Supplemental Fig. S1

The partial genomic DNA sequence of one LINE-1 allele: Clone #18

```
GTTCTAAAAGACCTGGAAAAATTGAATTACCAAAGAAGATCCAAAACGAA
CTTCTTGAAGAGAGAACAACATGTTCTAAAGAAACTGTGGCAGAATCCAA
ATTTAATATTGAAACCGGCAGATAAGGGAAGAGCCCTAGTGATGATGAAC
TCTGAATATTACAAGAAGAAGTGGAAAGAAAACTAGCAGATGAAGATAC
CTATCTGCAAATTCATGAAAACCCCACAGAAAAAATCCAGAAATTAATCA
AAACTATATTGGACGAAGCAGAAAATGATGAATTAATTAGTCATCACACC
AAACATTTCTTGATGAATGCACATCCATCGGTTCCAATTATATATATAAT
CCCGAAAGTGCACAAGAACTTAATTAATCCGCCAGGCAGACCCATCATTG
CAGCGAACAATAGGGTGCTGGAACCATTAGCACAATATATAGATCGAGCA
ATTCAACCCCTAACTCAGAAATGTAGAACCCACATTAAAGACACCAATGA
CTTTCTGAACAAATTGAACTCAATCGAAATTAATGAAGAGCAAGCTATCC
TCTTTACAATGGACGTCGTAAGTTTGTACACAAACATCACCCATGAAGGG
GGTTTAGAAGCCATGGAATGGCTTCTGTTGAAACCTGATTCAAATTGTGG
AGCTGATAAATTGTTCATCCTAAAACTGTTGAAGATTGTACTGCAGAACA
ACCTCTTCATGTTTGAAGAGAAATACTTCATACAAACATCGGGAACATCA
ATGGGGGCCGCGATGGCCCCAAGCTATGCAACCACATACATGGCTTATTT
GGAAGAAACTAACATCTTTAATGATGCAAGATGGACTGAACAACTCAAAT
GTATCTACAGATTCATTGAGGACATATTTGGTATTTGGTGGGGCTCACAT
GAAGAACTGGACACATTTTTTCAACATCTGAATCAAATGGCACCAAGGCT
CAGACTAATATCAAAAACAAGCAAAGAAACAATAGAATTTTTGGATGTAC
AAATATATAAGAAAAGAGGGAAATTGGAGACAACCATATACACAAAAGAA
ACAGACAGAAACAGCATATTGCATGCCAGCAGCTTTCATCCTAAAAAAAC
TGTAGAAAGCATACCATTCAGTCAATTTCTAAGATATAGAAGAATCATAT
CGGAAGAATCTGAATACATTAAAAAATCACGAGATCTGAAAGAAAAGTTT
GAGAAAAGAGGCTCTCAAGCAACAAATATAACAACTAGTGCAGAAAAGGT
TAGGAAAATCAGCAGAGAAGACGCTCTGAAACATAAAACTAAGAACAAAG
TGGACAATTTGGTATATGTTACTACTTTTCACAACAGAGTT
```

The partial LINE-1 ORF1 cDNA sequence (Clone #7-10)

```
AGGATTGGGACCACGGAGGATGAAGTACATGTGCTCCAGGGCACGGGCTC
TAACCTGGTGCGTGATATGAAACAGATCAAAGCGAAGTGCGACGATTTAG
AGTCCAGATCCCGCAGGAACAATATTCGCATTGTGGGGGGTTCCGGAGGCG
GCCCTCAAGGGCAAGATGGAACTCGCTGTTGAGACCCTTCTGAAGGACCT
CCTGGGAGATCCCCAACTCTCCCCGTTCTTCACCATTGAGCGCGCCCATC
GCTCACTTGCCCCGCGCCCCAAGCTGGGGGACTTCCCTAGACCAATTATA
GCCAAGGTCCTCAGCTTCCGGGATAGAGACCACATCCTACGCCTAGCCCG
CCTTTTCGGTCAATGTCCAAATGGAGCGCAGACAATTTAATGGTGTAAAG
AAAATGCTTAGAGAAAGGAAAGGGAATACGCTATGCTGTTCCGCGCAAG
GCTGAAGCTCACCCATCGTAATAAACTGTACTTTTTCACGGTCCCTGAGG
AGGCAGTGAAATTTATTGAATCTCATATTCCTATCCCTGGTCCGGCGGAC
AACCTGGTGGAGGAGGGTTGAGTCGC
```

The partial LINE-1 ORF2 cDNA sequence (Clone #6-5)

```
GCGATGACAGAGGGGGAGTGGAATAGCGCTTGCATTCCCCAAAGAGGTGT
CCAGAAATCATAGATTCCGACAAATACAGATGAATGTGTTGCACCGAACC
TACCTAACCCCGAAACGAATAGCTAAGTTTAACAAACAAGTGCAGTCACA
CTGCACCTGGTGCATGAGGGAGGAAGCGGATCTAACCCACATGATGTGGG
AATGCCCCAAGTCTAGGACGCTGTGGGATAGGGTAAAACAGACATGCGAG
AAAACAGGCATGACCAACTACAAATGGACACCTGAGGAATGCCTACTGGG
AATCTATCCTAGGTTAGCCAAACTGAAACACATAGTCAGGCTTATGGACA
TAACGTGCATACTGGCCAAAAGAACCATAGCCATGTCCTGGAAAAGACCC
GCAGGACCACAATACAAAGCATGGCACAGTGAAACAGAGCGATG
```

Supplemental Fig. S2

The primers used for genomic DNA PCR:

The primer derived from one of the putative LINE-1 ORF-2 piRNAs listed in Fig. 4 (the 25th small RNA from the top of the list). The sequence of the small RNA is: GCCCAGTAGGCATTCCTTGGGTGTCCACTCGT. The sequence of the primer (P25R) used in the genomic DNA PCR is the fragment from the 2nd base to the 27th base of this small RNA since this portion aligns with only 2 mismatches with its putative template, LINE-1 ORF-2 clone #6-5 shown in Supplemental Fig. S1: CCCAGTAGGCATTCCTTGGGTGTCCA.

The LINE-1 ORF-2-specific primer (P25F/26) derived from the partial ORF-2 cDNA sequence (clone #6-5): GCGCTTGCATTCCCCAAAGAGGTGT.

The LINE-1 ORF-2 cDNA sequence between these 2 primers, P25R and P25F/26 is 275 bases. It's a partial fragment of clone #6-5 we originally identified. The sequence of this partial clone #6-5 between P25R and P25F/26 is (the fragments corresponding to the 2 primers are in bold):

GCGCTTGCATTCCCCAAAGAGGTGTCCAGAAATCATAGATTCCGACAAAT
ACAGATGAATGTGTTGCACCGAACCTACCTAACCCCGAAACGAATAGCTA
AGTTTAACAAACAAGTGCAGTCACACTGCACCTGGTGCATGAGGGAGGAA
GCGGATCTAACCCACATGATGTGGGAATGCCCCAAGTCTAGGACGCTGTG
GGATAGGGTAAAACAGACATGCGAGAAAACAGGCATGACCAACTACAAA**T
GGACACCTGAGGAATGCCTACTGGG**

The 3 scrambled primers: GACTACAAAGACGATGACGACAAGGTG; ACC
ATGTACCCATACGATGTTCCAGATTAC; GCATCAATGCAGAAGCTGATCTCAGAG
GAGGAC

The DNA sequences of 3 different clones directly cloned from the genomic DNA PCR products primed by P25R and P25F/26 (the fragments of the 2 primers are in bold upper capital letters; the bases between the primers that are different from those in clone #6-5 represent LINE-1 genomic polymorphism and are underlined in bold lower capitals):

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Clone #1:
GCGCTTGCATTCCCCAAAGAGGTGTCCAGAAATCATAGATTCCGACAAATACAGATGAA
TGTGTTGCACCGAACCTACCTAACCCCGAAACGAATAGCTAA**a**TTTAACAAACAAG**c**GC
AGTCA**a**ACTGCACCTGGTGCATGAGGGAGGAAGC**a**GATCTAA**t**CCACATGATGTGGGAA
TG**t**CCCAA**aa**CTA**a**GACGCTGTGGGATA**a**GGT**g**AAACAGACATGCGAGAAAACAGGCAT
GACCAACTACAAA**TGGACACCCAAGGAATGCCTACTGGG**

Clone #2:
GCGCTTGCATTCCCCAAAGAGGTGTC**a**AGAAA**c**CATAGATTCCGACAAATACAGATGAA
TGTGTTGCACCGAACCTACCTAACCCCGAAACGAATAGC**c**AA**a**TTTAA**c**TAACAAG**aa**C
AGTCA**a**ACTGCACCTGGTGCATGAGGGAGGAAGC**a**GATCTAA**t**CCACATGATGTGGGAA
TGCCCCAAG**a**CTA**a**GACGCTGTGGGATA**t**GGTAAAACAGACATG**t**GAGAAAACAGGCAT
GACCAACTACAAA**TGGACACCCAAGGAATGCCTACTGGG**

Clone #3:
GCGCTTGCATTCCCCAAAGAGGTGTC**a**AGAAA**c**CATAGATTCCGACAA**t**TACAGAT**c**AA
TGTGTTGCACCGAACCTACCTAACCCCGAAACGAATAGC**c**AA**a**TTTAACAAACAAG**c**GC
AGTCA**a**ACTGCACCTGGTGCATGA**a**GGAGGAAGC**a**GATCTAA**t**CCACATGATGTGG**a**AA
TG**t**CCCAA**aa**CTA**a**GACGCTGTGGGATA**a**GGT**g**AAAC**g**GACATGCGAGAAAACAGGCAT
GACCAA**t**TACAAA**TGGACACCCAAGGAATGCCTACTGGG**

**Alignment of these 3 clones with the corresponding portion
in LINE-1 ORF-2 cDNA Clone #6-5 (the polymorphic
nucleotides found in these DNA fragments are highlighted in
bold):**

```
Clone1      GCGCTTGCATTCCCCAAAGAGGTGTCCAGAAATCATAGATTCCGACAAATACAGATGAAT  60
Clone2      GCGCTTGCATTCCCCAAAGAGGTGTCAAGAAACCATAGATTCCGACAAATACAGATGAAT  60
Clone3      GCGCTTGCATTCCCCAAAGAGGTGTCAAGAAACCATAGATTCCGACAATTACAGATCAAT  60
ORF2cDNA    GCGCTTGCATTCCCCAAAGAGGTGTCCAGAAATCATAGATTCCGACAAATACAGATGAAT  60
            ************************* ***** *************** ******* ***


Clone1      GTGTTGCACCGAACCTACCTAACCCCGAAACGAATAGCTAAATTTAACAAACAAGCGCAG  120
Clone2      GTGTTGCACCGAACCTACCTAACCCCGAAACGAATAGCCAAATTTAACTAACAAGAACAG  120
Clone3      GTGTTGCACCGAACCTACCTAACCCCGAAACGAATAGCCAAATTTAACAAACAAGCGCAG  120
ORF2cDNA    GTGTTGCACCGAACCTACCTAACCCCGAAACGAATAGCTAAGTTTAACAAACAAGTGCAG  120
            ************************************** ** ****** ******   ***


Clone1      TCAAACTGCACCTGGTGCATGAGGGAGGAAGCAGATCTAATCCACATGATGTGGGAATGT  180
Clone2      TCAAACTGCACCTGGTGCATGAGGGAGGAAGCAGATCTAATCCACATGATGTGGGAATGC  180
Clone3      TCAAACTGCACCTGGTGCATGAAGGAGGAAGCAGATCTAATCCACATGATGTGGAAATGT  180
ORF2cDNA    TCACACTGCACCTGGTGCATGAGGGAGGAAGCGGATCTAACCCACATGATGTGGGAATGC  180
            *** ****************** ********* ******* ******* ************* ****


Clone1      CCCAAAACTAAGACGCTGTGGGATAAGGTGAAACAGACATGCGAGAAAACAGGCATGACC  240
Clone2      CCCAAGACTAAGACGCTGTGGGATATGGTAAAACAGACATGTGAGAAAACAGGCATGACC  240
Clone3      CCCAAAACTAAGACGCTGTGGGATAAGGTGAAACGGACATGCGAGAAAACAGGCATGACC  240
ORF2cDNA    CCCAAGTCTAGGACGCTGTGGGATAGGGTAAAACAGACATGCGAGAAAACAGGCATGACC  240
            *****  *** ************** *** **** ****** *****************
```

```
Clone1       AACTACAAATGGACACCCAAGGAATGCCTACTGGG 275
Clone2       AACTACAAATGGACACCCAAGGAATGCCTACTGGG 275
Clone3       AATTACAAATGGACACCCAAGGAATGCCTACTGGG 275
ORF2cDNA     AACTACAAATGGACACCTGAGGAATGCCTACTGGG 275
             ** ************* ***************
```

Supplemental Fig.S3

Table 1

Cluster ID	Best hit	Gene	NR5 454	DL5 454	NR14 454	DL14 454	CTL 454	Function
Cluster_218328_Contig1	XP_945963	LOC651665	0.0	0.0	12.9	0.0	0.0	retrotransposon-like
Cluster_154450_Contig16	XP_945963	LOC651665	4.8	27.4	11.5	2.0	9.8	retrotransposon-like
Cluster_217452_Contig1	XP_935194	LOC647087	0.0	2.5	8.6	0.0	15.7	retrotransposon-like
Cluster_193687_Contig1	XP_931431	LOC642956	69.3	74.7	75.9	68.0	9.8	retrotransposon-like
Cluster_193687_Contig8	XP_931431	LOC642956	21.5	2.5	22.9	10.0	2.0	retrotransposon-like
Cluster_323661_Contig38	XP_931247	LOC642707	40.6	17.4	51.6	26.0	0.0	retrotransposon-like
Cluster_10953_Contig8	NP_055405	ERVWE1	4.8	14.9	0.0	1.0	0.0	retroviral component
Cluster_42238_Contig456	NP_055883	PEG10	40.6	2.5	10.0	3.0	11.8	retrovirus-like
Cluster_42238_Contig60	NP_055883	PEG10	7.2	34.9	37.3	10.0	27.5	retrovirus-like

Table 2

Ambystoma Contig	Annotation	amby seq Start	end	subject seq start	end	e-value
Mex_Nohits_1286_Contig_1	gi|41203814|ref|XP_370776.1| RTL1 PREDICTED: similar to retrotransposon-like 1 [Homo sapiens]	510	4	741	911	7.00E-11
EPTY8IW01DWBJX	gi|10047124|ref|NP_061333.1| RAG1AP1 recombination activating gene 1 activating protein 1 [Homo sapiens]	243	4	9	88	4.00E-25
Mex_NM_032862_Contig_1	gi|144922631|ref|NP_116251.3| tigger transposable element derived 5 [Homo sapiens]	380	559	1	60	2.00E-25
165619_1695_0737	gi|156627567|ref|NP_006506.2| SET domain and mariner transposase fusion [Homo sapiens]	182	9	115	172	1.00E-21
Cluster_25858_Contig1	gi|25777746|ref|NP_689808.2| PGBD4 piggyBac transposable element derived 4 [Homo sapiens]	388	2	446	585	3.00E-19
EQEDK3201D8MHF	gi|31542663|ref|NP_061952.2| ECAT11 LINE-1 type transposase domain containing 1 [Homo sapiens]	24	263	757	836	4.00E-09
EPTY8IW01CSQVN	gi|46397390|ref|NP_055915.2| POGZ pogo transposable element with ZNF domain isoform 1 [Homo sapiens]	239	3	1191	1269	4.00E-27
EPTY8IW01EIT9X	gi|46397394|ref|NP_997054.1| POGZ pogo transposable element with ZNF domain isoform 2 [Homo sapiens]	2	250	78	151	3.00E-27
Cluster_401840_Contig1	gi|4759258|ref|NP_004720.1| DHRSX Ac-like transposable element [Homo sapiens]	2	259	591	676	2.00E-29
Cluster_42238_Contig386	gi|89037862|ref|XP_945963.1| LOC651665 PREDICTED: similar to retrotransposon-like 1 [Homo sapiens]	87	905	633	907	5.00E-36