

The following supplement accompanies the article

Mitogenome analysis reveals a complex phylogeographic relationship within the wild tiger population of Thailand

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Fig. S1 Sites of sample collection

Fig. S2 The alignment of the control region of the WEFCOM and Malayan tigers reported in this study with previous reports. These sequences contain different lengths of the control region resulting in different sizes of the complete mitochondrial genome. The different lengths of the control region are a result of the variable number of tandem repeats in the repetitive sequence box 3 (RS-3). HVS = hypervariable site, RS = repetitive sequence, CCR = central conserved region, CSB = conserved sequence box.

Fig. S3 The mitogenome map of the tiger (*P. tigris*) including F2 *numt* (red curve). Fragment 9 of this study contained two distinct sequences; 9.1 (blue line) and 9.2 (blue dashed line), where the *numt* sequence was found (red box). The grey curve indicates the region containing two highly distinct sequences when compared with other reported complete mitogenomes.

Fig. S4 The alignment of confounding sequences near the 5' end of F2 *numt* (red arrow). The sequences of the WEFCOM tiger (fragment numbers 8, 9.1, 9.2 and 10) were aligned to HM569215 P27 of Zhang et al. (2011), JF357971 CORBETTI1 of Kitpith et al. (2012), *cymt* DQ151550 and F2 *numt* (DQ151551) reported by Kim et al. (2006). The sequences resembling F2 *numt* are labeled in red. Two distinct sequences contaminated with *numt* were found in fragment 9. The start point of the ambiguous sequences is at the last domain of the *COXI* gene. The alignment shows that the amplicon 9.1 was initially similar to *numt* and could not be aligned with the adjacent fragment (red dashed boxes). There is a turning point at the middle of *COX2* (red arrow head) where the amplicon 9.2 which was initially identical to *cymt* turned to the *numt* sequence and amplicon 9.1 turned to the *cymt* sequence. After the end of F2 *numt* at the *ATP6* gene, the 9.1 and 9.2 amplicons remain different (labeled cyan).

Table S1. The full details of the primers used in this study.

No.	Primer names	Primer sequences (5'-3')	Gene	Size of PCR product	T _a	Ref.
1	wTG3021F Dloopre	CTTATCCATCTTAATCTTAGCCAC CCTGAAGAAAGAACAGATGC	CR	951	58	This study (Ward et al. 1999)
2	TGDL1F wTG4940R	GATTAGAGCAGTTCTTCATGGAT TATATTAAAGCTACATTAACCAAGGC	CR	1,137	58	This study This study
3	wTG4753F wTG6290R	AGACTAAACCCGTATCTAGGCAC TTCATCCTGTAATAGATTGTTATCGG	CR - 12S rRNA	1,563	60	This study This study
4	TG6031F TG7276R	CTTGAGCTAGAGCTAGCCCACTA GGGTAACCTGTTCCGTTGATCACGC	16S rRNA	1,271	60	This study This study
5	H2513 wTG8870R	GCCTGTTACCAAAAACATCAC ACGGTTGATATAATGATGGTGAGG	16S rRNA - ND1	2,027	56	(Kitano et al. 2007) This study
6	wTG8191F wTG9920R	GAATACATCTGGCTCATCATCGCT GCTCTTGGTCTAGTTGACCCT	ND1 - ND2	1,729	60	This study This study
7	TG9711F TG11294R	TAGCCATAACAGCACTACTTAACGTA CCCAAAGCCCATAGTATAGCGCGA	ND2 - COX1	1,618	60	This study This study
8	wTG11001F wTG12044R	CCAGAAGTCTATATCTTAATCCTG AATGTATGATCATGGAAGTGTGAA	COX1 - COX2	1,049	60	This study This study
9.1	mtDNA6H mtDNA6L	GCTCATTATTTCACTAACAGCACT GGGCTACAGCAAATTCAAGGAT	COX2 - ATP6	1,856	58	(Delisle & Strobeck 2002) (Delisle & Strobeck 2002)
9.2	TG6H TG6L	ACAACTAATCTGAATGACTTGAC TCCTCCGATTAGGTGTATTAATTAA	COX2 - ATP6	1,667	58	This study This study
10	mtDNA7H mtDNA7L	TTGGCTCACTTCTACCTCAAGG GTGGGGATGATGATTTTAGCATTGTA	ATP6 – ND4L	1,890	60	(Delisle & Strobeck 2002) (Delisle & Strobeck 2002)
11	mtDNA8H mtDNA8L	CCAAAACAAATGATTCGACTCA GGTCCTAACAGACCAATGGATTACTCT	ND4L – ND4	1,889	60	(Delisle & Strobeck 2002) (Delisle & Strobeck 2002)
12	mtDNA9H wTG1680R	AAACCATCATTACACAGAGAAAAC GGTGCGGGTGATTGAGTGGTC	ND4- ND6	2,270	58	(Delisle & Strobeck 2002) This study
13	TND6-1 wTG3170R	CTATCCTCCATAATCACCTG GCCGATGGCAATAAAGGGGTGT	ND5 – CYT B	1,693	58	This study This study

Table S2. The list of reference sequences used in this study.

Accession No.	Species/subspecies	Haplotype/ individual	Length (bp)	Reference
NC_010638	<i>P. uncia</i>	-	16,773	Wei et al. 2010
EF551002	<i>P. pardus</i>	-	16,964	Wei et al. 2011
DQ257669	<i>N. nebulosa</i>	-	16,884	Wu et al. 2007
KF297576	<i>P. t. altaica</i>	-	16,996	Sun et al. 2014
DQ151550	<i>P. tigris</i>	-	12,912	Kim et al. 2006
DQ151551	<i>P. tigris</i>	F2 nuclear copy	12,559	Kim et al. 2006
HM589214	<i>P. t. amoyensis</i>	P25	16,957	Zhang et al. 2011
HM589215	<i>P. t. amoyensis</i>	P27	17,001	Zhang et al. 2011
JF357967	<i>P. t. tigris</i>	TIGRIS1	16,637	Kitpipit et al. 2012
JF357968	<i>P. t. tigris</i>	TIGRIS2	16,976	Kitpipit et al. 2012
JF357969	<i>P. t. sumatrae</i>	SUMATRA1	16,998	Kitpipit et al. 2012
JF357970	<i>P. t. sumatrae</i>	SUMATRA2	17,001	Kitpipit et al. 2012
JF357971	<i>P. t. corbetti</i>	CORBETTI1	16,602	Kitpipit et al. 2012
JF357972	<i>P. t. corbetti</i>	CORBETTI2	14,174	Kitpipit et al. 2012
JF357973	<i>P. t. altaica</i>	ALTAICA4	16,980	Kitpipit et al. 2012
JF357974	<i>P. t. altaica</i>	ALTAICA1	17,015	Kitpipit et al. 2012
AY736559– AY736808	All subspecies of extant <i>Panthera tigris</i>	ALT, AMO1-3, COR1-8, SUM1-8, TIG1-6	250 - 593	Luo et al. 2004
JN786601- JN786684	<i>P. tigris</i>	NHM	199 - 482	Mondol et al. 2013
KJ686500-KJ686533	<i>P. t. sondaica</i> , <i>P. t. balica</i>	SON, BAL	67 - 223	Xue et al. 2015

Table S3. The components of the WEFCOM and Ti2 (*P. t. jacksoni*) tiger mitochondrial genome.

Gene	Position				ORF		Strand	
	WEFCOM		Ti2 (<i>P. t. jacksoni</i>)		start	stop		
	start	stop	start	stop				
<i>tRNA</i> ^{-Phe}	1	71	1	71			H	
<i>12S rRNA</i>	72	1,031	72	1,031			H	
<i>tRNA</i> ^{-Val}	1,032	1,099	1,032	1,099			H	
<i>16S rRNA</i>	1,100	2,674	1,100	2,674			H	
<i>tRNA</i> ^{-Leu}	2,675	2,749	2,675	2,749			H	
<i>ND1</i>	2,752	3,707	2,752	3,707	ATG	TAA <u>A</u>	H	
<i>tRNA</i> ^{-Ile}	3,708	3,776	3,708	3,776			H	
<i>tRNA</i> ^{-Gln}	3,774	3,847	3,774	3,847			L	
<i>tRNA</i> ^{-Met}	3,848	3,916	3,848	3,916			H	
<i>ND2</i>	3,917	4,958	3,917	4,958	ATC	TAA <u>A</u>	H	
<i>tRNA</i> ^{-Trp}	4,959	5,026	4,959	5,026			H	
<i>tRNA</i> ^{-Ala}	5,042	5,110	5,042	5,110			L	
<i>tRNA</i> ^{-Asn}	5,112	5,184	5,112	5,184			L	
<i>tRNA</i> ^{-Cys}	5,218	5,282	5,217	5,281			L	
<i>tRNA</i> ^{-Tyr}	5,283	5,349	5,282	5,348			L	
<i>COX1</i>	5,351	6,895	5,350	6,894	ATG	TAA	H	
<i>tRNA</i> ^{-Ser}	6,893	6,961	6,892	6,960			L	
<i>tRNA</i> ^{-Asp}	6,968	7,036	6,967	7,035			H	
<i>COX2</i>	7,037	7,720	7,036	7,719	ATG	TAA	H	
<i>tRNA</i> ^{-Lys}	7,724	7,791	7,723	7,790			H	
<i>ATP8</i>	7,793	7,996	7,792	7,995	ATG	TAA	H	
<i>ATP6</i>	7,954	8,634	7,953	8,633	ATG	TAA	H	
<i>COX3</i>	8,634	9,417	8,633	9,416	ATG	TAA <u>A</u>	H	
<i>tRNA</i> ^{-Gly}	9,418	9,486	9,417	9,485			H	
<i>ND3</i>	9,487	9,833	9,486	9,832	ATA	TAA <u>A</u>	H	
<i>tRNA</i> ^{-Arg}	9,834	9,902	9,833	9,901			H	
<i>ND4L</i>	9,903	10,199	9,902	10,198	ATG	TAA	H	
<i>ND4</i>	10,193	11,570	10,192	11,569	ATG	TAA <u>A</u>	H	
<i>tRNA</i> ^{-His}	11,571	11,638	11,570	11,637			H	
<i>tRNA</i> ^{-Ser}	11,640	11,698	11,639	11,697			H	
<i>tRNA</i> ^{-Leu}	11,699	11,768	11,698	11,767			H	

Gene	Position				ORF		Strand	
	WEFCOM		Ti2 (<i>P. t. jacksoni</i>)		start	stop		
	start	stop	start	stop				
<i>ND5</i>	11,769	13,589	11,768	13,588	ATA	TAA	H	
<i>ND6</i>	13,573	14,100	13,572	14,099	ATG	TAA	L	
<i>tRNA</i> ^{-Glu}	14,101	14,169	14,100	14,168			L	
<i>CYT B</i>	14,173	15,312	14,172	15,311	ATG	AGA	H	
<i>tRNA</i> ^{-Thr}	15,313	15,382	15,312	15,381			H	
<i>tRNA</i> ^{-Pro}	15,383	15,449	15,382	15,448			L	
CR	15,450	16,954	15,449	17,008			H	

Table S4. The variable sites between the WEFCOM and Malayan (Ti2) haplotype. The variations between HVS-I of CR to first base of *tRNA^{Phe}* were excluded. The new mutation sites comparing to previous reports (Luo et al. 2004, Driscoll et al. 2009, Zhang et al. 2011, Kitppipit et al. 2012, Mondol et al. 2013, Sun et al. 2014, Xue et al. 2015) are indicated by the red marks. The red box indicates the position that was excluded from phylogenetic analysis as it may contain additional *numt*.

Gene	12S	16S	ND2	COI	COII	ATP6	COX III	ND3	ND4	ND5	ND6	Q	Cytb				CR				
Position on WEFCOM sequence	2 on WEFCOM sequence	8 0 3 0 3	1 4 8 4 2	1 3 9 2 2	2 6 0 9 7	2 3 3 4 5	7 7 8 8 8	8 8 8 8 9	9 0 0 2 2	1 2 2 3 4	1 3 4 7 0	1 2 3 4	1 1 4 4 4	1 1 4 4 4	1 1 4 4 4	1 1 4 5	1 1 5 5				
Position on Felis catus (NC_001700)	1 1 0 4	1 6 7 1	2 1 9 5	2 3 0 7	3 2 8 5	6 6 6 2	6 6 6 7	6 6 6 7	6 7 7 8	6 7 8 9	6 6 6 3	1 1 1 1	1 1 1 1	1 1 1 1	1 1 1 1	1 1 1 1					
WEFCOM Ti2 (<i>P.t.jacksoni</i>)	C T	C C	G T	C T	G T	C T	G A	T C	C C	A G	G T	T T	A A	T C	A T	T C	T T G T				
Luo et al. 2004 (AY736559-808)	-	T/C	-	-	-	T	-	C	-	-	-	-	-	G/A	-	A/G	-	-	C A/G C/T -	-	
Driscoll et al. 2009	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	A	-	-	-	G C -	-
Mondol et al. 2013 (JN786601-84)	-	-	-	-	-	-	-	-	-	-	-	-	-	A/G	-	-	-	C G C/T -	-		
Xue et al. 2015	-	-	-	-	-	-	T	-	-	-	-	-	-	A	-	G	-	-	-	G T -	-
Zhang et al. 2011 (HM589214-15)	T/C	C/T	C	G/A	T	C/T	T	G	C	T C A C T C C G	G G G C C G/A	T G T C C C G	T/C G/A C	T/C G/A C	T/C G/A C	T/C G/A C	T/C G/A C	T/C G/A C			
Kitppipit et al. 2012 (JF357967-74)	T/C	C/T	C	G	T	T	T	G	C	T C G C T C C G	G G G C C G/A	T G/A T C C C G	T/C G/A C	T/C G/A C	T/C G/A C	T/C G/A C	T/C G/A C				
Sun et al. 2014 (KF297576)	C	T	C	A	T	T	T	G	C	T C G C T C C G	G G G C C A	T A T C C C G	C C A C A C	T A T C C C G	T A T C C C G	T A T C C C G					

Fig. S1. Sites of sample collection.

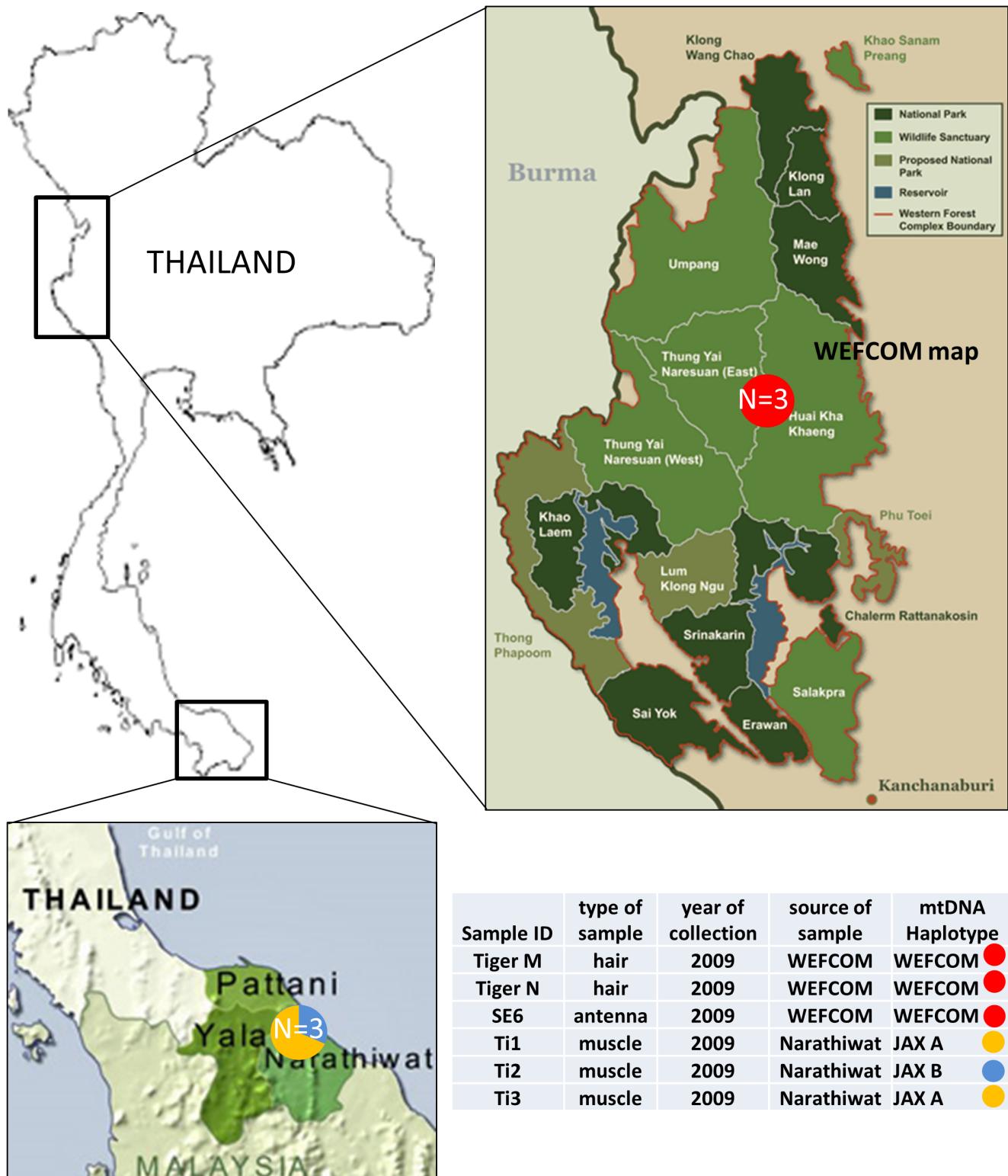


Fig. S2. The alignment of the control region of the WEFCOM and Malayan tigers reported in this study with previous reports. These sequences contain different lengths of the control region resulting in different sizes of the complete mitochondrial genome. The different lengths of control region are a result of the variable number of tandem repeats in the repetitive sequence box 3 (RS-3). HVS = hypervariable site, RS = repetitive sequence, CCR = central conserved region, CSB = conserved sequence box.

WEFCOM	CCAATACCAAAAAACAACCCCATGACTTCATAATTCATATATTGCATATACCGTACTGTGCTGCCAGTATGCTCATCC-CCACAAAAATAAGT	99
T12	-T.....	99
JF357971 CORBETTI1	T.....	99
JF357973 ALTAICA4	99
JF357974 ALTAICA1	..C.....	99
JF357969 SUMATRA1	99
JF357970 SUMATRA2	99
JF357967 TIGRIS1	98
JF357968 TIGRIS2	98
HM589215 amoyensis P27	99
HM589214 amoyensis P25	T.....	99
DQ151550 P.tigris	99
DQ151551 F2 Numt	100
	HVS-1 RS-2 CCA	
WEFCOM	GAAAAAATCCTCAATCCCCTTAACAGAACACACACGAAAT-AACCTGTTAACTACCGGACCCCCCCCCTCCCCCGTTAACATTACCGTAGG	198
T12	197
JF357971 CORBETTI1	197
JF357973 ALTAICA4	197
JF357974 ALTAICA1	197
JF357969 SUMATRA1	197
JF357970 SUMATRA2	197
JF357967 TIGRIS1T.....	195
JF357968 TIGRIS2T.....	195
HM589215 amoyensis P27C.....	198
HM589214 amoyensis P25	198
DQ151550 P.tigrisC.....	198
DQ151551 F2 Numt	.TG.....T.....C.....G.....TGTA...CC.....A.....G.....AATA.....G.....A.....	175
	RS-2 CCR 5	
WEFCOM	GCATACTATGGATATCGTCATTAATGCCGTGCCCCATGAATATTAAGCATGTACAGTAGTTATATATTACATAAGGCATACTATGGATATCGTC	298
T12T.....G.....	297
JF357971 CORBETTI1T.....G.....A.....	297
JF357973 ALTAICA4T.....G.....	297
JF357974 ALTAICA1T.....	297
JF357969 SUMATRA1T.....G.....T.....	297
JF357970 SUMATRA2T.....	297
JF357967 TIGRIS1T.....	295
JF357968 TIGRIS2T.....	295
HM589215 amoyensis P27T.....	298
HM589214 amoyensis P25T.....	298
DQ151550 P.tigris	A.....T.....	298
DQ151551 F2 Numt	A.....T.....CT.....T.....C.....A.....A.....A.....	298
	RS-2 CCR 5	
WEFCOM	ATTAATCGCTTGTCCCCATGAATATTAAGCATGTACAGTAGTTCATATATATTACATAAGACATAATAGTCTTAATCGCATATTGATTTAGAGC	398
T12T.....	397
JF357971 CORBETTI1T.....	397
JF357973 ALTAICA4T.....	397
JF357974 ALTAICA1T.....	397
JF357969 SUMATRA1T.....	397
JF357970 SUMATRA2T.....	397
JF357967 TIGRIS1T.....	395
JF357968 TIGRIS2T.....	395
HM589215 amoyensis P27T.....	398
HM589214 amoyensis P25T.....	398
DQ151550 P.tigrisC.....	398
DQ151551 F2 NumtT.....	375
	RS-2 CCR 5	
WEFCOM	AGTTCTTCATGGATCTCAACTATCGAAAGAGCTTAATCACCTGGCCTCGAGAACCAACAACCCTGCTCGAGCGTGTACCTCTT-CTCGCTCCGGC	497
T12	496
JF357971 CORBETTI1	496
JF357973 ALTAICA4C.....	497
JF357974 ALTAICA1	496
JF357969 SUMATRA1G.....A.....	496
JF357970 SUMATRA2G.....	496
JF357967 TIGRIS1	494
JF357968 TIGRIS2G.....	494
HM589215 amoyensis P27T.....	497
HM589214 amoyensis P25T.....	497
DQ151550 P.tigrisG.....CT.....	497
DQ151551 F2 NumtC.....C.....-....C.....G.....G.....CT.....	473

WEFCOM	-----ACGTACACACGTACACAGTATAACCGTACAC--GTACACACGTACACACGTACACACGTACACACGTACA	1149
T12	CGTAC.....C.A.....AC.....	1180
JF357971 CORBETTI1C.....	1150
JF357973 ALTAICA4T.....T.....	1151
JF357974 ALTAICA1C.A.....AC.....	1186
JF357969 SUMATRA1C.A.....AC.....	1169
JF357970 SUMATRA2G.....C.A.....AC.....	1172
JF357967 TIGRIS1G.....N.Y.--.	817
JF357968 TIGRIS2A.T.--.CGT.....	1156
HM589215 amoyensis P27T.....	1171
HM589214 amoyensis P25T.....	1127
DQ151550 P.tigrisT.G.....GTAC.C..TAC.....	1159
DQ151551 F2 Numt		864
	RS-3	HVS-2
WEFCOM	CACGTACACACGTACACACGTACACACGTAA-----TACACGTATAACGTATAACGTATAACCATGCAAACCTTTTGAT	1225
T12T.....TACACGTATAACGTATAACACGTAA.....	1280
JF357971 CORBETTI1CACACGTACACACGTATAACACGTAA.....	1241
JF357973 ALTAICA4TACACGTATAACGTATAACACGTAA.....	1251
JF357974 ALTAICA1T.....T.....TACACGTATAACGTATAACACGTAA.....	1286
JF357969 SUMATRA1T.....T.....TACCGTATAACGTATAACACGTAA.....	1269
JF357970 SUMATRA2T.....T.....TACACGTATAACGTATAACACGTAA.....	1272
JF357967 TIGRIS1T.....CACACGTACACACGTATAACACGTAA.....	909
JF357968 TIGRIS2T.....CACACGTACACACGTATAACACGTAA.....	1248
HM589215 amoyensis P27CACACGTACACACGTATAACACGTAA.....	1271
HM589214 amoyensis P25T.....TACACGTATAACGTATAACACGTAA.....	1227
DQ151550 P.tigrisCACACGTACACACGTACACACGTAA.....	1259
DQ151551 F2 Numt		900
	CSB II	CSB III
WEFCOM	TTAGTAAATAATTAGCTAACCAAAACCCCCCTACCCCCC-GTTAATCTTATTATTATAGTACGTGTTATTCTGTCTGCCAACCCCCAAAACAAG	1324
T12C.....	1379
JF357971 CORBETTI1		1241
JF357973 ALTAICA4		1350
JF357974 ALTAICA1		1385
JF357969 SUMATRA1		1368
JF357970 SUMATRA2		1371
JF357967 TIGRIS1		1008
JF357968 TIGRIS2		1347
HM589215 amoyensis P27		1370
HM589214 amoyensis P25		1326
DQ151550 P.tigris		1358
DQ151551 F2 NumtT.....A.....C.....C.....C.A.....C.....A.....	1000
WEFCOM	ACTAAACCCGTATCTAGGCACAAGGCCATAAGA-TTAACGTTACAAACTCTACCAACCCCATTACCAATTATTAATACTAAATCATAACTTCGTTCG	1423
T12	-----A.....C-----	1478
JF357971 CORBETTI1	-----A.....C-----	1249
JF357973 ALTAICA4	-----	1449
JF357974 ALTAICA1	-----	1484
JF357969 SUMATRA1	-----	1467
JF357970 SUMATRA2	-----	1470
JF357967 TIGRIS1	-----	1107
JF357968 TIGRIS2	-----	1446
HM589215 amoyensis P27	-----	1469
HM589214 amoyensis P25	-----	1425
DQ151550 P.tigris	-----T.....	1457
DQ151551 F2 NumtC.A..GT.....A.....T.....T.....C.....G.....T.....	1099
WEFCOM	CAGTTATCTATAGATACGACAACCGATCTAATTGTCCTATCGAACAAATTACATACCAACAACCCATGTCTTG	1505
T12	-----	1560
JF357971 CORBETTI1	-----	1249
JF357973 ALTAICA4	-----	1531
JF357974 ALTAICA1	-----	1566
JF357969 SUMATRA1C.....	1549
JF357970 SUMATRA2C.....	1552
JF357967 TIGRIS1C.....	1189
JF357968 TIGRIS2C.....	1528
HM589215 amoyensis P27	1551
HM589214 amoyensis P25	1507
DQ151550 P.tigrisC.....T.....A.....	1539
DQ151551 F2 NumtT.....C.....T.....A.....	1181

Fig. S3. The mitogenome map of the tiger (*P. t. tigris*) including F2 *numt* (red curve). Fragment 9 of this study contained two distinct sequences; 9.1 (blue line) and 9.2 (blue dashed line), where the *numt* sequence was found (red box). The grey curve indicates the region containing two highly distinct sequences when compared with other reported complete mitogenomes. The green curve indicates the sequence range used to construct the phylogenetic tree in Figure 2.

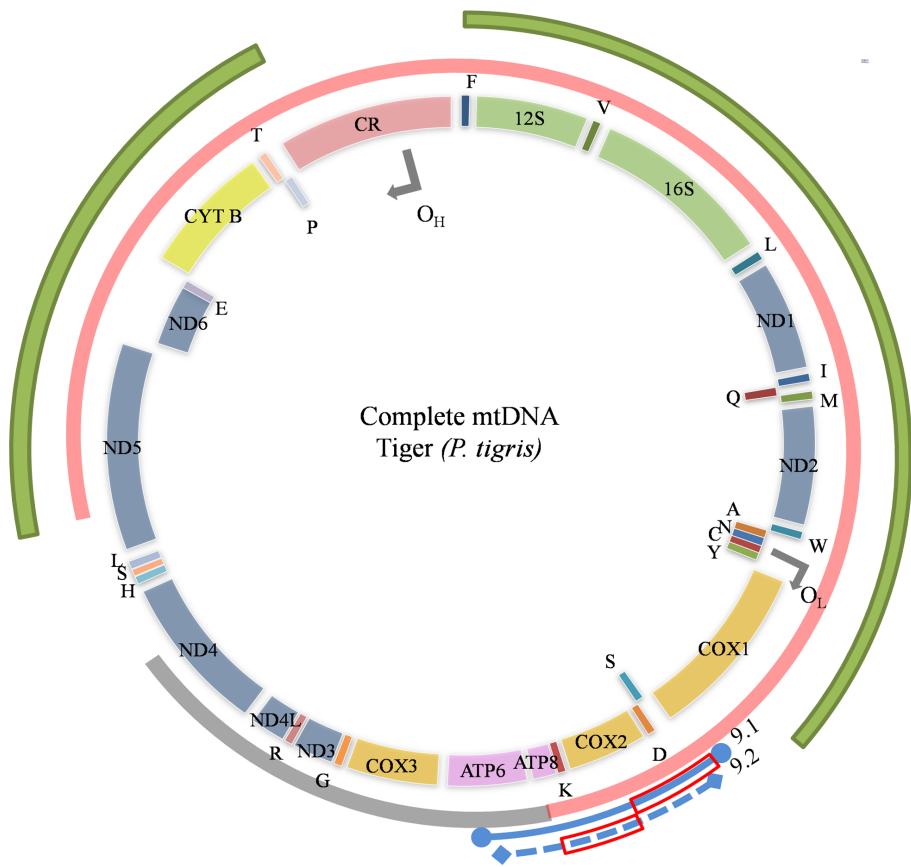


Fig. S4. The alignment of confounding sequences near the 5' end of F2 *numt* (red arrow). The sequences of the WEFCOM tiger (fragment numbers 8, 9.1, 9.2 and 10) were aligned to HM569215 P27 of Zhang et al. (2011), JF357971 CORBETTI1 of Kitpipit et al. (2012, *cymt* DQ151550 and F2 *numt* (DQ151551) reported by Kim et al. (2006). The sequences resembling F2 *numt* are labeled in red. Two distinct sequences contaminated with *numt* were found in fragment 9. The start point of the ambiguous sequences is at the last domain of the *COX1* gene. The alignment shows that the amplicon 9.1 was initially similar to *numt* and could not be aligned with the adjacent fragment (red dashed boxes). There is a turning point at the middle of *COX2* (red arrow head) where the amplicon 9.2 which was initially identical to *cymt* turned to the *numt* sequence and amplicon 9.1 turned to the *cymt* sequence. After the end of F2 *numt* at the *ATP6* gene, the 9.1 and 9.2 amplicons remain different (labeled cyan).

		<i>COX1</i>
HM589215	P27	ATG-TTCATAAACCGCTGAGTATTTCAACCAATCACAAGGATATTGAACTCTTACCTTTATTGGCGCTGGCTGGTATGGGGGACTGCCCTCAGTCTCCTAATTGAGCCGA
JF357971	CORBETTI1C.....G.....T.....T.....
DQ151550	G.....C.....G.....C.....A.....
DQ151551	F2 Numt	TATG.....C.....A.....T.....G.....C.....C.....A.....T.....T.....C.....G.....G.....
HM589215	P27	TGACCAAATTATAATGTGGTAGTTACTGCCATGCCCTTGATGATACTTTTATAGTAATGCCTATTATAATTGGAGGGTCGAAAAGCTGGCTAGTCCGTAATAATCGGGGCCCGATATGGCATCCCTCGAATGAATAACAT
JF357971	CORBETTI1A.....A.....A.....A.....
DQ151550	NA.....A.....A.....A.....
DQ151551	F2 Numt	C.....A.....C.....C.....A.....C.....G.....A.....AT.....G.....A.....T.....A.....T.....
HM589215	P27	AAGCTCTGACTCCTCCCCATCCTCCTACCTCTGCTCGATCGCTATGGTAGAACGCTGGGGCAGGAACCTGGGGACAGTATACCCACCCCTAGCTGGCAACCTAGCCATGAGGAGCATCCGTGGATCTAACATTTC
JF357971	CORBETTI1
DQ151550	
DQ151551	F2 Numt	G.....G.....T.....A.....G.....A.....T.....C.....T.....A.....
HM589215	P27	ACACCTAGCAGCGCTCCTCAATCTAGGTGCTATTAAATTATTAACTATTAAATAAAAACCGCCGCTATGTCCTAACACCAACACCCCTATTGTTGATCGGTTCTAAATTACTGCTGTGTTGCTACTCTATCACTGCC
JF357971	CORBETTI1
DQ151550	
DQ151551	F2 NumtG.....N.....N.....C.....C.....T.....A.....T.....C.....T.....C.....A.....A.....
HM589215	P27	AGTTTAGCAGCAGGCATCACCATGCTACTGACAGATCGAAATCTAAATACCACATTGGATCCT-GCTGGGGAGGAGACCCCATCTTA---TATCAACACCTATTGATTCTCGGTACCCAGAAGTCTATCTTAATCCTG
JF357971	CORBETTI1
DQ151550	
DQ151551	F2 NumtT.....A.....G.....C.....C.....C.....A.....G.....T.....T.....CTTA.....T.....C.....T.....TT.....A.....
HM589215	P27	CCGGGTTTGAATAATTACATATTGTCACCTACTCAGGAAAAAGAACCTTTGGCTACATGGGATAGTCTGAGCCATAATGTCATTGGCTTCTGGCTTATCGTATGGGCCATCACATGTTACTGTAGGGATAGAT
JF357971	CORBETTI1
DQ151550	
DQ151551	F2 NumtCT.....T.....A.....T.....T.....A.....A.....A.....G.....
WEFCOM	8	-----
HM589215	P27	GTGGATACAGCAGCATACTTACGTCACTACTATAATTACGCTATTCTACTGGGTAAAGTATTAGCTGATTGGCCACTCTCACGGGGTAAATTAAATGGCTCCCGTATACTATGGCTTGGGATTCAATTCTATT
JF357971	CORBETTI1
DQ151550	
DQ151551	F2 NumtC.....A.....T.....C.....C.....T.....A.....C.....C.....T.....G.....A.....C.....C.....
WEFCOM	8	-----
HM589215	P27	ACCGTAGGGGCTTAACAGGAATTGTATTAGCAAACCTCTCATTGGATATTGCTTCACGACACATACTACGTAGTAGCCCACCTCCACTACGTCTGTCAATAGGAGCAGTATTGCTATCATAGGGGCTTGTCACTGATTCCCC
JF357971	CORBETTI1
DQ151550	C.....
DQ151551	F2 NumtA.....C.....T.....A.....T.....T.....
WEFCOM	8T.....A.....C.....T.....

