The following supplement accompanies the article

Population genetic structure of *Lepidonotothen larseni* revisited: *cyb* and microsatellites suggest limited connectivity in the Southern Ocean

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We here present additional data not included in the main text: exact sampling locations of specimen (Table S1), likelihood values for the $\log_{10}$ Bayes Factor model comparison used to identify the most likely subsitution rate for the Bayesian Skyline Plots (Table S2), locus-specific microsatellite properties (Table S3), and Ln P(D) values resulting from the Structure analyses used to infer the most likely number of clusters (Table S4).

We further present Bayesian Skyline Plots based on cytochrome *b* substitution rates of 0.02 and 0.04 substitutions/site/million years (Fig. S1) and a graphical output of the analyses conducted with the software Geneland (Fig. S2).

Table S1. Exact locations of *Lepidonotothen larseni* specimen sampled in the Atlantic sector of the Southern Ocean and analysed in this study. Data includes cruise, sampling location, depth and number of collected individuals (n)

Area	Cruise	Latitude	Longitude	Depth [m]	n
South Orkney Islands					
	U.S. AMLR 2009	60° 25.77’ S	46° 26.16’ W	142	2
	U.S. AMLR 2009	61° 9.38’ S	43° 32.66’ W	455	1
	ANT-XXVII/3 2011	61° 9.62’ S	44° 2.37’ W	354	7
	ANT-XXVII/3 2011	61° 10.61’ S	45° 41.91’ W	337	27
South Georgia Island					
	ANT-XXVII/3 2011	54° 24.47’ S	35° 36.95’ W	275	14
	ANT-XXVII/3 2011	54° 25.06’ S	35° 37.94’ W	279	25
Bouvet Island					
	ANT-XXVII/3 2011	54° 28.23’ S	3° 11.10’ E	250	25
	ANT-XXVII/3 2011	54° 28.84’ S	3° 11.33’ E	300	17

Table S2. Log_{10} Bayes Factor model comparison for Bayesian Skyline Plots based on cytochrome *b* gene sequences with substitution rates of 0.01, 0.02, 0.04 and 0.08 substitutions/site/myr. Chosen model indicated by an asterisk

Rate	Likelihood	S.E. (+/-)	0.01	0.02	0.04	0.08
0.01	-1243.593	0.181	-	-0.180	-0.394	-0.420
0.02	-1243.180	0.205	0.180	-	-0.214	-0.240
0.04	-1242.686	0.218	0.394	0.214	-	-0.026
0.08*	-1242.627	0.183	0.420	0.240	0.026	-

Table S3. Locus specific microsatellite properties based on 115 *Lepidonotothen larseni* specimen collected at South Orkney Islands (35 individuals), South Georgia Island (39 ind.) and Bouvet Island (41 ind.). N_A=number of alleles, A_R=allelic richness standardized to the smallest sample size (35 ind.)

	Trne20	***Trne35***	***Trne37***	***Trne53***	***Trne55***	***Trne66***
Size Range (bp)	185-267	210-294	128-148	312-364	174-208	291-373
N_A	30	35	8	26	5	30
A_R	21.5	23.7	6.9	19.3	2.8	18.1

Table S4. STRUCTURE results for *Lepidonotothen larseni*. Reported are the mean Ln P(D) values (SD) and Delta *K* of 20 runs for *K*=1-4. Locprior=including information about sampling site. Highest Delta *K* values in **bold**

Parameter Set	***K***			
	1	**2**	**3**	**4**
Normal				
Ln P(D)	-3058.48 (0.73)	-3181.12 (61.77)	-3180.64 (62.29)	-3299.79 (93.29)
Delta *K*	NA	**1.99**	1.92	NA
Locprior				
Ln P(D)	-3058.54 (0.56)	-3023.13 (7.91)	-3077.86 (61.25)	-3091.81 (54.29)
Delta *K*	NA	**11.40**	0.67	NA

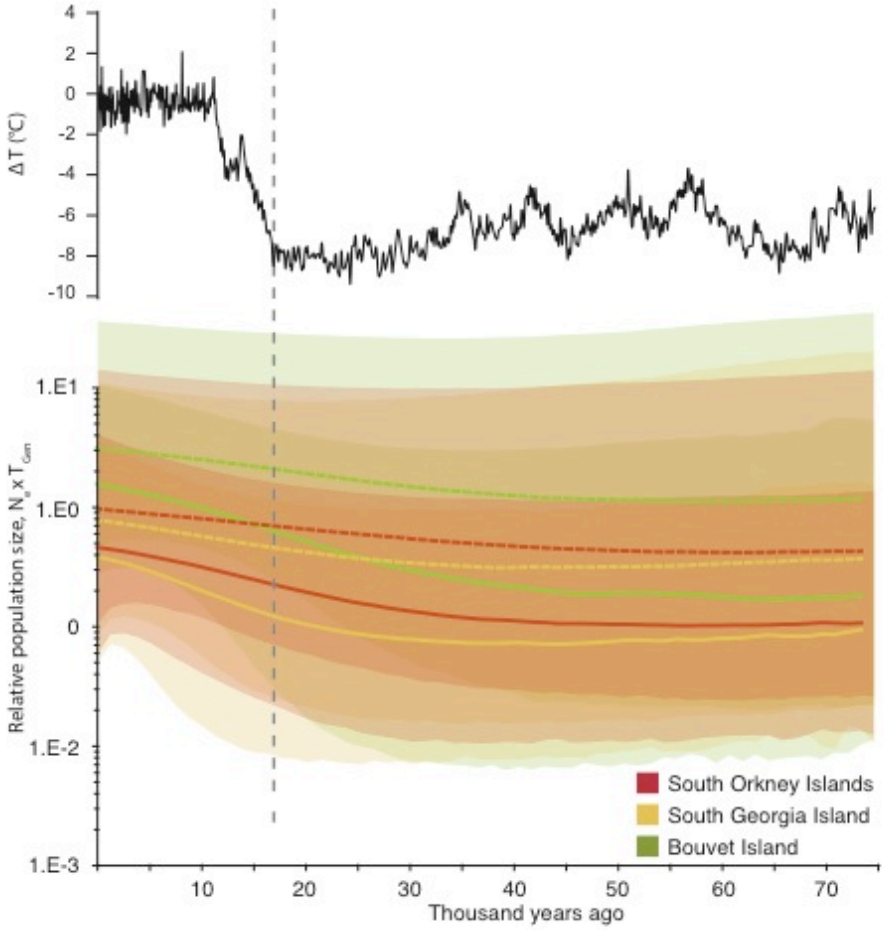

Fig. S1. Bayesian Skyline Plots of *Lepidonotothen larseni* populations reconstructed from substitution rates of 0.02 (dashed lines) and 0.04 (solid lines) substitutions/site/myr. Upper plot shows the temperature changes according to Petit et al. (1999). For additional information refer to Fig. 3 in the main text

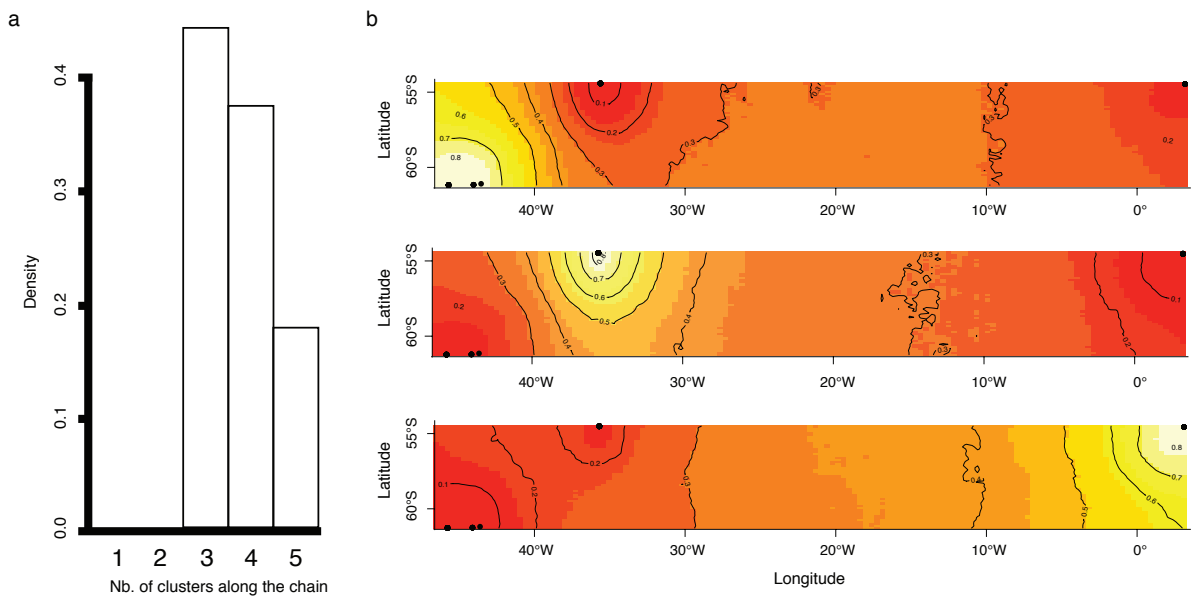

Fig. S2. GENELAND analyses for *Lepidonotothen larseni* based on microsatellite data with *K* varying from 1-5. Shown are (a) the inferred number of clusters along the chain for the run with the highest posterior probability and (b) spatial assignment probabilites for belonging to one of the identified clusters. The probabilities of cluster memberships increase from red to light-yellow. Black dots represent sampling localities. Maps for cluster 4 and 5 are not shown due to spatial homogeneities

LITERATURE CITED

Petit JR, Jouzel J, Raynaud D, Barkov NI and others (1999) Climate and atmospheric history of the past 420000 years from the Vostok ice core, Antarctica. Nature 399:429–436