

## Supplementary Tables

**Table S1.** Summary of the microsatellite loci used in this study, including literature sources and polymorphism characteristics for 83 Antarctic fur seals.

Locus	Reference	Multiplex	Number of alleles	Allelic size range (bp)	$H_o$	$H_e$
Aa4	<a href="#">Gemmell et al. (1997)</a>	1	6	204–218	0.767	0.749
Pv9	<a href="#">Allen et al. (1995)</a>	1	10	162–184	0.732	0.766
Hg6.3	<a href="#">Allen et al. (1995)</a>	1	11	215–245	0.866	0.851
Hg8.10	<a href="#">Allen et al. (1995)</a>	1	3	162–166	0.543	0.480
Hg1.3	<a href="#">Gemmell et al. (1997)</a>	1	10	234–266	0.864	0.867
M11a	<a href="#">Hoelzel et al. (1999)</a>	1	15	148–182	0.983	0.896
PvcA	<a href="#">Coltman et al. (1996)</a>	1	9	137–159	0.852	0.834
Zcwb07	<a href="#">Hoffman et al. (2007)</a>	1	11	180–200	0.756	0.858
Agaz2	<a href="#">Hoffman (2009)</a>	1	10	220–246	0.779	0.836
Ag3	<a href="#">Hoffman et al. (2008)</a>	2	2	147–149	0.291	0.315
Agaz6	<a href="#">Hoffman (2009)</a>	2	4	174–180	0.696	0.658
OrrFCB7	<a href="#">Buchanan et al. (1998)</a>	2	10	194–216	0.859	0.849
PvcE	<a href="#">Coltman et al. (1996)</a>	2	13	94–144	0.875	0.852
Ag2	<a href="#">Hoffman et al. (2008)</a>	2	7	212–236	0.756	0.767
OrrFCB2	<a href="#">Buchanan et al. (1998)</a>	2	13	108–136	0.772	0.866
Lw10	<a href="#">Davis et al. (2002)</a>	2	17	100–140	0.866	0.905
Zcwc01	<a href="#">Hoffman et al. (2007)</a>	2	13	131–163	0.897	0.849
Agaz5	<a href="#">Hoffman, (2009)</a>	2	4	192–198	0.487	0.622
ZcwCgDhB.14	<a href="#">Hernandez-Velazquez et al. (2005)</a>	2	6	230–258	0.810	0.784
SSL_301	<a href="#">Huebinger et al. (2007)</a>	3	14	258–286	0.924	0.883
Ag7	<a href="#">Hoffman et al. (2008)</a>	3	7	119–137	0.785	0.784
Agt10	<a href="#">Hoffman et al. (2008)</a>	3	4	211–217	0.342	0.326
ZcwCgDh4.7	<a href="#">Hernandez-Velazquez et al. (2005)</a>	3	13	250–276	0.859	0.881
Zcwe05	Unpublished	3	9	186–202	0.620	0.720
Ag1	<a href="#">Hoffman et al. (2008)</a>	3	11	101–123	0.861	0.873
OrrFCB8	<a href="#">Buchanan et al. (1998)</a>	3	8	172–202	0.705	0.778
Agt47	<a href="#">Hoffman and Nichols (2011)</a>	3	4	237–249	0.646	0.610

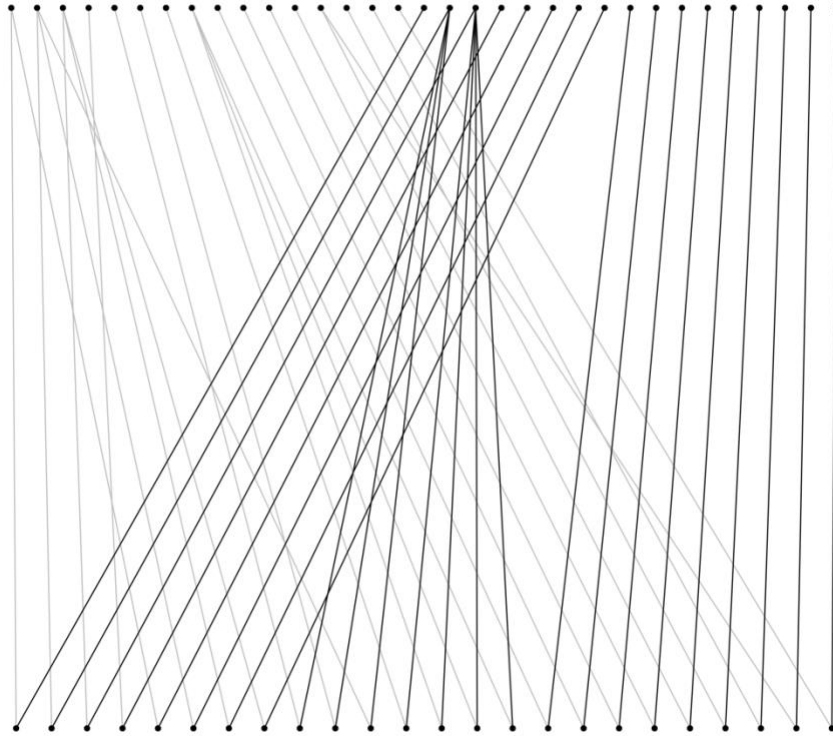
**Table S2.** Summary of the primer sequences used that successfully amplified 40 RAD derived SNP loci, including SNP genotype, primer sequence length, product sequence length and PCR melting temperature ( $T_m$ ).

Primer ID	SNP	Forward Primer	Reverse Primer	Forward Primer Length	Reverse Primer Length	Product Length	$T_m$
1_RAD	A/G	TGATGTCCTGTCACCTCTGG	AGCTCCTGAAAGTCCCTCGT	20	20	171	59-60
2_RAD	C/T	AACGTGCACCTATGGAGGAG	TTTAGCCACGTACCCCAGAC	20	20	151	59-60
3_RAD	C/T	CAGAAAGCAGCTGGGTGATTA	TTCCCCTGCTTTTCAAGCTA	21	20	176	59-60
4_RAD	G/T	TGCCCTTCCCTTTCTTATC	GTTCCAGGGTGTGGGCAGA	20	18	162	60
5_RAD	A/G	TTTGGTGGGCACATCCTC	AGGGACCCTTTGTGTCAGG	18	19	163	59-60
6_RAD	C/T	AAACCTGCAGGAACCGAGTA	CCCCCTCACCTTACAATCT	20	20	160	59-60
7_RAD	A/G	AAGGAAAATCAGGGTCAGCA	CCTGTCCACAGACATTGCTC	20	20	158	59
8_RAD	G/T	CTGGACGGGGTCCTTAGTCT	CTCGCCCCACAGACTTACA	20	19	201	59-60
9_RAD	C/T	TGCTGTTCTGTGACCTTGA	GGGACCCTCCTTCTAAATGC	20	20	178	59-60
10_RAD	A/G	AGGGCTGGCTGTATTGACC	AGACATTGGATCTGGCCTCA	19	20	154	60
11_RAD	A/G	CAGTCCAGCCGATAGGATA	TCTGCAGGAAGTCTGGTCCT	20	20	166	59-60
12_RAD	C/T	ACCATCCCCATTTACAGAC	GTCCGCGTTCTCCTACCTC	20	19	177	59
13_RAD	A/G	ATCTAACCAAAGAGGAATGGTCA	TGAGAGAGACATTTTCCCACCT	23	22	150	59-60
14_RAD	A/C	CCCATTTGTGTGATGATGGA	CAACTGGGGCTAGGAAGACA	20	20	162	60
15_RAD	C/T	TGTATGAGCACATAGAAATGACCA	TCAGTGCTTGTAGACGACTTGAG	24	23	151	59
16_RAD	A/G	TTCCTGATCTTAGGGAGAAAGC	AAAAATGCCTGAAAAGCAATAA	22	22	114	58
17_RAD	A/G	TTTCTTTTACTGTGGGTTGC	GCTAATCTACTCCATGGTACTGATGC	21	26	150	60-61
18_RAD	A/G	CGCATACTTGACGTGACCTG	CCCGTGGAACATAAATCACC	20	20	163	60
19_RAD	A/G	CAGCTTTGGAGGAGTGTGAA	CTCCTGAGGTGGGGTGTG	20	18	163	59-60
20_RAD	C/T	GCTTGCCCTCCTAGCAATTT	CCCACCTTCACAAATCCAAG	20	20	187	58-60
21_RAD	A/G	ATTCCCGAGCATCCAGGTAG	CCCCAGGGATCATGGATTA	20	19	184	60-61
22_RAD	C/T	CCTTCCTGTCCACCTCTTCA	ACAATGGCCAACCTCACTTC	20	20	151	59-60
23_RAD	A/G	CACAGTTCATGGACCCAAAA	CCCTGCAGGAACCTTGTTAT	20	20	119	59
24_RAD	C/G	TGGCATATAGGGAGCTTTGG	GCATGCATTTCTTCACATCC	20	20	183	59-60
25_RAD	A/C	AGGGAATCCCAGAAGAGGAA	TTTGTATGGTGGTTTATTATGTG	20	25	174	59-60
26_RAD	C/T	CAGGAGAAGGGTGGAGACAG	CCATCTTTGAAGGAGGGACA	20	20	158	59-60
27_RAD	C/T	CCAATCTTCCAAGCCTCAAA	CCCCTGACCTCTGCATCAT	20	20	150	60
28_RAD	A/G	ATGTGACCACAGGCCAGTCT	CCACATGGAAAGGCTGACT	20	19	152	58-60
29_RAD	C/T	TGAAAATACAAAAATGCCAATAGC	GCCCTCTTATAAATGAGGCTGA	24	22	157	59
30_RAD	C/T	GGGCAACAAGAAATTGAGTCG	ATTTCTGGTGGGAGGTCATTT	20	20	155	60
31_RAD	A/G	AGTCACCCAAAACGGTCATC	CCAATTTTCATCTTGTGGAAG	20	21	172	57-59
32_RAD	A/G	TCGAGACAGTAAGTGGTTATCAGG	TGTGAAAATGATACCGCCACT	24	21	161	59-60

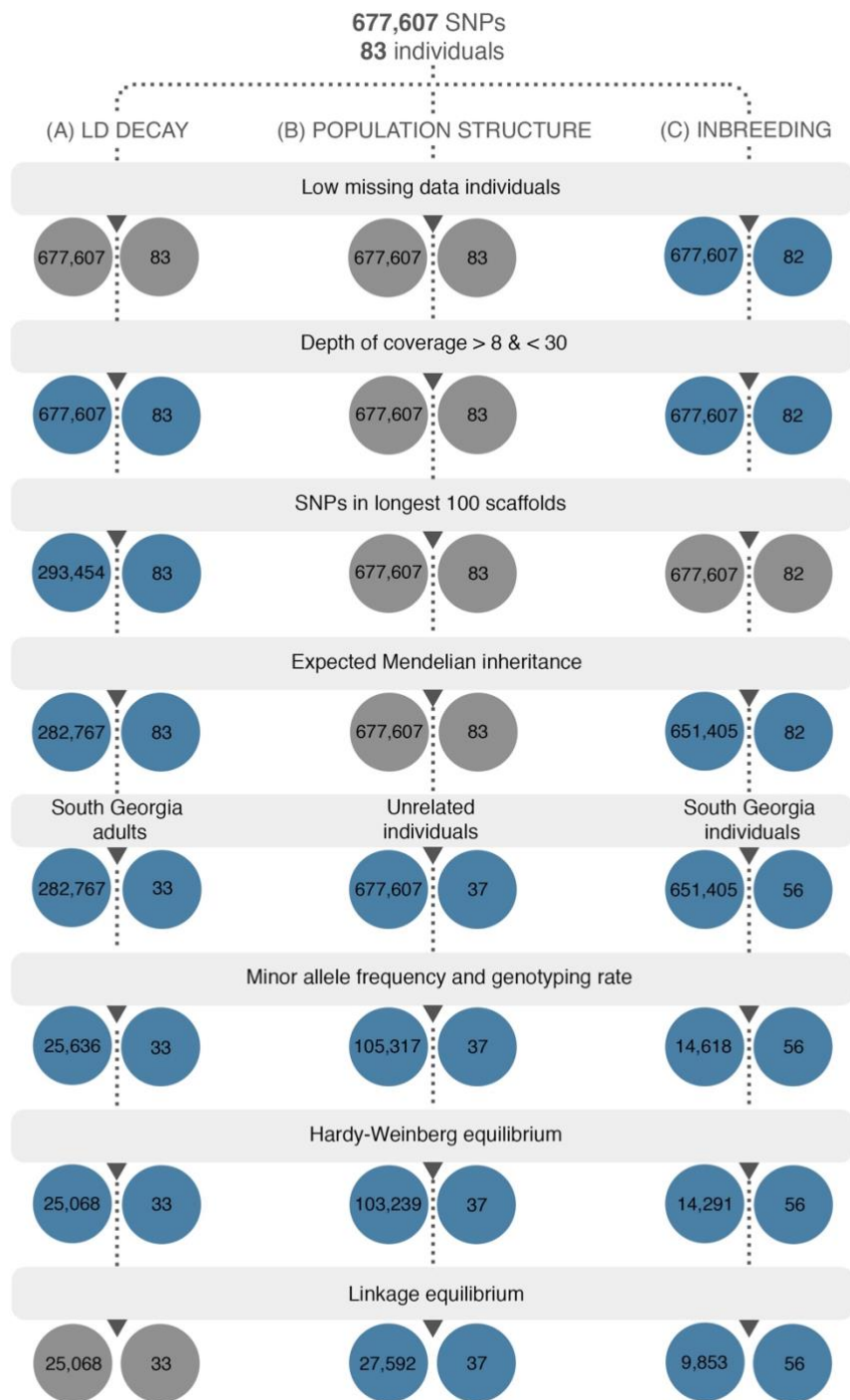
33_RAD	G/T	GGGTCAGGAAAAGTGGCTCT	CCACTGCCCATCACTCGTAT	20	20	154	60
34_RAD	C/T	ATTTAGTTCCAAACCCACCCACT	AACAGTCCAGGTGGGAGGTC	23	20	150	61
35_RAD	A/G	GCACCTTTACCATCCCAGAA	CGAGGAGAAACAAGGTCAGG	20	20	150	59
36_RAD	C/T	TGTATGACTATTCATGTCACTG	CTCATGACCTGAGCCAAAGG	24	20	150	58-60
37_RAD	C/T	GGCTAACTTCTTCTGTCAATCA	CAAGGAAACAAGTGAGCAAGG	23	21	152	59
38_RAD	A/G	AAAGACTTAACAAAGTGCCAGGTT	TTTCGCAGTGGCTAATCACA	24	20	153	59-60
39_RAD	G/T	TGCCTTATCTGGGAGAGAGG	GGAGGTGAAGGCAAATCAAA	20	20	182	59-60
40_RAD	C/T	CACAGGGTCAGCAGTGGTC	TTTTTGACCATGGATTATTCAGA	19	23	151	58-60

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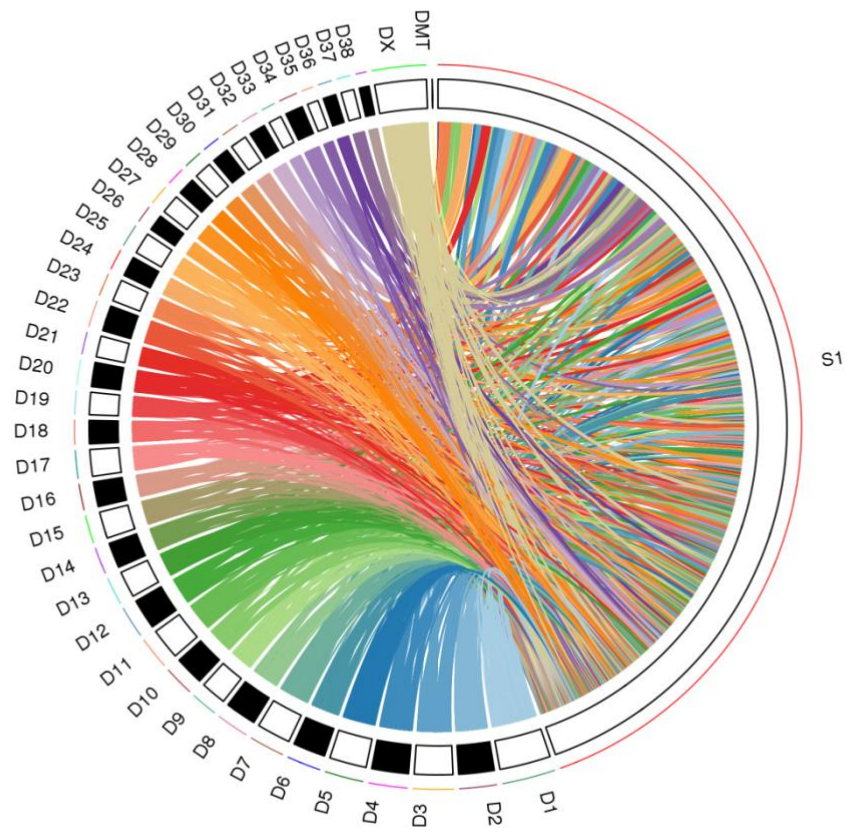
## Supplementary Figures



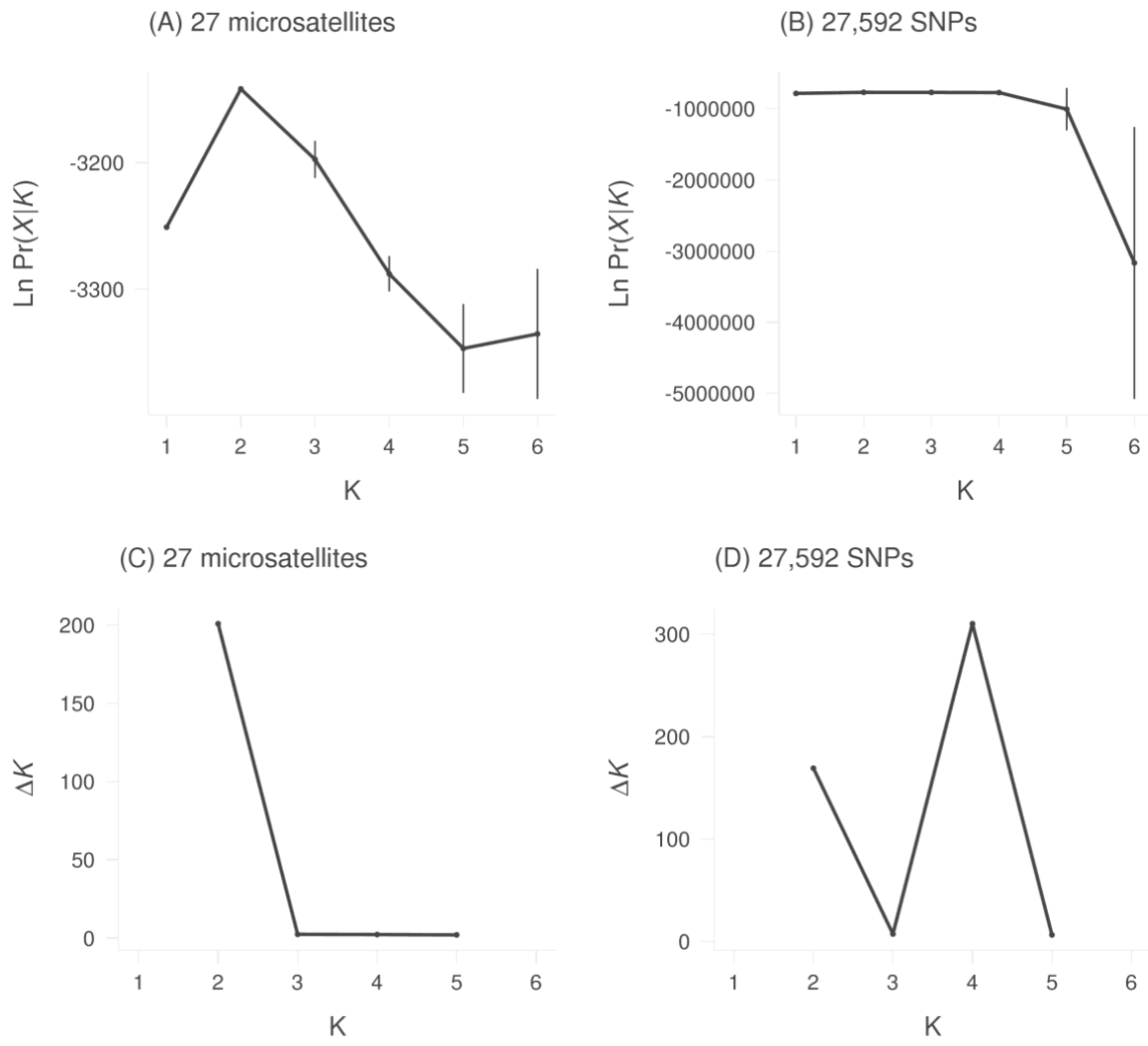
**Figure S1.** Graphical representation of the family structure of the 24 Antarctic fur seal triads from South Georgia. Maternities are represented by grey lines and paternities are represented by black lines.



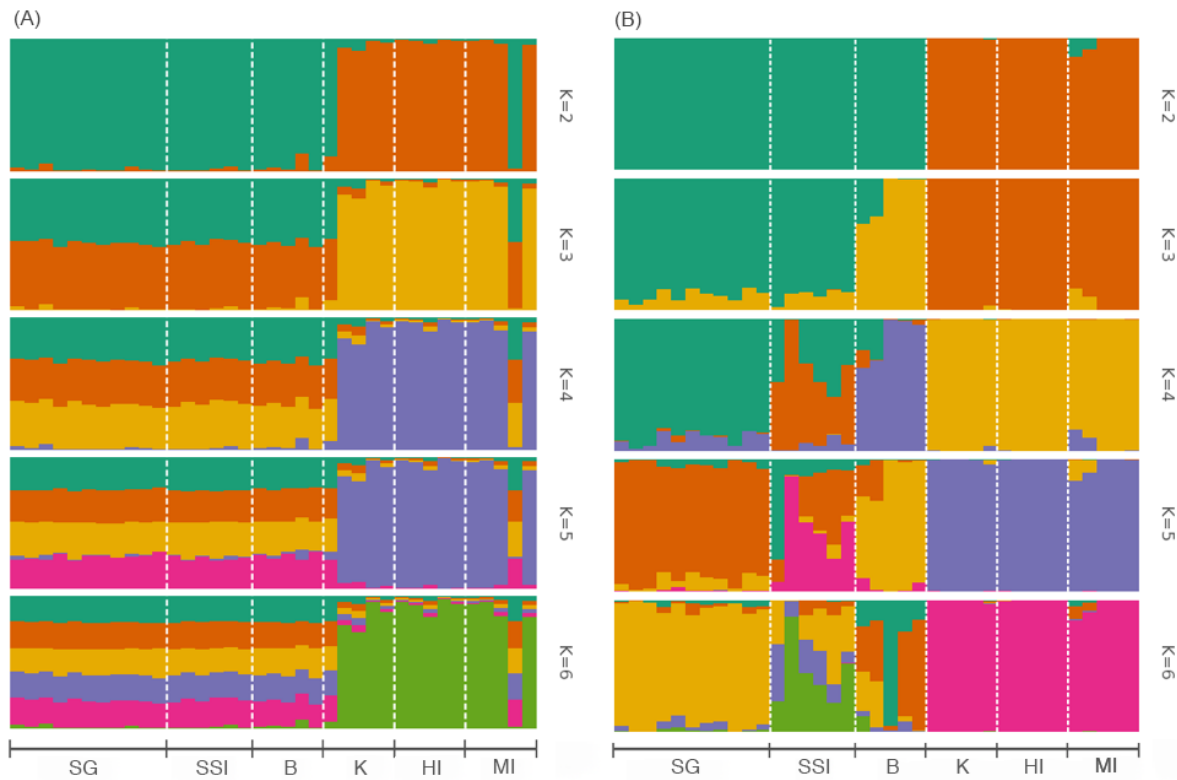
**Figure S2.** Flow diagram showing the number of SNPs (left hand circle) and the number of individuals (right hand circle) remaining after each step of the SNP filtering pipeline for the analysis of (A) LD decay; (B) population structure; and (C) inbreeding. Circles are coloured blue if a filtering step was applied and are coloured grey if it was not.



**Figure S3.** Synteny of the Antarctic fur seal scaffolds (right, prefixed S) with dog chromosomes (left, prefixed D). Alignment blocks were concatenated in the Antarctic fur seal to improve visualisation (S1). Mapping each fur seal scaffold to the dog genome resulted in multiple alignment blocks (mean = 2.1 kb, range = 0.1–52.8 kb) and alignments over 5 kb are shown.



**Figure S4.**  $\text{Ln Pr}(X | K)$  and Delta K values with standard errors calculated for 5 replicate runs of STRUCTURE for  $K = 1$  to  $K = 6$  using 27 microsatellites (panels A and C) and 27,592 SNPs (panels B and D).



**Figure S5.** Individual assignment to genetic clusters based on STRUCTURE analysis for  $K = 2$  to  $K = 6$  using (A) 27 microsatellites; and (B) 27,592 SNPs. Each vertical bar represents a different individual and the relative proportions of the different colours indicate the probabilities of belonging to each group. Individuals are separated by sampling locations. SG = South Georgia, SSI = South Shetland Islands, B = Bouvetøya, K = Kerguelen, HI = Heard Island and MI = Macquarie Island.