

Novel mitochondrial haplotype of spotted-tailed quoll (*Dasyurus maculatus*) present on Kangaroo Island (South Australia) prior to extirpation

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Supplementary methods

Table S1 | Details of the primer sets designed to amplify a region of the D-loop from ancient *Dasyurus maculatus* specimens.

Region	Primer name	Sequence (5'-3')	Target product size (bp)	Insert size (bp)
1	Dasymac_CR_1-20_F	GCACAATTTAATTTAATC	162	118
	Dasymac_CR_139-163_R	GAATATAAATGTATGCTCTATATAC		
2	Dasymac_CR_93-114_F	CATACATTACATTTTACATGTA	165	123
	Dasymac_CR_238-257_R	TTAAGATATGAATGTACTGT		
3	Dasymac_CR_177-197_F	GCATGTACATATTAATCATAT	159	118
	Dasymac_CR_316-335_R	GTCTATGTACGCCAACATTA		
4	Dasymac_CR_238-257_F	ACAGTACATTCATATCTTAA	164	125
	Dasymac_CR_383-402_R	AGGTAATCCTAATGGTTGTG		
5	Dasymac_CR_316-335_F	TAATGTTGGCGTACATAGAC	116	77
	Dasymac_CR_413-431_R	GTTGCTGATCTCTCGTGAG		
6	Dasymac_CR_383-402_F	CACAACCATTAGGATTACCT	143	103
	Dasymac_CR_H16498M_R	CCTGAAGTAGCAACCAAGTAG		

Figure S1 (next page) | Published 471 bp region of the *Dasyurus maculatus* control region (Firestone et al. 1999): bases conserved with the consensus are marked by a dot. The primer sets designed to amplify six short, overlapping fragments of the D-loop (regions 1-6) are shown.

SI I Changes to the NEBNext Quick Ligation protocol

End-repair was performed using 30-36 µl of purified library (approximately 300-903 ng of input DNA). End-repaired DNA was purified using a QIAquick PCR purification kit (QIAGEN), as per the manufacturer's instructions and eluting in 32 µl of EB Buffer. A-tailing was performed using 32 µl of the purified, end-repaired library, and the reaction was incubated for 30 minutes at 37 °C. A-tailed DNA was purified using a QIAquick PCR purification kit, as per the manufacturer's instructions and eluting in 30 µl of EB Buffer. The concentration of the purified A-tailed library was quantified using the QIAxpert following the manufacturer's instructions. For ligation, the ratio of Nextera adapter to template used was 3:1, and the volume of adapter used was 4.46-5.04 µl of a 2.5 µM concentration ($1.116-1.26 \times 10^{11}$ moles) coupled with 28 µl of purified, A-tailed library (approximately 13.4-29.4 ng/µl or a total of $3.72-4.2 \times 10^{12}$ moles of DNA). The ligation reaction was incubated for 15 minutes at 20 °C. The final ligated library was purified using a QIAquick PCR purification kit, as per the manufacturer's instructions and eluting in 30 µl of EB Buffer.

Supplementary results

Table S2 | Taxa identified from the amplification of a barcoding region of the mitochondrial *12S rRNA* gene. The number in the parentheses represents the number of unique reads assigning to that taxon.

Sample	Taxonomic assignment
P16-102 (modern)	<i>Dasyurus maculatus</i> (38) <i>Dasyurus hallucatus</i> (1) <i>Dasyurus</i> (6) Dasyuridae (5) <i>Homo sapiens</i> (1) Camelidae (1)
No-template control	<i>Homo sapiens</i> (32)
MB3660	<i>Dasyurus maculatus</i> (27) <i>Dasyurus</i> (1) <i>Homo sapiens</i> (1) <i>Rattus</i> (5) Peramelemorphia (1)
MB3661	<i>Dasyurus maculatus</i> (23)
MB3662	<i>Dasyurus maculatus</i> (2) <i>Homo sapiens</i> (41) Muroidea (1)
MB3663	<i>Dasyurus maculatus</i> (2) Dasyuridae (3) <i>Homo sapiens</i> (23)
MB3664	<i>Homo sapiens</i> (26) <i>Rattus</i> (3)

Table S3 | The total number of paired reads obtained per primer set for each sample (left), followed by the number of unique, filtered reads (post quality control). Asterisks indicate only one replicate of two amplified. The table below shows which samples amplified a sequence variant with an 11-bp deletion in Region 1: the number on the left of the slash shows how many unique reads were obtained for each variant, and the number to the right of the slash shows the read abundance of each variant.

Sample	Region 1	Region 2	Region 3	Region 4	Region 5	Region 6
P16-102 (modern)	4221 / 1	8616 / 5	17724 / 1	5290 / 1	58438 / 1	48184 / 1
MB3660	297 / 13	17095 / 6	3530 / 1	7200 / 1	18499 / 1	58027 / 1
MB3661	35 / 1	5299 / 3	16836 / 2	8377 / 1	9672 / 1	33609 / 1
MB3662	13886 / 1	3627 / 6	1942 / 4	1923 / 3	22353 / 1	83338 / 1
MB3663	29 / 2	NA / NA	NA / NA	19404 / 6	86960 / 1	63382 / 2
MB3664	33 / 2	NA / NA	3998 / 7	7288 / 1	41526 / 13	27280 / 8
No-template control	NA / NA	27 / 1*	NA / NA	NA / NA	373 / 17	NA / NA

Sample	Deletion	No deletion
P16-102 (modern)	-	1 / 3302
MB3660	9 / 229	4 / 10
MB3661	1 / 30	-
MB3662	-	1 / 11582
MB3663	2 / 23	-
MB3664	1 / 24	1 / 2

Supplementary information

Table S4 | Bootstrap support values (%) for relationships of interest in phylogenetic trees generated using Neighbour-Joining, UPGMA, Maximum Evolution, and Maximum Likelihood methods coupled with various genetic distance models (Tamura-Nei, Jukes-Cantor, HKY) using 5000 bootstrap replicates to test the statistical significance of the evolutionary relationships inferred. Phylogenetic analyses were carried out using Geneious Tree Builder v10.0.5 as well as MEGA v6 (Tamura *et al.* 2011) (asterisks).

Tree type	Genetic distance model	Bootstrap support (%)		
		Tasmanian monophyly	KI monophyly	Tasmanian/KI monophyly
UPGMA	HKY	86	100	89
UPGMA	JC	86	100	89
UPGMA	TN	87	100	89
NJ	HKY	89	98	90
NJ	JC	90	98	90
NJ	TN	89	98	89
Maximum likelihood*	HKY	27 / 1*	NA / NA	NA / NA
Maximum likelihood*	JC			
Maximum likelihood*	TN			
Minimum evolution*	JC	90	98	90
Minimum evolution*	TN	89	97	89

Figure S2 (next page) | Complete alignment, no sites masked

Figure S3 (page 6-7) | **A** Alignment with sites masked, **B** Alignment with masked sites deleted (see Figure 3 in the manuscript for the tree generated from these alignments).

Figure S2 displays two panels of sequence alignments, labeled A and B, showing consensus sequences and individual sample sequences (AF082774_Dasyurus viverrinus, MB3660, MB3661, MB3662, MB3663, MB3664, P16_102_Positive_control) across various positions (20, 40, 60, 80, 100, 120, 140, 160, 180, 200).

Panel A: Shows consensus sequences and individual sample sequences. The consensus sequence is GCACAATTTTAAT-----TTTAAATCACAAAATTCATTTTATATGCTATCTCAGTATTAAATTTTT---TACAAAAATTTTCAC--AAAATTTTAAATTCAAAC-ATACATTACAT-TTTACATGTATAT-AATGTACAAAAATTATTATTATGTATATAGAGCATACATTTTATATTCCTCTATAATATAAGCATGT. The individual sample sequences are aligned below the consensus, with positions 20, 40, 60, 80, 100, 120, 140, 160, 180, and 200 marked.

Panel B: Shows consensus sequences and individual sample sequences. The consensus sequence is ACATATTAATCATATATTACTAAATACATTAATATAATATATTGTTATCATTTGACAGTACATTCATATCTTTAACTAATACTCATAATAGTACATAATAACATAATATGTATATATTACATAAGACATATAATGTTGGCGTACATAGACATTAAATCCATGGAACGAGATCAACAAGCTAATTCCTCTAGCAGAT. The individual sample sequences are aligned below the consensus, with positions 220, 240, 260, 280, 300, 320, 340, 360, 380, and 400 marked.

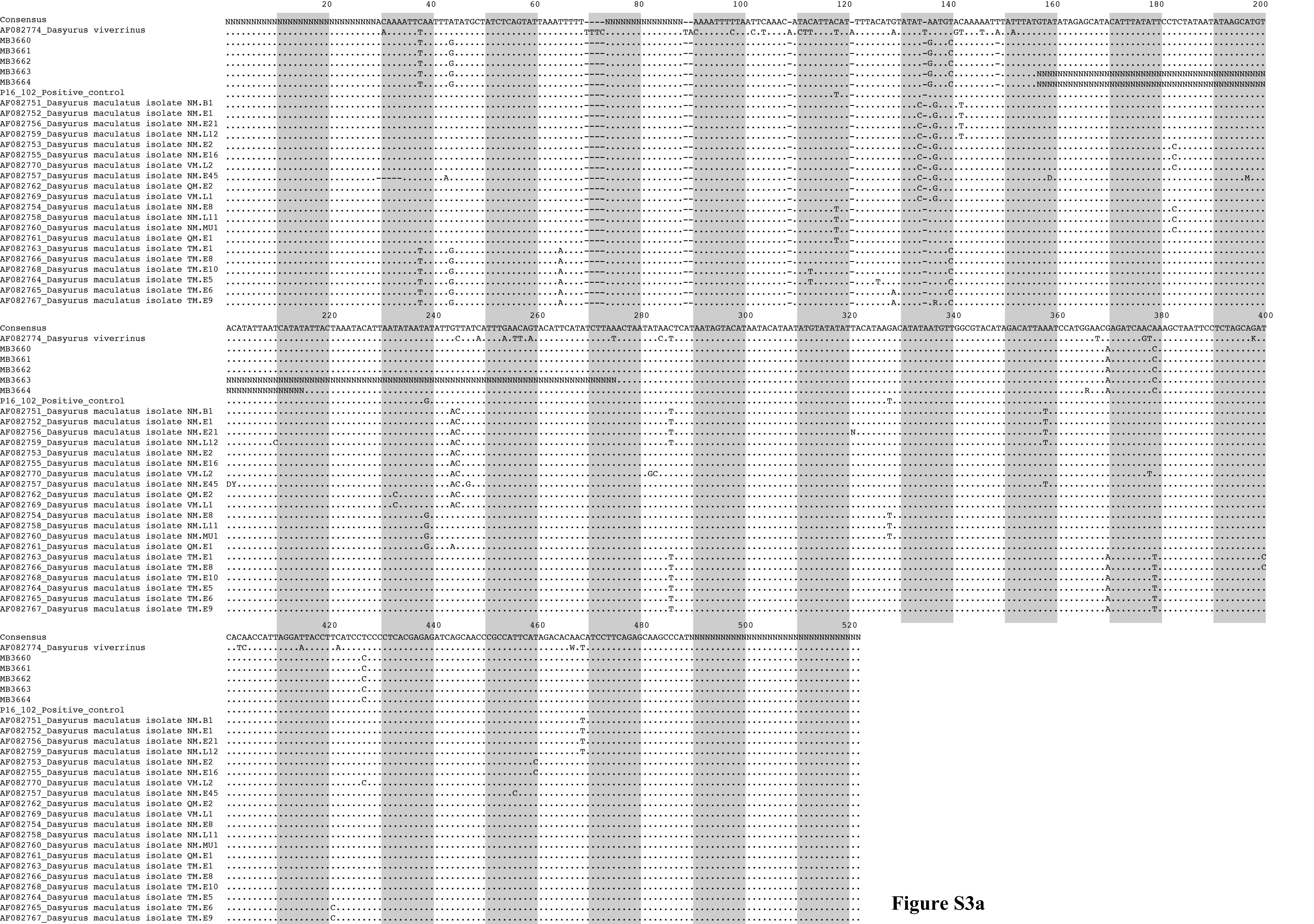


Figure S3a

				20	40	60	80	100	120	140	160	180	200
Consensus				ACAAAATTCATTTATATGCTATCTCAGTATTAATATTTT-----AAATTTTTTAATTCAAAC-ATACATTACAT-TTTACATGTATAT-AATGTACAAAAATTATTTATGTATATAGAGCATACATTTATATTCCCTCTATAATATAAGCATGTACATATTAAATCATATATTACTAAATACATTAATATAATATATTG									
AF082774_Dasyurus viverrinus				.A.....T.....TTTCTAC.....C...C.T...A.CTT...T..A.....A.....T.....GT...T..A..A.....									
MB3660				T.....G.....-G..C.....									
MB3661				T.....G.....-G..C.....									
MB3662				T.....G.....-G..C.....									
MB3663				T.....G.....-G..C.....									
MB3664				T.....G.....-G..C.....									
P16_102_Positive_control				T.....-G.....									
AF082751_Dasyurus maculatus isolate NM.B1				C..G...T.....									
AF082752_Dasyurus maculatus isolate NM.E1				C..G...T.....									
AF082756_Dasyurus maculatus isolate NM.E21				C..G...T.....									
AF082759_Dasyurus maculatus isolate NM.L12				C..G...T.....									
AF082753_Dasyurus maculatus isolate NM.E2				C..G...C.....									
AF082755_Dasyurus maculatus isolate NM.E16				C..G...C.....									
AF082770_Dasyurus maculatus isolate VM.L2				C..G...C.....									
AF082757_Dasyurus maculatus isolate NM.E45				-----..A.....C..G.....D.....M...DY.....									
AF082762_Dasyurus maculatus isolate QM.E2				C..G.....C.....									
AF082769_Dasyurus maculatus isolate VM.L1				C..G.....C.....									
AF082754_Dasyurus maculatus isolate NM.E8				T.....C.....									
AF082758_Dasyurus maculatus isolate NM.L11				T.....C.....									
AF082760_Dasyurus maculatus isolate NM.MU1				T.....C.....									
AF082761_Dasyurus maculatus isolate QM.E1				T.....C.....									
AF082763_Dasyurus maculatus isolate TM.E1				T.....G.....A.....C.....									
AF082766_Dasyurus maculatus isolate TM.E8				T.....G.....A.....C.....									
AF082768_Dasyurus maculatus isolate TM.E10				T.....G.....A.....T.....C.....									
AF082764_Dasyurus maculatus isolate TM.E5				T.....G.....A.....T.....C.....									
AF082765_Dasyurus maculatus isolate TM.E6				T.....G.....A.....A.....C.....									
AF082767_Dasyurus maculatus isolate TM.E9				T.....G.....A.....A.....R..C.....									

					220	240	260	280	300	320	340	360	380	400
Consensus					TTATCATTTTGAACAGTACATTCATATCTTAAACTAATATAA	CTCAATAAGTACATAATACATAATATGTATATATTACATAAGACATATAATGTTGGCGTACATAGACATTAAATCCATGGAACGAGATCAACAAAGCTAATTTCCTCTAGCAGATCACAACCATTAGGATTACCTTCATCCTCCCTCACGAGAGATCA								
AF082774_Dasyurus viverrinus					C...A...A.TT.A.....T.....C.T.....							T.....GT.....K...TC.....A.....A.....		
MB3660											A.....C.....			C.....
MB3661											A.....C.....			C.....
MB3662											A.....C.....			C.....
MB3663					NN						A.....C.....			C.....
MB3664											R..A.....C.....			C.....
P16_102_Positive_control								T.....						
AF082751_Dasyurus maculatus isolate NM.B1					C.....	T.....				T.....				
AF082752_Dasyurus maculatus isolate NM.E1					C.....	T.....				T.....				
AF082756_Dasyurus maculatus isolate NM.E21					C.....	T.....	N.....			T.....				
AF082759_Dasyurus maculatus isolate NM.L12					C.....	T.....				T.....				
AF082753_Dasyurus maculatus isolate NM.E2					C.....									
AF082755_Dasyurus maculatus isolate NM.E16					C.....									
AF082770_Dasyurus maculatus isolate VM.L2					C.....GC.....						T.....			C.....
AF082757_Dasyurus maculatus isolate NM.E45					C.G.....					T.....				
AF082762_Dasyurus maculatus isolate QM.E2					C.....									
AF082769_Dasyurus maculatus isolate VM.L1					C.....									
AF082754_Dasyurus maculatus isolate NM.E8								T.....						
AF082758_Dasyurus maculatus isolate NM.L11								T.....						
AF082760_Dasyurus maculatus isolate NM.MU1								T.....						
AF082761_Dasyurus maculatus isolate QM.E1														
AF082763_Dasyurus maculatus isolate TM.E1					T.....						A.....T.....			C.....
AF082766_Dasyurus maculatus isolate TM.E8					T.....						A.....T.....			C.....
AF082768_Dasyurus maculatus isolate TM.E10					T.....						A.....T.....			
AF082764_Dasyurus maculatus isolate TM.E5					T.....						A.....T.....			
AF082765_Dasyurus maculatus isolate TM.E6					T.....						A.....T.....			C.....
AF082767_Dasyurus maculatus isolate TM.E9					T.....						A.....T.....			C.....

					420	440
Consensus					GCAACCCGCCATT	CATAGACAACAATCCTTCAGAGCAAGCCCAT
AF082774_Dasyurus viverrinus						..W.T.....
MB3660						
MB3661						
MB3662						
MB3663						
MB3664						
P16_102_Positive_control						
AF082751_Dasyurus	maculatus	isolate	NM.B1		..T.....	
AF082752_Dasyurus	maculatus	isolate	NM.E1		..T.....	
AF082756_Dasyurus	maculatus	isolate	NM.E21		..T.....	
AF082759_Dasyurus	maculatus	isolate	NM.L12		..T.....	
AF082753_Dasyurus	maculatus	isolate	NM.E2		..C.....	
AF082755_Dasyurus	maculatus	isolate	NM.E16		..C.....	
AF082770_Dasyurus	maculatus	isolate	VM.L2			
AF082757_Dasyurus	maculatus	isolate	NM.E45		..C.....	
AF082762_Dasyurus	maculatus	isolate	QM.E2			
AF082769_Dasyurus	maculatus	isolate	VM.L1			
AF082754_Dasyurus	maculatus	isolate	NM.E8			
AF082758_Dasyurus	maculatus	isolate	NM.L11			
AF082760_Dasyurus	maculatus	isolate	NM.MU1			
AF082761_Dasyurus	maculatus	isolate	QM.E1			
AF082763_Dasyurus	maculatus	isolate	TM.E1			
AF082766_Dasyurus	maculatus	isolate	TM.E8			
AF082768_Dasyurus	maculatus	isolate	TM.E10			
AF082764_Dasyurus	maculatus	isolate	TM.E5			
AF082765_Dasyurus	maculatus	isolate	TM.E6			
AF082767_Dasyurus	maculatus	isolate	TM.E9			

Figure S4a (next page) | Alignment of 460 bp of the *Dasyurus maculatus* control region (i.e., with the deletion observed in Region 1 unmasked). Accession numbers of extant *D. maculatus* were taken from Firestone *et al.* (1999). *D. viverrinus* is included as an outgroup.

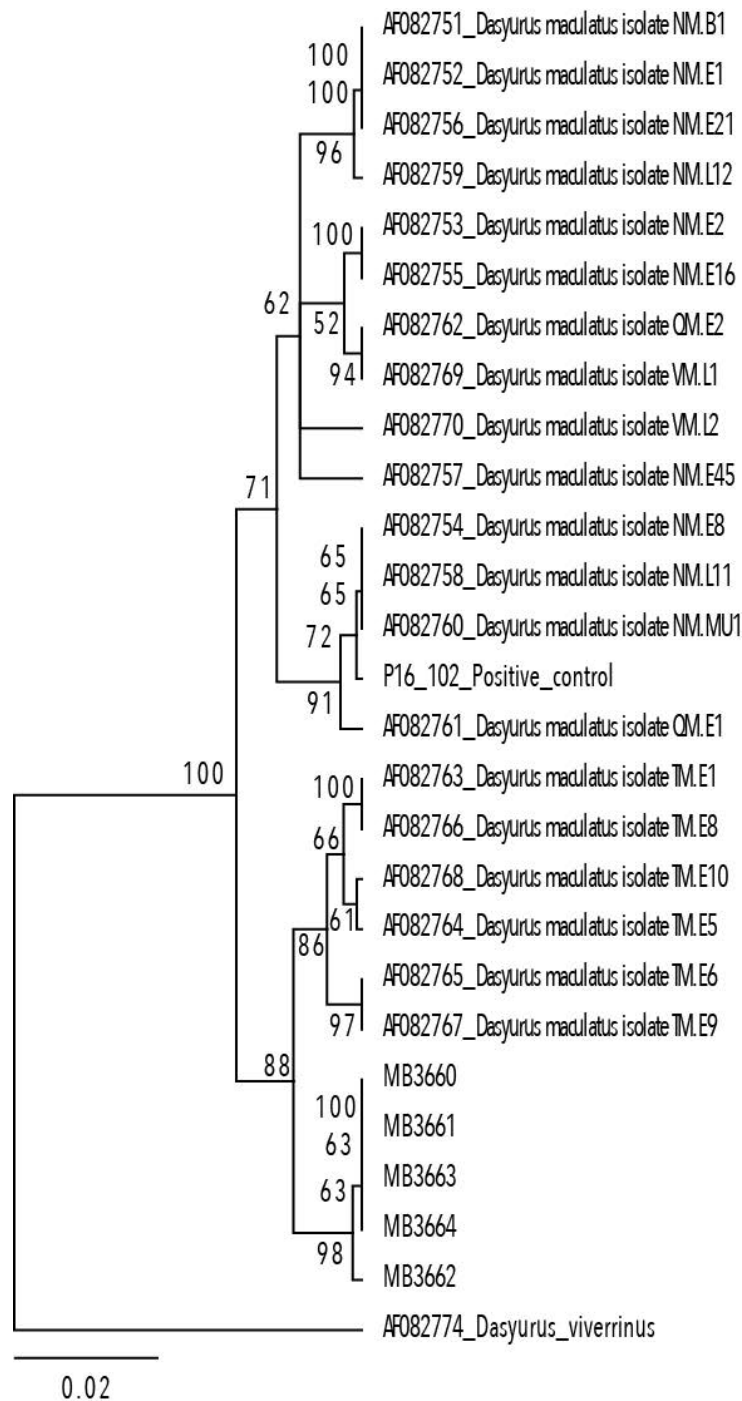


Figure S4b | Phylogenetic tree generated using 460 bp of the *Dasyurus maculatus* control region (i.e., with the deletion observed in Region 1 unmasked). The tree was generated in *Geneious* v10. Evolutionary history was inferred using UPGMA tree with evolutionary distances computed with the HKY model. 5000 bootstrap replicates were performed with bootstrap support displayed at each node as a percentage. The tree is drawn to scale, with branch lengths in the units of the number of base substitutions per site. Accession numbers of extant *D. maculatus* were taken from Firestone *et al.* (1999).

Figure S4a displays three panels of sequence alignments, each showing a consensus sequence and individual sample sequences (AF082774_Dasyurus viverrinus, MB3660, MB3661, MB3662, MB3663, MB3664, P16_102_Positive_control) across a range of positions (200-400, 200-400, 200-400).

The top panel shows the consensus sequence (ACAAAATTYAATTTTATGCTATCTCAGTATTAAATTTT) and individual sample sequences (AF082774_Dasyurus viverrinus, MB3660, MB3661, MB3662, MB3663, MB3664, P16_102_Positive_control) across a range of positions (200-400). The middle panel shows the consensus sequence (TAATATAATATATTRYTATCATTGTAACAGTACATTCATATCTTAACTAATATAAYTCATAATAGTACATAATACATAATATGTATATATTACATAAGACATATAATGTTGGCGTACATAGACATTAAATCCATGGAACRAGATCAACWAAGCTAATTCCTCTAGCAGATCACAACCATTAGGATTACCTTCATCCTCC) and individual sample sequences (AF082774_Dasyurus viverrinus, MB3660, MB3661, MB3662, MB3663, MB3664, P16_102_Positive_control) across a range of positions (200-400). The bottom panel shows the consensus sequence (CCTCACGAGAGATCAGCAACCCGCCATTTCATAGACACAACATCCTTCAGAGCAAGCCCCAT) and individual sample sequences (AF082774_Dasyurus viverrinus, MB3660, MB3661, MB3662, MB3663, MB3664, P16_102_Positive_control) across a range of positions (200-400).

Figure S5a (next page) | Alignment of 366 bp of the *Dasyurus maculatus* control region (i.e., with the deletion observed in Region 1 masked, as well as Region 2 and Region 5 excluded). Accession numbers of extant *D. maculatus* were taken from Firestone *et al.* (1999). *D. viverrinus* is included as an outgroup.

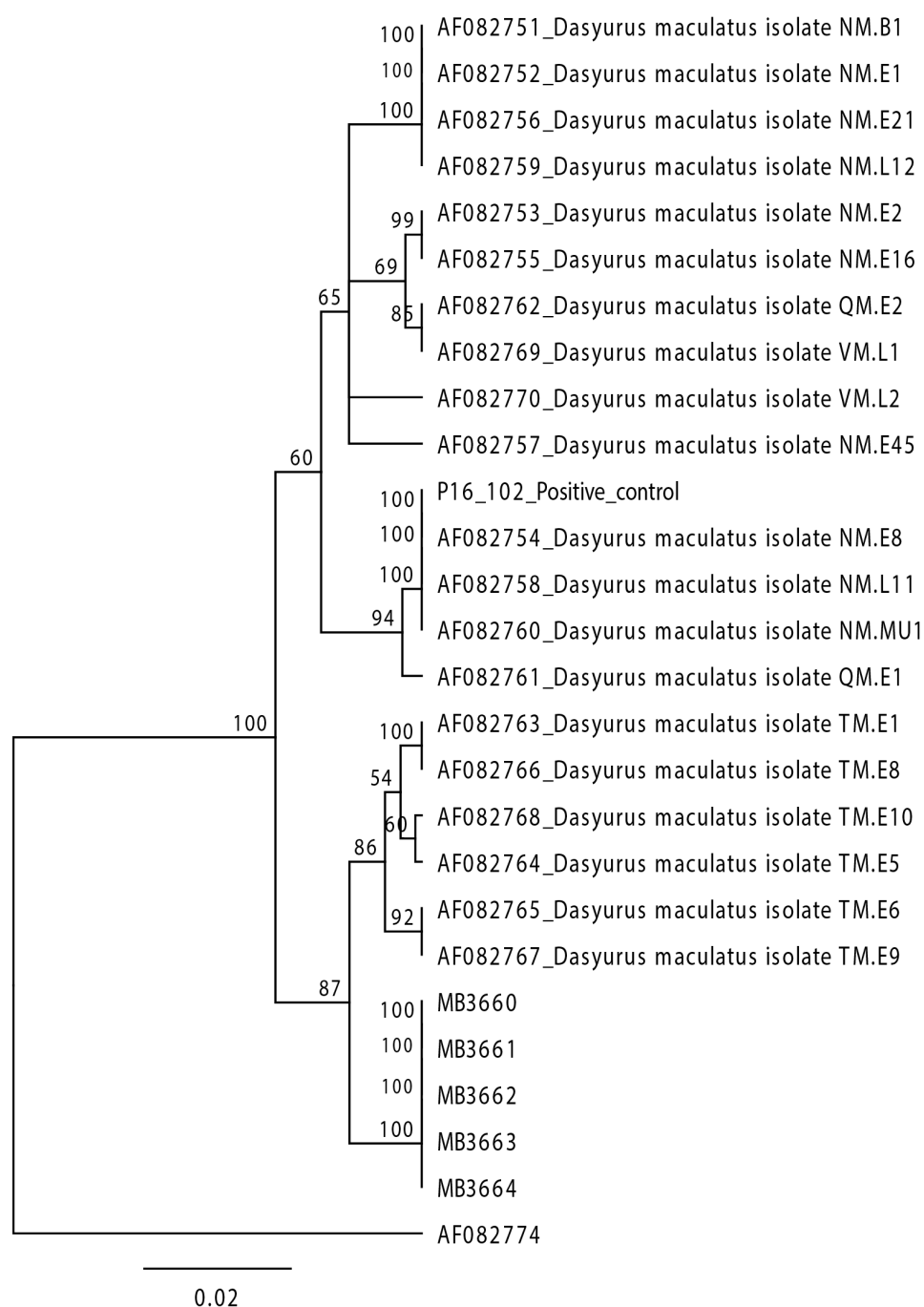


Figure S5b | Phylogenetic tree generated using 366 bp of the *Dasyurus maculatus* control region (i.e., with the deletion observed in Region 1 masked, as well as Region 2 and Region 5 excluded). The tree was generated in *Geneious* v10. Evolutionary history was inferred using UPGMA tree with evolutionary distances computed with the HKY model. 5000 bootstrap replicates were performed with bootstrap support displayed at each node as a percentage. The tree is drawn to scale, with branch lengths in the units of the number of base substitutions per site. Accession numbers of extant *D. maculatus* were taken from Firestone *et al.* (1999).

Figure S6 (page 12) | Complete alignment of the 471 bp region from *D. maculatus* *D-loop* (control region) described in Firestone *et al.* (1999) (including sequence data from the KI specimens sampled here) depicting variable sites (not including the deletion observed in Region 1).

Figure S5a displays two sequence alignment panels comparing various *Dasyurus viverrinus* isolates (AF082774, MB3660, MB3661, MB3662, MB3663, MB3664) against a positive control (P16 102) and a reference sequence (Consensus).

The top panel shows a sequence alignment from position 20 to 200. The reference sequence (Consensus) is: ACAAATTC AATTTATATGCTATCTCAGTATTAAATTTT-----AAAATTTT TAATTCAAAC-ATACATTACAT-TTTACATGTATAT-AATGTACAAAAATTTATT TATATTACTAAATACATTAATATAATATATTGTTATCATTTGAACAGTACATTTCATATCTTAAACTAATATAACTCATAATAGTACATAAT. The isolates are aligned below the reference, with gaps indicated by dashes. The isolates are: AF082774_Dasyurus viverrinus, MB3660, MB3661, MB3662, MB3663, MB3664, P16 102 Positive control, AF082751_Dasyurus maculatus isolate NM.B1, AF082752_Dasyurus maculatus isolate NM.E1, AF082756_Dasyurus maculatus isolate NM.E21, AF082759_Dasyurus maculatus isolate NM.L12, AF082753_Dasyurus maculatus isolate NM.E2, AF082755_Dasyurus maculatus isolate NM.E16, AF082770_Dasyurus maculatus isolate VM.L2, AF082757_Dasyurus maculatus isolate NM.E45, AF082762_Dasyurus maculatus isolate QM.E2, AF082769_Dasyurus maculatus isolate VM.L1, AF082754_Dasyurus maculatus isolate NM.E8, AF082758_Dasyurus maculatus isolate NM.L11, AF082760_Dasyurus maculatus isolate NM.MU1, AF082761_Dasyurus maculatus isolate QM.E1, AF082763_Dasyurus maculatus isolate TM.E1, AF082766_Dasyurus maculatus isolate TM.E8, AF082768_Dasyurus maculatus isolate TM.E10, AF082764_Dasyurus maculatus isolate TM.E5, AF082765_Dasyurus maculatus isolate TM.E6, AF082767_Dasyurus maculatus isolate TM.E9.

The bottom panel shows a sequence alignment from position 220 to 360. The reference sequence (Consensus) is: ACATAATATGTATATATTACATAAGACATAATTAATCCATGGAACGAGATCAACAAAGCTAATTCCTCTAGCAGATCACAACCATTAGGATTACCTTCATCCTCCCCTCACGAGAGATCAGCAACCCGCCATTTCATAGACACAACATCCTTCAGAGCAAGCCCAT. The isolates are aligned below the reference, with gaps indicated by dashes. The isolates are: AF082774_Dasyurus viverrinus, MB3660, MB3661, MB3662, MB3663, MB3664, P16 102 Positive control, AF082751_Dasyurus maculatus isolate NM.B1, AF082752_Dasyurus maculatus isolate NM.E1, AF082756_Dasyurus maculatus isolate NM.E21, AF082759_Dasyurus maculatus isolate NM.L12, AF082753_Dasyurus maculatus isolate NM.E2, AF082755_Dasyurus maculatus isolate NM.E16, AF082770_Dasyurus maculatus isolate VM.L2, AF082757_Dasyurus maculatus isolate NM.E45, AF082762_Dasyurus maculatus isolate QM.E2, AF082769_Dasyurus maculatus isolate VM.L1, AF082754_Dasyurus maculatus isolate NM.E8, AF082758_Dasyurus maculatus isolate NM.L11, AF082760_Dasyurus maculatus isolate NM.MU1, AF082761_Dasyurus maculatus isolate QM.E1, AF082763_Dasyurus maculatus isolate TM.E1, AF082766_Dasyurus maculatus isolate TM.E8, AF082768_Dasyurus maculatus isolate TM.E10, AF082764_Dasyurus maculatus isolate TM.E5, AF082765_Dasyurus maculatus isolate TM.E6, AF082767_Dasyurus maculatus isolate TM.E9.

Figure S6 displays two sequence alignment panels showing the alignment of various Dasyurus maculatus isolates (AF082751_Dasyurus maculatus isolate NM.B1 to AF082767_Dasyurus maculatus isolate TM.E9) against a reference sequence (P16_102_Positive_control).

The top panel shows the alignment of the reference sequence (P16_102_Positive_control) against the consensus sequence (GCACAATTTTAATTTTAATCACAAAATTCAATTTATATGCTATCTCAGTATTAAATTTTTCACAAAATTTTCAAAAATTTTAAATTCACACATACATTACATTTTACATGTATATAATGTACAAAATTTATTTATGTATATAGAGCATACTTTATATTCCTCTATAATATAAGCATGTACATATTAATCATATATT). The alignment is shown for positions 20 to 200.

The bottom panel shows the alignment of the reference sequence (P16_102_Positive_control) against the consensus sequence (ACTAAATACATTAATATAATATATTGTTATCATTTGAACAGTACATTCATATCTTAAACTAATATAACTCATAATAGTACATAATACATAATATGTATATATTACATAAGACATATAATGTTGGCGTACATAGACATTAAATCCATGGAACGAGATCAACAAAGCTAATTCCTCTAGCAGATCACAACCATTAGGATTAC). The alignment is shown for positions 220 to 400.

Key features of the alignment include:

- Consensus sequence: GCACAATTTTAATTTTAATCACAAAATTCAATTTATATGCTATCTCAGTATTAAATTTTTCACAAAATTTTCAAAAATTTTAAATTCACACATACATTACATTTTACATGTATATAATGTACAAAATTTATTTATGTATATAGAGCATACTTTATATTCCTCTATAATATAAGCATGTACATATTAATCATATATT.
- Reference sequence: P16_102_Positive_control.
- Isolates: AF082751_Dasyurus maculatus isolate NM.B1, AF082752_Dasyurus maculatus isolate NM.E1, AF082756_Dasyurus maculatus isolate NM.E21, AF082759_Dasyurus maculatus isolate NM.L12, AF082753_Dasyurus maculatus isolate NM.E2, AF082755_Dasyurus maculatus isolate NM.E16, AF082770_Dasyurus maculatus isolate VM.L2, AF082757_Dasyurus maculatus isolate NM.E45, AF082762_Dasyurus maculatus isolate QM.E2, AF082769_Dasyurus maculatus isolate VM.L1, AF082754_Dasyurus maculatus isolate NM.E8, AF082758_Dasyurus maculatus isolate NM.L11, AF082760_Dasyurus maculatus isolate NM.MU1, AF082761_Dasyurus maculatus isolate QM.E1, AF082763_Dasyurus maculatus isolate TM.E1, AF082766_Dasyurus maculatus isolate TM.E8, AF082768_Dasyurus maculatus isolate TM.E10, AF082764_Dasyurus maculatus isolate TM.E5, AF082765_Dasyurus maculatus isolate TM.E6, AF082767_Dasyurus maculatus isolate TM.E9.

The alignment shows high sequence identity between the isolates and the reference sequence, with minor variations observed in some positions.

Supplementary information

References

1.
Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. & Kumar, S. (2011). MEGA5: Molecular Evolutionary Genetics Analysis Using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. *Molecular Biology and Evolution*, 28, 2731-2739.