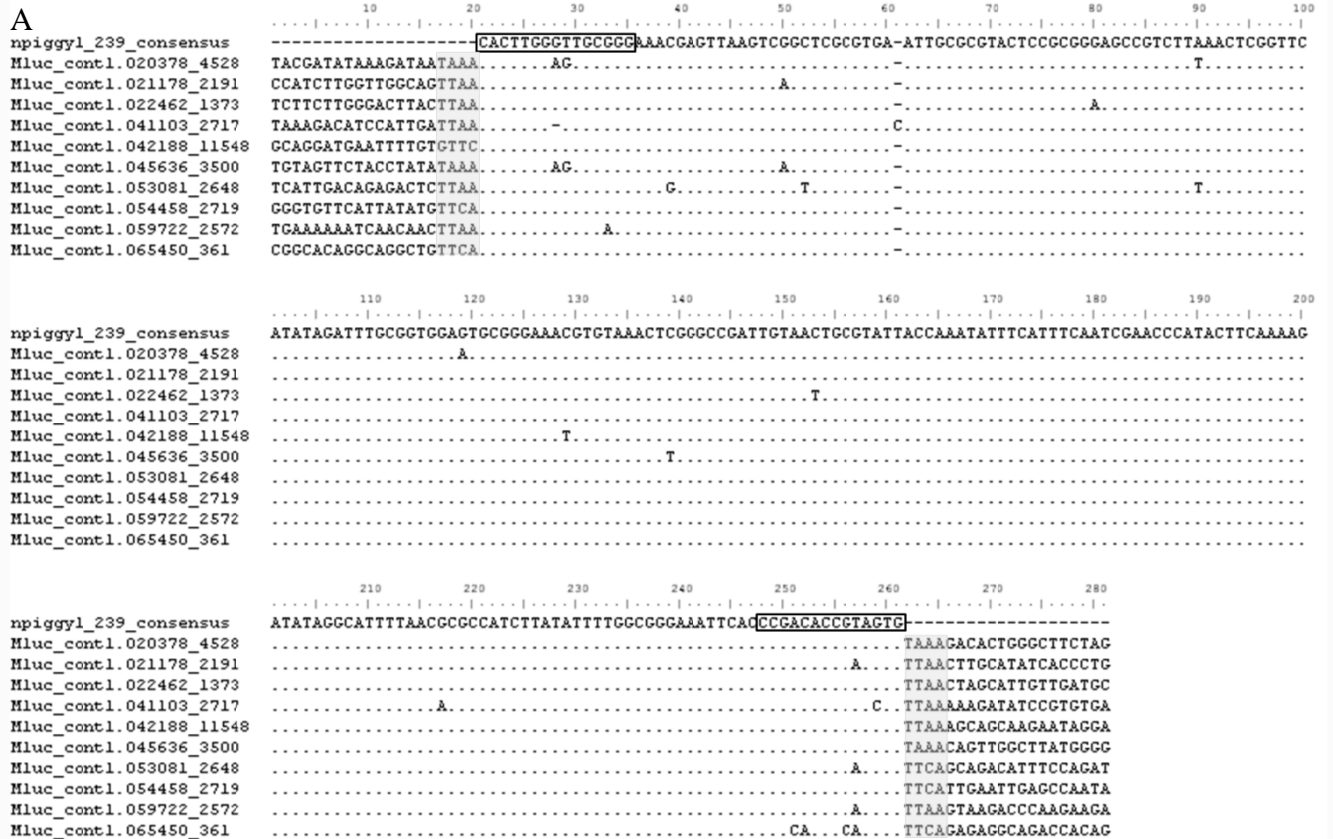**Supplemental Figure**

Supplemental Figure S1. Representative alignments for three subfamilies recovered during this analysis: A) a nonautonomous piggyBac1_ML element; B) a nonautonomous hAT1_ML element; C) a non-autonomous Tc2 element. For all, the presumed TSD is outlined in black and the TSDs that are characteristic of the family are shaded in gray. Identical residues below the consensus are indicated by "." and indels are indicated by "-".

A

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                      10        20        30        40        50        60        70        80        90       100
                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
npiggy1_239_consensus    --------------------CACTTGGGTTGCGGGAAACGAGTTAAGTCGGCTCGCGTGA-ATTGCGCGTACTCCGCGGGAGCCGTCTTAAACTCGGTTC
Mluc_cont1.020378_4528   TACGATATAAAGATAATAAA.......AG....................................-..............................T..........
Mluc_cont1.021178_2191   CCATCTTGGTTGGCAGTTAA.................................A...........-.....................................
Mluc_cont1.022462_1373   TCTTCTTGGGACTTACTTAA............................................-..............A.......................
Mluc_cont1.041103_2717   TAAAGACATCCATTGATTAA.......-.................................C.......................................
Mluc_cont1.042188_11548  GCAGGATGAATTTTGTGTTC............................................-.....................................
Mluc_cont1.045636_3500   TGTAGTTCTACCTATATAAA.......AG........................A...........-.....................................
Mluc_cont1.053081_2648   TCATTGACAGAGACTCTTAA.................G.............T.........-..........................T..........
Mluc_cont1.054458_2719   GGGTGTTCATTATATGTTCA............................................-.....................................
Mluc_cont1.059722_2572   TGAAAAAATCAACAACTTAA...........A................................-.....................................
Mluc_cont1.065450_361    CGGCACAGGCAGGCTGTTCA............................................-.....................................

                     110       120       130       140       150       160       170       180       190       200
                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
npiggy1_239_consensus    ATATAGATTTGCGGTGGAGTGCGGGAAACGTGTAAACTCGGGCCGATTGTAACTGCGTATTACCAAATATTTCATTTCAATCGAACCCATACTTCAAAAG
Mluc_cont1.020378_4528   ...................A...............................................................................
Mluc_cont1.021178_2191   ..................................................................................................
Mluc_cont1.022462_1373   .........................................................T........................................
Mluc_cont1.041103_2717   ..................................................................................................
Mluc_cont1.042188_11548  .............................T....................................................................
Mluc_cont1.045636_3500   ...................................T.............................................................
Mluc_cont1.053081_2648   ..................................................................................................
Mluc_cont1.054458_2719   ..................................................................................................
Mluc_cont1.059722_2572   ..................................................................................................
Mluc_cont1.065450_361    ..................................................................................................

                     210       220       230       240       250       260       270       280
                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|.
npiggy1_239_consensus    ATATAGGCATTTTAACGCGCCATCTTATATTTTGGCGGGAAATTCACCCGACACCGTAGTG-------------------
Mluc_cont1.020378_4528   ...................................................TAAAGACACTGGGCTTCTAG
Mluc_cont1.021178_2191   ...............................................A....TTAACTTGCATATCACCCTG
Mluc_cont1.022462_1373   ...................................................TTAACTAGCATTGTTGATGC
Mluc_cont1.041103_2717   ...............A...................................C..TTAAAAAGATATCCGTGTGA
Mluc_cont1.042188_11548  ...................................................TTAAAGCAGCAAGAATAGGA
Mluc_cont1.045636_3500   ...................................................TAAACAGTTGGCTTATGGGG
Mluc_cont1.053081_2648   ...............................................A....TTCAGCAGACATTTCCAGAT
Mluc_cont1.054458_2719   ...................................................TTCATTGAATTGAGCCAATA
Mluc_cont1.059722_2572   ...............................................A....TTAAGTAAGACCCAAGAAGA
Mluc_cont1.065450_361    .............................................CA...CA....TTCAGAGAGGCAGACCACAG
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B

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                              10        20        30        40        50        60        70        80        90        100
                         ...|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
nhAT1_239a_consensus     -------------------CAGTGATGGCGAACCTATGACACGCGTGTCAGAGGTGACACGCGAA-CTCATTTTTTT---GGTTGATTTTTCTT----T
Mluc_cont1.000608_2072   TCTAATACCTGATCCTAAGT...............................................A..-...........G---...........----.
Mluc_cont1.001009_6307   CTTTAGGTCAAGGTCTAGGC.........T...................................T...-..........T--...........----.
Mluc_cont1.005237_1270   AACACCACCTTCCACTAGAA.........A.......A.....................T...-G..........---...........----.
Mluc_cont1.014030_9544   TGCCTAGTGACATCATAGCC......................C...................T.....-..........TTT...........----.
Mluc_cont1.046453_18410  TTCTTCTCTTTAGTCTAGTG.............................................A..-..........---A...........----.
Mluc_cont1.083381_63     CAAAATTAGATGGTCTATAG................................................G.......A..........T--...........----.
Mluc_cont1.094254_1495   TTGAGAACCCCTGCCTAGGG............................................-..........---.....G.........----.
Mluc_cont1.104958_1817   AGTAAGGCCTGAACCTAGAG..........A.................C............T.....-..........T--...........TGAT.
Mluc_cont1.115850_12906  TATTCCCGAACTGCCTAAAT.............T.........T..A..A..--..C.........-..........---...........----.
Mluc_cont1.132846_1554   CTGATCAACTCAGTCTGCCC..........G...........................T...G..-..........---...........----.
```

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                              110       120       130       140       150       160       170       180       190       200
                         ...|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
nhAT1_239a_consensus     GTTAAATGGC----ATTTAAATATATAAAATAAATATCAAAAA-TATA----ADTCTTTGTTTTACTATGG-----TTGCAAATATCAAAAAATTT-CTA
Mluc_cont1.000608_2072   ..........----...................T-....----...........-----..........-...
Mluc_cont1.001009_6307   ..........----...................-....AGTA...........-----..........-...
Mluc_cont1.005237_1270   ..........----...................-....----..........TAAAA.AT...............-...
Mluc_cont1.014030_9544   ..........----...................-....----..........G----...........A.GT...
Mluc_cont1.046453_18410  ..........ATTC...................-....----...A...........-----C..........-...
Mluc_cont1.083381_63     ..........----...................A....----...A...........-----..........T...
Mluc_cont1.094254_1495   ..........----...................-....----..........-----..........-...
Mluc_cont1.104958_1817   T..CTT....----...................-....----..........-----..........-...
Mluc_cont1.115850_12906  ..........----...................-....----..........T.-----..........G.........-...
Mluc_cont1.132846_1554   ..........----...................T-....----...C..........-----..........-...
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                              210       220       230       240       250       260       270       280       290       300
                         ...|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
nhAT1_239a_consensus     -TATGTGACACGGCACCAGAG-----TTAAGTTAGGG-TTTTT-CAAAA--TGCTGACACGCC-GAGCTC-AAAAGGTTCG-CCATCACTG--------
Mluc_cont1.000608_2072   -..................TTAAG...-T......-......--........-......-..........-.T.......TCCTAAGTC
Mluc_cont1.001009_6307   -..................T..-----......-....--........A...-..........T.........GTCTAGGCT
Mluc_cont1.005237_1270   -..................-----....-..--.....A.....-..........-T.......CAGTAGAAT
Mluc_cont1.014030_9544   -..................-----....G.....-....---........T-......-......C-.-..........TCGTAGCCT
Mluc_cont1.046453_18410  -.........TT.........-----.....G...-....--........-......-.........GTCTAGTGA
Mluc_cont1.083381_63     -.........T..........-----......-....--........-......-........T.-.........GTCTATAGC
Mluc_cont1.094254_1495   -..................A-GAG......-....-....--........A...-......-.........GCCTAGGGC
Mluc_cont1.104958_1817   -..................-----......-....--........-......-..........TTCTAGAGT
Mluc_cont1.115850_12906  A..................-----.AG..G.....-....A.C.C.CG.....-....GA.....C.........CT.........GGCCTAAAT
Mluc_cont1.132846_1554   -..................TCAAG....A...A..-.....-.C...--.....C......-A.....-.....A...A-.........GCCCTAGAC
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                              310
                         ...|....|.
nhAT1_239a_consensus     -----------
Mluc_cont1.000608_2072   ATCAAGGATGG
Mluc_cont1.001009_6307   CAGATGTGCAG
Mluc_cont1.005237_1270   GTCTTCCTCAG
Mluc_cont1.014030_9544   CTGATGTAGTC
Mluc_cont1.046453_18410  GATGGCTGAGC
Mluc_cont1.083381_63     CTCCTAAACAC
Mluc_cont1.094254_1495   ATCGTGTCCAA
Mluc_cont1.104958_1817   GTGTCCTGCTC
Mluc_cont1.115850_12906  TATCAAATTAC
Mluc_cont1.132846_1554   ACTCGCTTTGG
```

C

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                    10        20        30        40        50        60        70        80        90       100
             ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
nTc2_527_consensus   -------------------CCGTATTTTTCCGTGTATAAGACGCTA----TTTTTTTCTAAAATCGTTAGACTGAAAATCGAGGGGCGTCTTATACACG
Mluc_cont1.087472_2447  TGTGATTATCTGCTGAATTA.........A..........A...TTTT..........A......A.....A....T.....C...GA
Mluc_cont1.111057_5805  CCCAAAGCCCAAGAGATTTA..........A.....A..----.C...............T......A....A...A
Mluc_cont1.018722_481   GCTCTCTTAATCACTAAGTA..........T..........A...---T..........T....CT...................TT.
Mluc_cont1.060466_101   GTGTTAACTTTTGCTTTATA...........T.....----........A..T.T.........A.T..........A.
Mluc_cont1.020727_688   TTTCTTTATTGAGTGTCATA.........T......A....---T.......CT....A......G.C..A..A...........
Mluc_cont1.215841_1303  AGGGGGGAAAAGGGAACATA..A......A......A...T....----..C..........A.........A...A..A..
Mluc_cont1.286269_519   TAAGAGCTTCCAGGGACATA....C.......A....AA.....----...A...........A..A...AC..C....T.
Mluc_cont1.061271_2901  TTAGCATTGAAGACAAACTA.T.......T........C.T....----....C......C....A...........A.
Mluc_cont1.232421_7894  ATAAGTAGAATTATATAGTA..A........A.........A...--TT.......A..A....TC................A
Mluc_cont1.288193_1284  ACTTCAGAAATCACAAACTA....C.......T....C.......A....----.........................T.........
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Figure C. Sequence alignment of nTc2_527_consensus with Myotis lucifugus contig sequences.