Friesen *et al.*, Appendix 1

a) *M. capensis*

CATTCAA**T**TA TAACCCATAT CATACATTA**A** CTTTTTTCCT AGTTTGATAA (50)

CT**G**AATTTAT GG**A**TTAAACA CAT**A**GAAATA C**T**ATCGGATA A**T**ACCAAA**C**T (100)

T**T**A**T**CC**T**CT**G** A**CC**AACCAA**A** C**C**A**C**T**G**TAAA TGAAATG**CC**C TACCA**A**CAG**C** (150)

TAC**T**C**T**TTTG **GC**CTCGA**A**CC **C**A**A**ACCATCC TAGA**A**TAAA**T** AA**C**CTGTAC**T** (200)

TT**A**ATATCTT TAATG**A**TACG GCAGTGCTGT AG**CA**TACTAA CC**C**CTGAATG (250)

GTTACTCGAC ATAC**T**CTCTC AACAA**T**TCTC GAAGTACCGG TTTCTGAAGT (300)

ATTAGGTTAT CTATTGATCG AGCTTCTCAC GTGAAATCAG CAACGCGCCG (350)

F BOX

CATAGAAGAT CCT**A**CGTTAC TAGCTTCAGG ACCATTCTTT CCCCCTACAC (400)

CCCTAGCAC**T** TCTTGCACTT TTGCGCCTCT GGTTCCTCGG TCAGGGCCAT (450)

D BOX

AACTTGATTA A**C**TCCTA**T**GT TTCTCACCTT TCACAGAGTC ATCTGGTTGG (500)

C BOX

CTATTGATCA TCAT**C**GTCTC TCTTAATCGC GTCACCTAAA CTT**C**TCCTCT (550)

TTTGGTTCTC TTTTTTTTTG GGCGTCTTCA CAGGTGACTT CTCCCAGTGC (600)

AGAGCGGAGA ACTTACAATC TAGGTCTGAA CATACACTGG TATGCGTCCG (650)

GGCCTCGCCG TC**A**AGAGTTG ATTA (674)

b) *M. serrator*

CATTCAACTA TAACCCATAT CATACATTAA CTTTTTTCCT AGTTTGATAA (50)

CTCAATTTAT GGATTAAACA CATAGAAATA CCATCGGATA A**T**AC**C**AAACT (100)

TTACCCTCTA AC**T**A**A**CCAA**A** CCATTATAAA TGAAATG**TT**C T**A**CCAAC**A**G**T** (150)

CAC**C**C**CT**TTG **A**CCTCGAACC CAAACCATCC TAGAATAAAT AA**T**CTGTACC (200)

TTAATATCTT TAATGATACG GCAGTGCTG**T** AGCATACTAA CCCCTGAATG (250)

GTTACTCGAC ATA**C**CCTCTC AACAA**C**TCTC GAAGTACCGG TTTCTGAAGT (300)

ATTAGGTTAT CTATTGATCG AGCTTCTCAC GTGAAATCAG CAACGCGCCG (350)

F BOX

CATAGAAGAT CCTACGTTAC TAGCTTCAGG ACCATTCTTT CCCCCTACAC (400)

CCCTAGCAC**T** **T**CTTGCACTT TTGCGCCTCT GGTTCCTCGG TCAGGGCCAT (450)

D BOX

AACTTGATTA ACTCCTATGT T**C**CTCAC**T**TT TCACAGAGTC ATCTGGTTGG (500)

C BOX

CTATTGATCA TCAT**T**GTCTC TCTTAATCGC GTCACCTAAA CTT**C**TCCTCT (550)

TTTGGTTCTC TTTTTTTTTG GGCGTCTTCA CAGGTGACTT CTCCCAGTGC (600)

AG**A**GCGGAGA ACTTACAATC TAGGTCTGAA CATACACTGG TATGCGTCCG (650)

GGCCTCGCCG TCAAGAGTTG ATTA (674)

c) *M. bassanus*

CATTCAATTA TAA**C**CCATAT TATACATTAA CTTT**T**TT**C**CT AG**T**TTGACAA (50)

TCTAATTTAT GG**A**TTAAACA CATA**GT**AA**C**A C**C**ATCGGATA ATAC**C**A**A**A**C**T (100)

TTATCC**C**CT**G** AC**C**AACCAA**A** CCA**T**TATAAA TGAA**A**TG**C**CC TACCAAC**A**G**C** (150)

TAC**T**C**T**TTTG **GT**CTCGAACC CAAACCATCC TAGAATAAAT AA**TC**TGTAC**T** (200)

TTA**A**TATCTT TAATGATACG GCAGTGCCGC GG**T**ATGCTA**A** CCC**C**TGAATG (250)

GTCGC**TC**GAC ATACACTCTC **A**ACA**AT**TCT**C** GAAGT**A**CCGG TTTCTGAAGT (300)

ATTAGGTTAT CTATTGATCG AGCTTCTCAC GTGAAATCAG CAACGC**G**CCG (350)

F BOX

CATAGAAGAT CCT**A**CGTTAC TAGCTTCAGG ACCATTCTTT CCCCCTACAC (400)

CCCTAGCAC**C** **T**CTTGCACTT TTGCGCCTCT GGTTCCTCGG TCAGGGCCAT (450)

D BOX

AACTTGATT**A** A**C**TCCTATGT T**C**CTCAC**T**TT TCACAGAGTC ATCTGGTTGG (500)

C BOX

CTATTGATCA TCAT**C**GTCTC TCTTAATCGC GTCACCTA**A**A CTT**T**TCCTCT (550)

TTTGGTTCTC T**T**TTTTTT**T**G GGCGTCTTCA CAGGTGACTT CTCCCAGTGC (600)

AG**A**GCGGAGA ACTTACAATC TAGGTCTGAA CATACACTGG TATGCGTCCG (650)

GGCCTCGCCG TC**AA**GAGTTG ATTA (674)

Fig. S1. Mitochondrial control region sequence examples for a) *M. capensis*, b) *M. serrator,* and c) *M. bassanus* individuals. Variable sites are bolded and underlined.

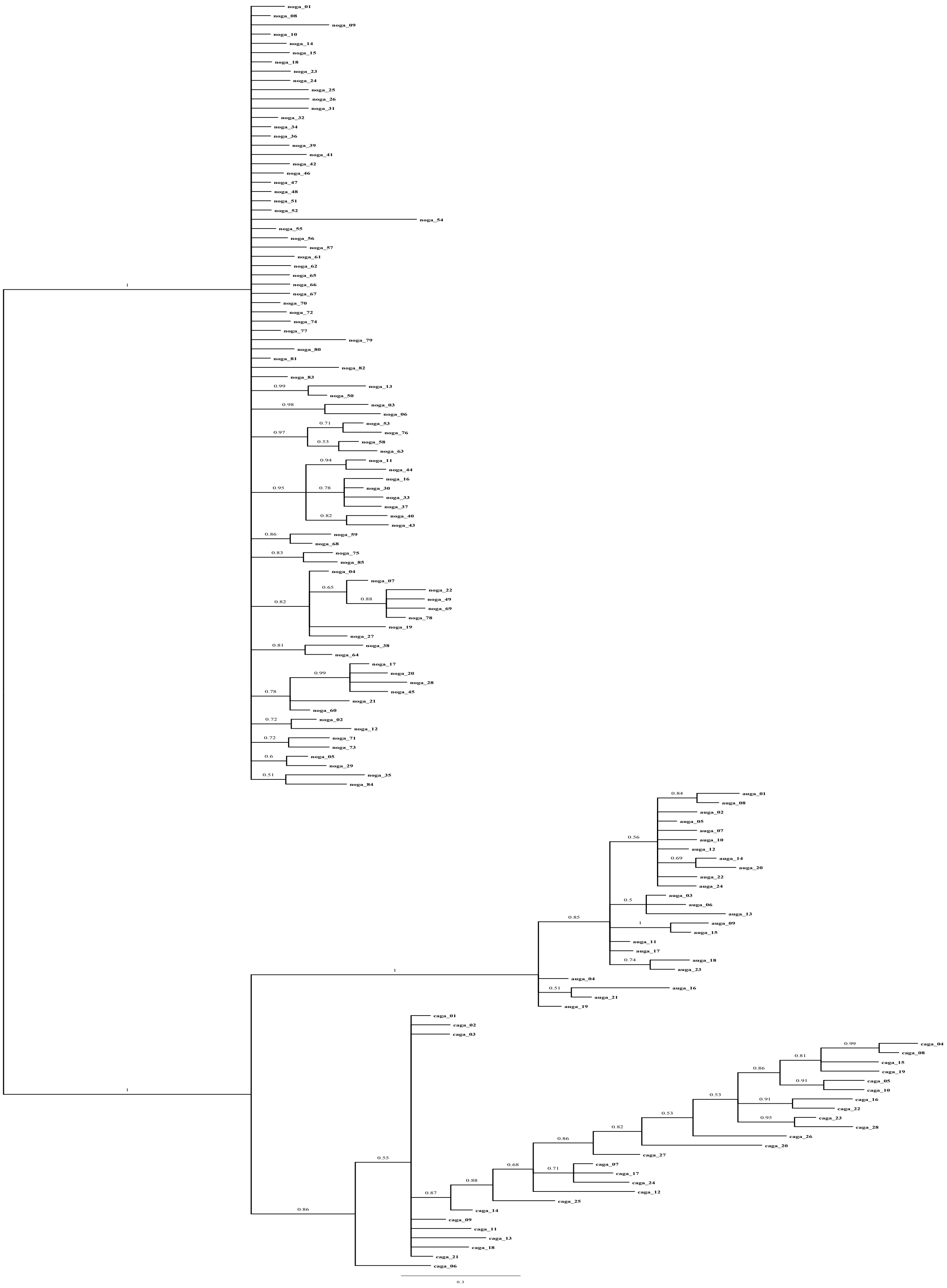


Fig. S2. Bayesian gene tree for control region haplotypes of gannets. Labels at branch tips are haplotype names, and numbers on branches are posterior probabilities.

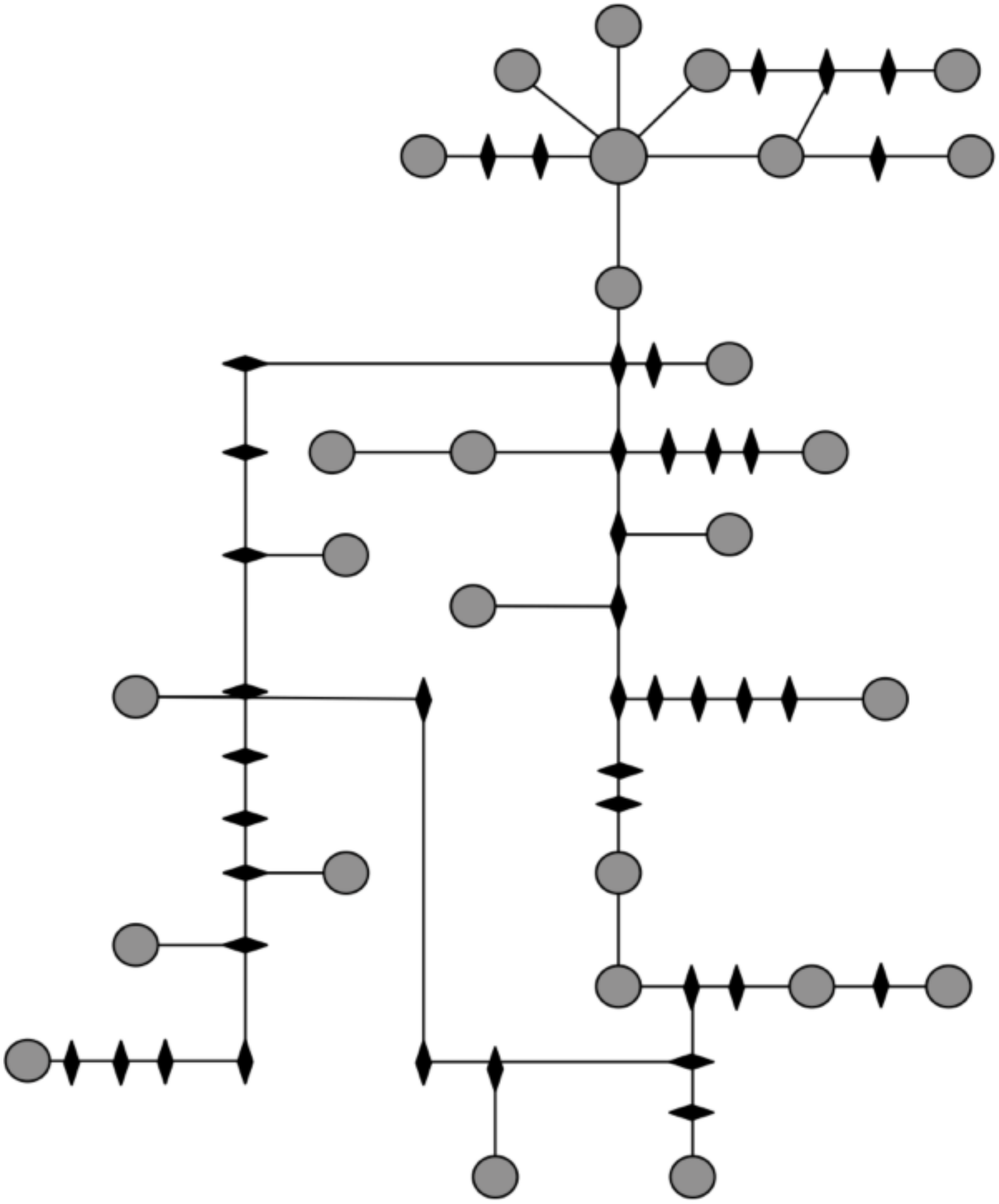


Fig. S3. Mitochondrial control region haplotype network for *M. capensis*. Each branch represents one mutational step and diamonds represents missing haplotypes.

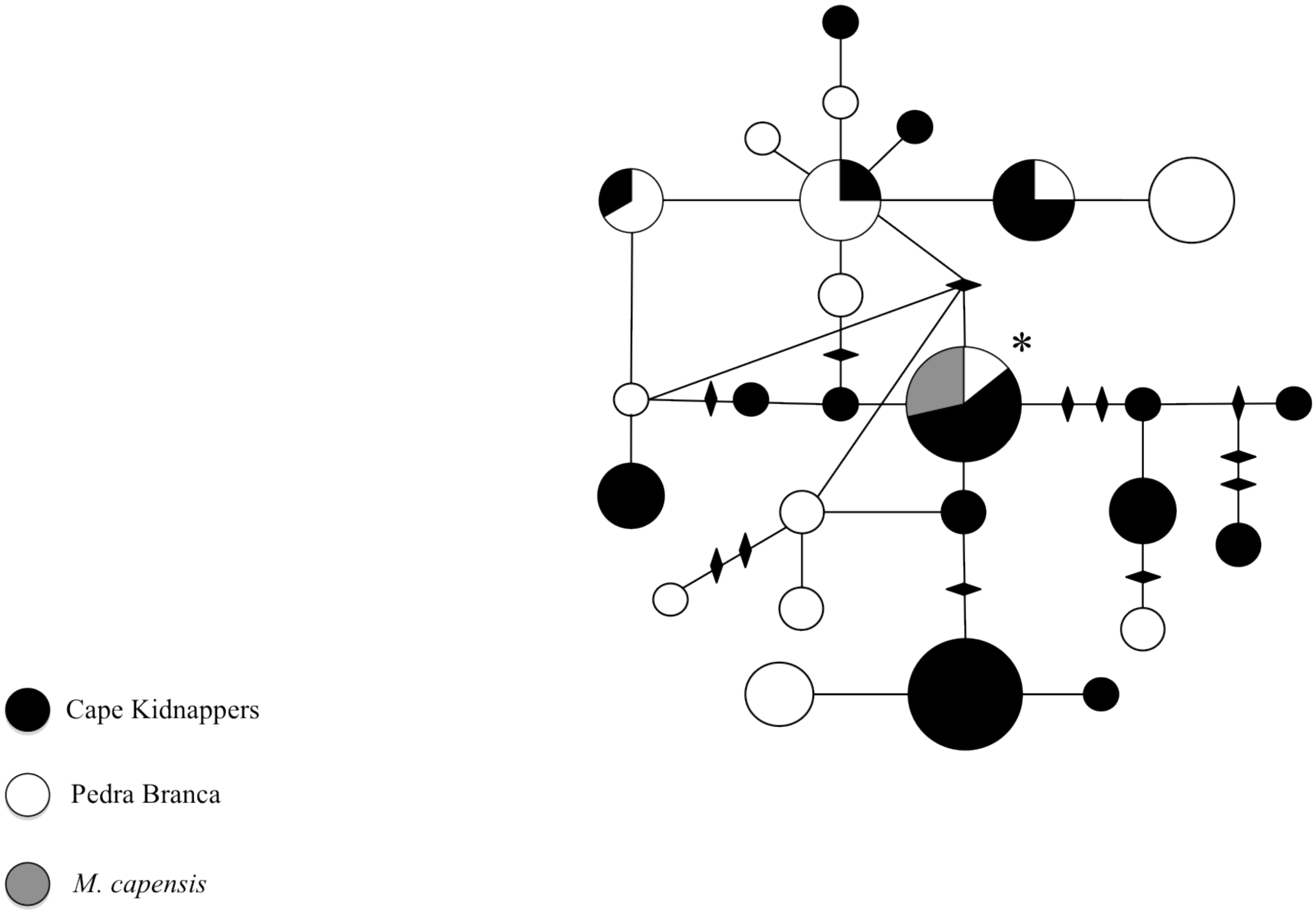


Fig. S4. Mitochondrial control region haplotype network for Australasian Gannets sampled in this study. *M. serrator*. Shades represent the population in with the haplotype is found, and circle size is proportional to the frequency of the haplotype in that population. Each branch represents one mutational step and diamonds represent missing haplotypes. The haplotype with the asterisk was found in two phenotypic Australasian Gannets sampled at Malgas Island, South Africa.

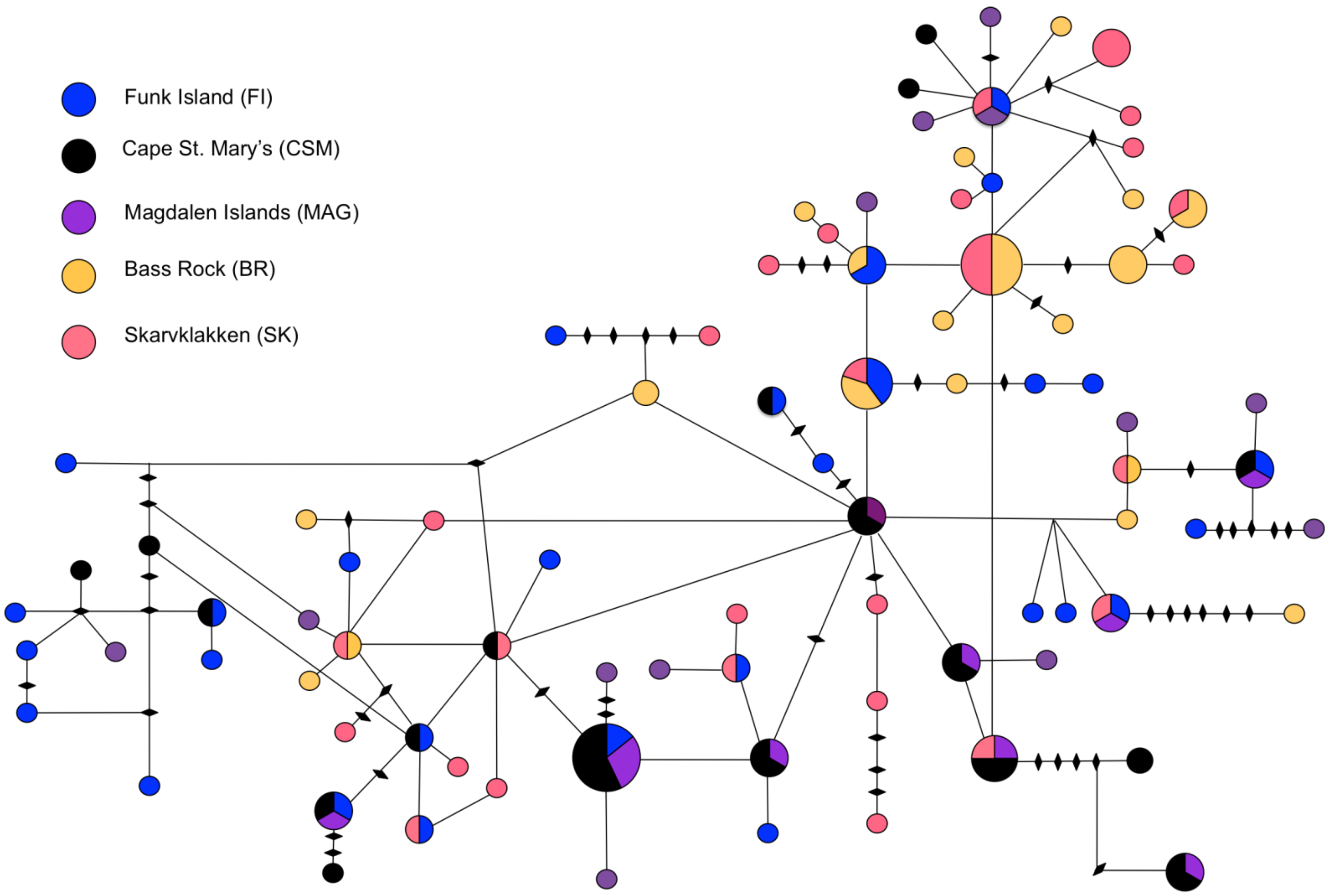
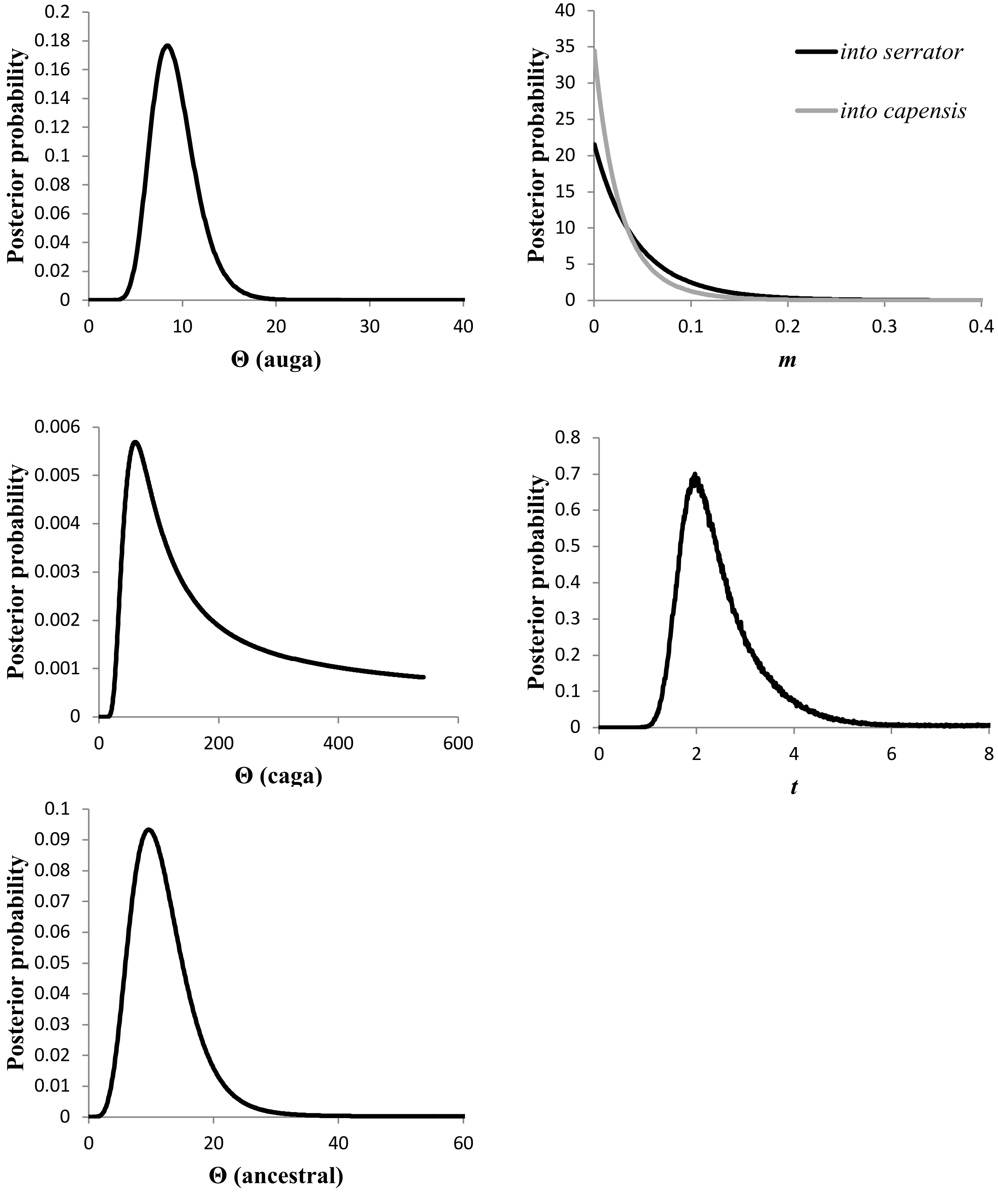


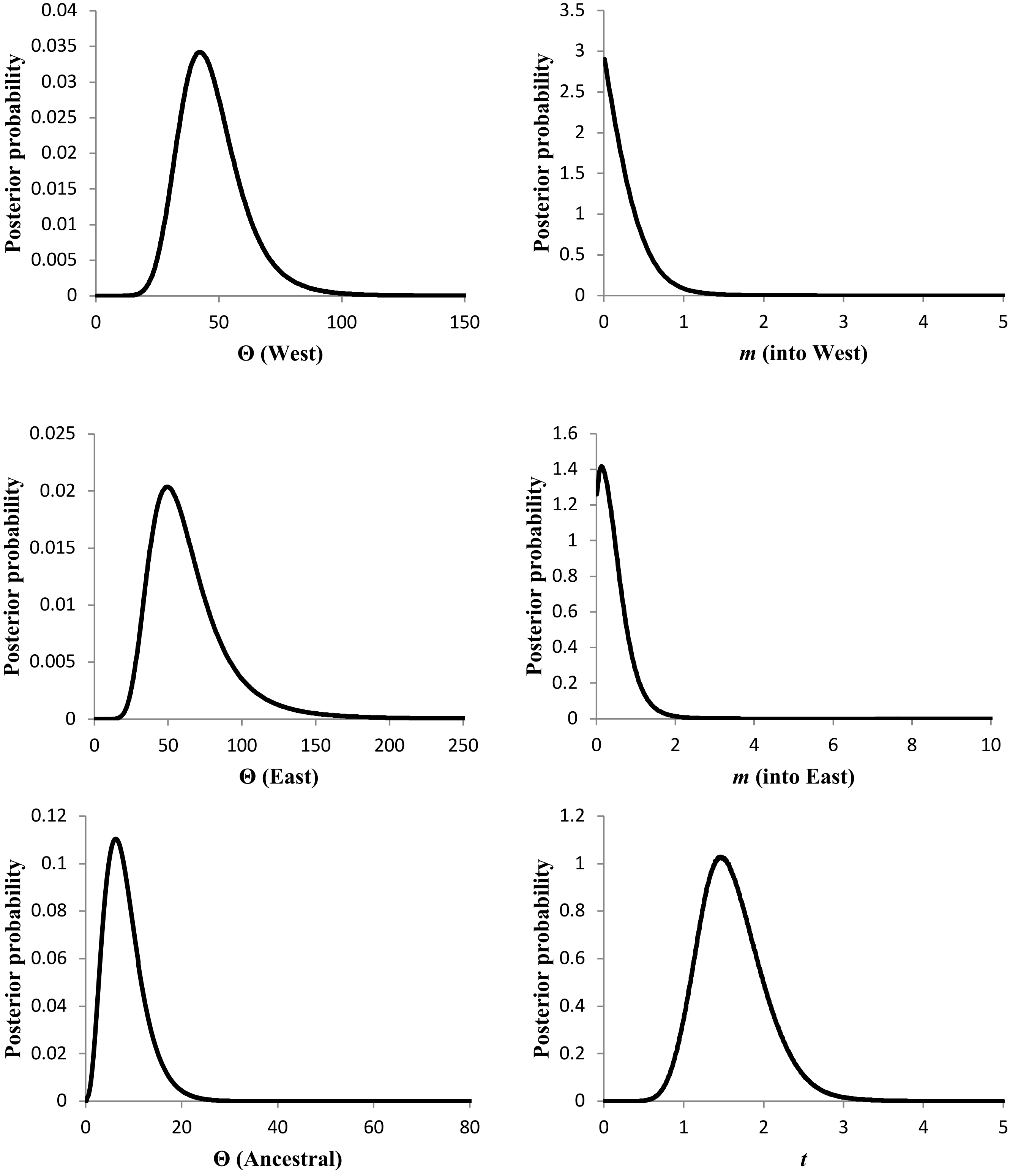
Fig. S5. Mitochondrial control region haplotype network for *M. bassanus*. Colours represent the population in with the haplotype is found, and circle size is proportional to the frequency of the haplotype in that population. Each branch represents one mutational step and diamonds represents missing haplotypes.

(a)



Posterior probability
0.2
0.18
0.16
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0
10
20
30
40
Θ (auga)
Posterior probability
40
35
30
25
20
15
10
5
0
0
0.1
0.2
0.3
0.4
m
into serrator
into capensis
Posterior probability
0.006
0.005
0.004
0.003
0.002
0.001
0
0
200
400
600
Θ (caga)
Posterior probability
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
0
2
4
6
8
t
Posterior probability
0.1
0.09
0.08
0.07
0.06
0.05
0.04
0.03
0.02
0.01
0
0
20
40
60
Θ (ancestral)

(b)


Posterior probability
0.04
0.035
0.03
0.025
0.02
0.015
0.01
0.005
0
0
50
100
150
Θ (West)
Posterior probability
3.5
3
2.5
2
1.5
1
0.5
0
0
1
2
3
4
5
m (into West)
Posterior probability
0.025
0.02
0.015
0.01
0.005
0
0
50
100
150
200
250
Θ (East)
Posterior probability
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
0
2
4
6
8
10
m (into East)
Posterior probability
0.12
0.1
0.08
0.06
0.04
0.02
0
0
20
40
60
80
Θ (Ancestral)
Posterior probability
1.2
1
0.8
0.6
0.4
0.2
0
0
1
2
3
4
5
t

(c)

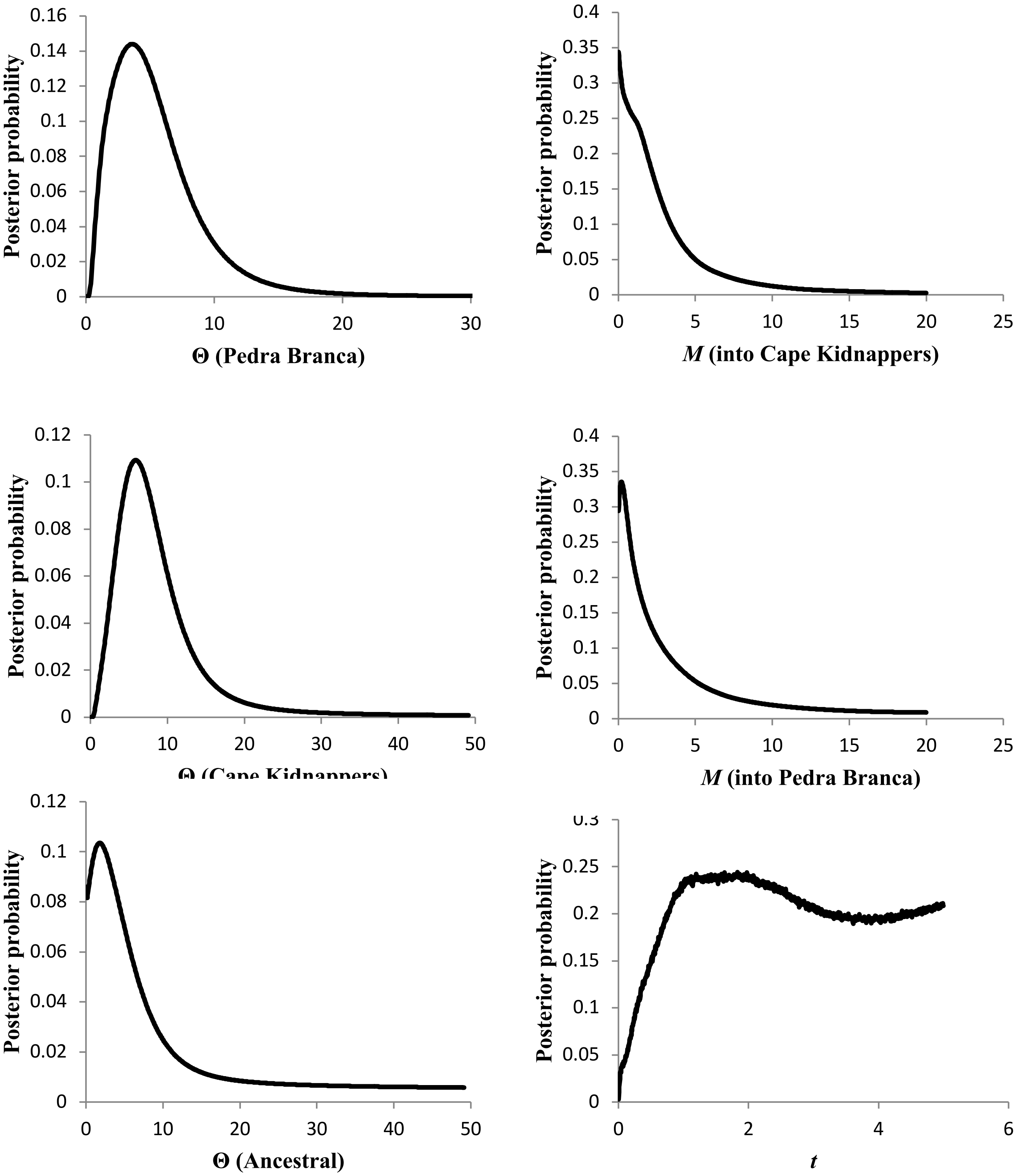


Fig. S6. Results of estimates of Θ, *t* and *m* from IMa for (a) Cape vs. Australasian gannets, (b) eastern vs. western Atlantic Northern Gannets, and (c) Australasian Gannets from Tasmania vs. New Zealand.

TABLE S1

Table of mitochondrial control region haplotype frequencies by population[a]

Haplotype	MAL	PED	CAK	FUN	MAG	BON	BAS	SKA	Total
caga-1	2								**2**
caga-2	1								**1**
caga-3	1								**1**
caga-4	1								**1**
caga-5	1								**1**
caga-6	1								**1**
caga-7	1								**1**
caga-8	1								**1**
caga-9	1								**1**
caga-10	1								**1**
caga-11	1								**1**
caga-12	1								**1**
caga-13	1								**1**
caga-14	1								**1**
caga-15	1								**1**
caga-16	1								**1**
caga-17	1								**1**
caga-18	1								**1**
caga-19	1								**1**
caga-20	1								**1**
caga-21	1								**1**
caga-22	1								**1**
caga-23	1								**1**
caga-24	1								**1**
caga-25	1								**1**
caga-26	1								**1**
caga-27	1								**1**
auga_PB-A		5							**5**
auga_PB-B		1							**1**
auga_PB-C		2							**2**
auga_PB-D		2							**2**
auga_PB-E		2							**2**
auga_PB-F		2							**2**
auga_PB-G		4							**4**
auga_PB-H		1							**1**
auga_PB-I		1							**1**
auga_PB-J		1							**1**
auga_CK-A			7						**7**
auga_CK-B			2						**2**
auga_CK-C			2						**2**
auga_CK-D			1						**1**
auga_CK-E			3						**3**
auga_CK-F			3						**3**
auga_CK-G			1						**1**
auga_CK-H			1						**1**
auga_CK-I			1						**1**
auga_CK-J			1						**1**
auga_CK-K			1						**1**
auga_CK-L			1						**1**
auga-A		3	1						**4**
auga-B		1	3						**4**
auga-C_caga	2	1	4						**4**
auga-D		2	1						**6**
noga_FI-A				1					**1**

noga_FI-B	1					**1**
noga_FI-C	1					**1**
noga_FI-D	1					**1**
noga_FI-E	1					**1**
noga_FI-F	1					**1**
noga_FI-G	1					**1**
noga_FI-H	1					**1**
noga_FI-I	1					**1**
noga_FI-J	1					**1**
noga_FI-K	1					**1**
noga_FI-L	1					**1**
noga_FI-M	1					**1**
noga_FI-N	1					**1**
noga_FI-O	1					**1**
noga_FI-P	1					**1**
noga_MAG-A		1				**1**
noga_MAG-B		1				**1**
noga_MAG-C		1				**1**
noga_MAG-D		1				**1**
noga_MAG-E		1				**1**
noga_MAG-F		1				**1**
noga_MAG-G		1				**1**
noga_MAG-H		1				**1**
noga_MAG-I		1				**1**
noga_MAG-J		1				**1**
noga_MAG-K		1				**1**
noga_MAG-L		1				**1**
noga_BON-A			2			**2**
noga_BON-B			1			**1**
noga_BON-C			1			**1**
noga_BON-D			1			**1**
noga_BON-E			1			**1**
noga_BON-F			1			**1**
noga_BON-G			1			**1**
noga_BR-A				1		**1**
noga_BR-B				3		**3**
noga_BR-C				1		**1**
noga_BR-D				2		**2**
noga_BR-E				1		**1**
noga_BR-F				1		**1**
noga_BR-G				1		**1**
noga_BR-H				1		**1**
noga_BR-I				1		**1**
noga_BR-J				1		**1**
noga_BR-K				1		**1**
noga_BR-L				1		**1**
noga_BR-M				1		**1**
noga_SK-A					1	**1**
noga_SK-B					1	**1**
noga_SK-C					3	**3**
noga_SK-D					1	**1**
noga_SK-E					1	**1**
noga_SK-F					1	**1**
noga_SK-G					1	**1**
noga_SK-H					1	**1**
noga_SK-I					1	**1**
noga_SK-J					1	**1**
noga_SK-K					1	**1**
noga_SK-L					1	**1**
noga_SK-M					1	**1**

noga_SK-N								1	**1**
noga_SK-O								1	**1**
noga-1				2			2	1	**5**
noga-2				2			1		**3**
noga-3				1	1	1			**3**
noga-4				1				1	**2**
noga-5				1		1			**2**
noga-6				1	1	1			**3**
noga-7				1			1	1	**3**
noga-8				1					**1**
noga-9				1	2	4			**7**
noga-10				1		1			**2**
noga-11				1				1	**2**
noga-12				1		1			**2**
noga-13				1	1			1	**3**
noga-14					1	2			**3**
noga-15					1	2			**3**
noga-16					1	2			**3**
noga-17					1	2			**3**
noga-18					1	2		1	**4**
noga-19						1		1	**2**
noga-20							3	3	**6**
noga-21							2	1	**3**
noga-22							1	1	**2**
noga-23							1	1	**2**
Total	**30**	**28**	**33**	**31**	**22**	**28**	**27**	**30**	**229**

[a] Population name abbreviations can be found in Table 2