The following supplement accompanies the article

When two oceans meet: regional population genetics of an exploited coastal shark *Mustelus mustelus*

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Table S1 Summary of genetic diversity estimates at 12 microsatellite loci in eight *Mustelus mustelus* sampling sites in southern Africa. Number of alleles per locus (A_N); allelic richness (A_R); observed heterozygosity (H_O); expected heterozygosity (H_E); polymorphic information content (*PIC*); inbreeding coefficient (F_{IS}) with statistically significant deviations from Hardy-Weinberg expectations indicated by * ($P < 0.01$) and ** ($P < 0.001$); null allele frequency (Fr_{NULL}) with [b] indicating the presence of null alleles at statistical significance at the 5% nominal level.

Population	Locus	A_N	A_R	H_O	H_E	*PIC*	F_{IS}	Fr_{NULL}
Angola	*Mh1*	3	1.5	0.273	0.255	0.228	-0.071	-0.023
	Mh2	3	2.2	0.3	0.611	0.492	0.522	0.177
	Mh9	5	2.6	0.556	0.712	0.617	0.231	0.07
	Mh25	6	2.8	0.273	0.749	0.669	0.647**	0.258[b]
	Mca25	4	2	0.455	0.463	0.411	0.02	-0.009
	McaB39	2	1.9	1	0.524	0.375	-1.000**	-0.333
	McaB5	6	2.7	0.583	0.717	0.641	0.194	0.062
	McaB6	5	2.5	0.75	0.674	0.59	-0.119	-0.063
	McaB22	10	3.3	0.75	0.877	0.823	0.150*	0.049
	McaB27	1	1	0	0	0	0	0
	Mca33	2	1.8	0.5	0.464	0.346	-0.082	-0.039
	McaB37	1	1	0	0	0	0	0
	Average	4	2.1	0.453	0.504	0.433	0.041	0.012
Langebaan Lagoon Marine Protected Area	*Mh1*	1	1	0	0	0	0	0
	Mh2	3	1.9	0.391	0.474	0.39	0.178	0.05
	Mh9	3	1.9	0.391	0.474	0.39	0.178	0.05
	Mh25	5	2.5	0.174	0.657	0.594	0.740**	0.285[b]
	Mca25	4	1.8	0.348	0.378	0.347	0.081	0.016
	McaB39	2	1.9	1	0.511	0.375	-1.000**	-0.333
	McaB5	7	2.7	0.913	0.733	0.671	-0.252	-0.114
	McaB6	4	2.4	0.455	0.644	0.571	0.299	0.107
	McaB22	10	3.3	0.857	0.875	0.838	0.02	-0.002
	McaB27	2	1.1	0.043	0.043	0.042	0	-0.001
	Mca33	3	1.3	0.174	0.165	0.154	-0.054	-0.011
	McaB37	3	1.3	0.174	0.165	0.154	-0.054	-0.011
	Average	3.9	1.9	0.41	0.427	0.377	0.011	0.003

Robben Island	*Mh1*	1	1	0	0	0	0	0
	Mh2	2	1.5	0.111	0.286	0.239	0.618*	0.13
	Mh9	3	1.6	0.19	0.324	0.279	0.418	0.096
	Mh25	6	2.9	0.316	0.78	0.721	0.602**	0.252[b]
	Mca25	3	1.5	0.318	0.28	0.247	-0.14	-0.035
	McaB39	3	2	1	0.534	0.407	-0.913**	-0.314
	McaB5	7	2.8	0.773	0.761	0.71	-0.016	-0.017
	McaB6	5	2.8	0.773	0.768	0.71	-0.006	-0.012
	McaB22	10	3.4	0.955	0.885	0.851	-0.081	-0.048
	McaB27	5	1.4	0.182	0.175	0.168	-0.037	-0.009
	Mca33	3	1.4	0.182	0.173	0.163	-0.05	-0.011
	McaB37	2	1.6	0.05	0.296	0.247	0.835**	0.185[b]
	Average	4.2	2	0.404	0.439	0.395	0.103	0.018
False Bay	*Mh1*	2	1.1	0.063	0.063	0.059	0	-0.002
	Mh2	4	2	0.188	0.466	0.417	0.605**	0.182[b]
	Mh9	2	1.5	0.167	0.29	0.239	0.436	0.087
	Mh25	7	2.6	0.385	0.683	0.625	0.447**	0.164[b]
	Mca25	5	2.1	0.438	0.51	0.462	0.146	0.038
	McaB39	2	1.9	1	0.516	0.375	-1.000**	-0.333
	McaB5	6	2.7	0.647	0.725	0.66	0.111	0.034
	McaB6	5	2.5	0.647	0.679	0.61	0.049	0.007
	McaB22	14	3.4	0.882	0.889	0.853	0.008	-0.01
	McaB27	6	1.9	0.471	0.414	0.385	-0.143	-0.049
	Mca33	3	2	0.824	0.542	0.436	-0.545*	-0.195
	McaB37	5	1.6	0.176	0.275	0.258	0.364	0.071
	Average	5.1	2.1	0.49	0.504	0.448	0.04	-0.001
Kalk Bay	*Mh1*	2	1.1	0.063	0.063	0.059	0	-0.002
	Mh2	4	1.8	0.385	0.403	0.363	0.048	0.002
	Mh9	3	2.3	0.25	0.607	0.468	0.625	0.184
	Mh25	5	2.5	0.214	0.656	0.584	0.682**	0.256[b]
	Mca25	3	1.9	0.467	0.503	0.396	0.076	0.014
	McaB39	2	1.9	1	0.516	0.375	-1.000**	-0.333
	McaB5	6	2.8	0.688	0.758	0.696	0.096	0.027
	McaB6	5	2.5	0.875	0.657	0.588	-0.346	-0.146
	McaB22	10	3.4	1	0.901	0.86	-0.114	-0.068
	McaB27	6	2.4	0.813	0.615	0.558	-0.336	-0.136
	Mca33	4	2.2	0.875	0.597	0.51	-0.489	-0.188
	McaB37	2	1.1	0.063	0.063	0.059	0	-0.002
	Average	4.3	2.2	0.558	0.528	0.46	-0.063	-0.033
Struis Bay	*Mh1*	3	2.3	0.294	0.633	0.532	0.543*	0.198[b]
	Mh2	3	2	0.556	0.503	0.404	-0.111	-0.054
	Mh9	4	2.3	0.588	0.62	0.522	0.053	0.009
	Mh25	5	2.5	0.941	0.679	0.603	-0.403**	-0.17
	Mca25	2	1.8	0.706	0.471	0.352	-0.524**	-0.171
	McaB39	2	1.9	1	0.515	0.375	-1	-0.333
	McaB5	6	2.8	1	0.759	0.695	-0.330**	-0.151
	McaB6	5	2.8	1	0.75	0.684	-0.347**	-0.157
	McaB22	9	3.1	1	0.822	0.772	-0.225**	-0.113
	McaB27	1	1	0	0	0	0	0
	Mca33	3	1.2	0.118	0.116	0.109	-0.016	-0.005
	McaB37	2	1.8	0.647	0.451	0.342	-0.455	-0.146
	Average	3.8	2.1	0.654	0.527	0.449	-0.234	-0.091

Jeffreys Bay	*Mh1*	5	1.6	0.313	0.29	0.271	-0.079	-0.024
	Mh2	3	2.4	0.636	0.671	0.567	0.054*	0.003
	Mh9	2	1.8	0.625	0.458	0.337	-0.4	-0.137
	Mh25	5	2.6	0.333	0.683	0.626	0.521**	0.197[b]
	Mca25	5	2.6	0.563	0.7	0.638	0.201**	0.069
	McaB39	5	2.5	1	0.677	0.593	-0.500**	-0.208
	McaB5	6	2.5	0.813	0.653	0.599	-0.254	-0.11
	McaB6	6	2.6	0.5	0.69	0.616	0.281	0.101
	McaB22	11	3.5	0.813	0.921	0.883	0.122**	0.042
	McaB27	6	1.8	0.438	0.391	0.366	-0.123	-0.043
	Mca33	3	1.8	0.5	0.417	0.367	-0.206	-0.068
	McaB37	5	2.2	0.467	0.611	0.507	0.243	0.078
	Average	5.2	2.3	0.583	0.597	0.531	-0.012	-0.008
Durban	*Mh1*	5	1.9	0.278	0.43	0.396	0.361**	0.099
	Mh2	4	2.3	0.444	0.601	0.522	0.273**	0.079
	Mh9	4	1.9	0.412	0.437	0.385	0.059	0.009
	Mh25	5	2.3	0.5	0.595	0.542	0.164**	0.05
	Mca25	3	1.6	0.368	0.317	0.275	-0.167	-0.046
	McaB39	2	1.9	1	0.514	0.375	-1.000**	-0.333
	McaB5	6	2.5	0.563	0.681	0.612	0.179**	0.059
	McaB6	6	3	0.429	0.812	0.75	0.482**	0.199[b]
	McaB22	12	3.5	0.875	0.913	0.874	0.043	0.005
	McaB27	1	1	0	0	0	0	0
	Mca33	4	2.5	0.467	0.674	0.587	0.315*	0.112
	McaB37	3	1.7	0.267	0.343	0.294	0.228	0.048
	Average	4.6	2.2	0.467	0.526	0.468	0.078	0.023
Overall Populations	*Mh1*	2.8	1.4	0.161	0.217	0.193	-0.025	0.007
	Mh2	3.3	2.0	0.376	0.502	0.424	0.159	0.055
	Mh9	3.3	2.0	0.397	0.490	0.405	0.200	0.046
	Mh25	5.5	2.6	0.392	0.685	0.621	0.425	-0.060
	Mca25	3.6	1.9	0.458	0.453	0.391	0.003	-0.016
	McaB39	2.5	2.0	1.000	0.538	0.406	-1.000	-0.315
	McaB5	6.3	2.7	0.748	0.723	0.661	-0.020	-0.026
	McaB6	5.1	2.6	0.679	0.709	0.640	0.026	-0.023
	McaB22	10.8	3.4	0.892	0.885	0.844	-0.025	-0.018
	McaB27	3.5	1.5	0.243	0.205	0.190	-0.080	-0.030
	Mca33	3.1	1.8	0.455	0.394	0.334	-0.150	-0.051
	McaB37	2.9	1.5	0.231	0.276	0.233	0.047	0.005
	Average	4.4	2.1	0.502	0.507	0.445	-0.005	-0.010

Table S2. Polymorphic nucleotide positions for *Mustelus mustelus* mtDNA *ND4* haplotypes. A dot indicates that the base in that position is the same as the base in Haplotype 1

Haplotype number	Nucleotide positions														GenBank Accession number
		014	017	024	055	230	347	381	387	407	445	503	640	738	791	
CSH01	C	G	C	A	T	A	T	G	T	C	C	C	T	A	T	KU523351
CSH02	T	.	.	.	.	.	.	.	.	.	.	.	.	.	.	KU523352
CSH03	T	.	.	.	.	.	.	A	.	T	.	T	.	.	.	KU523353
CSH04	T	.	.	.	.	.	.	.	.	.	.	.	.	T	.	KU523354
CSH05	T	.	.	.	.	G	.	.	.	.	.	.	.	.	.	KU523355
CSH06	T	.	T	.	.	.	.	.	C	.	.	.	.	.	.	KU523356
CSH07	T	A	.	.	.	.	.	.	.	.	.	.	.	.	.	KU523357
CSH08	T	.	.	.	.	.	.	.	.	.	T	.	.	.	.	KU523358
CSH09	T	.	T	.	.	.	.	.	.	.	.	.	.	.	.	KU523359
CSH10	T	.	.	.	.	.	.	.	.	.	.	.	C	.	.	KU523360
CSH11	T	.	.	G	.	.	.	.	.	.	.	.	.	.	.	KU523361
CSH12	T	.	.	.	C	.	.	.	.	.	T	.	.	.	.	KU523362
CSH13	T	.	.	.	.	.	C	.	.	.	.	.	.	.	.	KU523363
CSH14	T	.	.	.	.	.	.	.	.	.	.	.	.	.	C	KU523364
CSH15	T	.	.	.	.	.	.	.	.	T	.	T	.	.	.	KU523365

Table S3. Pairwise Jost's D_{est}-values among populations based on eight microsatellite loci with *P*-values shown above diagonal

	D_{est}							
	A	**LL**	**RI**	**FB**	**KB**	**SB**	**JB**	**D**
Angola (ANG)		0.001**	0.001**	0.002**	0.009**	0.001**	0.001**	0.001**
Langebaan (LMPA)	0.048		0.119	0.003**	0.001**	0.001**	0.001**	0.001**
Robben Island (RI)	0.054	0.006		0.009**	0.001**	0.001**	0.003**	0.001**
False Bay (FB)	0.071	0.025	0.020		0.462	0.001**	0.004**	0.001**
Kalk Bay (KB)	0.080	0.053	0.056	0.002		0.001**	0.001**	0.001**
Struis Bay (SB)	0.204	0.198	0.158	0.233	0.295		0.001**	0.001**
Jeffreys Bay (JB)	0.091	0.075	0.044	0.046	0.082	0.124		0.002**
Durban (DUR)	0.216	0.174	0.123	0.147	0.214	0.126	0.061	

*Statistical significance at the 5% nominal level and ** statistical significance at the 1% nominal level.

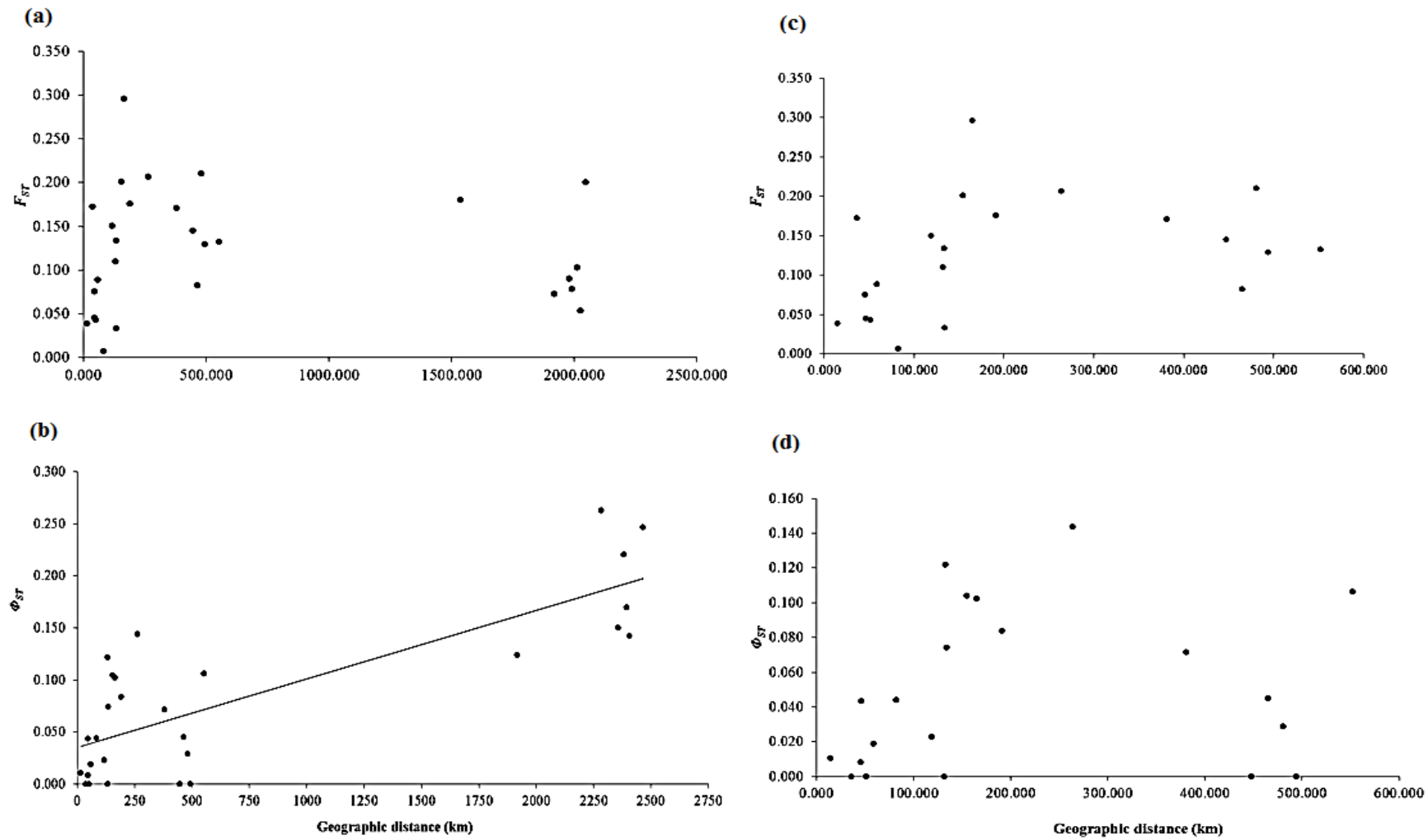

Fig. S1. Isolation by distance scatterplots with all sampling locations (a, microsatellites and b, mitochondrial DNA) and excluding samples from Angola (c, microsatellites and d, mitochondrial DNA).

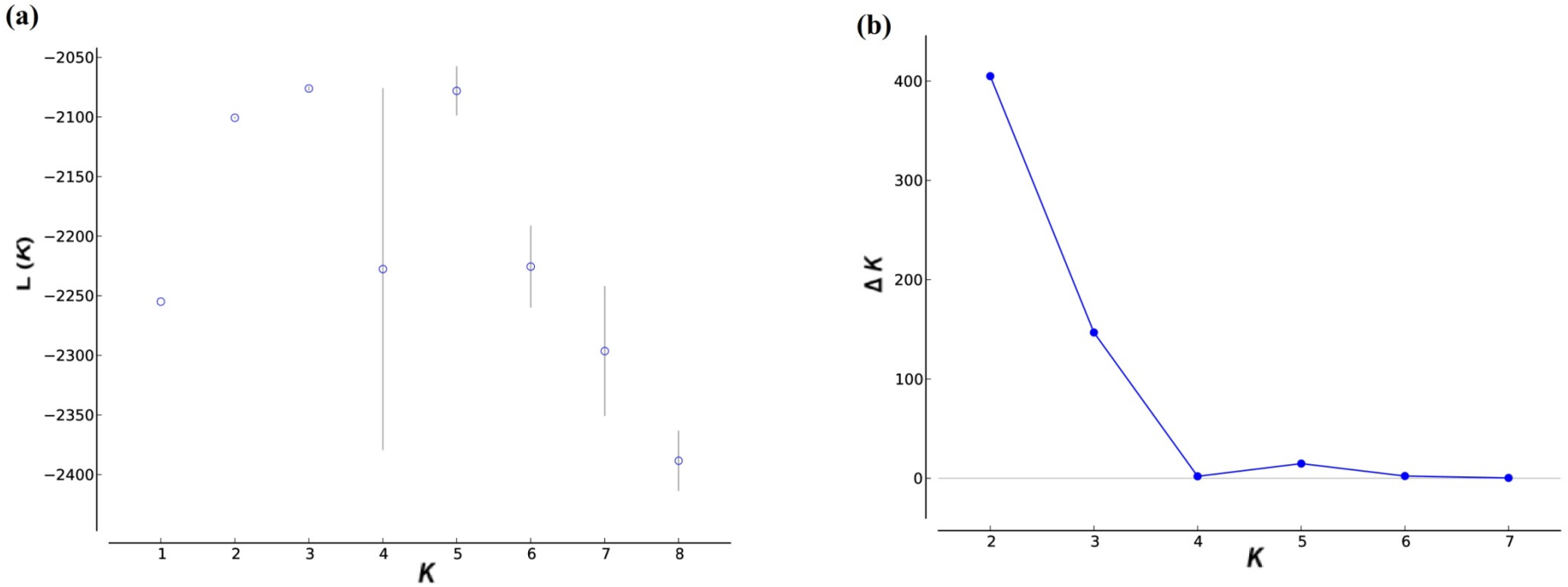

Fig. S2. Bayesian clustering analyses (STRUCTURE) of all samples at eight microsatellite loci. (a) Likelihood probability profile estimated from STRUCTURE at *K*1-8 showing the mean and variance at each K. (b) Δ*K* at each value of *K*, averaged across 10 replicates.

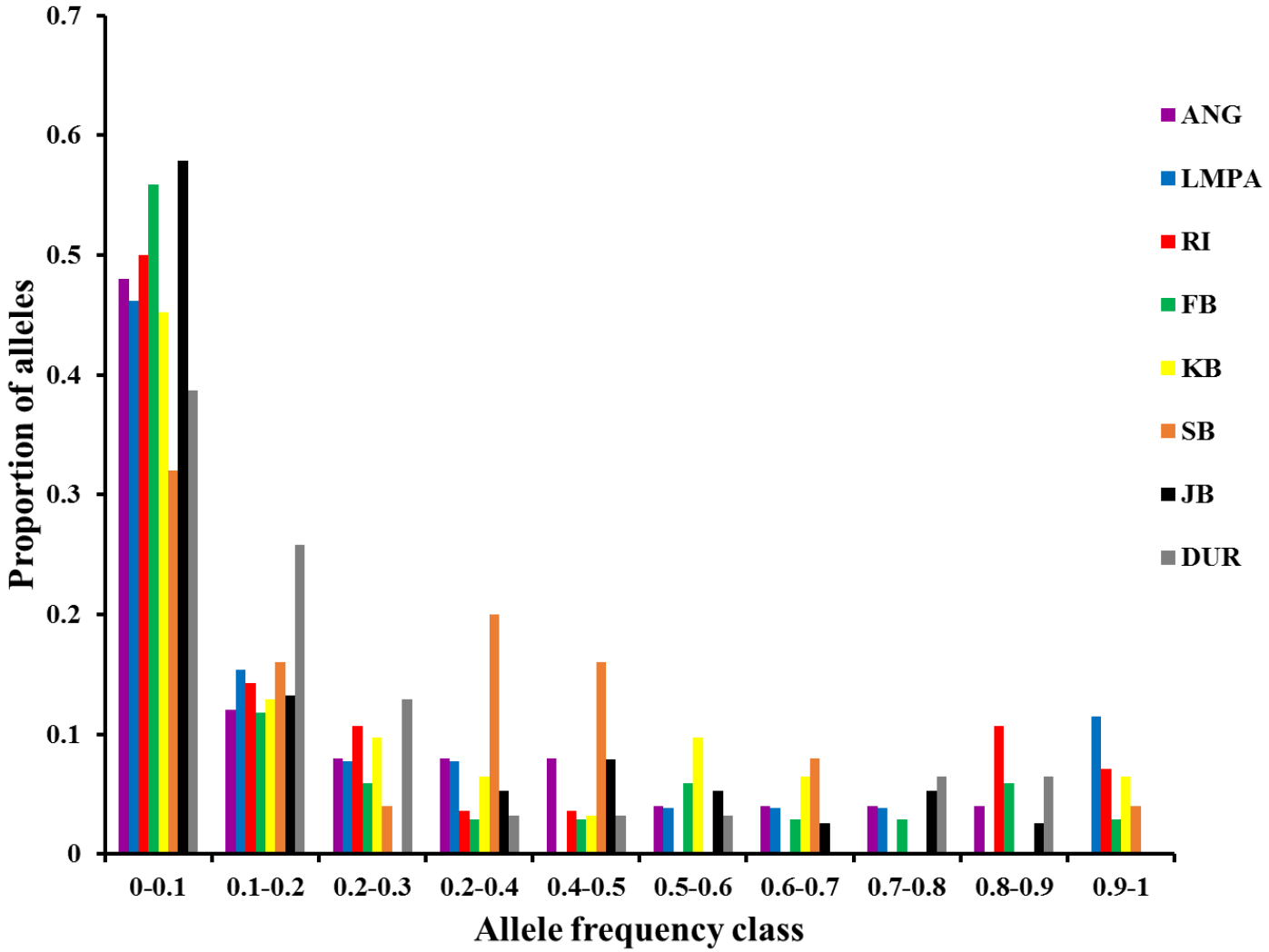

Fig. S3. Allele frequency spectra of *Mustelus mustelus* populations in southern Africa showing normal L-shaped distribution and absence of recent genetic bottleneck.