b	5
Dde09	F: GAA GAT TTT ACC CTG CCT GTC R: GAT CTG TGC TCC TTA GGG AAA	$(CTAT)_{10}$	55	221−245	1	-	-	10	-	-	8a	5

Locus	Primer sequence	Repeat motif	T_a (°C)	Size range (bp)	N_a	H_O	H_E	n	PI	PIsib	Pooled after amplification for loading	Reference
Dde059	F: TAC ACA GCT TAC TTA CCT TAC CAA R: GTC CCT TTG AGC AGA GTT CTA	(GATA)$_n$	55	384–432	1	-	-	10	-	-	8b	5
Mean					11.69	0.8664	0.7102		0.1362	0.4257		
SD					5.736	0.0875	0.1154					

T_a stands for annealing temperature, bp for allele sizes, and N_a represents the number of alleles examined within each putative population where observed (H_O) and expected (H_E) heterozygosities were estimated; n indicates the number of individuals used in calculations; dash (-) indicates loci which were not polymorphic, PI stands for Probability of Identity per locus, and *PIsibs* indicates Probability of Identity for genetic similarity among siblings per locus. Locus SCA22 did not amplify and loci Dde09 and Dde059 were monomorphic.

References:

1. Chen L, Yang G (2008). A set of polymorphic dinucleotide and tetranucleotide microsatellite markers for the Indo-Pacific humpback dolphin (*Sousa chinensis*) and cross-amplification in other cetacean species. *Conservation Genetics* **10**, 697–700.
2. Mirimin L, Coughlan J, Rogan E, Cross TF (2006). Tetranucleotide microsatellite loci from the striped dolphin (*Stenella coeruleoalba* Meyen, 1833). *Molecular Ecology Notes* **6**, 493–5.
3. Valsecchi E, Amos W (1996). Microsatellite markers for the study of cetacean populations. *Molecular Ecology* **5**, 151–6.
4. Rosel P, Forgetta V, Dewar K (2005). Isolation and characoiszation of twelve polymorphic microsatellite markers in bottlenose dolphins (*Tursiops truncatus*). *Molecular Ecology Notes* **5**, 830–3.
5. Coughlan J, Mirimin L, Dillane E, Rogan E, Cross TF (2006). Isolation and characterization of novel microsatellite loci for the short-beaked common dolphin (*Delphinus delphis*) and cross-amplification in other cetacean species. *Molecular Ecology Notes* **6**, 490–2.

Table S2 Genetic variability estimates in mtDNA control region sequences excluding singletons ($n = 27$) for haplotype diversity (h) and nucleotide diversity (π)

Location	Haplotype diversity (h)	Nucleotide diversity (π)
Table Bay	0.6106 ±0.0669	0.002106 ±0.001515
St. Helena Bay	0.7749 ±0.0554	0.006995 ±0.004011
Lambert's Bay	0.7631 ±0.0435	0.006938 ±0.003896
Hondeklipbaai	0.8807 ±0.0246	0.005766 ±0.003369
Port Nolloth	0.8920 ±0.0186	0.005671 ±0.003278
Luderitz	0.7136 ±0.0443	0.002797 ±0.001861
Walvis Bay	0.8727 ±0.0272	0.005797 ±0.003354
Overall	0.7868 ±0.0401	0.005152 ±0.003040

Table S3 Summary of genetic variation based on 13 microsatellite loci in the Heaviside's dolphin

Locus		Table Bay ($n = 54$)	St. Helena Bay ($n = 55$)	Lambert's Bay ($n = 63$)	Hondeklipbaai ($n = 40$)	Port Nolloth ($n = 66$)	Luderitz ($n = 62$)	Walvis Bay ($n = 55$)
				Research sites (putative populations)				
SCO11	N_a	5	5	6	4	4	8	5
	H_O	0.6111	0.8000	0.9365	0.9500	0.8636	0.8871	0.8363
	H_E	0.5152	0.5466	0.6600	0.6642	0.6051	0.6656	0.5950
	HWE	0.8757	1.0000	1.0000	1.0000	1.0000	0.9965	0.9954
SCA17	N_a	11	10	13	13	14	17	17
	H_O	0.7407	0.6181	0.9365	0.9750	0.9090	0.9032	0.7818
	H_E	0.7464	0.6944	0.8005	0.8265	0.7800	0.8535	0.7749
	HWE	0.2871	0.0074	1.0000	1.0000	0.9982	0.8190	0.0970
SCA37	N_a	10	7	9	8	9	10	10
	H_O	0.5555 [§*]	0.6363	0.9682	1.0000	0.8939	0.8709	0.9090
	H_E	0.7371	0.7031	0.8213	0.8209	0.8030	0.7651	0.8367
	HWE	0.0000	0.0798	1.0000	1.0000	0.9958	0.8652	0.7487
SCO28	N_a	3	2	2	2	4	4	3
	H_O	0.5925	0.4909	0.8095	0.7750	0.7272	0.8387	0.6727
	H_E	0.4823	0.4379	0.4958	0.4807	0.4959	0.5222	0.4909
	HWE	0.6754	0.7426	1.0000	1.0000	1.0000	0.0154	0.9347
SCA9	N_a	5	6	6	8	9	7	7
	H_O	0.7037	0.8363	0.9047	0.9750	0.9545	0.9193	0.8546
	H_E	0.6955	0.7122	0.7439	0.7911	0.8009	0.7870	0.7701
	HWE	0.2139	0.9903	1.0000	1.0000	0.9991	0.6943	0.8827
SCA27	N_a	11	12	8	8	10	8	9
	H_O	1.0000	0.9818	1.0000	1.0000	0.9848	1.0000	1.0000
	H_E	0.7895	0.8038	0.7147	0.7614	0.7626	0.7348	0.7473
	HWE	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000

Locus		Research sites (putative populations)						
		Table Bay ($n = 54$)	St. Helena Bay ($n = 55$)	Lambert's Bay ($n = 63$)	Hondeklipbaai ($n = 40$)	Port Nolloth ($n = 66$)	Luderitz ($n = 62$)	Walvis Bay ($n = 55$)
SCA39	N_a	5	9	7	7	8	7	7
	H_O	0.8703	0.9090	1.0000	1.0000	0.9697	0.9839	0.9818
	H_E	0.5443	0.7497	0.6794	0.7092	0.7575	0.7322	0.7785
	HWE	1.0000	0.1317	1.0000	1.0000	0.9995	1.0000	0.9997
EV14	N_a	10	9	11	8	11	10	8
	H_O	0.6851[*]	0.6181[*]	1.0000	0.9750	0.9242	0.8387	0.8909
	H_E	0.8043	0.7668	0.8397	0.8307	0.8109	0.8146	0.7807
	HWE	0.0221	0.0192	1.0000	0.9596	0.9961	0.3241	0.9555
Ttr11	N_a	5	5	8	4	9	8	8
	H_O	0.8888	0.9636	0.9841	1.0000	0.9393	0.9677	0.9818
	H_E	0.7613	0.7578	0.8133	0.6535	0.7317	0.8436	0.8634
	HWE	0.9507	0.9999	1.0000	1.0000	1.0000	0.9892	0.9858
Ttr63	N_a	10	10	10	10	12	11	13
	H_O	0.5925[§*]	0.7272[*]	1.0000	0.9750	0.9849	0.8548	0.8909
	H_E	0.8200	0.8517	0.7845	0.8098	0.7573	0.8631	0.8734
	HWE	0.0019	0.0199	1.0000	1.0000	1.0000	0.0354	0.0869
EV37	N_a	4	4	5	4	6	5	8
	H_O	0.6666	0.5636	1.0000	1.0000	0.9090	0.8709	0.8181
	H_E	0.5637	0.4946	0.6646	0.7237	0.6981	0.6448	0.7269
	HWE	0.0111	0.9224	1.0000	1.0000	0.9997	0.9928	0.4015
SCA54	N_a	3	3	2	3	3	3	3
	H_O	0.4074	0.2363	0.9365	0.9750	0.7576	0.8709	1.0000
	H_E	0.3456	0.2163	0.5019	0.5503	0.5259	0.5642	0.6198
	HWE	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000

Locus		Research sites (putative populations)						
		Table Bay ($n = 54$)	St. Helena Bay ($n = 55$)	Lambert's Bay ($n = 63$)	Hondeklipbaai ($n = 40$)	Port Nolloth ($n = 66$)	Luderitz ($n = 62$)	Walvis Bay ($n = 55$)
Dde66	N_a	4	4	5	5	7	5	3
	H_O	0.9814	0.9818	1.0000	1.0000	0.8636	1.0000	1.0000
	H_E	0.6941	0.6333	0.6318	0.6095	0.6174	0.6746	0.6059
	HWE	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000	1.0000
Average (SD)	N_a	6.615 (3.203)	6.615 (3.124)	7.077 (3.252)	6.462 (3.126)	8.154 (3.288)	7.923 (3.639)	7.769 (4.045)
	H_O	0.715 (0.176)	0.720 (0.222)	0.959 (0.056)	0.969 (0.060)	0.898 (0.080)	0.908 (0.060)	0.894 (0.101)
	H_E	0.654 (0.148)	0.644 (0.177)	0.704 (0.114)	0.710 (0.113)	0.703 (0.107)	0.728 (0.109)	0.728 (0.116)

N_a indicates the number of alleles examined per each sampling site where observed (H_O) and expected (H_E) heterozygosities were estimated, HWE stands for Hardy-Weinberg equilibrium; n indicates the number of individuals used in calculations, § denotes loci out of HWE (≤ 0.05) and * indicates evidence for null allele. Locus SCA22 did not amplify and loci Dde09 and Dde059 were monomorphic

Table S4 Sex-biased dispersal results for males and females with respect to F_{IS}, F_{ST}, Ho, Hs, mean assignment and variance assignment

	N	F_{IS}	F_{ST}	Ho	Hs	Mean assignment	Variance of mean assignment
Males	173	–0.2619	0.0277	0.8692	0.6888	0.3567	12.0338
Females	222	–0.2347	0.0219	0.8638	0.6996	–0.2780	15.1182
Overall	395	–0.2468	0.0248	0.8662	0.6947	0.0000	0.0000
P-value		0.9440	0.8870	0.2860	0.9260	0.9640	0.9000

Table S5 Haplotype frequencies per sampling location of 51 haplotypes identified in biopsy samples of Heaviside's dolphins obtained at seven locations off the southwest African coast

	Table Bay	St. Helena Bay	Lambert's Bay	Hondeklipbaai	Port Nolloth	Luderitz	Walvis Bay	Total
TBH1	27	4		4	6		1	**42**
TBH2	2							**2**
TBH3	1	3		2	4	4	2	**16**
TBH4	9	2						**11**
TBH7	1							**1**
TBH8	6	12	6	7	6	16		**53**
TBH11	2	2						**4**
TBH18	1							**1**
TBH35	1							**1**
TBH38	1							**1**
TBH40	1							**1**
TBH54	1							**1**
TBH55	1							**1**
SHB1		2		1	7	27	5	**42**
SHB8		1						**1**
SHB14		1						**1**
SHB15		16	27					**43**
SHB16		10	5	4	4	2		**25**
SHB20		1	11	1	3			**16**
SHB32		1						**1**
LBH10			5	7	7	4		**23**
LBH21			3					**3**
LBH24			2	6	15		6	**29**
LBH27			1					**1**
LBH34			3				1	**4**
HKB3				1	6		2	**9**
HKB11				1				**1**

	Table Bay	St. Helena Bay	Lambert's Bay	Hondeklipbaai	Port Nolloth	Luderitz	Walvis Bay	Total
HKB19				2	3			**5**
HKB30				1				**1**
HKB34				1				**1**
HKB35				1				**1**
HKB37				1				**1**
PNH5					1			**1**
PNH17					2			**2**
PNH33					1			**1**
PNH65					1			**1**
CH2LDZ						4		**4**
CH5LDZ						1		**1**
CH7LDZ						1	7	**8**
CH19LDZ						1		**1**
CH45LDZ						1	1	**2**
CH54LDZ						1		**1**
CH2WB							14	**14**
CH4WB							1	**1**
CH9WB							1	**1**
CH16WB							4	**4**
CH18WB							1	**1**
CH26WB							1	**1**
CH29WB							5	**5**
CH33WB							1	**1**
CH49WB							2	**2**
TOTAL	**54**	**55**	**63**	**40**	**66**	**62**	**55**	**395**

Table S6 Proportion of Heaviside's dolphin individuals from each of the seven sampling locations assigned to each of the two clusters inferred from STRUCTURE analysis

Sampling location (sample size)	Inferred population clusters	
	1	2
Table Bay (54)	**0.680**	0.320
St. Helena Bay (55)	**0.698**	0.302
Lambert's Bay (63)	0.434	**0.566**
Hondeklipbaai (40)	0.362	**0.638**
Port Nolloth (66)	0.458	**0.542**
Luderitz (62)	0.425	**0.575**
Walvis Bay (55)	0.424	**0.576**
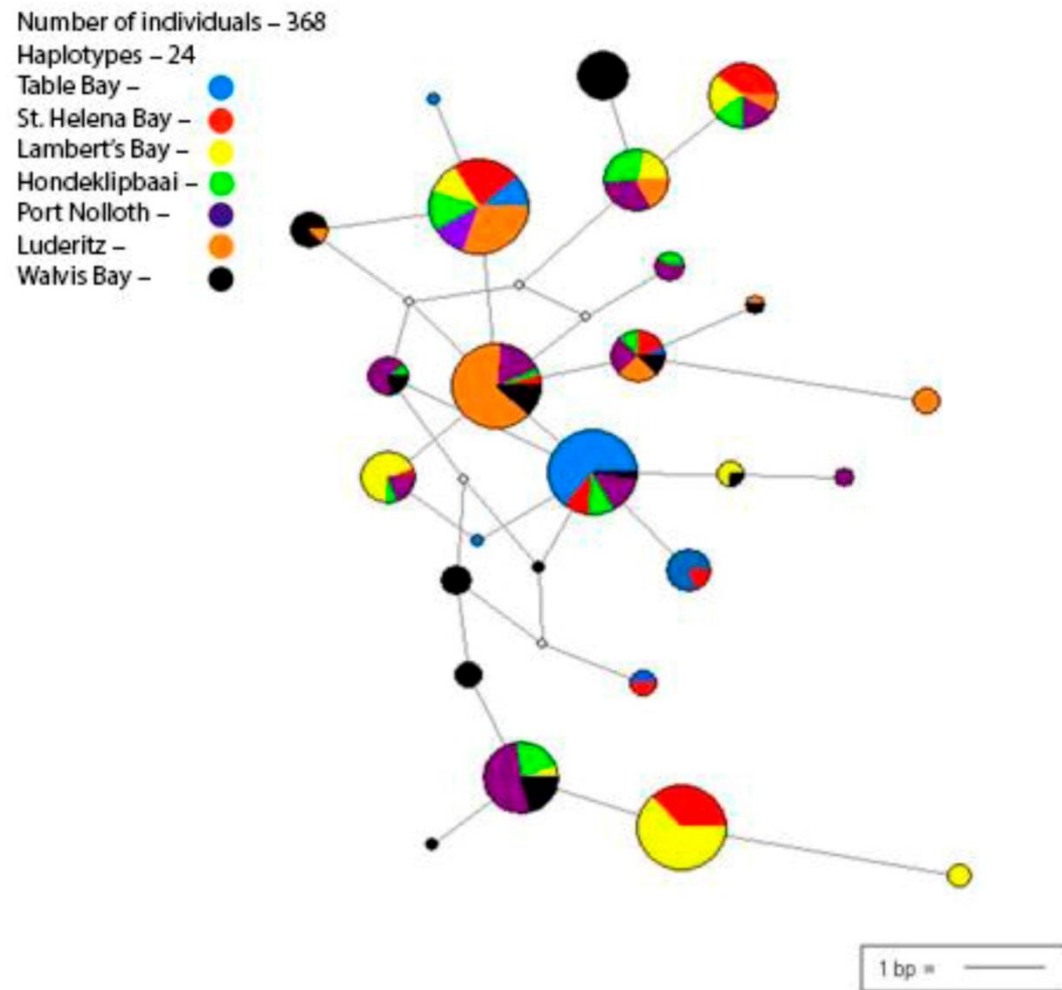
Figure S1 Median-joining network of mtDNA control region haplotypes without singletons for Heaviside's dolphins found off the southwest coast of southern Africa.
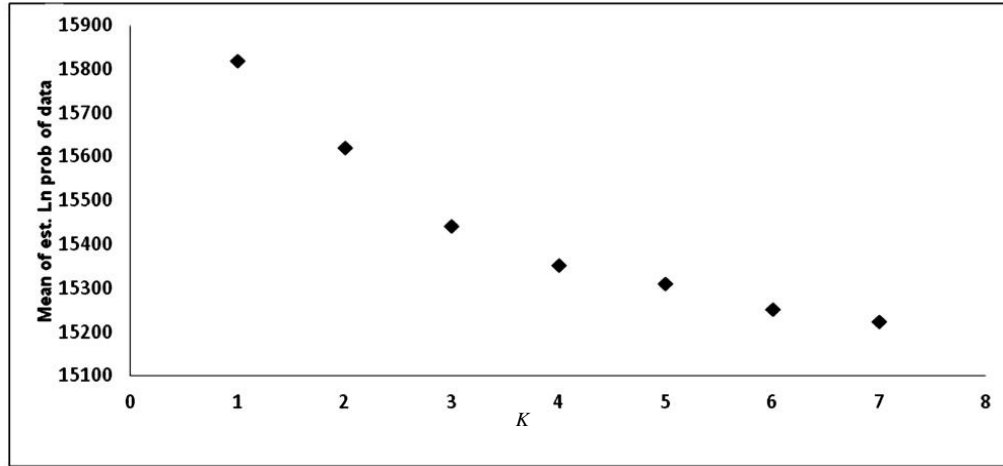
Figure S2 Average posterior probability (ln K) for each of the seven clusters (i.e., K 1 to 7) from 15 independent runs.
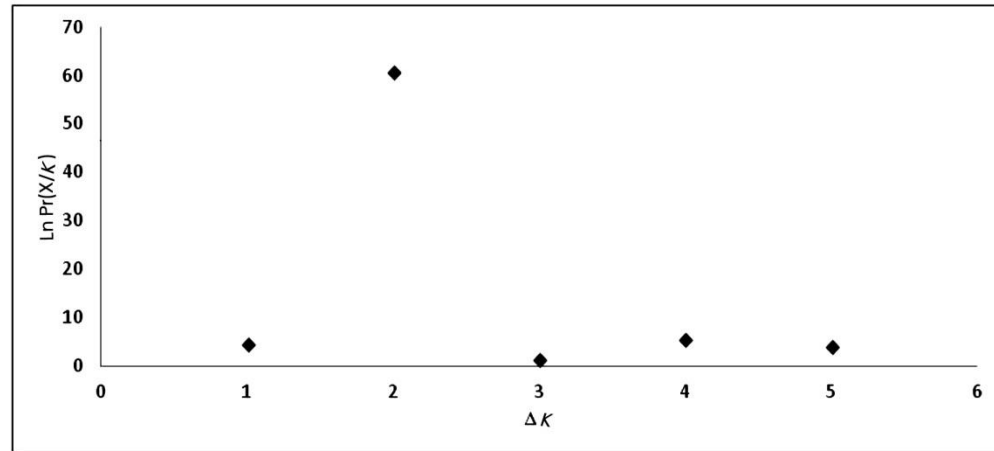

Figure S3 Log-likelihood values (Ln Pr(X/K)) from 15 independent runs, where the ad hoc statistic delta K (ΔK) shows the most probable number of genetic clusters (K).
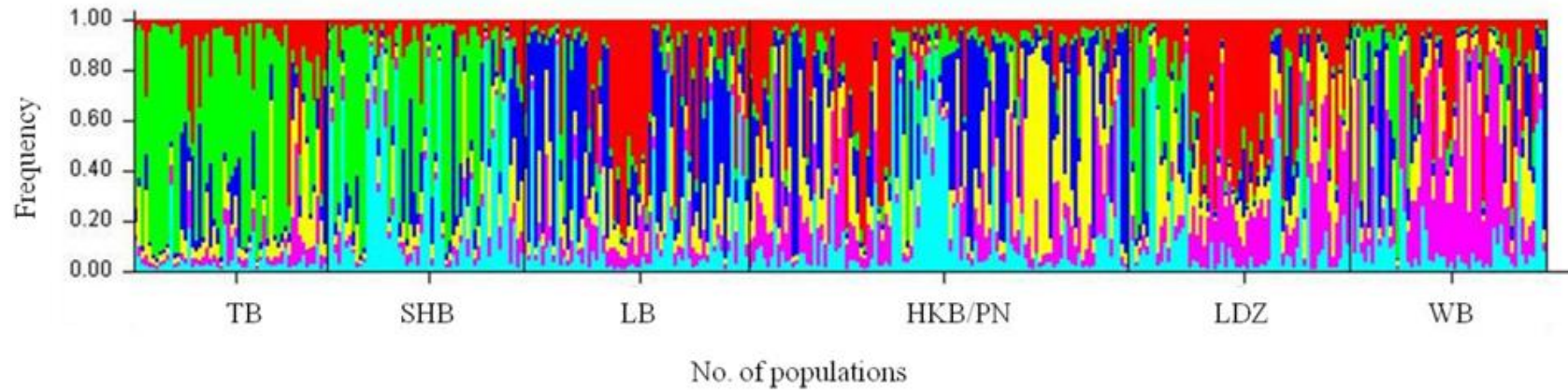
Figure S4 Bayesian assignment probabilities where $K = 6$ clusters were inferred from STRUCTURE analysis. Two sampling sites, Hondeklipbaai and Port Nolloth, are grouped together as in the AMOVA results using mtDNA control region data. Each individual is represented by a thin vertical line, which is portioned into K coloured segments that represent the individual's estimated membership fractions in K clusters. Black lines separate individuals of different populations. The six putative populations are labelled below the figure.