

Table S1. Species names, mitochondrial genome sequences used for phylogenetic analysis

		Species	Accession number
Torpediniformes	Narcinidae	<i>Narcine timlei</i>	This study
		<i>Narcine tasmaniensis</i>	JN171594.1
		<i>Narcine entemedor</i>	NC 025512.1
		<i>Narcine bancroftii</i>	NC 034772.1
		<i>Narcine brasiliensis</i>	NC 034771.1
	Torpedinidae	<i>Torpedo marmorata</i>	NC 059941.1
		<i>Tetronarce macneilli</i>	JN184080.1
	Narkidae	<i>Narke japonica</i>	MZ417389.1
		<i>Typhlonarke aysoni</i>	JN184082.1
Myliobatiformes	Gymnuridae	<i>Gymura poecilura</i>	NC 024102.1

Table S2. Structural characteristics of the mitochondrial genomes of species used in this study

Accession number	Species	Length	ND1	ND2	COX1	COX2	ATP8	ATP6	COX3	ND3	ND4L	ND4	ND5	ND6	CYTB	All 13 PCGs	%A	%C	%G	%T	G+C	A+T	Skew_AT	Skew_GC	#CDS	#tRNA	#rRNA	#CR
This study	<i>Narcine timlei</i>	17964	975	1047	1557	699	168	684	786	351	297	1378	1827	516	1143	11428	36.19	22.68	11.92	29.21	34.6	65.4	0.10673	-0.311	13	22	2	1
NC 025512.1	<i>Narcine entemedor</i>	17081	975	1047	1557	693	168	684	786	351	297	1383	1827	516	1143	11427	36.22	21.95	11.94	29.89	33.89	66.11	0.09575	-0.2954	13	22	2	0
NC 034772.1	<i>Narcine bancroftii</i>	16971	975	1044	1560	693	168	687	786	351	297	1383	1818	516	1140	11418	34.29	22.82	12.98	29.92	35.8	64.21	0.06806	-0.2749	13	22	2	1
NC 034771.1	<i>Narcine brasiliensis</i>	16997	975	1044	1560	693	168	684	786	351	297	1383	1824	516	1140	11421	34.45	22.64	12.88	30.02	35.52	64.47	0.06871	-0.2748	13	22	2	0
JN171594.1	<i>Narcine tasmaniensis</i>	11188	975	1044	1542	693	158	683	786	351	290	1383	1822		366	10093	27.76	21.48	11.33	29.47	32.81	57.23	-0.0299	-0.3094	12	0	0	0
NC 059941.1	<i>Torpedo marmorata</i>	17810	972	1047	1554	693	168	684	786	351	297	1383	1824	516	1143	11418	34.33	22.05	12.26	31.35	34.31	65.68	0.04537	-0.2853	13	22	2	0
JN184080.1	<i>Tetronarce macneilli</i>	9716	805	1046	1542	693	158	683	785	351	290	1383	984			8720	27.23	19.45	11.25	29.55	30.7	56.78	-0.0409	-0.2671	11	0	0	0
MZ417389.1	<i>Narke japonica</i>	17990	975	1053	1557	693	168	684	786	351	297	1386	1827	519	1143	11439	34.87	22.28	11.98	30.87	34.26	65.74	0.06085	-0.3006	13	22	2	0
JN184082.1	<i>Typhlonarke aysoni</i>	10408	671	1047	1542	693	155	683	786	351	290	1383	1812			9413	27.69	20.84	10.17	28.24	31.01	55.93	-0.0098	-0.3441	11	0	0	0
NC 024102.1	<i>Gymura poecilura</i>	17874	975	1047	1557	693	168	684	786	351	297	1383	1821	522	1143	11427	28.46	30.07	14.99	26.49	45.06	54.95	0.03585	-0.3347	13	22	2	1

Table S3: Description of tandem repeats found in the control region of the assembled mitogenomes.

Indices	Period	Copy	Consensus	Percent	Percent	Score	A	C	G	T	Entropy
	Size	Number	Size	Matches	Indels						(0-2)
270--360	47	1.9	47	86	4	130	34	26	5	34	1.8
1403--1427	10	2.5	10	100	0	50	40	0	0	60	0.97
1714--1758	22	2	23	83	12	58	40	17	4	37	1.7

The summary table includes the following information:

1. Indices of the repeat relative to the start of the sequence.
2. Period size of the repeat.
3. Number of copies aligned with the consensus pattern.
4. Size of consensus pattern (may differ slightly from the period size).
5. Percent of matches between adjacent copies overall.
6. Percent of indels between adjacent copies overall.
7. Alignment score.
8. Percent composition for each of the four nucleotides.
9. Entropy measure based on percent composition.

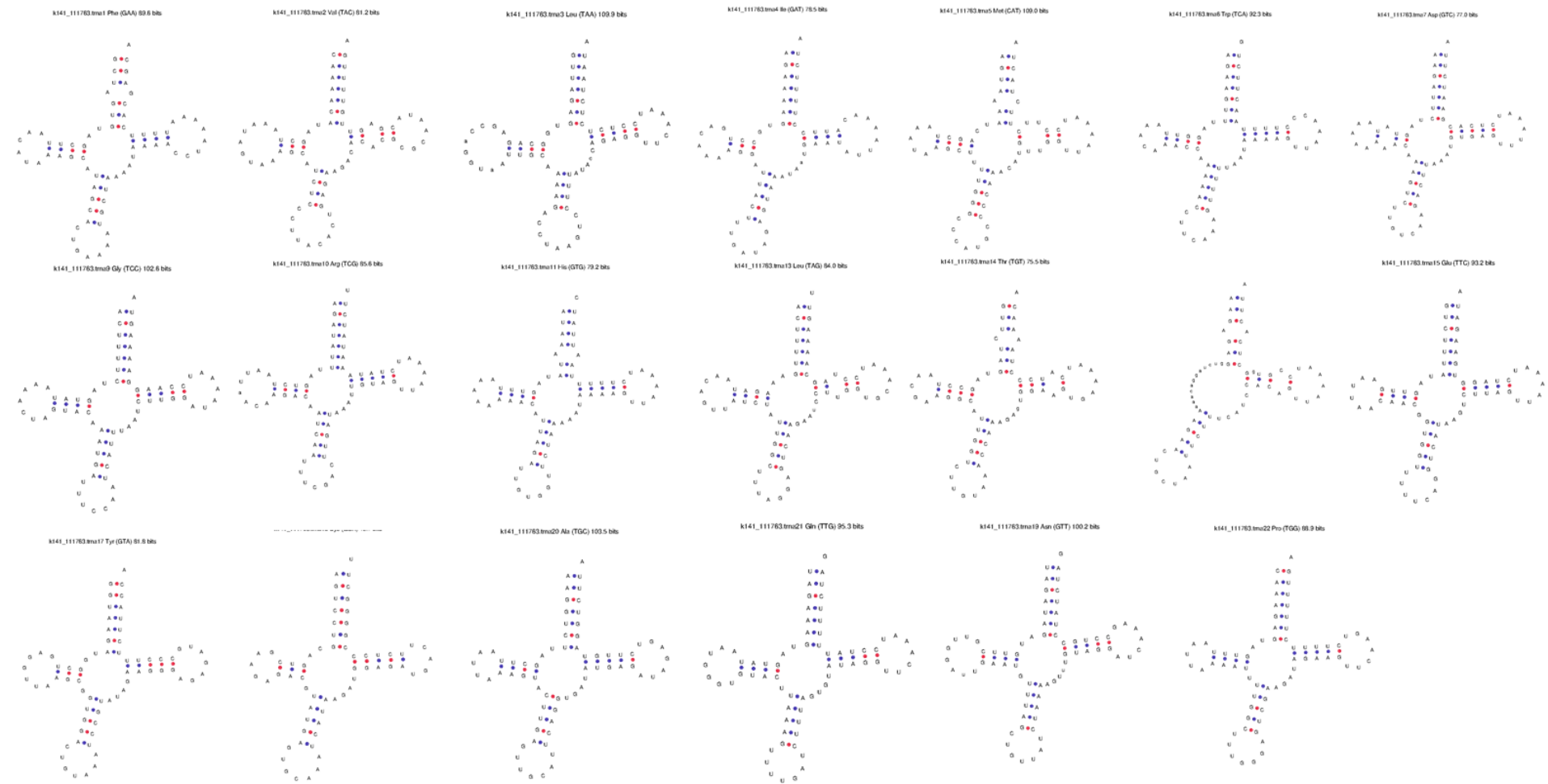
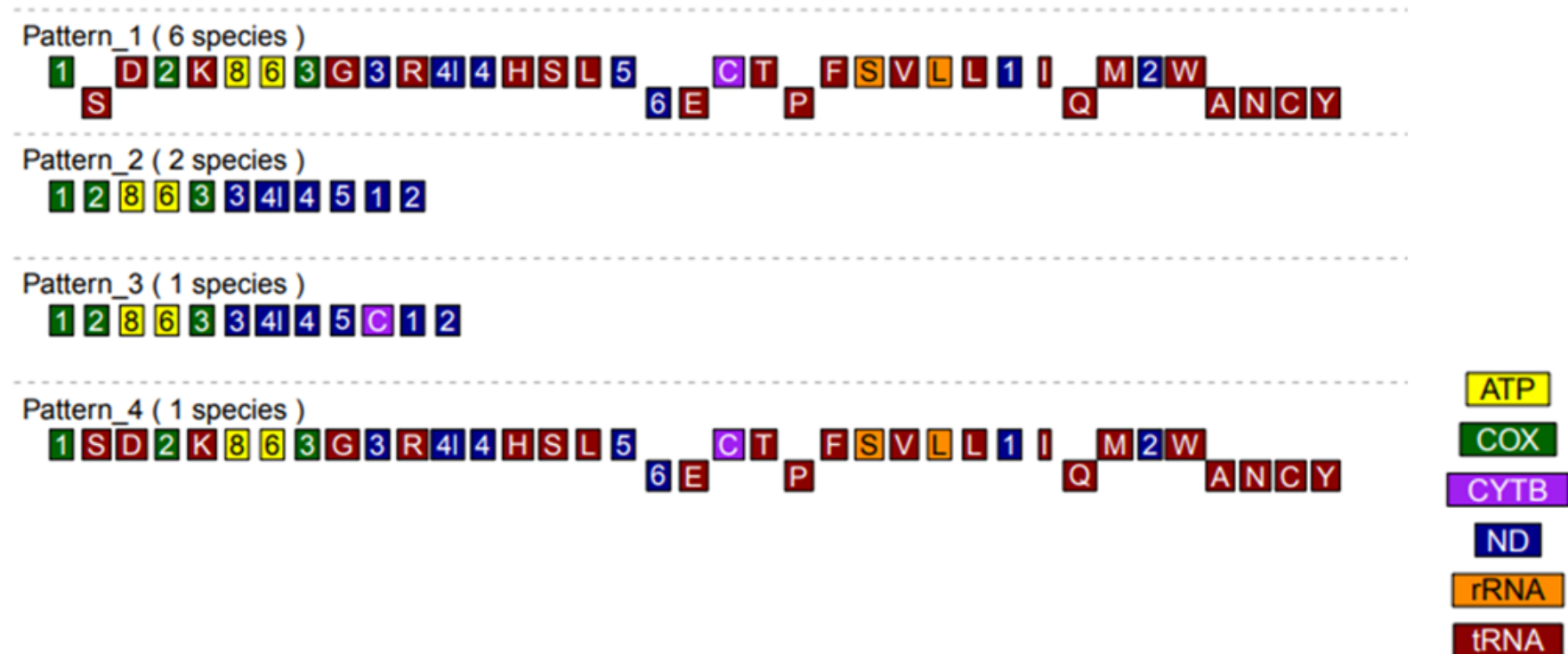


Figure S1. Secondary structure of tRNAs in the mitochondrial genome of *N. timlei* predicted by tRNAscan-SE v2.0.



Pattern – 1	Pattern- 2	Pattern- 3	Pattern- 4
<i>Gymnura poecilura</i>			
<i>Narcine bancroftii</i>			
<i>Narcine brasiliensis</i>	<i>Tetronarce macneilli</i>	<i>Narcine tasmaniensis</i>	<i>Narke japonica</i>
<i>Narcine entemedor</i>	<i>Typhlonarke aysoni</i>		
<i>Narcine timlei</i>			
<i>Torpedo marmorata</i>			

Figure S2. Gener order, patterns in *N. timlei*, and other Torpediniformes.

AAATATACACCACTAAAAAGGCACATAACAACCTAGTTGGTCACCAACATACGTGCCAACAACAACCAACTTCCGCC
ACATCAGTACAATCAAATACTCACCCCATGCTCCTACAGCTCCTTAATAAAACATTAACCATTACCAACCTACAAA
ATAACACCAAAAACCCATAGTATGCCAAATCAATTTCTATCACGTTAGTTGTTTTACACAACAATAGCAATTTTCAGTG
AGAAGCACCACGCCAATAGTATAGTTATATAAACACA

CTATGTATAATCAGCATTAACAGACATTCCCCATATTCATTACATCCCTATGTATAATACCCATTAATAGACATTCTCATCTTCATTACA

TANDEM REPEAT 1

CTTAAGTTTTTAAATCCTAACAAATCTAATTTCCAAAATTCATTACATAATTCCATAAAACTACCTCATTTTCATTAAATTA
ATCGTTATTCCATTCCATATTATTCTAATTAATAATTTAACAGTATTATCCAACCATTATGTGGGTTGGCGAGAAATCAG
CAATGACCTATTCTATCCACCTTTGTACGTTTGTAGCACAGATTAAAGATTAATCCCTTATAATTGCTTAAATGCCGGC
ATTTGGCAACCTTGTAATACATACGGTTCTGCTCGTATCACGAATTTATTACCCCTAGTTACCATTATTGACACTTTACT
CTTACCTGATGTCTGTCCCACGACAGACGGTAAGAGTACTCTTAATTGTCTCAAGATTTATTTCCCTCCCAGTTTTTTT
CTTCTTGGTATGCGAGCAATCGCTAGCCGGGTCGAAGGCCCGTTCAGGTCATTATCTTAGATTTGCGTTATCCTCGAC
ATATCATATATTAATCCATTACTAATTCATTCATGAATTATGATTGTCAAGTAACTTTAGTGGTAGGCTTCCTTTAATAT
TGTTATCATCATTGACAAGCGCAACGTAGGTTTAGTTGTACGCTGAATAATTTCACTACTTTCACTAATTAATTGTGAA
ACGAGTTTCACAATGAAATAGTGAATGACAAGAAGATATTAGGTAGTGGAAATATACTCATAATAACAGGTATTAATT
ATCGTCTAATGTAAATTCGTTATCAAATCTTAGGAACATTTAAAGATTTATTGGACATTATTATTATATATATGCCCCCTC
TTTCGAAAACGAACGAAAAAACAACACTTTTACAAATTTTTTCGAAAAACCCCCCTCCCCCTGCACTTC
GAGTTATTCTCGAAAAACCCCTAAACGAGGACTGGAAGTGCATTTTCCGGGCGATGCAAAAGCAATCAAAAACGC
CATTTTTATTGTGACATGCCATTTTTGACACATCACTGATATCAACCAATTTTGGGCAAAAAAAGTGAAAAATT
TTCA

TTTTTTTTTTTTTTTTTAAAAATTTTAAAAATTTTT

TANDEM REPEAT 2

TTCATTTTTTTTTTAAACAAAAAATAGGAACAAAATCCATATTTTTTGAAAATGTTTTAAAATGATTTTAAAAATAAAA
ACTTTAACTAATCTTACCTCAAAAACAAGAGCGAATATTATATATATAACCACAAAACCAAGATAATAAGTATAATGGA
ATAATAAACTTATATATTATTATCTTAAGTAGAATGGAATATACACATAACAAAATTAATACACTAAAAACGGAAATGA
GGTACACACGTATAATACAATAAACAGCACATACACTGCCATACACAA

ATATACATGTATTAAACCCTATCATATAATGTTTAAACTCATATC

TANDEM REPEAT 3

CTTAGTTATTAACTCCCATCGCCATATATAGGACTAAATCAGTACACCATGTATCTCTAAAAACTTAAAAATAAGAGT
TACATAATCATTATTAAACCACAATATACATTATCCTACTTAAAAATTTAACGTATAAATCAATTATAGTGTGTAACAT

Figure S3: Sequence of mitochondrial putative control region highlighting tandem repeats.