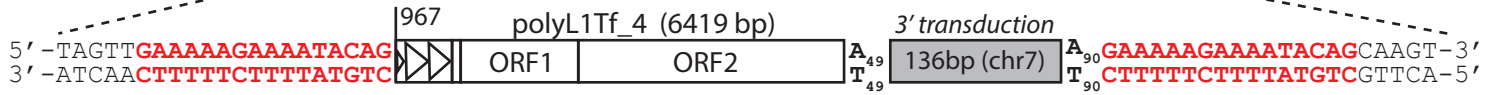


Supplemental Figure 3 (cont'd)

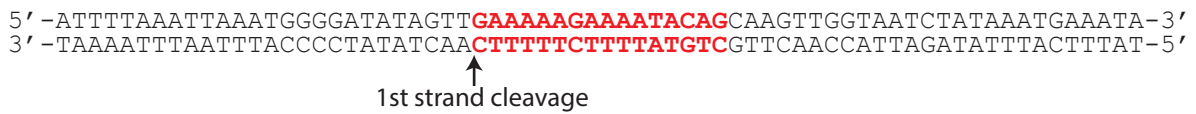
Poly_L1Tf_4 chr17 (qB2), +strand



Filled site:



Empty site:

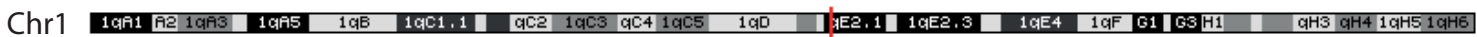


L1 subfamily: Tf
Monomers: 2 + 83 bp

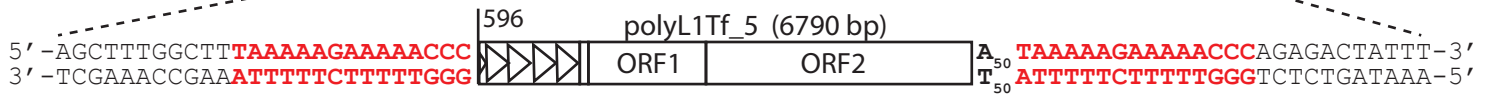
TSD: 16 bp
(Chr17; 41,334,114 - 41,334,129)

EN motif: 5'-TTTC/AA-3'

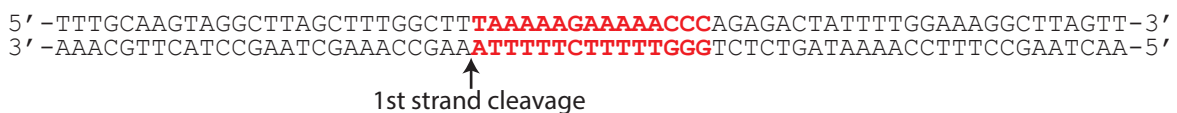
Poly_L1Tf_5 chr1 (qE2.1), -strand



Filled site:



Empty site:



L1 subfamily: Tf
Monomers: 4 + 34 bp

TSD: 15 bp
(Chr1, 104,818,661 - 104,818,675)

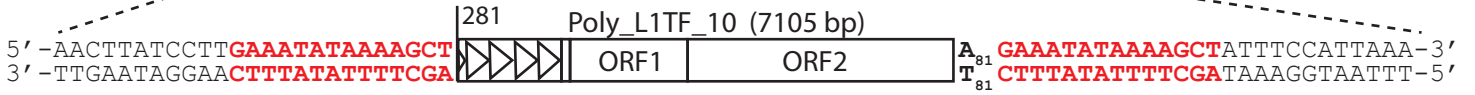
EN motif: 5'-TTTA/AA-3'

Supplemental Figure 3 (cont'd)

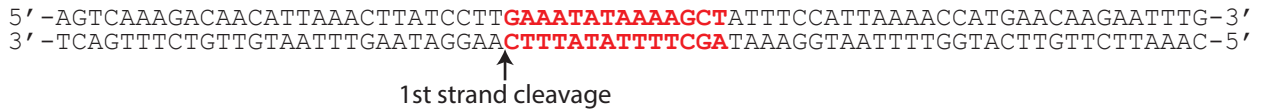
Poly_L1Tf_10 chr10 (qB1), +strand



Filled site:



Empty site:



L1 subfamily: Tf

Monomers: 4 + 96 bp

TSD: 14 bp

(Chr10, 36,022,472 - 36,022,486)

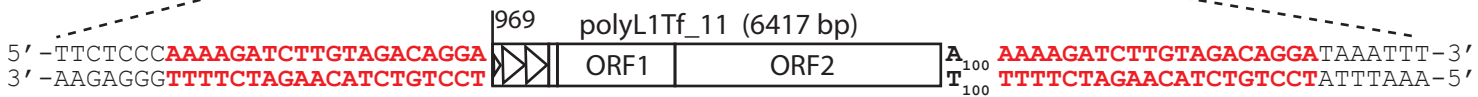
EN motif: 5'-TTTC/AA-3'

polyL1Tf_11

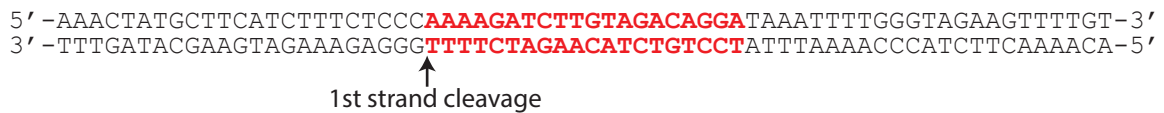
chr15 (qB3.1), +strand



Filled site:



Empty site:



L1 subfamily: Tf

Monomers: 2 + 81 bp

TSD: 20 bp

(Chr15, 45,572,157 - 45,572,177)

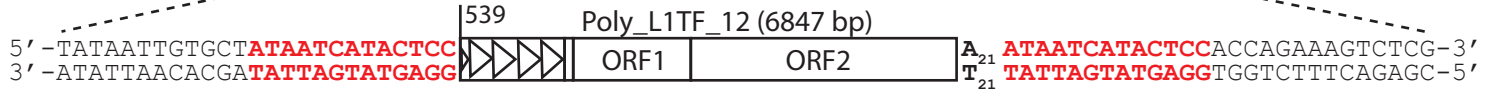
EN motif: 5'-TTTT/GG-3'

Poly_L1Tf_12

chr5 (qC3.1), +strand



Filled site:



Empty site:



L1 subfamily: Tf

Monomers: 4 + 61 bp

TSD: 13 bp

(Chr5, 69,153,918 - 69,153,936)

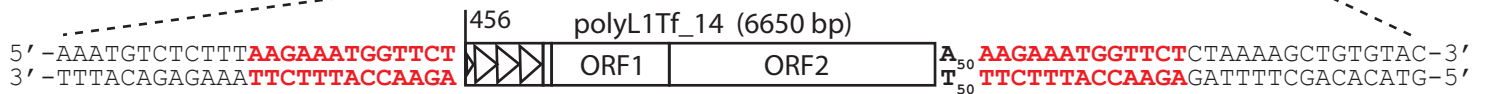
EN motif: 5'-TTAT/AG-3'

polyL1Tf_14

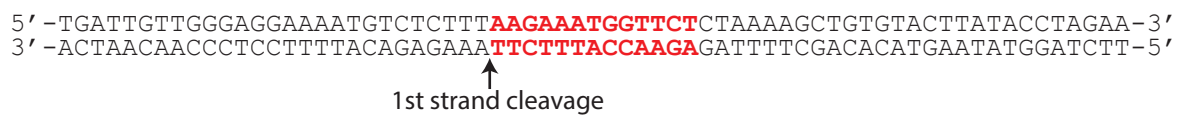
chr11 (qD), +strand



Filled site:



Empty site:



L1 subfamily: Tf

Monomers: 3 + 101 bp

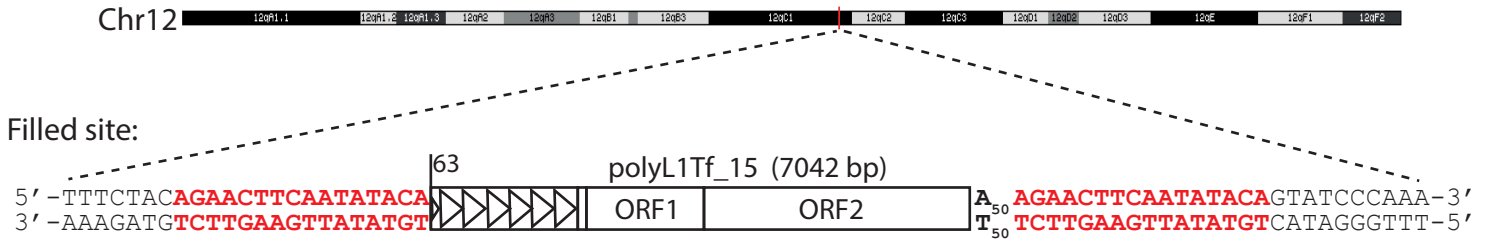
TSD: 13 bp

(Chr11, 91,759,570 - 91,759,583)

EN motif: 5'-TCTT/AA-3'

polyL1Tf_15

chr12 (qC1), +strand



Empty site:

5' -GTTGCTGACTTAAATTTTTTTTCTACAGAACTTCAATATACA-3'

3' -CAACGACTGAATTTAAAAAAAAGATGTCTTGAAGTTATATGT-5'

↑

1st strand cleavage

L1 subfamily: Tf

Monomers: 6 + 78 bp

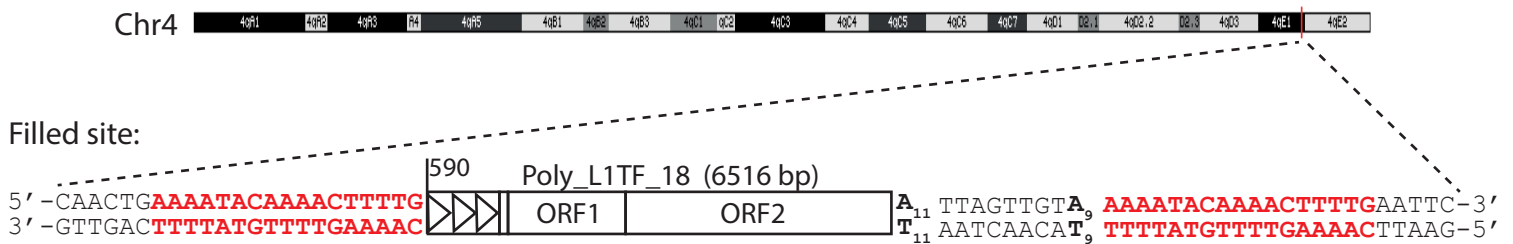
TSD: 16 bp

(Chr12, 64,779,624 - 64,779,640)

EN motif: 5'-TTCT/GT-3'

Poly_L1Tf_18

chr4 (qE1), -strand



Empty site:

5' -CTCGTGAATCTATTACTGGCACAAC T GAAAATACAAAACTTTTGAATTCACCAATATTCTTCTTTATTAT-3'

3' -GAGCACTTAGATAATGACCGTGTGAC T TTTTATGTTTTGAAAAC TTAAGTGGTTATAAGAAGAGAAATAATA-5'

↑

1st strand cleavage

L1 subfamily: Tf

Monomers: 3

TSD: 17 bp

(Chr4, 147,497,685 - 147,497,704)

EN motif: 5'-TTTT/CA-3'

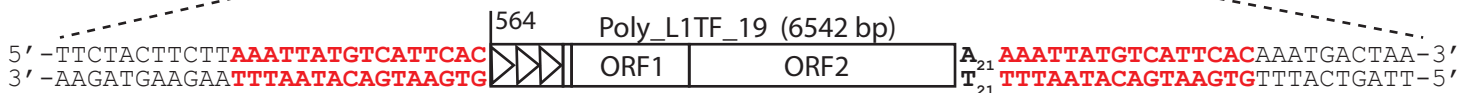
Supplemental Figure 3 (cont'd)

Poly_L1Tf_19

chr7 (qC), +strand



Filled site:



Empty site:

5' -GCATCTTCTGCGTTTATAAGAAATCTTCTACTTCTTAAATTATGTCATTCACAAATGACTAATCCATGTTG-3'
 3' -CGTAGAAGACGCAAATATTCTTTAGAAAGATGAAGAA TTTAATACAGTAAGTGTTTACTGATTAAGGTACAAC-5'

↑
1st strand cleavage

L1 subfamily: Tf
 Monomers: 3

TSD: 16 bp
 (Chr7, 62,347,340 - 62,347,358)

EN motif: 5'-ATTT/AA-3'

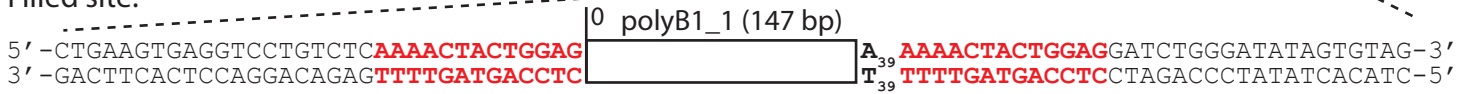
Supplemental Figure 3 (cont'd)

Poly_B1_1

chr16 (qC3.3), +strand



Filled site:



Empty site:



↑
1st strand cleavage

SINE family: B1

TSD: 13 bp
(Chr16, 91599058 - 91599070)

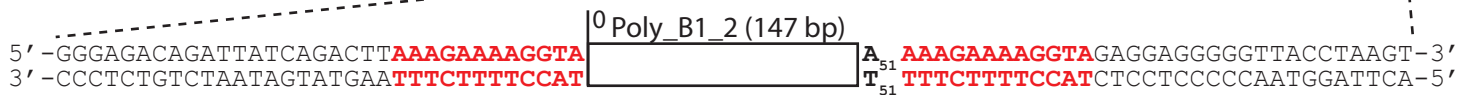
EN motif: 5'-TTTT/GA-3'

Poly_B1_2

chr4 (qE1), -strand



Filled site:



Empty site:



↑
1st strand cleavage

SINE subfamily: B1

TSD: 12 bp
(Chr4, 146,430,138 - 146,430,150)

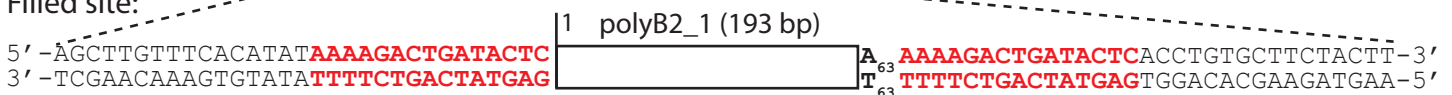
EN motif: 5'-CTTT/AA-3'

Poly_B2_1

chrX (qA4), +strand



Filled site:



Empty site:



↑
1st strand cleavage

SINE family: B2

TSD: 15 bp
(Chr5, 41,903,727-41,903,741)

EN motif: 5'-TTTT/AT-3'

Supplemental Figure 3 (cont'd)

Poly_B2_2

chr5 (qE3), +strand



Filled site:

5' -CATGGACAGATCTTTT**AAAACATGACCATCC** [0 polyB2_2 (193 bp)] **A**₁₀₀ **AAAACATGACCATCC**AAAAATAGAAGCAAGAT-3'
 3' -GTACCTGTCTAGAAAA**TTTTGTACTGGTAGG** **T**₁₀₀ **TTTTGTACTGGTAGG**TTTTATCTTCGTTCTA-5'

Empty site:

5' -ATATTGAAGACATGGACAGATCTTTT**AAAACATGACCATCC**AAAAATAGAAGCAAGATGTTAGGGAGC-3'
 3' -TATAACTTCTGTACCTGTCTAGAAAA**TTTTGTACTGGTAGG**TTTTATCTTCGTTCTACAATCCCTCG-5'

↑
1st strand cleavage

SINE subfamily: B2

TSD: 15 bp
(Chr5, 98060042 - 98060056)

EN motif: 5'-TTTT/AA-3'

Poly_B2_3

chr4 (qE1), +strand



Filled site:

5' -TGACTCCCACTGTGCTATCAAAAATTAAAA**TA** [2 Poly_B2_3 (192 bp)] **A**₁₀ **TA**AGCCAGGCAGTGGTGACACATGCCTTTA-3'
 3' -ACTGAGGGTGACACGATAGTTTTTAATTTT**AT** **T**₁₀ **AT**TCGGTCCGTACCACCTGTGTACGGAAAT-5'

Empty site:

5' -GCCAAAAACTCTGACTCCCACTGTGCTATCAAAAATTAAAA**TA**AGCCAGGCAGTGGTGACACATGCCTTTAATC-3'
 3' -CGTTTTTTGAGACTGAGGGTGACACGATAGTTTTTAATTTT**AT**TCGGTCCGTACCACCTGTGTACGGAAATAG-5'

↑
1st strand cleavage

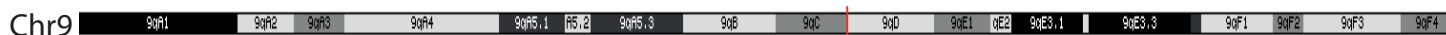
SINE subfamily: B2

TSD: 2 bp
(Chr4, 146,493,190 - 146,493,204)

EN motif: 5'-TTTT/AT-3'

Poly_B2_4

chr9 (qD), +strand



Filled site:

5' -GGTTCATAAGTTTTTCGTTGTC**AAAACTGCT** [2 Poly_B2_4 (192 bp)] **A**₁₀ **AAAACTGCT**AAGAAATGTTAGTCTCATAT-3'
 3' -CCAAGATTTCAAAAAGCAACAG**TTTTTGACGA** **T**₁₀ **TTTTTGACGA**TTCTTTACAATCAGAGTATA-5'

Empty site:

5' -TCAAAAAACAGAGGTTCTAAAGTTTTTCGTTGTC**AAAACTGCT**AAGAAATGTTAGTCTCATATCTAGCTTACT-3'
 3' -AGTTTTTTTGTCTCCAAGATTTCAAAAAGCAACAG**TTTTTGACGA**TTCTTTACAATCAGAGTATAGATCGAATGA-5'

↑
1st strand cleavage

SINE subfamily: B2

TSD: 10 bp
(Chr9, 69,742,273 - 69,742,283)

EN motif: 5'-TTTT/GA-3'

Supplemental Figure S3. Structures of polymorphic retrotransposon insertions absent from the C57BL/6J reference genome (GRCm38/mm10).

For each structure, the relative location of the insertion is shown on the chromosome. The filled-site diagram denotes target-site duplications (TSDs), promoter monomer units for L1 insertions are shown as triangles, ORF1 and ORF2 are indicated as open rectangles. The truncation point for each insertion relative to the L1MdTf_I consensus(Sookdeo et al. 2013) is indicated. A_n/T_n indicates poly(A) sequence length. Below, the sequence of the empty site is shown, with TSDs and the site of first-strand cleavage indicated. Characteristics of each insertion (retroelement family, monomer number for L1 insertions, TSD length and chromosomal location, and endonuclease (EN) cleavage motif) are summarized below. 3' transductions are indicated as filled grey rectangles.