

ACTCTCCGCAAGTGGCTTTT--AAGAGCCACTGGTTACACTTCAAGTCCATCTCAAGGCGCGGACCA--CATCTCCCTCTCTAGCTTTTCCAAAGCCCTTTGGTGCGAACCGGTTATATGGTGACATACACCTCATGTCTTT--ATACAGC--TGCAGCATGT
 ACTCTCTCCAGAGTGCCTTT--AAGAGCCACTGGTTACACTTCAAGTCCATCTCAAGGCGCGGACCACTCTCCCTACTAGCTTTTCCAAAGCCCTTTGGTGCGAACCGGTTATATGGTGACATACACCTCATGTCTTT--ATACAGC--TGCAGCATGT
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 ACCCTCTCCAGTGTGACTTT--AAGAGCCACTGGTTACACTTCAAGTCCATCTCAAGGCGCGGACCACTCCCGGCTCATAGCTTTTCCAAAGCCCTTTGGTGCGAACCGGTTATATGGTGACATACACCTCATGTCTTT--ATACAGC--TGCAGTGTAGTG
 ACCCTCTCCAGTGTGACTTT--AAGAGCCACTGGTTACACTTCAAGTCCATCTCAAGGCGCGGACCACTCCCGGCTCATAGCTTTTCCAAAGCCCTTTGGTGCGAACCGGTTATATGGTGACATACACCTCATGTCTTT--ATACAGC--TGCAGTGTAGTG
 ACTCTCTCCAGTGTGACTTT--AAGAGCCACTGGTTACACTTCAAGTCCATCTCAAGGCGCGGACCACTCTCCCTACTAGCTTTTCCAAAGCCCTTTGGTGCGAACCGGTTATATGGTGACATACACCTCATGTCTTT--ATACAGTGTATGAGAAC
 ACTCTCTCCGCAAGTGGCTTTT--AAGAGCCACTGGTTACACTTCAAGTCCATCTCAAGGCGCGGACCACTCTCCCTACTAGCTTTTCCAAAGCCCTTTGGTGCGAACCGGTTATATGGTGACATACACCTCATGTCTTT--ATACAGTGTATGAGAAC
 ACTCTCCGCTTTATGTGTTT--AAGAGCCACTGGTTACACTTCAAGTCCATCTCAAGGCGCGGACCACTCCCGGCTCATAGCTTTTCCAAAGCCCTTTGGTGCGAACCGGTTATATGGTGACATACACCTCATGTCTTT--ATACAGTATGTCGAGTG
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 C--CCCTCTCTCTTGGCTTTT--CCAAAGCCGCTGGTTACACTTCAAGATCATCTCGAATGTCGGGACCACTCCCTCATACTAGCTTTTCCAAAGCCCTTTGGTGCGAACCGGTTATAT--TGTGACATATACACCTCATGTCTTG--ATACAGTATGTCGAGTG

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TAATAAAACAATACGAGATTGATATACAATA
TTAATAAAACAAATACGAGATTAAATATATAAAAT
TATGCGGAAATTAATAAATACTCTGAGCGCTATC
ACCGATAAATTAAACTACCCCAACCCATCTTCAACCCATAACCCATGAACCAT

[--repeat sequence
--TTATAAAATAATCGAGATTAAATATAAATATATTCTCCACCAGCCTCCTCCCAAAAAAAGGTACAAGCATGTTTCGTTCGATG
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TAATTTTTTATCCAGTTTTTACTATTATTAGTTCTAACAGCCTATTTAAAAATATTAAATTACTTCTCACACTACTATAGCATTTTTACCTTTAA} 10 tandem repeats of 190bp sequence
GTTTTTATTATTATTATCTAAAACTATTAAAGAAATTTAAATCACTCTCAGCGTATTATAGCTATTTTATCTTTACTTTATAAAACAATACGAGATTAAATATATA} 8 tandem repeats of 197bp sequence
TAGAATTTATCGCATTGTAGCTTTAATTCAGTTTATTATTAAAGTTTCTAAAACTATTAGGAATATTAAATTACTCTCGCGCTATTATAGCGATTTTAT} 13 tandem repeats of 198 bp sequence
TAGAATTTATCGCATTGTAGCTTTAATTCAGTTTATTATTAAAGTTTCTAAAACTATTAGGAATATTAAATTACTCTCGCGCTATTATAGCGATTTTAT} 14 tandem repeats of 198 bp sequence
TTATTATTGTTTATTCTAAAACTATTAAAGAAATTTAAATTATCTCACACTATTATTAGCGCTTTTATCTTTATTATAAAACAATACGAGATTAAATATATAAAAT} 4 tandem repeats of 199 bp sequence
ATTACAATACTGATTTTTTATAATAAAAACTACTATAAAAAACCAATAAGACTTAGATAAATTTACGATAAAATAACCACTCCCCCTCAATAATTGTATTAAATGCAAAATCTTCCCCACTAATATAGTTATTTTATCCCATGCTTACAG} 2 tandem

->][-- tRNA-Phe ->]
GTTATCA-TA-GCTT-ACAACC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CTT---ACC--TGATAACA--ACCCACAGTGAATAATGCTATTACAACCCATTATTAAATACAACACTAA

repeats of 241 bp sequence

AAACCGCCTACTTTATTGAAGTAGGTCTCTATTACATGGCTACTCAAATATCTTATACATTATCTCATGATCTAAGCAACCAACCTCTAACAAGCAATACGCGCATCATATAGTATTTTATAAAGACCGCACGTAAACCTACTCTTTATAN

[illegible][illegible]

(CSB-1)

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CTTTACCTGACACACATATATGCTGTGTTACC-GTTACCCCT-ACCGGGGTGGACAACCTT-AGTCCGGGTGGCGCTAATTTCTGTGCTACGATCTTCCTC-TATAGAGTACA--TTCTCTCCATGTTTTAGACATA--TTTTCTCTGGCAC
CTTTACCTGACACACCATATATGCCGCTTTACC-GTTACCCCT-ACCGGGGTGGACAACCTT-AGTCCGGGTGGCGCAATTTCTGTGCTACGATATTCCTC-TATAGAGTACA--TTCTCTCCAGTATTTTAGACATA--TTTTCTCTATGCC

CTTTCACTGACACCAATATATGCCCGGTATCC- GTTATCCCT- ACCGGGGGTAGACACTTT- AGTCACGGGTGGAGCTGATTTGTGGCTTCAGACATCC- TATATGGATACA- TCTCTT- CARGCTGTATAGACATA- TTTTCTCTCCGAC
 TTTTCACTGACACCAATATATGCCCGGTATCC- GTTATCCCTCACTGGGGGTAGACATTT- AGTACAGAGTGGAGCTGATTTGTGGCTCAGACATATCC- TATATGGATACA- TCTCTT- CARGATTTATAGACATA- TTTTCTCTCTCTC
 CTTTCACTGACACCAATATATGCCCGGTATCC- GTTATCCCTCACTGGGGGTAGACACTTT- AGTACAGAGTGGAGCTGATTTGTGGCTTCAGACATCC- TATATGGATACA- TCTCTT- CARGATTTATAGACATA- TTTTCTCTCCGAC
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 CTTTCACTGACACCAATATATGCCCGGTATCC- GTTATCCCT- ACCGGGGGTAGACACTTT- AGTCCGGGTGGAGCTAATTTGTGGCTAGACATATCC- TATATGGATACA- TTTCTT- CARGCTGTGTAGAGACA- TTTATCTTCCGAC
 CTTTCACTGACCACTCACTT- GCGGCTGATCC- GTTCTCCC- CACTGGGGGTAGACACTCACTGACGGGTGGAGCTAATTTGTGGCTCAGACATATCC- TATACGGATACA- TCTCTT- CARGCTGTGTAGAGACA- TTTTCTCTCTGAG
 CTTTCACTGACACCAATATATGCCCGGTATCC- GTTATCCCTCACTGGGGGTAGACACTTT- AGTCACGGGTGGAGCTGATTTGTGGCTCAGACATCC- TATATGGATACA- TCTCTT- CARGATTTATAGACATA- TTTATCTCTACAC
 CTTTCACTGACCACTCAATATATGACACACAGTTAGGATTTAGTCCG- GG- GTT- -AGACATA- TGTATGCTCTCCACCACTCCCTTGAAGGCTA- CA- -TCTC- TTAAGCTGTGTAGAGACA- TATCTTTTTCTCCG

[CSB-3]

[illegible]

ATGTTATCTTTGAATACCCCTACATCACACTTAACATATTTAACCCGGGTTTCACACTTTTAACTCCTAAAAGCTATTAAAAATAAAAACTTCCCACTACGCTACTATAGCATTTTATCTTTAA-----
 TATACCCCAACAGCCGCTTTATATATT-----
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[illegible]

TGGCTGATTTTATATAGTAATAA-
 AGATTTTATATACAAAT-----
 GAAATTCATATATAAAAAAT---
 TTTTATATATAAAATTTATTTTACCTACCAAAATTAACAGCAAAAAATTCCTATAAAAATTATCTCTGAGAGATGATTTTACATTTTAAATTTTTTTTCTCTCAAAAAAGTGCCCAATTTCCCGCTGCTTTCAACACTATGCGGAGATTAATAATA
 AATTGGAGACTATTTATATAAAA-
 TATTGGCAGTCATAATACGGGGAATTTGTATACTGAATCTACAACAAAAAT-
 ATGCTAAATTTCTTACAACATTATAACTTTCAACTTATATTTTAGCCCATAAAAGTACT-
 ATCTCAAAATTTTATACAATTTTTPAAAAGCTTACTGTTAAAGGCATCAAAATATTAATTTCAATACTATATAATCTCAACAAAAACCCTTAATTTATTAACATAAA-
 ATCTCAACACTCTCCCGAATTTTATATAA-
 CTAAATCTCTGTAGTCTCAAAATTTTATATATA-
 TTTCAACCAACACCGGAATTTCTATATAATTGCG-
 GGAAAACCAACCTCTTAATCAGCATTTGACGTTTGCTTCTTATATAAATTACTCTTATCTACACACTCAAAAGCAAAATCCAACATCATCCACTTTCTCTACACACCCCAAAA-

[illegible]

TATAAACATATTCTATTAT-CACCTTTTT---ACTCTTCCCTTGAGAAGCAACACAATATATTTTAA--TTCCGAGTTTTTATTATTATAAATCTCAAAAATCTTCAGAATATTAAACCACCTCTCACACTATTATAGCGCTTTTATCTTTATTATATAAATATATTATTGT-CACCTTTTT---ACTCTTCCCTTGAGAAGTAACACAATANATTTTA--TTCCGAGTTTTTATTATTATTATTCTCAAAAATCTTAAGAATATTAAAAATCTCTCACACTATTATGGTGATTTTATCTTTATTATCTAATAATATATTCTCCACCTTTTTTTACTACTCCCCCGAAAAACAACAACAACATACTTTA-ATCCC-ATTTTATTATTATTAGGTACCTTAAAA-CTTAAGAACAATT--AAATCACTCTCACACTACTGTAATGATTCTATTCTTATCA

AG--GCAAGCAG-GCAGGCAGATT-----GAGTTGCTCACAGAATCACAGATTCATTCTAGAGATCTATCTATCTGCATCGGCT-AGCTCAGTCTGTACATAAAAATTGCTTGCAGCAAACTCA-----CAAAATTAATCT

[illegible][illegible]

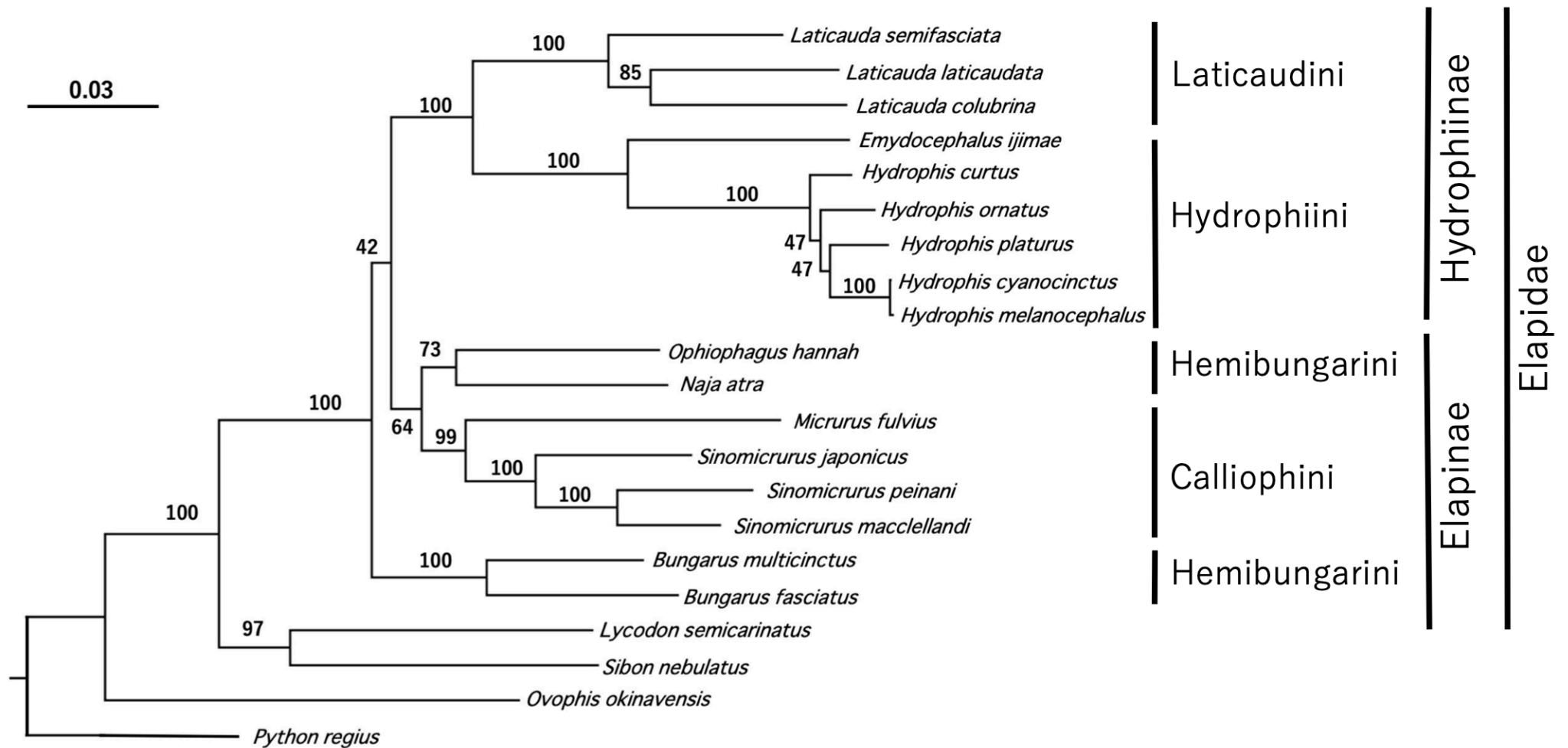
Supplementary figure S3. Sequence comparison of the MNCR2 region among 21 snake species. The control region sequences were aligned with the aid of ClustalX software after identifying common sequence blocks (C-rich, CSB-1, CSB-3, and coreTAS sequences). Transfer RNA genes were aligned based on their clover-leaf secondary structures. The red line indicates the anticodon of each tRNA gene. Sequences for tandemly duplicated regions are represented by a single repetitive unit sequence with a note on repetitive numbers.

scientific name	Accession number	[+ tRNA-Ile →]
1. Emydocephalus ijimae	LC648431	GGAAGCG-TG-CCCG-AGC-----AAGG-A-CTACA-TTGATAG-AGTAG-ACAC--GGAG--ACCATAAA-----CTCC-CACCTTCCC
2. Hydrophis ornatus	LC648430	GGAAGCG-TG-CCCG-AGT-----AGGG-G-CTACA-TTGATAG-AGTAG-CCAC--GGAG--ACCGAAAA-----CTCC-CACCTTCCC
3. Hydrophis melanocephalus(1)	LC648429	GGAAGTG-TG-CCCG-AGT-----AGGG-A-CTACA-TTGATAG-AGTAG-ACAC--GGAG--ACCGAAAA-----CTCC-CACCTTCCC
4. Hydrophis melanocephalus(2)	LC648429	AGGAAGTG-TG-CCCG-AGT-----AGGG-A-CTACA-TTGATAG-AGTAG-ACAC--GGAG--ACCGAAAA-----CTCC-CACCTTCCC
5. Hydrophis curtus	MK953549	GGAAGTG-TG-CCCG-AGT-----AAGG-G-CTACA-TTGATAG-AGTAG-ACAC--GGAG--ACCGAAAA-----CTCC-CACCTTCCC
6. Hydrophis platurus	MK775530	GGAAGCG-TG-CCCG-AGT-----AGGG-A-CTACA-TTGATAG-AGTAG-CCAC--GGAG--ACCGAAAA-----CTCC-CACCTTCCC
7. Hydrophis cyanocinctus	NC046795	GGAAGTG-TG-CCCG-AGT-----AGGG-A-CTACA-TTGATAG-AGTAG-ACAC--GGAG--ACCGAAAA-----CTCC-CACCTTCCC
8. Laticauda semifasciata	KY496325	AGGAAGCG-TG-CCCG-AATTA---AAGG-A-CTACC-TTGATAG-CGTAG-ACAT--GGAG--CTCCCTCA-----ACCA-CAACCAACA
9. Laticauda colubrina	KY496324	GGAACCG-TG-CCCG-AGT-----AGGG-G-CTACC-TTGATAG-AGTAG-ACAC--GGAG--ACCAACAAA-----CTCC-CGCTTCCCT
10. Laticauda laticaudata	KY496323	GGAAGCG-TG-CCCG-AGCA---AAGG-A-CTACA-CTGATAA-AGTAG-ACAC--GGAG--CCTATAAA-----CTCC-CGCTTCCC
11. Sinomicrurus japonicus	LC648432	GGAGGCG-TG-CCCG-AGCA---CAGG-G-CTACC-TTGATAG-AGTAG-ATAC--GGAA--CCCATAAA-----TTCC-CACCTTCCC
12. Sinomicrurus peianii	MZ230594	GAAGACG-TG-CCTG-AGT-----AAGG-A-CTACC-TTGATAG-AGTAG-ACAC--GGAA--CCCATAAA-----TTCC-CGCTTCCC
13. Sinomicrurus mecklelandi	MT547176	GGAGGTG-TG-CCTG-AGA---AAGG-A-CTACA-TTGATAA-AGTAG-ACAC--GGAG--CCATACCTCCAC-CTCC-CACCTTCCC
14. Micrurus fulvius	GU045453	GGAAGCG-TG-CCCG-AGAA---AAGG-A-CTACC-TTGATAG-CGTAG-ACAC--GGAG--CCATATAA-----CTCC-CGCTTCCC
16. Ophiophagus hannah	EU921899	GGAAGTG-TG-CCCG-AGT-----AAGG-A-CTACA-TTGATAG-CGTAG-ACAC--GGAG--CCCAAAA-----CTCC-CGCTTCCC
15. Naja atra	EU913475	GGAAGCG-TG-CCTG-AGT-----AAGG-A-CTACC-TTGATAG-TGTAG-ACAC--GGAA--CCCAAAA-----TTCC-CGCTTCCC
18. Bungarus multicinctus	EU579522	GGAAGTG-TG-CCTG-AGT-----AAGG-A-CTACC-TTGATAG-CGTAG-ACAC--GGAA--CCCAATAA-----TTCC-CACCTTCCC
17. Bungarus fasciatus	EU579523	GGAAGTG-TG-CCCG-AGCT---AAGG-A-CTACC-TTGATAG-AGTAG-ACAC--GGAA--CCATATAA-----TTCC-CACCTTCCC
19. Lycodon semicarinatus	AB008539	GGGGGTG-TG-CCCG-AGT-----AGGG-A-CTACC-TTGATAG-AGTAG-ACAC--GGAA--CCATATAA-----CTCC-CACCTTCCC
20. Sibon nebulatus	NC013985	GGAAATG-TG-CCCG-AGTC---AAGG-A-CTACC-TTGATAG-AGTAG-ATAC--GGAA--CCATATAA-----CTCC-CACCTTCCC
21. Oviphis okinavensis	AB175670	GGAAGTG-TG-CCTG-AGAACAC-AAGG-A-CTACC-TTGATAG-AGTAG-ACAC--GGGA--ACCCACA-----ACCC-CACCTTCCC
22. Python regius	AB177878	GGAAGTG-TG-CCCG-AGAC---AGGG-A-TTACC-TTGATAG-AGTAA-ACAC--AGGA--TTACAA-----CCCT-CACCTTCCC

Supplementary figure S4. Sequence comparison of tRNA^{Ile} genes among 21 snake species based on their clover-leaf secondary structures. *Hrdrophis melanocephalus* mtDNA encodes two copies of tRNA^{Ile} genes (noted with 1 and 2) that correspond to I₁ and I₂ in Fig. 3, respectively. The red line indicates the anticodon.

scientific name	Accession number	[+ tRNA-Phe →]
1. Hydrophis melanocephalus(1)	LC648429	GTTATC-A-TA-GCTT-ACAACC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CCT---ACC--TGATAACA
2. Hydrophis melanocephalus(2)	LC648429	GTTATC-A-TA-GCCC-TTATT---AAGC-G-CAGCA-CTGAAAA--TGCTA-AATT-ACC-CCA---ACT--TTATAACA
3. Hydrophis melanocephalus(3)	LC648429	GTTATC-A-TA-GCCC-TTATT---GGG-G-CAGCA-CTGAAAA--TGCTA-AATT-ACC-CCA---ACT--TCATAACA
4. Hydrophis melanocephalus(4)	LC648429	GTTATC-A-TA-GCCC-TTATT---AAGC-G-CAGCA-CTGAAAA--TGCTA-AATT-ACC-CCA---ACT--TCATAACA
5. Hydrophis melanocephalus(5)	LC648429	GTTATC-A-TA-GCCC-TTATT---GGG-G-CAGCA-CTGAAAA--TGCTA-AATT-ACC-CCA---ACT--TCATAACA
6. Hydrophis melanocephalus(6)	LC648429	GTTATC-A-TA-GCCC-TTATT---AAGC-G-CAGCA-CTGAAAA--TGCTA-AATT-ACC-CCA---ACT--TCATAACA
7. Hydrophis ornatus(1)	LC648430	GTTATC-A-TA-GCCC-TTATT---AAGC-G-CAGCA-CTGAAAA--TGCTA-AATT-ACC-CCA---CCT--TATTAAACA
8. Hydrophis ornatus(2)	LC648430	GTTATC-A-TA-GCCC-TTATT---AAGC-G-CAGCA-CTGAAAA--TGCTA-AATC-ACC-CTA---ACT--TTATAACA
9. Hydrophis ornatus(3)	LC648430	GTTATC-A-TA-GCCC-TTATT---AAGC-G-CAGCA-CTGAAAA--TGCTA-AATC-ACC-CTA---ACT--TTATAACA
10. Hydrophis cyanocinctus	NC046795	GTTATC-A-TA-GCTT-ACAACC---AAGC-A-YAGCA-CTGAAAWN-TGCTA-AAAC-GGT-CTT---ACC--TGATAACA
11. Hydrophis platurus	MK775530	GTTATC-A-TA-GCCC-TTATT---AAGC-A-TAGCA-CTGAAAA--TGCTA-AATT-ACC-CC---AAT--TTATAACA
12. Hydrophis curtus	MK953549	GTTATC-A-TA-GCTT-ACAACC---AAGC-A-CAGCA-CTGAAAA--TGCTA-AGAC-AGC-CCA---ACT--TTATAACA
13. Emydocephalus ijimae	LC648431	GTTATC-A-TA-GCTT-ACAACC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CCC---ACC--TAATAACA
14. Laticauda semifasciata	KY496325	GTTATT-A-TA-GCTT-ATAATC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAT-GGT-CTAC---TCC--TGATAACA
15. Laticauda colubrina	KY496324	GTTGTC-A-TA-GCTT-AAAATC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAT-GGC-CCAC---TCC--TGATAACA
16. Laticauda laticaudata	KY496323	GTTATT-A-TA-GCTT-ATATC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAT-GGT-CCAC---CCC--TAGTAACA
17. Sinomicrurus japonicus	LC648432	GTTATC-A-TA-GCTT-ACCTTC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CTA---CCC--TGATAACA
18. Sinomicrurus peianii	MZ230594	GTTATC-A-TA-GCTT-ACCTTC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CCT---ACC--TGATAACA
19. Sinomicrurus mecklelandi	MT547176	GTTATC-A-TA-GCTT-ACAATC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CTC---CCC--TGATAACA
20. Micrurus fulvius	GU045453	GCTATC-A-TA-GCTT-ACCTTC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CT---TCC--TGATAGCA
21. Ophiophagus hannah	EU921899	GTTATC-A-TA-GCTT-ACACTC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CCC---CCC--TGATAACA
22. Naja atra	EU913475	GTTGTC-A-TA-GCTT-ACCTATC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CAAT---GCC--TGACAGCA
23. Bungarus multicinctus	EU579522	GT-ACG-G-TA-GCTT-ACGATTA---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-CTC---GCC--TGATAACA
24. Bungarus fasciatus	EU579523	GTTATT-A-TA-GCTT-ACCTATC---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-ATTC---ACC--TGATAACA
25. Sibon nebulatus	NC013985	GTTATC-A-TA-GCTT-ACCTATC---AAGC-G-TAGCA-CTGAAAA--TGCTA-AGAC-GGC-ACAGC-CTGA-TC--TAACA
26. Lycodon semicarinatus	AB008539	GTTATC-A-TA-GCTT-ACGAATTA---AAGC-A-TAGCA-CTGAAAA--TGCTA-AGAT-GGT-CTAC---ACC--TGATTTAA
27. Oviphis okinavensis	AB175670	GTTGTCG-TA-GCTT-AAAGCTTA---AAGT-A-TAGCA-CTGAAAA--TGCTA-AGAT-GGT-CCA---ACC--CTCCAACA
28. Python regius	AB177878	GTTATT-G-TA-GCTT-ACACCA---AAGC-A-CAGCA-CTGAAAA--TGCTG-AGAC-GGT-ATTAC-ACCC-AAATAACA

Supplementary figure S5. Sequence comparison of tRNA^{Phe} genes among 21 snake species based on their clover-leaf secondary structures. *Hydrophis ornatus* mtDNA encodes three copies of tRNA^{Phe} genes (noted with 1-3) that correspond to F₁-F₃ in Fig. 3, respectively. *Hrdrophis melanocephalus* mtDNA encodes six copies of tRNA^{Phe} genes (noted with 1-6) that correspond to F₁-F₆ in Fig. 3, respectively. The red line indicates the anticodon.



Supplementary figure S7. Maximum likelihood tree using amino acid sequences of 13 mitochondrial protein genes. Numbers at each node represent bootstrap probabilities from 5000 replications. Note that the monophyly of Hemibungarini is not seen in this tree and inter-species relationships within Hydrophiini in this tree are different from those in Fig. S6.