

(A) *SINE1-1\_EBu*

TGTTTCATAGTGGTTTGTAAATACCAACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----AGTGTGTTGTAATAACATTAACATT  
ATACATCACTGTTTATATAGCTTGTATACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----ATGTGTTATAGCTTGGATTAATCA  
TGTCCTGGCCATAGTGGTTTGGGGCCACCAGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAACAAC-----ACATAGTGTGTTGGGGCCATCTCTCA  
ACCCCTCACTTCACTGATGGGAAAACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAACAAC-----ACCTTCACTGATGGGAAAATTAAGAT  
NNNNATATATATATATGGGGTTAGCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----ATGTGTTGGGGTCTGTACACATTTG  
TTGTCAAGTTGACATGGCAGATGAGAACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----ACATGGCAGATGAGGAGGAGGCT  
ATCTAAAGTTAACCACTAGTATGACACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----AACCATTAGTATGATGATGATGATG  
GAAGGTTGACATCATCTTCTTAACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----ACATATAGGAGCTGTAACCTAGGAA  
TCCTCCATAGGAATGCTCTGCTGGAACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GTGGCAGCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----AGGAATGCTCTGCTGGTGGTGGT  
AATTTATGATGTAGGAGTGTGTAAACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GTGGCAGCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----ATGTAGTGTGTGTAAACAATAG  
CACCGATATATATGTTAGCCCTCTGACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GTGGCAGCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----ATATCTGTAGCTTCTAATCTGTT  
TGCTTTGACACCTTTTGTGATTTACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----ACCTTTTATGATTTCCAAAGTATGG  
GGGAAATATATCAATATATAGTGGCACCAGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAACAAC-----ATCAATATAGTGGCTAGGTTTCA  
AATCTTGACTTTGGTTTCACTTTTACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAACAAC-----ACTTGGTTTCACTTTTATGTTTTC  
AACAGCATATGATGCTGATCACTAACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAACAAC-----ACATGATGCTGATCACTAATTTAAC  
AAATGATACACACCGCGATGTAACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAACAAC-----ATACACCGCGGATGACACTTTTA  
TCACATATACATCGGCTGCTTACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAAC-----ACATGGGTGATGTTTCACTCTTCA  
ACTTCTCAACTTGGACATGAATATACCGGGCGTAGTGGCGTGGCCGTGTAATCCGGCTACTCGGAGGCT//GCACCCCTAACGGGAGCAGCCGAAAGACGAACAACAACAAC-----GTGACATGAATGGAAAACCTCAGC

(B) *RTE-2\_EBu*

GGATCCGTTAGGAGTCTTGTGTTAAACCCAGCCACTGTGGTTGCACAAGTTAGTGCACTCTCAGCCGCG//GCAACCCCTAATGGAAGCAGCCGAATGAAGAAGAAG-----AGGAGTCTTGTGATGATGCTCAAGAG  
TATTTAAATGATGATGATGACAAAACCCAGCCACTGTGGTTGCACAAGTTAGTGCACTCTCAGTGGCG//GCACCCCTAACGGGAGCAGCCGAAATGAAG-----AGGATGATGACAAAATGAATTTGAG  
GTGAATCATCAATGTTCTTCTGACACCCAGCCACTGTGGTTGCACAAGTTAGTGCACTCTCAGTGGCG//GCACCCCTAATGGAAGCAGCCGAAAGAGAAG-----ATTCATGTTCTTCTCCGTAARA

(C) *RTE-4\_EBu*

ACCCGTGCTTCACTGAATAGTTTCCGGCGTGTGCCCAAGTTAGAAATAGGTACACCGTACCCTGTGT//CCCCTCTTGCAGGAAAATGGCCCTTAAAAA-TGCCCTTTGTGTGTT----GTGCTCTGTGAATATGGGAAGGG  
GGAAATTTCTCTCATTCATCCACCTGGTGTGTGCCCAAGTTAGAAATAGGTACACCGTACCCTGTGT//CCCCTCTTGCAGGAAAATGGCCCTTAAAAATCCTGTTGTGTGTGTTG-TCATCCCTGTTTCTACCTGTGTAC

(D) *SINE2-1\_EBu*

TCCTTACCCTGGCCTAATATATATATGCTGGTGTGGTGCAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GTGACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----CCCTGGCCTAATATATCCAAATTT  
CCCCACATCCAGCTGATAGTGGAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGAAGAT-----CCAGCTGATAGTGGTTAAAAGGA  
TACCATGCTCTGACAGAGTATAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGA-----GCTCTGACAGAGTATGTTGCTGTC  
ATTAATACGCTAAGCCATATTTATGCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGAAG-----ACCTAAGCCATATTTGGTGGAGCT  
ATTGGTGGTATGATATTTGGCAGCCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----ATGGTGGTATGATGATGATGATATAT  
AATTAGGAGGTTGACAGCCCTGATGCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGA-----GAGGTTGAGCCGCTTTAAGAGAT  
GAAACACATTCATCACTCAGAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGAAG-----ATTCATCACTCAGAAATACAGAA  
CCATTTAATATAGATACTTCTCAAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGAAGACTTCTTCACTGGCAGGCGATTGGG  
GTGCTACTTAACTCAGATTTGAGAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGAAG-----ACTTAACTCAGATTTGTGGCACTG  
ACCACTACTGTGCAGAGCAATGAAAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGAAG-----ACTGTGCAAGCAATTTGTGCTGC  
TTGTATATCACTCACTTTGTAAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----ATCCATCACTAATGGGAACAATG  
ATGTGCTATGATACCACTATGAGCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----ATGTATACCATCTGATATATCAT  
AATATCTGATCACTATCTTACCTTACCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----GCTATATATCTTCTGGGCCAATC  
AGGCTGCTTTTGAACCTCAAAAAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCTGAAGAAGAAGAAGAATA-----TGCTTTTGAACCTCAAGTGTGCTG  
CACATTTACAGGTTATACAGAGGCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGAAG-----ATATACAGGTTATACACACACAT  
TAGTGTGGAGCTGTTATGCCAAGGCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAGAAG-----GACTGTTATGCCAATCTATGTTT  
CAGGACAGATACCGAGGATTTGATGCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----AGATACCGGAGGATTTGAGAGTATG  
AGATCTGTCAGTCACTTTGATAGCCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----ATTCGTGATCACTTTGATATAGC  
ATACATACATATATTGTGGACCGGAGCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----ATGATTTGGGCCCGGGGCTGGTGT  
AACAGCTACATGGCATTACCAGGCTGGTGTGGCGTAGTGGTTAGGCGAGCGGCTTGGATCCAAG//GCACCCCTAACGGGAGCAGCCGAAAGAAAGAAGAAG-----GGGCATTACCAAAATGGCAGCCAA

Figure S1. Target site duplications (TSDs). TSDs are shown in red. (A) *SINE1-1\_EBu* and (D) *SINE2-1\_EBu*, only the representative 20 copies are shown. (B) *RTE-2\_EBu* and (C) *RTE-4\_EBu*, all full-length copies are shown.

```

UCON3 [78-131]                CCAG-CAGGGTTAACTCAGCCCTTCATCCTTCTAA-GGTAGATAAAATGAGTTCCA Euteleostomi
UCON3_CM [64-116]            CCGG--TGGGTCCACTCAGCCCTTCACCCCTTTGA-GGTGATAAAAATGAGTACCA Callorhynchus (shark)
SINE2-1_EBu [88-140]        CCAG--GGGGTTGACTCAGCCCTTCATCCTTCCGA-GGTGCGGAAAATGAGTACCA Eptatretus (hagfish)
SINE2-1B_EBu [91-143]      CCAG--GAGGTTGACTCAGCCCTTCATCCTTCCGA-GGTGCGGAAAATGAGTACCA
SINE2-2_EBu [88-142]        CCAGGTGGGGTTGACTCGGCCCTTCATCCTTCCGA-GGTGCGGAAAATGAGTGCCA
SINE2-2B_EBu [90-144]      CCAGGTGGGGTTAACTCAGCCCTTCATCCTTCCGA-GGTGCGGAAAATGAGTGCCA
SINE2-2C_EBu [88-142]      CCAGGTGGGGTTGACTCTGCCCTTCATCCTTCCGA-GGTGCGGAAAATGAGTGCCA
SINE2-3_EBu [87-139]      CCAG--GGGGTTGACTCAGCCCTTCATCCTTCCGA-GGTGCGGAAAATGAGTACCA
SINE2-3B_EBu [90-144]      CCAGGTAGGGTTGACTCAGCCCTTCATCCTTCCGA-GGTGCGGAAAATGAGTACCA
SINE2-3C_EBu [87-141]      CCAGGTGGGGTTGACTCAGCCCTTCATCCTTCTGA-GGTGCGGAAAATGAGTACCA
SINE2-4_EBu [88-140]      CCAG--GGGGTTGACTCAGCCCTTCATCCTTCCGA-GGTGCGGAAAATGAGTACCA
SINE2-9_EBu [85-139]      TCAG-GGGGTTGACTCAGCCCTTCATCCTTCCGAAGGTGCGTAAAATGAGTACCA
SINE2-10_EBu [86-138]     CCAG--GGGGTTGACTCAGCCCTTCATCCTTCCGA-GGTGCGTAAAATGAGTACCA
SINE2-5_PM [64-113]        -----GGGGTTGACTCAGCCCTTCATCCTTCCGA-GGTGCGTAAAATGAGTACCA Petromyzon (lamprey)
SINE2-1_CrH [84-131]       -----AGGTTGACTCAGCCCTTCATCCTTCCGA-GGTGCGTAAAATGAGGACCC Crotalus (snake)
SINE2-1_NAm [67-113]       -----GTGCTCACCAGCCCTTCATCCTTCCGG-GGTGATAAAATG-GTACCA Necator (hookworm)
SINE2-2_NAm [72-118]       -----GTCAAACAAGCCCTTCATCCTTCCGG-GGTGATAAAATG-GTACCA
SINE2-15_ADi [104-151]     -----AAGTTCACTCAGCTTTCATCCTTCCGA-GGTGCGTAAAATGAGTACCA Acropora (coral)
SINE2-21_ADi [127-174]    -----AAGTTCATCAGCTTTCATCCTTCCGT-GGTGGTAAAATGAGTACCA
SINE2-1_XB [98-144]        -----AGGCCAACTCAGCCCTTCATCCTTCCGG-GGTGCGTAAAATGAGTACCG Xenoturbella
SINE2-2_NW [68-114]        -----GGGTCCACTCAGCCCTTCATCCTTCCGA-GGTGCGTAAAATGAGTACCA Nemertoderma

```

**Figure S2. Sequence alignment of UCON3 domains of SINEs.** Nucleotides identical to those of *UCON3* are colored in red. The positions inside of Repbase entries are shown in parentheses. Abbreviations for organism names are as follows: ADi, *Acropora digitifera* (coral); CM, *Callorhynchus milii* (elephant shark); CrH, *Crotalus horridus*, timber rattlesnake; NAm, *Necator americanus* (hookworm); NW, *Nemertoderma westbladi* (acora); PM, *Petromyzon marinus* (sea lamprey), XB, *Xenoturbella bocki*.

```

                                     A-Box                                     B-Box
SINE2-1_EBu [1-70]  ----GCCTGGT--GTTGG-----CGCAGTGGTTAGGG---CAGCGGCTTGGGATCCAAG-AGGTCTGAGTTSAA----GCCCGTTGG
SINE2-1B_EBu [1-70] ----GCCTGGT--GTTGG-----CGTAGTGGTTAGGG---TAGCGGCTTGGGATCCAAA-AGGTCTGAGTTCAA----GCCCGTTGG
SINE2-9_EBu [1-70]  ----AGCCTGGT--G-TGG-----CTCAGTGGTTAAGG---CGGTGGCTTGGGATCCTTG-GGGTCTGAGTTCA----GCCCGCTGG
SINE2-10_EBu [1-71] ----AGCCTGGT--GTTGG-----CTTAGTGGTTAGGG---TGGCTGGCTTGGGATCCTA-GGGTCTGAGTTTGA----GCCCGTTT
SINE2-2_EBu [1-72]  --ATGCCTGGT--GTTGG-----CTTAATGGTTAGGG---TGGTGGCTTGGGATCCTA-GGATCCTGAGTTCAA----ATCCCGCTCG
SINE2-2B_EBu [1-74] ATATGCCTGGT--GTTGG-----CTTAATGGTTAGGG---TGGCGGGCTTGGGATCCTA-GGGTCTGAGTTCAA----ATCCCGCTCA
SINE2-2C_EBu [1-72] --ATGCCTGGT--GTTGG-----CTTAATGGTTAGGG---TGGTGGCTTGGGATCCGA-GGATCCTGAGTTCAA----ATCCCACTCG
SINE2-3_EBu [1-70]  --AGCCTGGT--GTTGG-----CTCAGTGGTTAGGG---TGGC-GGCTTGGGATCCTA-GGGTCTGAGTTCAA----GCCCGCTCGG
SINE2-3B_EBu [1-73] -CAGGCCTGGT--GTTGG-----CTTAACGGTTAAGG---TGGCTGGCTTAAGATCCTA-GGGTCTGAGTTCAA----GCCCTGTGCG
SINE2-3C_EBu [1-72] --AAGCCTGGT--GTTGG-----CTTAGTGGTTAGGG---TGGCTGGCTTGGGATCCTA-GGGTCTGAGTTTGA----GCCCTGTGG
SINE2-4_EBu [1-73]  TTGAACCTGGT--GTTGG-----CTTAGCGGTTAGGG---TGGT-GGCTTGGGATCCTA-GGGTCTGAGTTCAA----GCCCGTTGG
EptSINE1 [1-72]     ----CCAGACTTGGTGG-----TGTAATGGTTGGAG---CGTCCGCTCCGAGTCTGGGAAGGTCCGGGTTCAA----ACCCGGCCG
EptSINE1B_EBu [1-71] ----CCAGACTCGGTGG-----TGTAATGGTTAGAG---CGTCCGCTCCGAGTCTGGG-AGGTCCGGGTTCAA----ACCCGGCCG
EptSINE1C_EBu [1-74] ----AGACTCGGTGG-----CATAATGGTTAGAG---CGTCCGCTCTGAGTCTGGG-AGGTCCGGGTTCCGATCCGACCTGGCCG
SINE2-5_EBu [1-72]  ----ACCAGACTCGGTGG-----CGTAATGGTTAGAG---CGTCCGCTCTGAGTCTGGG-AGGTCCGGGTTCAA----ACCCGGCCG
SINE2-5B_EBu [1-70] ----CAGACTCGGTGG-----TGTAATGGTTGGAG---CGTCCGCTCTGAGTCTGGG-AGGTCCGGTGGTTCAA----ACCCGGCCG
EbuSINE1 [1-72]     ---GGGCTGACAGGATGG-----CTTAGAGGTACGCA---CACTCACCTCTAAGCTGTC-TAGCC-TGGGTTTGA----ATCCCGACCC
EbuSINE2 [1-74]     ----GGCAGGATGGCCTAAACCTAGAGGCACGCA---CACTCRCCTCTAAGCTGTC-TAGCC-TGGGTTTGA----ATCCCGACCC
SINE2-6_EBu [1-71]  ----GGCTGGCAGGATGG-----CCAAGAGGTACGCA---CACTCGCCTCTAAGCTGTC-TAGCC-TGGGTTTGA----ATCCCGACCC
SINE2-7_EBu [1-60]  -----AG-----CTCAGTTGGTATGC---GTGCTGCCTCTGAGCTGTC-TGGTCATGGATTTGT----TCCCTGTGG
SINE2-7B_EBu [1-59] -----AG-----CTCAGTTGGTAGCG---TGCTCGCCATTGAGCTGTC-TAGTC-TGGGTTTGA----TCCCGACGG
SINE2-11_EBu [1-75] ---GAGCTGGCTGTTTGG-----TCGAGTGGTTAAAGACTTGTTCCTTCTCCACTGGC-TGGTG-TGGGTTTGA----TCCCATGGC
SINE2-8_EBu [1-67]  -----ATGTT--GGTGG-----CTTGTGGTGAGGA---CACTGGACTGGCATCCAG-AGGTTGTGGGTTCAA----ATCCAGCTGA

```

**Figure S3. Sequence alignment of tRNA-derived head regions of hagfish SINEs.** Two conserved regions for transcription promoter (A- and B-boxes) are indicated. The positions inside of Repbase entries are shown in parentheses.

### Deu domain

```
EbuSINE1 [126-267] GTGCCGTCCTCGGAT--GGACGTTAAACTGGGCGTCCCGTCTGCCGGCATTAGTTGGTG
EbuSINE2 [128-268] GTGCCGTCCTCAGAT--GGACGTTAAACT-GGCGTCCCGTCTGCCGGCATTAGTTGGTG
SINE2-6_EBu [125-266] GTGCCGTCCTCGGAT--GGACGTTAAACTGGGCGTCCCGTCTGCCGGCATTAGTTGGTG
SINE2-7_EBu [72-211] ATGCCGTCCTCAGATGGGGACGTAAGCCGGCTGTCCCGTCTGC---ATTAGTTGGTG
AmnSINE1_HS [213-343] GTGCCGTCCTCGGAT-GAGACGTAAAACC-GAGTCTGACCAC-----TTGCG

EbuSINE1 [126-267] GACGTTAAAGATCCCACGGTGCCTTCGCGAAGAGTAGGCGAGCTATCGCCGGCACCTG
EbuSINE2 [128-268] GACGTTAAAGATCCCACGGTGCCTTCGCGAAGAGWAGGCGAGCTATCGCCGGCACCTG
SINE2-6_EBu [125-266] GACGTTAAAGATCCCACGGTGCCTTCGCGAAGAGTAGGCGAGCTATCGCCGGCACCATG
SINE2-7_EBu [72-211] GACGTTAAAGATCCCACGGTATCTCTGAA-AAGAGTAGGCCATTGTGTGCCGGTACCCTG
AmnSINE1_HS [213-343] GTCATTAAAGATCCCATGGCACCTTTTCGT-AAGAGTAGGGGTGTTAACCCCGGTGTCTG

EbuSINE1 [126-267] AACAAATTCCAAATTCCTGCCCTA
EbuSINE2 [128-268] AACAAATTCCAAATTCYTGCCCTG
SINE2-6_EBu [125-266] AACAAATTCCAAATTCCTGCCCTA
SINE2-7_EBu [72-211] GCTAAATTCCTGCCTAGAGATTA
AmnSINE1_HS [213-343] GCCAAATTCCAATTCGGGTAATTA
```

### Meta domain

```
EptSINE1 [83-150] AAGACTTTAAAAATGGTACGTGCTGCTTCCTTGCTTGATGCTCAGCATTAAAAGGATAAGAGCACGG
EptSINE1B_EBu [82-149] AAGACTTTAAAAATGGTACGTGCTGCTTCCTTGCTTGACGTTTCAGCATTAAAAGGATAAGAGCATGG
EptSINE1C_EBu [85-151] AAGACTTTAAAAATGGTACATGCTGCTTCCTTGCTTGACGCTCAGCATTGAAAGGAT-AGAGCATGG
Meta-domain consensus AAGACTTTAAAAATGGTACTTGCTGCTTCCTTGCTTGCGCTCAGCATT--AAGGGTTAGAGTAGG
```

**Figure S4. Sequence alignments of body domains of hagfish SINEs.** Nucleotides identical to those of one representative sequence are colored in red. The positions inside of Repbase entries are shown in parentheses. Abbreviations for organism names are as follows: HS, *Homo sapiens* (human). Sequences without the abbreviations shown above are families from the seashore hagfish.

### RTE-11\_EBu-like

```
RTE-38_CPB [263-304]      GAACATCAGGCCTGGCCAGCCGGTTTGTAAAAGTTGTGCCAA-----  
SINE2-6_EBu [276-385]    GAACGTCAGGCCTGGCCAGCCGGTTCTGTAAAGACTTGGGCCAAGCTTCCCCTGGCCAAC  
RTE-11_EBu [1017-1073]  -----GGCCGAC  
  
RTE-38_CPB [263-304]      -----  
SINE2-6_EBu [276-385]    CCCCACAAGAAGCTGGGATAATTGTGGCCTTAAGAAGAAGAAGAGAA  
RTE-11_EBu [1017-1073]  CCCCACAAGAAGGTGGGATAATTGTGGCCATGAGTACTAGTAGTAGTAGTAG
```

### CR1-3\_EBu-like

```
SINE2-4_EBu [212-268]    GGCGCAGGCATGATGGGCCGAATGGCCTCCTCCTGCGCATAA-TTTCCTTGTAA-TCCTT  
SINE2-5_EBu [178-273]    GTGCAGGCTTGATGGGCTAATTGGCCTCCTCCTGCGTCGAAG-TTCCTTGTAA-GGGA  
SINE2-5B_EBu [172-234]   GCACAGGCTTGATGGGCTAATTGGCCTCCTCCTGCGTTGAAG-TTCCTTGTAA-GGGA  
SINE2-7_EBu [373-421]    AGCCAGGCATGATGGGCCAAATTGGCCTCCTCCTGTGTCTAAGTTTCCT-----  
SINE2-7B_EBu [313-365]   GGCCAGGCATGATGGGCCAAATTGGCCTCCTCCTGTGTCTAAGTTTCCTTGCA-----  
CR1-3_EBu [3949-4008]    CGCGCAGGCATGATGGGCTGAATGGCCTCCACTGTGTFGA-TTTCCTTGTATTCCTT  
CR1-4_CM [4458-4528]     GGCCAGACTCGATGGGCCAAATTGGCCTCCTCCTGTGTCCGTA-ACATTCTATGA-ATCTA  
CR1-1_CM [4063-4123]     GGGGCAGGCWCGAGGGGCCAAATTGGCCTACTCCTGTCTCTAA-TTCTTATGTC-TTATG  
CR1-11_CM [211-266]      GGACAGGCTCGATGGGCTGAATGGCCTCCTCCTGTTTCCTGT-TTCCT---A-TGTTC  
CR1-5_CM [4387-4455]     GGCCAGACCAGATGGGCCAAATTGGCCTCCTCCTGTGTGTGA-TAATTCTATGA-TTCTA  
CR1-1_LCh [3984-4037]    ---GCAGGCTGTTGGGCTAATTGGCCTTTTCCTGTCTCTAA-AATTCTTATG-TTCT-
```

### CR1-7\_EBu-like

```
EptSINE1C_EBu [365-410]  TGTGTGCAGCTCCTCCATGAGCCTTAGACCCT-GTAGAAAAAAAAA  
EptSINE1B_EBu [367-412]  TGTGTGGCAGCTCCACTACGAGCCTTAGATCCT-GTAAAAAAAAA  
CR1-7_EBu [2400-2445]    TGTCATTTAGCTCCTCCATGAGCCT-AGACCCTTGTAAAAAAAAAA
```

### EbuSINE1-like

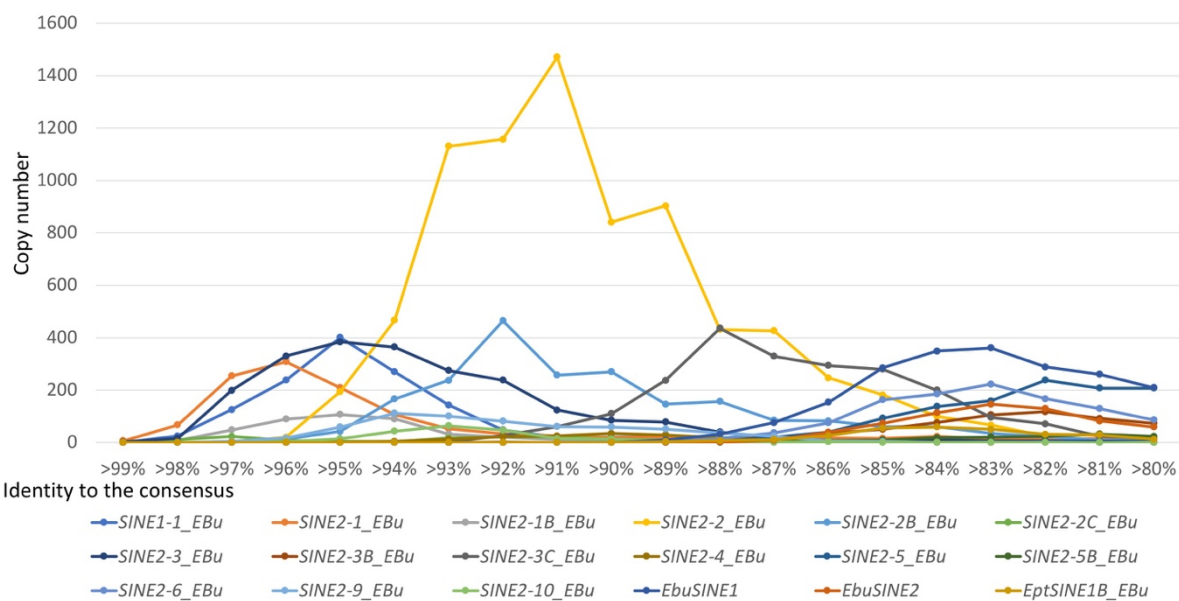
```
EbuSINE1 [277-347]       GGGCATTGCATCAGCGGCACAGCCGCGCCCTCAGCCAATRAT-GCTACCCCGCAGCGTTGTGCTG-CATACGA  
SINE2-3_EBu [164-234]    GGGCACTGCATCAGCGCACAGTCGCGCTTCAAGAATGATA-GCTACCCCGCAGCTAAGCTGC-CATACGA  
SINE2-3B_EBu [158-228]   GGGCACTGCATCAGCGGCACAGTGCACCCCAGAAATGAT-GCAGCCAAGCAGCCAGGCTG-CATACGA  
SINE2-3C_EBu [156-226]   GGGCACAGCATCAGCGGCACAGCCGCGCCCCAGAAATGATGCTACCCGGCAGCCAA--GCTGCCATATGC
```

### EbuSINE2-like

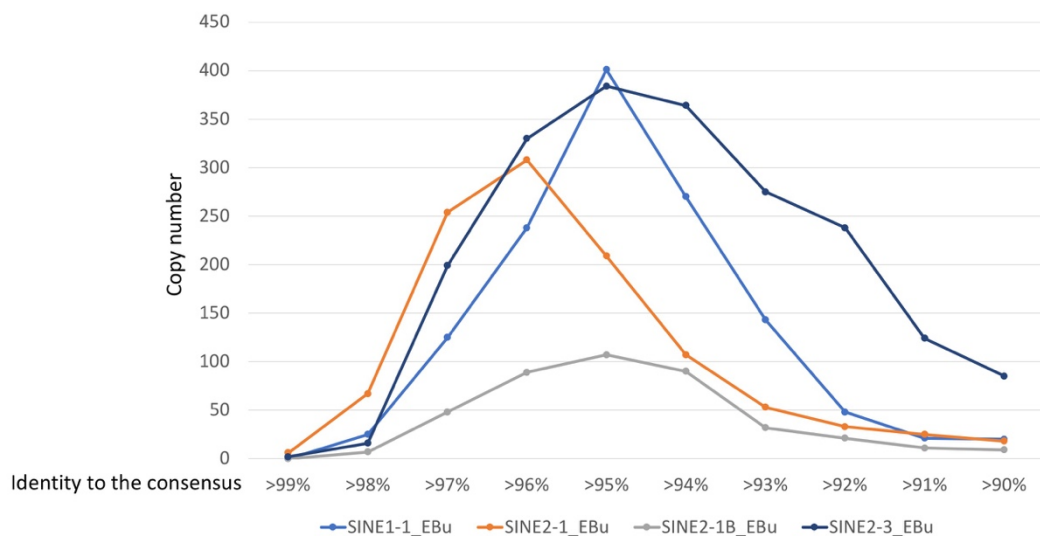
```
SINE2-2_EBu [197-253]    CCAAGGAGACTGCTTAGGCAGCACCAACGCTCTG-CACAGAGTATGGTCCCCAATGGAT  
SINE2-2B_EBu [199-255]   CCAAGGAGACTGCTTAGGCAGCACCAACGCTCTG-CACAGAGTATGGTCCCCAATGGAT  
SINE2-2C_EBu [197-253]   CCAAGGAGACTGCTTCGGCAGCACCAACGCTCTG-CACAGAGTATGGTCCCCATGGAT  
EbuSINE2 [314-370]       CCAAG-AAACTGCTTCGGCAGCATGCACGCTCTGTCACAGAGTATGGTACTACGAAT
```

**Figure S5. Sequence alignments of tails of hagfish SINEs.** Nucleotides identical to those of one representative sequence are colored in red. The positions inside of Repbase entries are shown in parentheses. Abbreviations for organism names are as follows: CM, *Callorhynchus milii* (elephant shark); CPB, *Chrysemys picta bellii* (western painted turtle); LCh, *Latimeria chalumnae* (coelacanth). Sequences without the abbreviations shown above are families from the seashore hagfish.

**A**



**B**



**Figure S6. Age distribution of hagfish SINE families.** (A) All families except four families whose copy numbers are lower than 100 (*SINE2-7\_EBu*, *SINE2-7B\_EBu*, *SINE2-8\_EBu*, and *EptSINE1*). (B) The most recently active 4 families.