```
                         10        20        30        40        50        60        70        80        90       100       110       120
                                          5' TSD                          Pol A Box                                                  Pol B Box
Consensus      TGATGCTATATTAAAATGATTAGTAGAAAGCAGTCAAGAAAATGGGGGGCCTGGGTGGGGCAGTCGGTTAAGGGTCCGAATTCAGCCAGGTCACGATTTNGCGGTCCGTGAGTTCGAGCCCAGGGTCAGG
L. canadensis  ···················································································································T······························
L. lynx        ···················································································································G······························
L. pardinus    ·······················-----------------------------------------------------------------------------------------------------------

                        140       150       160       170       180       190       200       210       220       230       240       250
                                                            >>>>>>>>>>CT Rich Region>>>>>>>>>>>>>>>>>>>>>>>****************Poly AT tail*********
Consensus      GTTTGGGGTGATGGGTCAGAGCCTGGAGCCCGTTTTGATTTTGNGTTTCCCTTTTTTTTTGCCCCTCCCCCGTTCATGGTTTGTTTTTTTTTGTCCCAAAAATAAATAAACGTTGAAAAAAAAAAAAATTT
L. canadensis  ···········································G······································································
L. lynx        ···········································T······································································
L. pardinus    ---------------------------------------------------------------------------------------------------------------------------------·

                        270       280       290       300
                       3' TSD
Consensus      AGAAAGCAGTCAAGAAGAGATTCAGAAACGTAAGACACTT
L. canadensis  ········································
L. lynx        ········································
L. pardinus    ········································
```

Figure S4. Alignment of lynx lineage individuals at locus 134463 reveals, a Can-SINE insert in all 7 *L. canadensis* and 3 *L. lynx* individuals examined, yet absent from all 5 *L. pardinus* individuals examined. Yellow-highlighted regions mark target site duplications and gray-shaded regions denote the A and B RNA polymerase III recognition sequences.