

Supplemental Materials

Supplemental Table 1

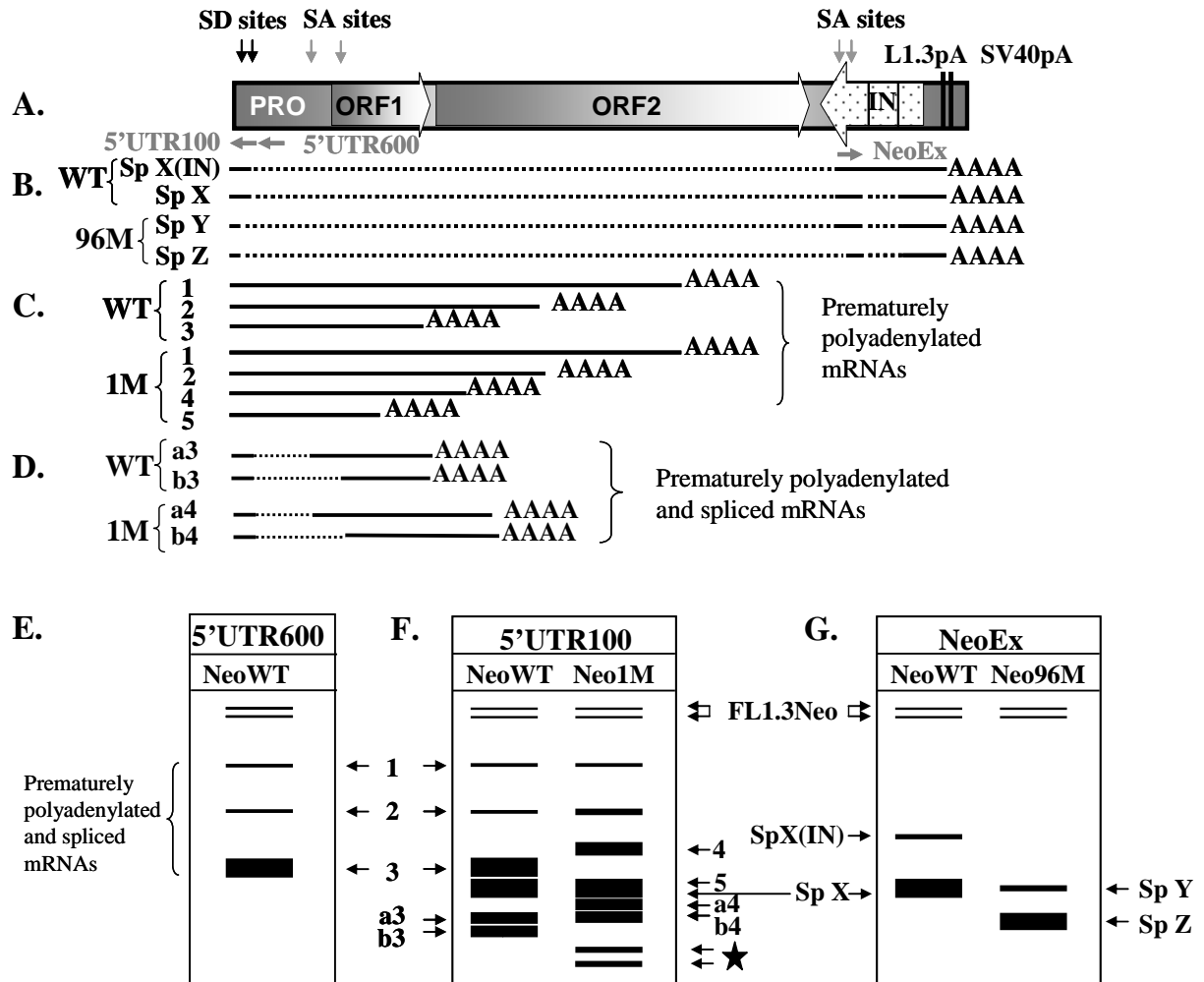
Retrotransposed spliced L1.3 copies in the human genome

SD	SA	Chromosome #	Accession #
97	976	14	AL163952
		3	AC093115
		12	AF188024
		6	AL133472
		1	AL138900
		4	AC093808
		X	AL807813
		8	AC079018
		9	AL353590
		2	AC0099487

Retrotransposed spliced L1 spa copies in the mouse genome

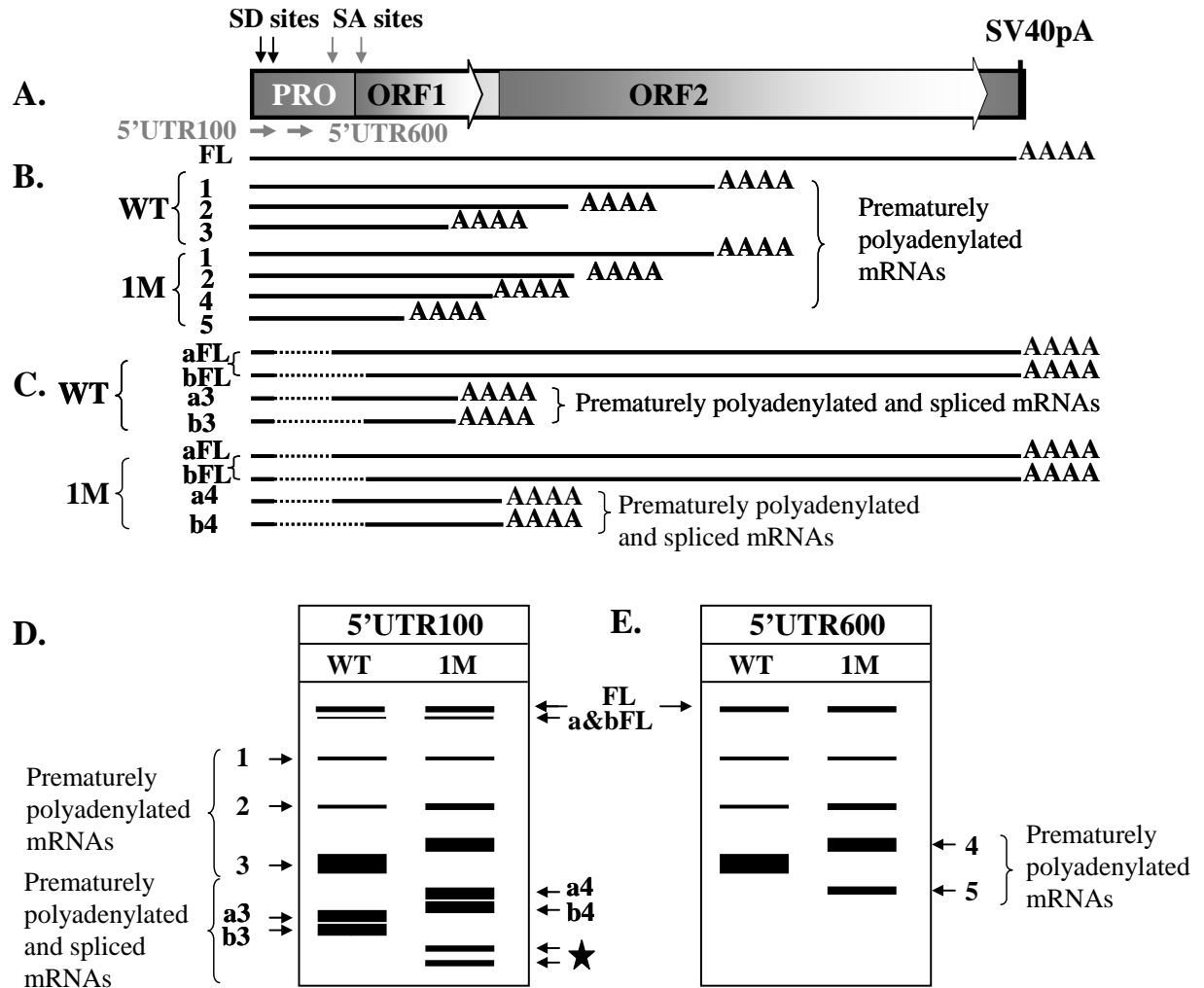
SD	SA	Chromosome #	Accession #
27	1514	12	CA125142
		7	AC102220
		6	AC078790
		X	AL954355
		18	AC125166
		14	AC133495
27	1597	X	AL662923
		11	AL646046
		5	AC036146
		2	AL845483
		1	AC107832
		14	AC124709
		15	AC122834
		12	AC122029
		10	AC153559
27	1702	X	BX119996
			AC133213
239	1597	5	AC036146
		X	AL671880
		15	AC122834
		14	AC124709
		2	AL845483

Supplemental table 1. Examples of the spliced retrotransposed L1 elements in the human and mouse genomes. SD and SA columns indicate the positions of the splice donor and acceptor sites in either L1.3 or L1spa genomes. Chromosomal location and accession numbers are listed for each retrotransposition event.



Supplemental figure 1. Schematic representation of the mRNA species produced by L1.3 expression vector tagged with the neomycin (Neo) resistance cassette and driven by CMV promoter. **A.** A diagram of the L1.3Neo expression cassette containing L1.3 5'UTR (PRO), open reading frames 1 and 2 (ORF1 and ORF2) as depicted in figure 1B. The neomycin resistance gene is positioned in the reverse orientation relative to the L1.3 expression and is interrupted by the intron that can be spliced out during L1.3 transcription (IN). Black and gray vertical arrows represent functional splice donor (SD) and splice acceptor (SA) sites, respectively. Gray horizontal arrows indicate relative positions of the strand-specific RNA probes complementary to the first 100 bp (5'UTR100), positions 583 to 698 (5'UTR600) of the L1.3 sequence or to the second exon of the Neo resistance gene (NeoEx). Note that the 5'UTR100 probe would detect both spliced and unspliced mRNAs while 5'UTR600 probe would only detect mRNA species that did not have that region removed by splicing. **B.** Splice products produced by L1.3Neo expression vector transiently transfected in NIH 3T3 cells and detected by RT-PCR and northern blot analysis with the strand-specific probe to the second exon. Solid black lines represent part of the L1.3 sequence included in the transcripts. Dotted lines represent portions of the L1.3 element that are spliced out during L1.3 transcription and are not present in the mature mRNAs. A major splice product produced by the wild type

(WT) L1.3Neo, SpX, is a result of the usage of the splice donor site in the 5' UTR at position 97 of L1.3 sequence and splice acceptor site at the end of the second exon of the neomycin resistance gene. SpX mRNA also does not contain any intronic sequences of the neo resistance gene. A less abundant product, SpX(IN), produced by the wt L1.3Neo construct results from the usage of the same splice donor and acceptor sites as SpX, but contains unspliced intron of the neo resistance cassette. **C.** Schematic representation of the previously reported prematurely polyadenylated mRNA species produced by L1.3Neo WT and 1M. 1M contains a double mutation in the conserved hexamer of the strongest polyA signal located at the end of ORF1 of the L1.3 element. Usage of this polyA signal during transcription of the wt L1.3 element produces mRNA species 3 that is absent in the 1M mutant. Instead, the 1M element makes mRNAs "a" and "b"⁴ and 5 by utilization of the polyA signals located downstream and upstream, respectively, of the mutated one. 3' ends of the solid black lines representing prematurely polyadenylated mRNAs correspond to the relative positions of the polyA signals in the L1.3 sequences responsible for their production. **D.** A diagram of the prematurely polyadenylated and spliced mRNAs species produced by the WT and 1M L1.3Neo elements. Solid and dotted black lines represent L1.3 sequences included in or spliced out of the mRNA molecules respectively. 3' ends of these spliced and polyadenylated mRNAs correspond to the relative positions of the polyA signals in the L1.3 sequences responsible for their production. Spliced, prematurely polyadenylated mRNAs are labeled by combining the splice junction name (a or b) with the name of the polyA signal used for termination of the spliced mRNA species (a3 and b3 for the WT construct and a4, b4 for the 1M construct). **E.** A virtual northern blot representing mRNAs produced by the NeoWT L1.3 expression cassette. mRNAs were detected with 5'UTR600 probe that visualizes only the unspliced, prematurely polyadenylated molecules (described in C). **F.** A virtual northern blot representing mRNAs produced by NeoWT and Neo1M L1.3 expression vectors. mRNAs were detected with 5'UTR100 probe that visualizes the unspliced and spliced prematurely polyadenylated molecules (described in C and D) and splice variants between L1.3 sequence and neo resistance gene (described in B). Unspliced prematurely polyadenylated mRNAs are labeled 1-5. Spliced prematurely polyadenylated mRNAs are labeled by combining the splice junction name (a or b) with the name of the polyA site used for termination of the spliced mRNA species (a3 and b3 for the WT construct and a4, b4, for the 1M construct). The star denotes bands seen in the actual northern for which the appropriate combination of splicing and polyadenylation has not been determined. **G.** A virtual northern blot representing mRNAs produced by NeoWT and the mutant of the major SD site position 97 of the L1.3 sequence, Neo97M, L1.3 expression cassette. mRNAs were detected with the strand-specific probe to the second exon of the neo resistance gene (NeoEx) that visualizes splice variants between the L1.3 sequence and the neo resistance gene (described in B) in addition to the previously described full-length L1.3 mRNAs (FL1.3Neo) with spliced (faster migrating band of the doublet) and unspliced (slower migrating band of the doublet) neo intron. Note the similarity in size between the splice variants SpX and Y most likely resulting from the usage of the SD site located only about 50 bp upstream of the mutated SD site (A of this figure and also see figure 6 for the actual northern blot).



Supplemental figure 2. Schematic representation of the mRNA species produced by the L1.3notag expression vector driven by CMV promoter. **A.** A diagram of the L1.3notag expression cassette containing the L1 promoter (PRO), open reading frames 1 and 2 (ORF1 and ORF2) and an SV40 polyadenylation signal as depicted in figure 3A. Black and gray vertical arrows represent functional splice donor (SD) and splice acceptor (SA) sites, respectively. Gray horizontal arrows indicate relative positions of the strand-specific RNA probes complementary to the first 100 bp (5'UTR100) or positions 583 to 698 (5'UTR600) of the L1.3 sequence. **B.** Schematic representation of the previously reported full-length (FL) and prematurely polyadenylated mRNA species produced by L1.3notag WT and a mutant of this construct that lacks the strongest polyA site (1M). 1M of L1.3notag contains the same mutation as described for the 1M mutant of the L1.3Neo expression vector. Prematurely polyadenylated mRNA species produced by the WT and 1M L1.3notag are identical to those observed for the WT and 1M L1.3Neo expression vector (Figure 2B and schematized in supplemental figure 1). 3' ends of the solid black lines representing prematurely polyadenylated mRNAs correspond to the relative positions of the polyA signals in the L1.3 sequences responsible for their production. **C.** A diagram of the prematurely polyadenylated and spliced mRNAs species produced by

the WT and 1M L1.3notag elements. Solid and dotted black lines represent L1.3 sequences included in or spliced out of the mRNA molecules respectively. 3' ends of these spliced and polyadenylated mRNAs correspond to the relative positions of the polyA signals in the L1.3 sequences responsible for their production. a3 and b3; a4, b4 mRNA species produced by the WT and 1M L1.3notag, respectively, are the same products that were described for the WT and 1M L1.3Neo constructs. The letter corresponds to the splice junction and the number represents the polyA site characteristic to a particular transcript. In addition to these spliced and prematurely polyadenylated products L1.3notag also makes mRNAs that undergo splicing at the SD and SA sites described for a3 and b3 mRNAs but terminate at the end of the L1.3 sequence, aFL and bFL (Figure 4). These spliced products are retrotranspositionally competent (see text for details). **D.** A virtual northern blot representing mRNAs produced by WT and 1M L1.3notag expression vectors. mRNAs were detected with 5'UTR100 probe that visualizes the unspliced and spliced prematurely polyadenylated molecules (described in B and C) and "aFL" and "bFL" splice variants that terminate at the end of the L1.3 sequence (described in C). Unspliced prematurely polyadenylated mRNAs are labeled 1-5. Spliced prematurely polyadenylated mRNAs are labeled by combining the splice junction name (a or b) with the name of the polyA site used for termination of the spliced mRNA species (a3 and b3 for the WT construct and a4, b4v for the 1M construct). The star denotes bands with as yet uncharacterized splicing and polyadenylation. **E.** A virtual northern blot representing mRNAs produced by WT and 1M L1.3notag expression vectors. mRNAs were detected with 5'UTR600 probe that visualizes only the unspliced polyadenylated molecules (described in B).

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-----+-----+-----+-----+-----+-----+
          10         20         30         40         50         60         70
-----+-----+-----+-----+-----+-----+
1 GGGGGAGGAGCCAAGATGGCCGAATAGGAACAGCTCCGGTCTACAGCTCCCAGCGTGAGCGACGCAGAAG
L1.3splice790
1 -----T..... AC093006
1 -----C..... AL031985
1 -----AL137022
1 -----AP000560

-----+-----+-----+-----+-----+-----+
          80         90         100        110        120        130        140
-----+-----+-----+-----+-----+-----+
71 AC-GGTGATTTCATTCATCTGAGACCTGCAGCTGAGGGTCCTGTCTGTTAGAAGGAAAACTAACA
L1.3splice790
59 ..-..... AC093006
65 ..C..... AL031985
65 ..A.....A..... AL137022
57 ..G..... AP000560

-----+-----+-----+-----+-----+-----+
          150        160        170        180        190        200        210
-----+-----+-----+-----+-----+-----+
140 ACCAGAAAGGACATCTACACCGAAAACCCATCTGTACATCACCATCATCAAAGACCAAAGTAGATAAAA
L1.3splice790
128 ..... AC093006
135 .A.....C.....A.....C..... AL031985
135 .A.....C.....A.....C..... AL137022
127 .A.....C..... AP000560

-----+-----+-----+-----+-----+-----+
          220        230        240        250        260        270        280
-----+-----+-----+-----+-----+-----+
210 CCACAAAGATGGGGAAAAACAGAACAGAAAACTGGAACTCTAAAACGCAGAGCGCCTCTCCTCCTCC
L1.3splice790
198 .....A..... AC093006
205 .....G...C...AT..... AL031985
205 .....TC..... AL137022
197 .....C..T.....G..... AP000560

-----+-----+-----+-----+-----+-----+
          290        300        310        320        330        340        350
-----+-----+-----+-----+-----+-----+
280 AAAGGAACGCAGTTCCTCACCAGCAACGGAACAAAGCTGGATGGAGAATGATTTTGACGAGCTGAGAGAA
L1.3splice790
268 .....A..... AC093006
275 .....C.....A.....C..... AL031985
275 .....A.....AA..A.....C..... AL137022
267 ..... AP000560

-----+-----+-----+-----+-----+-----+
          360        370        380        390        400        410        420
-----+-----+-----+-----+-----+-----+
350 GAAGGCTTCAGACGATCAAATTA CTCTGAGCTACGGGAGGACATTCAAACCAAAGCAAAGAAGTTGAAA
L1.3splice790
338 ..... AC093006
345 ..... AL031985
345 .....T.....A... AL137022
337 ..... AP000560

-----+-----+-----+-----+-----+-----+
          430        440        450        460        470        480        490
-----+-----+-----+-----+-----+-----+
420 ACTTTGAAAAAATTTAGAAGAATGTATAACTAGATAACCAATACAGAGAAGTGCCTTAAAGGAGCTGAT
L1.3splice790
408 ..... AC093006
415 ..... AL031985
415 .....T..... AL137022
407 .....T..... AP000560

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-----+-----+-----+-----+-----+-----+
          500      510      520      530      540      550      560
-----+-----+-----+-----+-----+-----+
490 GGAGCTGAAAACCAAGGCTCGAGAACTACGTGAAGAATGCAGAAGCCTCAGGAGCCGATGCGATCAACTG
L1.3splice790
478 ..... AC093006
485 ..... AL031985
485 .....C.....C..... AL137022
477 .....T.....A..... AP000560

-----+-----+-----+-----+-----+-----+
          570      580      590      600      610      620      630
-----+-----+-----+-----+-----+-----+
560 GAAGAAAGGGTATCAGCAATGGAAGATGAAATGAATGAAATGAAGCGAGAAGGGAAGTTTAGAGAAAAA
L1.3splice790
548 ..... AC093006
555 .....G.....G..... AL031985
555 ..... AL137022
547 .....G..... AP000560

-----+-----+-----+-----+-----+-----+
          640      650      660      670      680      690      700
-----+-----+-----+-----+-----+-----+
630 GAATAAAAAGAAATGAGCAAAGCCTCCAAGAAATATGGGACTATGTGAAAAGACCAAATCTACGTCTGAT
L1.3splice790
618 ..... AC093006
625 ..G.....A..... AL031985
625 .....C..... AL137022
617 ..... AP000560

-----+-----+-----+-----+-----+-----+
          710      720      730      740      750      760      770
-----+-----+-----+-----+-----+-----+
700 TGGTGTACCTGAAAGTGATGTGGAGAATGGAACCAAGTTGGAAAACACTCTGCAGGATATTATCCAGGAG
L1.3splice790
688 ..... AC093006
695 .....G..... AL031985
695 .....G..... AL137022
687 ...A.....G..... AP000560

-----+-----+-----+-----+-----+-----+
          780      790      800      810      820      830      840
-----+-----+-----+-----+-----+-----+
770 AACTTCCCAATCTAGCAAGGCAGGCCAACGTTTCAGATTCAGGAAATACAGAGAACGCCACAAAGATACT
L1.3splice790
758 ..... AC093006
765 .....T..... AL031985
765 .....T.....A..... AL137022
757 ..... AP000560

-----+-----+-----+-----+-----+-----+
          850      860      870      880      890      900      910
-----+-----+-----+-----+-----+-----+
840 CCTCGAGAAGAGCAACTCCAAGACACATAATTGTCAGATTCACCAAAGTTGAAATGAAGGAAAAAATGTT
L1.3splice790
828 ..... AC093006
835 ..... AL031985
835 ..... AL137022
827 ..... AP000560

-----+-----+-----+-----+-----+-----+
          920      930      940      950      960      970      980
-----+-----+-----+-----+-----+-----+
910 AAGGGCAGCCAGAGAGAAAGGTCGGGTTACCCCTCAAAGGAAAGCCCATCAGACTAACAGTGGATCTCTCG
L1.3splice790
898 .....C..... AC093006
905 .....G.....C.....A AL031985
905 .....G.....C..... AL137022
897 .....G.....C..... AP000560

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          990      1000      1010      1020      1030      1040      1050
-----+-----+-----+-----+-----+-----+-----+
 980 GCAGAAACCCCTACAAGCCAGAAGAGAGTGGGGCCAAATATTC AACATTCTTAAAGAAAAGAATTTTCAAC
L1.3splice790
 968 ..... AC093006
 975 ..... AL031985
 975 ..... AL137022
 959 .....A.....G..... AP000560

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          1060      1070      1080      1090      1100      1110      1120
-----+-----+-----+-----+-----+-----+
1050 CCAGAAATTTTCATATCCAGCCAAACTAAGCTTCATAAGTGAAGGAGAAATAAAATACTTTATAGACAAGCA
L1.3splice790
1038 ..... AC093006
1045 .....G.....C..... AL031985
1045 .....C..... AL137022
1029 .....G.....C.....C..... AP000560

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          1130      1140      1150      1160      1170      1180      1190
-----+-----+-----+-----+-----+-----+
1120 AATGTTGAGAGATTTTGTACCACCAGGCCCTGCCCTAAAAGAGCTCCTGAAGGAAGCGCTAAACATGGAA
L1.3splice790
1108 .....C.....A..... AC093006
1115 ....C.....A..... AL031985
1115 ....C.....A..... AL137022
1099 ....C..... AP000560

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          1200      1210      1220      1230      1240      1250      1260
-----+-----+-----+-----+-----+-----+
1190 AGGAACAACCGGTACCAGCCGCTGCAAAATCATGCCAAAATGTAAAGACCATCGAGACTAGGAAGAAACT
L1.3splice790
1178 ..... AC093006
1185 .....C.....A..... AL031985
1185 ..... AL137022
1169 .....T..... AP000560

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          1270      1280      1290      1300      1310      1320      1330
-----+-----+-----+-----+-----+-----+
1260 GCATCAACTAATGAGCAAAATCACCAGCTAACATCATAATGACAGGATCAAATTCACACATAACAATATT
L1.3splice790
1248 ..... AC093006
1255 .....C..... AL031985
1255 .....C..... AL137022
1239 .....C..... AP000560

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          1340      1350      1360      1370      1380      1390      1400
-----+-----+-----+-----+-----+-----+
1330 AACTTTAAATATAAATGGACTAAATCTGCAATTTAAAAGACACAGACTGGCAAGTTGGATAAAGAGTCAA
L1.3splice790
1318 ..... AC093006
1325 .....G.....G..C.....A..... AL031985
1325 .....G.....G..C.....A..... AL137022
1309 .....G.....C.....T..... AP000560

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          1410      1420      1430      1440      1450      1460      1470
-----+-----+-----+-----+-----+-----+
1400 GACCCATCAGTGTGCTGTATTTCAGGAAACCCATCTCACGTGCAGAGACACATAGGCTCAAATAAAAG
L1.3splice790
1388 ..... AC093006
1395 ..... AL031985
1395 ..... AL137022
1379 ..... AP000560

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          1480      1490      1500      1510      1520      1530      1540
-----+-----+-----+-----+-----+-----+

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-----+-----+-----+-----+-----+-----+
1470 GATGGAGGAAGATCTACCAAGCCAATGGAAAACAAAAAAGGCAGGGTTGCAATCCTAGTCTCTGATAA
L1.3splice790
1458 ..... AC093006
1465 ..... A ..... AL031985
1465 ..... A ..... AL137022
1449 ..... A ..... G ..... AP000560
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```
-----+-----+-----+-----+-----+-----+
                1550      1560      1570      1580      1590      1600      1610
-----+-----+-----+-----+-----+-----+
1540 AACAGACTTTAAACCAACAAAGATCAAAAGAGACAAAGAAGGCCATTACATAATGGTAAAGGGATCAATT
L1.3splice790
1528 ..... AC093006
1535 ..... AL031985
1535 ..... T ..... AL137022
1519 ..... AP000560
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```
-----+-----+-----+-----+-----+-----+
                1620      1630      1640      1650      1660      1670      1680
-----+-----+-----+-----+-----+-----+
1610 CAACAAGAGGAGCTAACTATCCTAAATATTTATGCACCCAATACAGGAGCACCCAGATTCATAAAGCAAG
L1.3splice790
1598 ..... AC093006
1605 ..... A ..... A ..... AL031985
1601 ..... A ..... A ..... AL137022
1589 ..... A ..... AP000560
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-----+-----+-----+-----+-----+-----+
                1690      1700      1710      1720      1730      1740      1750
-----+-----+-----+-----+-----+-----+
1680 TCCTCAGTGACCTACAAAGAGACTTAGACTCCCACACATTAATAATGGGAGACTTTAACACCCCACTGTC
L1.3splice790
1668 ..... AC093006
1675 ...G..... A ..... AL031985
1671 ...G..... AL137022
1659 ...G..... AP000560
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```
-----+-----+-----+-----+-----+-----+
                1760      1770      1780      1790      1800      1810      1820
-----+-----+-----+-----+-----+-----+
1750 AACATTAGACAGATCAACGAGACAGAAAGTCAACAAGGATACCCAGGAATTGAACTCAGCTCTGCACCAA
L1.3splice790
1738 ..... A ..... AC093006
1745 ..... AL031985
1741 ..... T ..... A ..... AL137022
1729 ..... AP000560
```

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-----+-----+-----+-----+-----+-----+
                1830      1840      1850      1860      1870      1880      1890
-----+-----+-----+-----+-----+-----+
1820 GCAGACCTAATAGACATCTACAGAACTCTCCACCCCAATCAACAGAATATACCTTTTTTTCAGCACCC
L1.3splice790
1808 ..... A ..... AC093006
1815 ..G..... A ..... AL031985
1811 ..TG..... AC ..... AL137022
1799 ..G..... A ..... AP000560
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-----+-----+-----+-----+-----+-----+
                1900      1910      1920      1930      1940      1950      1960
-----+-----+-----+-----+-----+-----+
1890 ACCACACCTATTCCAAAATTGACCACATAGTTGGAAGTAAAGCTCTCCTCAGCAAATGTAAAAGAACAGA
L1.3splice790
1878 ..... AC093006
1885 ..... C ..... AL031985
1881 ..... AL137022
1869 ..... A ..... AP000560
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-----+-----+-----+-----+-----+-----+
                1970      1980      1990      2000      2010      2020      2030
-----+-----+-----+-----+-----+-----+
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1960 AATTATAACAAACTATCTCTCAGACCACAGTGCAATCAAAC TAGAACTCAGGATTAAGAATCTCACTCAA
 L1.3splice790
 1948 AC093006
 1955 AL031985
 1951 AL137022
 1939 T..... AP000560

-----+-----+-----+-----+-----+-----+-----+
 2040 2050 2060 2070 2080 2090 2100
 -----+-----+-----+-----+-----+-----+-----+

2030 AGCCGCTCAACTACATGGAAACTGAACAACCTGCTCCTGAATGACTACTGGGTACATAACGAAATGAAGG
 L1.3splice790
 2018 AC093006
 2025 AL031985
 2021 A..... C..... T..... AL137022
 2009 AP000560

-----+-----+-----+-----+-----+-----+-----+
 2110 2120 2130 2140 2150 2160 2170
 -----+-----+-----+-----+-----+-----+-----+

2100 CAGAAATAAAGATGTTCTTTGAAACCAACGAGAACAAGACACCACATACCAGAATCTCTGGGACGCATT
 L1.3splice790
 2088 AC093006
 2095 A..... T..... AL031985
 2091 C..... A..... A..... AL137022
 2079 C..... A..... AP000560

-----+-----+-----+-----+-----+-----+-----+
 2180 2190 2200 2210 2220 2230 2240
 -----+-----+-----+-----+-----+-----+-----+

2170 CAAAGCAGTGTGTAGAGGGAAATTTATAGCACTAAATGCCTACAAGAGAAAGCAGGAAAGATCCAAAATT
 L1.3splice790
 2158 C..... AC093006
 2165 T..... C..... AL031985
 2161 C..... C..... C..... AL137022
 2149 T..... G..... C..... AP000560

-----+-----+-----+-----+-----+-----+-----+
 2250 2260 2270 2280 2290 2300 2310
 -----+-----+-----+-----+-----+-----+-----+

2240 GACACCCTAACATCACAATTTAAAGAACTAGAAAAGCAAGAGCAAACACATTCAAAGCTAGCAGAAGGC
 L1.3splice790
 2228 AC093006
 2235 AL031985
 2231 AL137022
 2219 AP000560

-----+-----+-----+-----+-----+-----+-----+
 2320 2330 2340 2350 2360 2370 2380
 -----+-----+-----+-----+-----+-----+-----+

2310 AAGAAATAACTAAAAATCAGAGCAGAACTGAAGGAAATAGAGACACAAAAACCCTTCAAAAAATCAATGA
 L1.3splice790
 2298 AC093006
 2304 A..... G..... AL031985
 2301 G..... AL137022
 2289 C..... T..... AP000560

-----+-----+-----+-----+-----+-----+-----+
 2390 2400 2410 2420 2430 2440 2450
 -----+-----+-----+-----+-----+-----+-----+

2380 ATCCAGGAGCTGGTTTTTTGAAAGGATCAACAAAATTGATAGACCGCTAGCAAGACTAATAAAGAAAAA
 L1.3splice790
 2368 AC093006
 2374 AL031985
 2371 C..... C..... AL137022
 2359 A..... AP000560

-----+-----+-----+-----+-----+-----+-----+
 2460 2470 2480 2490 2500 2510 2520
 -----+-----+-----+-----+-----+-----+-----+

2450 AGAGAGAAGAATCAAATAGACACAATAAAAAATGATAAAGGGGATATCACCACCGATCCCACAGAAATAC
L1.3splice790
2438 AC093006
2444G..... AL031985
2441T.....A.....A..... AL137022
2429A..... AP000560

-----+-----+-----+-----+-----+-----+-----+
2530 2540 2550 2560 2570 2580 2590
-----+-----+-----+-----+-----+-----+-----+

2520 AAACTACCATCAGAGAATACTACAAACACCTCTACGCAAATAAACTAGAAAATCTAGAAGAAATGGATAC
L1.3splice790
2508T.....G.....C..... AC093006
2514A..... AL031985
2511T.....A..... AL137022
2499A..... AP000560

-----+-----+-----+-----+-----+-----+-----+
2600 2610 2620 2630 2640 2650 2660
-----+-----+-----+-----+-----+-----+-----+

2590 ATTCTCGACACATACACTCTCCAAGACTAAACCAGGAAGAAGTTGAATCTCTGAATAGACCAATAACA
L1.3splice790
2578C..... AC093006
2584T..... AL031985
2581T.....C..... AL137022
2569C..... AP000560

-----+-----+-----+-----+-----+-----+-----+
2670 2680 2690 2700 2710 2720 2730
-----+-----+-----+-----+-----+-----+-----+

2660 GGCTCTGAAATTGTGGCAATAATCAATAGTTTACCAACCAAAAAGAGTCCAGGACCAGATGGATTACAG
L1.3splice790
2648 AC093006
2654 ..AG.....C.....T..... AL031985
2651 ..AG.....A..... AL137022
2639 ..AG..... AP000560

-----+-----+-----+-----+-----+-----+-----+
2740 2750 2760 2770 2780 2790 2800
-----+-----+-----+-----+-----+-----+-----+

2730 CCGAATTCTACCAGAGGTACATGGAGGAACGGTACCATTCTCTGAAACTATTCCAATCAATAGAAAA
L1.3splice790
2718A..... AC093006
2724A..... AL031985
2721A..... AL137022
2709AA..... AP000560

-----+-----+-----+-----+-----+-----+-----+
2810 2820 2830 2840 2850 2860 2870
-----+-----+-----+-----+-----+-----+-----+

2800 AGAGGGAATCCTCCCTAACTCATTTTATGAGGCCAGCATCATCTGATACCAAAGCCGGGCAGAGACACA
L1.3splice790
2788 AC093006
2794 AL031985
2791T.....T..... AL137022
2779G..... AP000560

-----+-----+-----+-----+-----+-----+-----+
2880 2890 2900 2910 2920 2930 2940
-----+-----+-----+-----+-----+-----+-----+

2870 ACCAAAAAGAGAATTTTAGACCAATATCCTTGATGAACATTGATGCAAAAATCCTCAATAAAATACTGG
L1.3splice790
2858 AC093006
2864 ..A..... AL031985
2861 AL137022
2849 AP000560

-----+-----+-----+-----+-----+-----+-----+
2950 2960 2970 2980 2990 3000 3010
-----+-----+-----+-----+-----+-----+-----+

2940 CAAACCGAATCCAGCAGCACATCAAAAAGCTTATCCACCATGATCAAGTGGGCTTCATCCCTGGGATGCA
L1.3splice790
2928 AC093006
2934 AL031985
2931 ...A.....C.....A..... AL137022
2919A..... AP000560

-----+-----+-----+-----+-----+-----+
3020 3030 3040 3050 3060 3070 3080
-----+-----+-----+-----+-----+-----+

3010 AGGCTGGTTCAATATACGCAAATCAATAAATGTAATCCAGCATATAAACAGAGCCAAAGACAAAACCAC
L1.3splice790
2998 AC093006
3004A..... AL031985
3001 AL137022
2989C..... AP000560

-----+-----+-----+-----+-----+-----+
3090 3100 3110 3120 3130 3140 3150
-----+-----+-----+-----+-----+-----+

3080 ATGATTATCTCAATAGATGCAGAAAAAGCCTTTGACAAAATCAACAACCCTTCATGCTAAAACTCTCA
L1.3splice790
3068 AC093006
3074 AL031985
3071 AL137022
3059 AP000560

-----+-----+-----+-----+-----+-----+
3160 3170 3180 3190 3200 3210 3220
-----+-----+-----+-----+-----+-----+

3150 ATAAATTAGGTATTGATGGGACGTATTTCAAATAATAAGAGCTATCTATGACAAACCCACAGCCAATAT
L1.3splice790
3138 AC093006
3144T..... AL031985
3141C..... AL137022
3129C..... AP000560

-----+-----+-----+-----+-----+-----+
3230 3240 3250 3260 3270 3280 3290
-----+-----+-----+-----+-----+-----+

3220 CATACTGAATGGGCAAAAACCTGGAAGCATTCCTTTGAAAACCGGCACAAGACAGGGATGCCCTCTCTCA
L1.3splice790
3208T..... AC093006
3214T..... AL031985
3211T..... AL137022
3199T..... AP000560

-----+-----+-----+-----+-----+-----+
3300 3310 3320 3330 3340 3350 3360
-----+-----+-----+-----+-----+-----+

3290 CCGCTCCTATTCAACATAGTGTGGAAGTTCTGGCCAGGGCAATCAGGCAGGAGAAGGAAATAAAGGGTA
L1.3splice790
3278 AC093006
3284 ..A.....T..... AL031985
3281 ..A.....T..... AL137022
3269 ..A.....A..... AP000560

-----+-----+-----+-----+-----+-----+
3370 3380 3390 3400 3410 3420 3430
-----+-----+-----+-----+-----+-----+

3360 TTCAATTAGGAAAAGAGGAAGTCAAATTGTCCTTGTTCAGACGACATGATTGTATATCTAGAAAACCC
L1.3splice790
3348T..... AC093006
3354T..... AL031985
3351 AL137022
3339T..... AP000560

-----+-----+-----+-----+-----+-----+
3440 3450 3460 3470 3480 3490 3500
-----+-----+-----+-----+-----+-----+

3430 CATCGTCTCAGCCAAAATCTCCTTAAGCTGATAAGCAACTTCAGCAAAGTCTCAGGATACAAAATCAAT
L1.3splice790
3418 AC093006
3424 ...T..... AL031985
3421 ...T.....G..... AL137022
3409 ...T..... AP000560

-----+-----+-----+-----+-----+-----+-----+
3510 3520 3530 3540 3550 3560 3570
-----+-----+-----+-----+-----+-----+-----+

3500 GTACAAAAATCACAAGCATTCTTATACACCAACAACAGACAAACAGAGAGCCAAATCATGGGTGAAGTCC
L1.3splice790
3488A..... AC093006
3494A..... AL031985
3491A.....A..... AL137022
3479A..... AP000560

-----+-----+-----+-----+-----+-----+-----+
3580 3590 3600 3610 3620 3630 3640
-----+-----+-----+-----+-----+-----+-----+

3570 CATTTCGTAATTGCTTCAAAGAGAATAAAATACCTAGGAATCCAACCTTACAAGGGATGTGAAGGACCTCTT
L1.3splice790
3558AC..... AC093006
3564AC..... AL031985
3561AC..... AL137022
3549AC.....T..... AP000560

-----+-----+-----+-----+-----+-----+-----+
3650 3660 3670 3680 3690 3700 3710
-----+-----+-----+-----+-----+-----+-----+

3640 CAAGGAGAACTACAAACCACTGCTCAAGGAAATAAAAGAGGACACAAACAAATGGAAGAACATTCCATGC
L1.3splice790
3628G..... AC093006
3634T..... AL031985
3631C.....T..... AL137022
3619C.....T..... AP000560

-----+-----+-----+-----+-----+-----+-----+
3720 3730 3740 3750 3760 3770 3780
-----+-----+-----+-----+-----+-----+-----+

3710 TCATGGGTAGGAAGAATCAATATCGTGAAAATGGCCATACTGCCCAAGGTAATTTACAGATTCAATGCCA
L1.3splice790
3698 AC093006
3704T..... AL031985
3701 AL137022
3689 AP000560

-----+-----+-----+-----+-----+-----+-----+
3790 3800 3810 3820 3830 3840 3850
-----+-----+-----+-----+-----+-----+-----+

3780 TCCCCATCAAGCTACCAATGACTTTCTTCACAGAATTGGAAAAACTACTTTAAAGTTCATATGGA----
L1.3splice790
3768---- AC093006
3774---- AL031985
3771---- AL137022
3759CGGC AP000560

-----+-----+-----+-----+-----+-----+-----+
3860 3870 3880 3890 3900 3910 3920
-----+-----+-----+-----+-----+-----+-----+

3846 -----
L1.3splice790
3834 ----- AC093006
3840 ----- AL031985
3837 ----- AL137022
3829 CGGGCGGGTGGCTCACGCTGTAATCCAGCACTTTGGGAGGCCAAGGTGGGCGGATCACGAGGTCAGG AP000560

-----+-----+-----+-----+-----+-----+-----+
3930 3940 3950 3960 3970 3980 3990
-----+-----+-----+-----+-----+-----+-----+

3846 -----
L1.3splice790
3834 ----- AC093006
3840 ----- AL031985
3837 ----- AL137022
3899 AGATCGAGACCATCCCCGCTAAAACAGTGAAACCCCGTCTCTACTAAAAATACAAAAAAAATTAGCCGG AP000560

-----+-----+-----+-----+-----+-----+
4000 4010 4020 4030 4040 4050 4060
-----+-----+-----+-----+-----+-----+

3846 -----
L1.3splice790
3834 ----- AC093006
3840 ----- AL031985
3837 ----- AL137022
3969 GCGTAGTGGCGGGCGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAATGGCGTGAAACCGGGA AP000560

-----+-----+-----+-----+-----+-----+
4070 4080 4090 4100 4110 4120 4130
-----+-----+-----+-----+-----+-----+

3846 -----
L1.3splice790
3834 ----- AC093006
3840 ----- AL031985
3837 ----- AL137022
4039 GGCGGAGCTTGACAGTGAGCCGAGATCCCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGTCT AP000560

-----+-----+-----+-----+-----+-----+
4140 4150 4160 4170 4180 4190 4200
-----+-----+-----+-----+-----+-----+

3846 -----ACCAAAAAAGAGCCCGCATTGCCAAGTCAATCCTAAGCCAAAAG
L1.3splice790
3834 ----- AC093006
3840 ----- .A...C..... AL031985
3837 -----CA..... AL137022
4109 CAAAAAAAAAAAAAGTTCATATGGA.....C.....A AP000560

-----+-----+-----+-----+-----+-----+
4210 4220 4230 4240 4250 4260 4270
-----+-----+-----+-----+-----+-----+

3890 AACAAAGCTGGAGGCATCACACTACCTGACTTCAAACATACTACAAGGCTACAGTAACCAAAACAGCAT
L1.3splice790
3878 AC093006
3884T.....A..... AL031985
3881 AL137022
4179 AP000560

-----+-----+-----+-----+-----+-----+
4280 4290 4300 4310 4320 4330 4340
-----+-----+-----+-----+-----+-----+

3960 GGTACTGGTACCAAAACAGAGATATAGATCAATGGAACAGAACAGAGCCCTCAGAAATAATGCCGCATAT
L1.3splice790
3948 AC093006
3954C.....C AL031985
3951C.....C..... AL137022
4249C.....C..... AP000560

-----+-----+-----+-----+-----+-----+
4350 4360 4370 4380 4390 4400 4410
-----+-----+-----+-----+-----+-----+

4030 CTACAACCTATCTGATCTTTGACAAACCTGAGAAAAACAAGCAATGGGGAAAGGATTCCCTATTTAATAAA
L1.3splice790
4018G..... AC093006
4024G.....A..... AL031985
4021T..... AL137022
4319 .A..... AP000560

-----+-----+-----+-----+-----+-----+
4420 4430 4440 4450 4460 4470 4480
-----+-----+-----+-----+-----+-----+

4100 TGGTGTGGGAAACCTGGCTAGCCATATGTAGAAAGCTGAACTGGATCCCTTCCTTACACCTTATACAA
L1.3splice790
4088 AC093006
4094 AL031985
4091 AL137022
4389 AP000560

-----+-----+-----+-----+-----+-----+-----+
4490 4500 4510 4520 4530 4540 4550
-----+-----+-----+-----+-----+-----+-----+

4170 AAATCAATTCAAGATGGATTAAGATTTAAACGTAAACCTAAAACCATAAAAACCTAGAAAGAAAACCT
L1.3splice790
4158 AC093006
4164G..... AL031985
4161G...G..... AL137022
4459G..... AP000560

-----+-----+-----+-----+-----+-----+-----+
4560 4570 4580 4590 4600 4610 4620
-----+-----+-----+-----+-----+-----+-----+

4240 AGGCATTACCATTTCAGGACATAGGCGTGGGCAAGGACTTCATGTCCAAAACACCAAAGCAATGGCAACA
L1.3splice790
4228 AC093006
4234A.....A..... AL031985
4231C...A...G..... AL137022
4529 AP000560

-----+-----+-----+-----+-----+-----+-----+
4630 4640 4650 4660 4670 4680 4690
-----+-----+-----+-----+-----+-----+-----+

4310 AAAGACAAAATTGACAAATGGGATCTAATTAAGCTAAAGAGCTTCTGCACAGCAAAAGAACTACCATCA
L1.3splice790
4298 AC093006
4304 AL031985
4301C..... AL137022
4599 AP000560

-----+-----+-----+-----+-----+-----+-----+
4700 4710 4720 4730 4740 4750 4760
-----+-----+-----+-----+-----+-----+-----+

4380 GAGTGAACAGGCAACCTACAACATGGGAGAAAATTTTCGCAACCTACTCATCTGACAAAGGCTAATATC
L1.3splice790
4368T..... AC093006
4374A..... AL031985
4371A..... AL137022
4669AC...A..... AP000560

-----+-----+-----+-----+-----+-----+-----+
4770 4780 4790 4800 4810 4820 4830
-----+-----+-----+-----+-----+-----+-----+

4450 CAGAATCTACAATGAACCTAAACAAATTTACAAGAAAAAACAACAACCCCATCAAAAAGTGGGCGAAG
L1.3splice790
4438C..... AC093006
4444C..C.....A... AL031985
4441C.....C..... AL137022
4739C.....A... AP000560

-----+-----+-----+-----+-----+-----+-----+
4840 4850 4860 4870 4880 4890 4900
-----+-----+-----+-----+-----+-----+-----+

4520 GACATGAACAGACACTTCTCAAAAGAAGACATTTATGCAGCAAAAAACACATGAAGAAATGCTCATCAT
L1.3splice790
4508 AC093006
4514A..... AL031985
4511A..... AL137022
4809 ..T.....A.....C... AP000560

-----+-----+-----+-----+-----+-----+-----+
4910 4920 4930 4940 4950 4960 4970
-----+-----+-----+-----+-----+-----+-----+

4590 CACTGGCCATCAGAGAAATGCAAATCAAACCCTATGAGATATCATCTCACACCAGTTAGAATGGCAAT
 L1.3splice790
 4578 AC093006
 4584A.....C..... AL031985
 4581A.....C..... AL137022
 4879 AP000560

-----+-----+-----+-----+-----+-----+
 4980 4990 5000 5010 5020 5030 5040
 -----+-----+-----+-----+-----+-----+

4660 CATTAAAAAGTCAGGAAACAACAGGTGCTGGAGAGGATGCGGAGAAATAGGAACACTTTTACACTGTTGG
 L1.3splice790
 4648 AC093006
 4654T.....T..... AL031985
 4651T..... AL137022
 4949T..... AP000560

-----+-----+-----+-----+-----+-----+
 5050 5060 5070 5080 5090 5100 5110
 -----+-----+-----+-----+-----+-----+

4730 TGGGACTGTAAACTAGTTCAACCATTGTGGAAGTCAGTGTGGCGATTCTCAGGGATCTAGAACTAGAAA
 L1.3splice790
 4718 AC093006
 4724 AL031985
 4721 AL137022
 5019 AP000560

-----+-----+-----+-----+-----+-----+
 5120 5130 5140 5150 5160 5170 5180
 -----+-----+-----+-----+-----+-----+

4800 TACCATTTGACCCAGCCATCCCATTTACTGGGTATATACCCAAATGAGTATAAATCATGCTGCTATAAAGA
 L1.3splice790
 4788 AC093006
 4794C..... AL031985
 4791T.....G..C..... AL137022
 5089T...G..C..... AP000560

-----+-----+-----+-----+-----+-----+
 5190 5200 5210 5220 5230 5240 5250
 -----+-----+-----+-----+-----+-----+

4870 CACATGCACACGTATGTTTATTGCGGCACTATTTCACAATAGCAAAGACTTGGAAACCAACCCAAATGTCCA
 L1.3splice790
 4858 AC093006
 4864T..... AL031985
 4861A.....T..... AL137022
 5159C.....T..... AP000560

-----+-----+-----+-----+-----+-----+
 5260 5270 5280 5290 5300 5310 5320
 -----+-----+-----+-----+-----+-----+

4940 ACAATGATAGACTGGATTAAGAAAATGTGGCACATATACCCATGGAATACTATGCAGCCATAAAAAATG
 L1.3splice790
 4928 AC093006
 4934 AL031985
 4931 AL137022
 5229 AP000560

-----+-----+-----+-----+-----+-----+
 5330 5340 5350 5360 5370 5380 5390
 -----+-----+-----+-----+-----+-----+

5010 ATGAGTTCATATCCTTTGTAGGGACATGGATGAAATGGAAACCATCATTCTCAGTAAACTATCGCAAGA
 L1.3splice790
 4998 AC093006
 5004G.....T.....T.....A..... AL031985
 5001G.....T.....A..... AL137022
 5299G.....C..... AP000560

-----+-----+-----+-----+-----+-----+
 5400 5410 5420 5430 5440 5450 5460
 -----+-----+-----+-----+-----+-----+

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5080 ACAAAAACCAAACACCGCATATTCCTCACTCATAGGTGGGAATTGAACAATGAGATCACATGGACACAGG
L1.3splice790
5068 ..... AC093006
5074 ..... AL031985
5071 .....G.....A..... AL137022
5369 ..... AP000560

-----+-----+-----+-----+-----+-----+
          5470      5480      5490      5500      5510      5520      5530
-----+-----+-----+-----+-----+-----+
5150 AAGGGGAATATCACACTCTGGGGACTGTGGTGGGGTCGGGGAGGGGGAGGGATAGCATTGGGAGATAT
L1.3splice790
5138 ..... AC093006
5144 .....A..... AL031985
5141 .G.....G.....A..... AL137022
5439 .....C.....G..... AP000560

-----+-----+-----+-----+-----+-----+
          5540      5550      5560      5570      5580      5590      5600
-----+-----+-----+-----+-----+-----+
5220 ACCTAATGCTAGATGACACATTAGTGGGTGCAGCGCACCAGCATGGCACATGTATACATATGTAAC TAAC
L1.3splice790
5208 ..... AC093006
5214 .....GAG..... AL031985
5211 .....GAG..... AL137022
5509 .....GAG..... AP000560

-----+-----+-----+-----+-----+-----+
          5610      5620      5630      5640      5650      5660      5670
-----+-----+-----+-----+-----+-----+
5290 CTGCACAATGTGCACATGTACCCTAAAACCTTAGAGTATAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
L1.3splice790
5278 .....TGCC. AC093006
5284 .....A.....G...G... AL031985
5281 .....A.....GG.TTTCT.CTTCT--- AL137022
5579 .....A.....T...T...T...G...TTGC---C AP000560

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Supplemental figure 3. Alignment of the spliced L1 elements identified in the human genome. Sequences of the full-length human L1 elements that underwent splicing (SD and SA sites at positions 97 and 790 L1.3 sequence respectively) and retrotransposed were extracted from the human genome and aligned by ClustalW method against L1.3 sequence spliced in the same manner (L1.3 spliced790). Nucleotides that do not match L1.3 sequence are shown. Accession numbers corresponding to each contig containing these sequences are shown on the right. AC093006 L1 belongs to the Ta family, the rest of the elements are non-Ta (Boissinot *et.al.* Mol Biol Evol. 2000 Jun;17(6):915-28)

```

-----+-----+-----+-----+-----+-----+
          10         20         30         40         50         60         70
-----+-----+
1 GGGGGAGGAGCCAAGATGGCCGAATAGGAACAGCTCCGGTCTACAGCTCCCAGCGTGAGCGACGCAGAAG L1.3spliced
1 -----T...C..... AC079018
1 .....T.....A..... AC093115
1 .....C.....A..... AF188024
1 ..... AL133472
1 --.....C.....T.....A..... AL138900
1 ..... AL163952
1 -----C.....A.....A...T...T..... AL353590
1 -----T.....A...T..... AL807813
1 -----T.....A..... AC093808

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-----+-----+-----+-----+-----+
          80         90         100        110        120        130        140
-----+-----+
71 ACGG-TGATTTCTGCATTTCCATCTGAGGAACGCAGTTCCTCACCAGCAACGGAACAAAGCTGGATGGAG L1.3spliced
65 ..A.G.....AT..A.....T...C.....A..... AC079018
71 ...G..... AC093115
71 ...G.....T.....C.... AF188024
71 ...G.....T.....T.....C.... AL133472
69 .T.G.....CA... AL138900
70 ...G..... AL163952
65 ...G.....A.....T..C.....T..... AL353590
64 .T.G.....A.....T..... AL807813
64 .T.G.....A.....C..... AC093808

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-----+-----+-----+-----+-----+
          150        160        170        180        190        200        210
-----+-----+
140 AATGATTTTGACGAGCTGAGAGAAGAAGGCTTCAGACGATCAAATTACTCTGAGCTACGGGAGGACATTC L1.3spliced
135 ..C..C.....T.....C.....C.....C.....A.....A.... AC079018
141 ..... AC093115
141 .....C.....G.....CA.....A.... AF188024
141 .....C.....T.....A.G...A.....CA.....TA.....A.... AL133472
139 .....C.....T.....T..... AL138900
140 .....C..... AL163952
135 ...A.C.....T.....C..A..C.....AA.....AG... AL353590
132 .....C.....T.....T.....C..C.....A.....A.... AL807813
134 .....C.--.....T.....C.....A.....A.... AC093808

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-----+-----+-----+-----+-----+
          220        230        240        250        260        270        280
-----+-----+
210 AAACCAAAGGCAAAGAAGTTGAAAACTTTGAAAAAATTTAGAAGAATGTATAACTAGAATAACCAATAC L1.3spliced
205 .....C.....A.....G.....A.....C.....G.....G. AC079018
211 ..T..... AC093115
211 .....A.....A.....A..... AF188024
211 .....CA.....A.C..... AL133472
206 .....C..... AL138900
210 ..... AL163952
205 G....C.T.....A.....A.....T....GC..G.....G. AL353590
202 .....T.....A.....T.....G.....A..... AL807813
202 .....A.....C..A.....C..... AC093808

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-----+-----+-----+-----+-----+
          290        300        310        320        330        340        350
-----+-----+
280 AGAGAAGTGCCTTAAAGGAGCTGATGGAGCTGAAAACCAAGGCTCGAGAACTACGTGAAGAATGCAGAAGC L1.3spliced
275 .....C.....A.....G.....T..... AC079018
281 ..... AC093115
281 ..... AF188024
281 .....G.....T..T.....C..... AL133472
276 .....T.....A..... AL138900
280 .....A..... AL163952
275 .....C.....C.....AT.....T...C.....C.... AL353590
272 .....G.....C.GG...A..... AL807813
272 .....G.....G..... AC093808

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          360      370      380      390      400      410      420
-----+-----+-----+-----+-----+-----+-----+
350 CTCAGGAGCCGATGCGATCAACTGGAAGAAAGGGTATCAGCAATGGAAGATGAAATGAATGAAATGAAGC L1.3spliced
345 .....A....A.....TG...C....CT.....AC079018
351 .....AC093115
351 .....A.....G.....AF188024
351 .....A....T.....TG.....AL133472
346 .....G.....TG.....G.....AL138900
350 .....T.....AL163952
345 .....T...A...T.....TG.....C...G.....AL353590
342 .....TT.....C...ATG.....AL807813
342 .....T....A.....TG.....T.....AC093808

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          430      440      450      460      470      480      490
-----+-----+-----+-----+-----+-----+
420 GAGAAGGGAAGTTTAGAGAAAAA-GAATAAAAAGAAATGAGCAAAGCCTCCAAGAAATATGGGACTATG L1.3spliced
415 .....A....T.....AC079018
421 .....A.....AC093115
421 .....C.C.....AF188024
421 .....C.A...A.....AL133472
416 A.....C.....AL138900
420 .....G.....AL163952
414 ---.A.....A.....AL353590
412 A.....A.G.....C.AT.....A.....AL807813
412 .....C.A.....AC093808

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          500      510      520      530      540      550      560
-----+-----+-----+-----+-----+-----+
489 TGAAAAGACCAAATCTACGTCTGATTGGTGTACCTGAAAGTGTATGTTGGAGAATGGAACCAAGTTGGAAAA L1.3spliced
484 .....A....C.....C.G.....G.....AC079018
490 .....T.....C.....AC093115
490 .....A.....C.G.....AF188024
490 .....G.....C.G.....AL133472
485 .....T.....C.....A.....AL138900
489 .....AG.....AL163952
480 .....A.....C.G.....AL353590
482 .....G.....G.....A.....AL807813
481 .....C.G....C....C.....AC093808

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          570      580      590      600      610      620      630
-----+-----+-----+-----+-----+-----+
559 CACTCTGCAGGATATTATCCAGGAGAACTTCCCAATCTAGCAAGGCAGGCCAACGTTTCAGATTCAGGAA L1.3spliced
554 .....A.....AC079018
560 .....G.....AC093115
560 .....A.....AF188024
559 .....A.....AL133472
554 .....T.TA.....AL138900
559 .....AL163952
550 .....G.....T.....A.....AL353590
552 .....G.....C.....A.....AL807813
551 .....AC093808

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          640      650      660      670      680      690      700
-----+-----+-----+-----+-----+-----+
629 ATACAGAGAACGCCACAAGATACTCCTCGAGAAGGCAACTCCAAGACACATAATGTTCAGATTCACCA L1.3spliced
624 .....T.....T.....AC079018
630 .....T.....A.....AC093115
630 .....AF188024
629 .....A.....AL133472
624 .....A.....T.....AL138900
629 .....G.....AL163952
620 .....T.....A.....AL353590
622 .....T.....A.....AL807813
621 .....A.....AC093808

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          710      720      730      740      750      760      770
-----+-----+-----+-----+-----+-----+

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-----+-----+-----+-----+-----+-----+
699 AAGTTGAAATGAAGGAAAAAATGTTAAGGGCAGCCAGAGAGAAAGGTCGGGTTACCCTCAAAGGAAAGCC L1.3spliced
694 .....A.....A.....G..... AC079018
700 .....G..... AC093115
700 .....G..... AF188024
699 .....A.....A.....G..... AL133472
694 .....A.....G..... AL138900
699 .....G..... AL163952
690 ..A.....G.....A.....G..... AL353590
690 .....A.....AA.....G..... AL807813
691 .....A.....A.....G..... AC093808

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-----+-----+-----+-----+-----+-----+
              780       790       800       810       820       830       840
-----+-----+-----+-----+-----+-----+
769 CATCAGACTAACAGTGGATCTCTCGGCAGAAACCCCTACAAGCCAGAGAGTGGGGGCCAATATTCAAC L1.3spliced
764 .....C.....T.....C...C..... AC079018
770 .....C..... AC093115
770 .....CA.....A.....T..... AF188024
769 ..A.....T.....T..... AL133472
764 .....C.....T.G.....T.G..... AL138900
769 .....C..... AL163952
760 .....G.C.....CT.....TG..... AL353590
760 .....CAA.....A.....T.....CA..... AL807813
761 .....CT.....T..... AC093808

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-----+-----+-----+-----+-----+-----+
              850       860       870       880       890       900       910
-----+-----+-----+-----+-----+-----+
839 ATTCTTAAAGAAAAGAATTTTCAACCCAGAATTTTCATATCCAGCCAAACTAAGCTTCATAAGTGAAGGAG L1.3spliced
834 ..... AC079018
840 ..... AC093115
840 ..... AF188024
839 .....A..... AL133472
834 .....T..... AL138900
839 ..... AL163952
830 .....G..... AL353590
830 .....G..... AL807813
831 ..C.....T.....A..... AC093808

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-----+-----+-----+-----+-----+-----+
              920       930       940       950       960       970       980
-----+-----+-----+-----+-----+-----+
909 AAATAAAATACTTTATAGACAAGCAAATGTTGAGAGATTTTGTCCACCAGGCCTGCCCTAAAAGAGCT L1.3spliced
904 ...C.....C.....C.....T..... AC079018
910 ...C.....C.....G.C.....A..... AC093115
910 .....T...C.....C.....T..... AF188024
909 .....C.....C..... AL133472
904 .....C...C.....C.....G..... AL138900
909 .....C.C.....C.....T..... AL163952
900 .....C...C.....C.....A.....T..... AL353590
900 .....C...C.....C.....A..... AL807813
901 .....C...C.....C.....T...C..... AC093808

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-----+-----+-----+-----+-----+-----+
              990       1000      1010      1020      1030      1040      1050
-----+-----+-----+-----+-----+-----+
979 CCTGAAGGAAGCGCTAAACATGGAAAGGAACAACCGGTACCAGCCGCTGCAAATCA-----TGCCA L1.3spliced
974 .....A.....A.....T.A..... AC079018
980 .....A..... AC093115
980 .....A..... AF188024
979 .....A.....C.....T..... AL133472
974 .....A..... AL138900
979 .....T..... AL163952
970 .....A.....T.....A.....A..... AL353590
970 .....A.....C.....A.....AA.AAAAAAA..... AL807813
971 .....A.....T.....A..... AC093808

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-----+-----+-----+-----+-----+-----+
              1060      1070      1080      1090      1100      1110      1120
-----+-----+-----+-----+-----+-----+

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1041 AAATGTAAAGACCATCGAGACTAGGAAGAACTGCATCAACTAATGAGCAAAATCACCAGCTAACATCAT L1.3spliced
1036 ..C.....G..A..G.....G.....A.....C AC079018
1042 .....C.....C.....C.....C.....C AC093115
1042 .....A.....T.....A..... AF188024
1041 .....T.....C.....A..A..... AL133472
1036 .....C.....A..... AL138900
1041 .....G.C..... AL163952
1032 ..T.....G.....A.....G. AL353590
1040 ..T.....A..T..G.....C..G...A...A..... AL807813
1033 ..T.....G..A.....C.....A..... AC093808

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-----+-----+-----+-----+-----+-----+
          1130      1140      1150      1160      1170      1180      1190
-----+-----+-----+-----+-----+
1111 AATGACAGGATCAAATTCACACATAACAATATTAACTTTAAATATAAATGGACTAAATCTGCAATTAAA L1.3spliced
1106 .....G....C.....T.....G.....G.C..G.G..C..... AC079018
1112 .....C.....G.....G.....G.....C..... AC093115
1112 .....G.....G.....G..C..... AF188024
1111 .....G.....G.....G..C..... AL133472
1106 .....G.....G.....G..C..... AL138900
1111 .....G.....G..C..... AL163952
1102 .....C....GG.....G.....G..C..... AL353590
1110 .....G.....G.....GA.T..... AL807813
1103 .....G.....G.....G..C..... AC093808

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-----+-----+-----+-----+-----+-----+
          1200      1210      1220      1230      1240      1250      1260
-----+-----+-----+-----+-----+
1181 AGACACAGACTGGCAAGTTGGATAAAGAGTCAAGACCCATCAGTGTGCTGTATTTCAGGAAACCCATCTCA L1.3spliced
1176 .....A...C.....C..... AC079018
1182 .....A.....A.....A..... AC093115
1182 .....A..A..... AF188024
1181 .....A.....A.....G..... AL133472
1176 .....A.....C..... AL138900
1181 .....A..A..... AL163952
1172 .....A..... AL353590
1180 .....A.....TA.....G..... AL807813
1173 .....A.....T..... AC093808

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-----+-----+-----+-----+-----+-----+
          1270      1280      1290      1300      1310      1320      1330
-----+-----+-----+-----+-----+
1251 CGTGCAGAGACACACATAGGCTCAAATAAAAAGGATGGAGGAAGATCTACCAAGCCAATGGAAAACAAAA L1.3spliced
1246 T.....A.....G..... AC079018
1252 .....A.....A..... AC093115
1252 .....A..... AF188024
1251 T.....A..... AL133472
1246 .....AA..... AL138900
1251 .....G.....A..... AL163952
1242 T.G.....TG.....A..... AL353590
1250 .....G..A.....T..... AL807813
1243 .A.....A..... AC093808

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-----+-----+-----+-----+-----+-----+
          1340      1350      1360      1370      1380      1390      1400
-----+-----+-----+-----+-----+
1321 AAA-GGCAGGGGTTGCAATCCTAGTCTCTGATAAAACAGACTTTAAACCAACAAGATCAAAGAGACAA L1.3spliced
1316 .....A..... AC079018
1322 .....A..... AC093115
1322 ..A.....T..... AF188024
1321 .....T..G..... AL133472
1316 ..G--..... AL138900
1321 .....A..... AL163952
1312 ..-A.....C..... AL353590
1320 ..A.....G.....G..... AL807813
1313 ..... AC093808

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```

-----+-----+-----+-----+-----+-----+
          1410      1420      1430      1440      1450      1460      1470
-----+-----+-----+-----+-----+
1390 AGAAGGCCATTACATAATGGTAAAGGATCAATTCACAAGAGGAGCTAACTATCCTAAATATTTATGCA L1.3spliced

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1385 A . A A AC079018
 1391 A AC093115
 1392 T . C A AF188024
 1390 .. G A AL133472
 1384 A . . A . A A AL138900
 1390 A A AL163952
 1381 G A A AL353590
 1390 G A A G . A AL807813
 1382 A G . . A A AC093808

-----+-----+-----+-----+-----+-----+-----+
 1480 1490 1500 1510 1520 1530 1540
 -----+-----+-----+-----+-----+-----+-----+
 1460 CCCAATACAGGAGCACCAGATTCATAAAGCAAGTCCTCAGTGACCTACAAAGAGACTTAGACTCCCACA L1.3spliced
 1455 G AC079018
 1461 G C AC093115
 1462 G T AF188024
 1459 A T G T AL133472
 1454 A T . G C AL138900
 1460 G AL163952
 1451 T T . A AL353590
 1460 G A . . T AL807813
 1452 G T . T AC093808

-----+-----+-----+-----+-----+-----+-----+
 1550 1560 1570 1580 1590 1600 1610
 -----+-----+-----+-----+-----+-----+-----+
 1530 CATTAATAATGGGAGACTTTAACACCCCACTGTCAACATTAGACAGATCAACGAGACAGAAAGTCAACAA L1.3spliced
 1525 .. A . . . G T G T AC079018
 1531 G AC093115
 1532 .. A G AF188024
 1529 .. A A C TC T AL133472
 1524 T T AL138900
 1530 G AL163952
 1521 .. A G T AL353590
 1530 .. A T C . . . CT AL807813
 1522 .. A T T AC093808

-----+-----+-----+-----+-----+-----+-----+
 1620 1630 1640 1650 1660 1670 1680
 -----+-----+-----+-----+-----+-----+-----+
 1600 GGATACCCAGGAATTGAACTCAGCTCTGCACCAAGCAGACCTAATAGACATCTACAGAACTCTCCACCCC L1.3spliced
 1595 AC079018
 1601 A G AC093115
 1602 A T G T AF188024
 1599 G A AL133472
 1594 T C G AL138900
 1600 C T G AL163952
 1591 T T G G AL353590
 1600 T T G AL807813
 1592 A A T G T AC093808

-----+-----+-----+-----+-----+-----+-----+
 1690 1700 1710 1720 1730 1740 1750
 -----+-----+-----+-----+-----+-----+-----+
 1670 AAATCAACAGAAATATACCTTTTTTT-CAGCACCACACCACCTATTCCAAAATTGACCACATAGTTGGA L1.3spliced
 1665 .. C A . C AC079018
 1671 A AC093115
 1672 G A C AF188024
 1669 A G AL133472
 1664 A C AL138900
 1670 A AL163952
 1661 A . C AL353590
 1670 A . C AL807813
 1662 A T T . C AC093808

-----+-----+-----+-----+-----+-----+-----+
 1760 1770 1780 1790 1800 1810 1820
 -----+-----+-----+-----+-----+-----+-----+
 1739 AGTAAAGCTCTCCTCAGCAAATGTAAGAAGACGAAATATAACAACCTATCTCTCAGACCACAGTGCAA L1.3spliced
 1734 A G . . G A AC079018

2090 ...C..... AF188024
 2088A..... AL133472
 2083 AL138900
 2089 AL163952
 2080G.....G..... AL353590
 2088A..... AL807813
 2082 AC093808

-----+-----+-----+-----+-----+-----+-----+
 2180 2190 2200 2210 2220 2230 2240
 -----+-----+-----+-----+-----+-----+
 2159 ATAGAGACACAAAAA-CCCTTCAAAAAATCAATGAATCCAGGAGCTGGTTTTTTTGAAGGATCAACAAA L1.3spliced
 2154--.....T.....T.....T.....A.....C.. AC079018
 2160-.....G..... AC093115
 2160A.....A.....T.....C.....A..... AF188024
 2158A.....AT.....T..... AL133472
 2153 G.....T.....-..... AL138900
 2159-..... AL163952
 2150C.....-.....T.....CA.....A..... AL353590
 2158T.....-.....-.....T.....G..... AL807813
 2152-.....T..... AC093808

-----+-----+-----+-----+-----+-----+
 2250 2260 2270 2280 2290 2300 2310
 -----+-----+-----+-----+-----+-----+
 2228 ATTGATAGACCCTAGCAAGACTAATAAAGAAAAAAGAGAGAAGAAATCAAATAGACACAATAAAAAATG L1.3spliced
 2222T.....A.....G.....G.....TG..... AC079018
 2229-----G..... AC093115
 2230A.....G.....G..... AF188024
 2228T.....-----A.A.....TG.....C. AL133472
 2222 .C..... AL138900
 2228A..... AL163952
 2219 ...T...A.....TA.G.-GA.A..GAG...G...TG..... AL353590
 2226G.....TG..... AL807813
 2221G.....G.....TGT..... AC093808

-----+-----+-----+-----+-----+-----+
 2320 2330 2340 2350 2360 2370 2380
 -----+-----+-----+-----+-----+-----+
 2298 ATAAAGGGGATATCACCACCGATCCCACAGAAATACAAACTACCATCAGAGAATACTACAAACACCTCTA L1.3spliced
 2292T.....A.....T.....A..... AC079018
 2295 AC093115
 2300C.....T.....T.....A..... AF188024
 2293A..... AL133472
 2292A.....T..... AL138900
 2298T..... AL163952
 2288T.....T..... AL353590
 2296A.....A..... AL807813
 2291A.....A.....C..... AC093808

-----+-----+-----+-----+-----+-----+
 2390 2400 2410 2420 2430 2440 2450
 -----+-----+-----+-----+-----+-----+
 2368 CGCAAATAAAGTGAATACTAGAAATGATACATTCCTCGACACATACACTCTCCCAAGACTAAAC L1.3spliced
 2362C.....A.....C..... AC079018
 2365 .A..... AC093115
 2370 T.....A.....T..... AF188024
 2363A.....C..... AL133472
 2362A.....A.....T..... AL138900
 2368A.....A..... AL163952
 2358 .A.....C.....CA.....G.....C..... AL353590
 2366A.....A.....C.....T..... AL807813
 2361 T.....A.....A.A.....G.C..... AC093808

-----+-----+-----+-----+-----+-----+
 2460 2470 2480 2490 2500 2510 2520
 -----+-----+-----+-----+-----+-----+
 2438 CAGGAAGAAGTTGAATCTCTGAATAGACCAATAACAGGCTCTGAAATTGTGGCAATAATCAATAGTTTAC L1.3spliced
 2432A.....G.....C..... AC079018
 2435AG..... AC093115
 2440G.....AG.....C..... AF188024

2433A.....C... AL133472
 2432A.....C... AL138900
 2438AG.....A.....G.C... AL163952
 2428C.....T.....CA.....T.....C... AL353590
 2436 ..A.....A.....C.....C.A... AL807813
 2431C..... AC093808

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-----+-----+-----+-----+-----+-----+
      2530      2540      2550      2560      2570      2580      2590
-----+-----+-----+-----+-----+
2508 CAACCAAAAAGAGTCCAGGACCAGATGGATTACAGCCGAATTCTACCAGAGGTACATGGAGGAACCTGGT L1.3spliced
2502 ..G.....A..G.....G.....A.....G.... AC079018
2505 .....A..... AC093115
2510 .....G.....A..... AF188024
2503 ...T.....AA.....A..... AL133472
2502 .....C.....A.....A.A..... AL138900
2508 .....G.....A..... AL163952
2498 .....A.....A.....A.....G.... AL353590
2506 .....T.....A...A...CA.....A.....T... AL807813
2501 .....A..... AC093808
  
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```

-----+-----+-----+-----+-----+
      2600      2610      2620      2630      2640      2650      2660
-----+-----+-----+-----+
2578 ACCATTCTCTTCTGAAACTATTCCAATCAATGAAAAAGAGGAATCCTCCCTAACTCATTTTATGAGGCC L1.3spliced
2572 ..... AC079018
2575 ..... AC093115
2580 .....C..... AF188024
2573 .....T..... AL133472
2572 .....A.....C.....A..... AL138900
2578 .....C..... AL163952
2568 .....G.....G..... AL353590
2576 .....G.....T..... AL807813
2571 .....A...A.....T.....G..... AC093808
  
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-----+-----+-----+-----+-----+
      2670      2680      2690      2700      2710      2720      2730
-----+-----+-----+-----+
2648 AGCATCATTCTGATACCAAAGCCGGGCAGAGACACAACCAAAAAAGAGAATTTTAGACCAATATCCTTGA L1.3spliced
2642 .A.....C.....T..... AC079018
2645 .....G.....G..... AC093115
2650 .....C.....A.....A..... AF188024
2643 .....C.....T.....C..... AL133472
2642 .....C...G.....A..... AL138900
2648 .....T..... AL163952
2638 .....C.....T.....C... AL353590
2646 .....C.....T..A.....G.....C..... AL807813
2641 .....C...T..T.....A..... AC093808
  
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-----+-----+-----+-----+-----+
      2740      2750      2760      2770      2780      2790      2800
-----+-----+-----+-----+
2718 TGAACATTGATGCAAAAATCCTCAATAAAAATACTGGCAAACCGAATCCAGCAGCACATCAAAAAGCTTAT L1.3spliced
2712 .....G..C.....T.....T-..... AC079018
2715 ..... AC093115
2720 .....G.....T... AL188024
2713 .....C.....T.....A..... AL133472
2712 .....T.....A..... AL138900
2718 .....A..... AL163952
2708 .....T.....T.....C... AL353590
2716 G...ACA.....A.....G..... AL807813
2711 .....G.....G..... AC093808
  
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-----+-----+-----+-----+-----+
      2810      2820      2830      2840      2850      2860      2870
-----+-----+-----+-----+
2788 CCACCATGATCAAGTGGGCTTCATCCCTGGGATGCAAGGCTGGTTCAATATACGCAAATCAATAAATGTA L1.3spliced
2781 .....C..T..... AC079018
2785 .....C..... AC093115
2790 .....A..... AF188024
2783 .....A..... AL133472
  
```

2782A..... AL138900
 2788 AL163952
 2778 ..G.....C...A..... AL353590
 2786T..... AL807813
 2781 AC093808

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-----+-----+-----+-----+-----+-----+
      2880      2890      2900      2910      2920      2930      2940
-----+-----+-----+-----+-----+
2858 ATCCAGCATATAAACAGAGCCAAAGACAAAAACCACATGATTATCTCAATAGATGCAGAAAAAGCCTTTG L1.3spliced
2851 .....A.....G..... AC079018
2855 .....C..... AC093115
2860 .....A.....C.....G..... AF188024
2853 .....A.....G..... AL133472
2852 .....T.....A.....G...T... AL138900
2858 .....A.....A..... AL163952
2848 .....G.....A.....T.....A...A...G..... AL353590
2856 .....A.....G..... AL807813
2851 .....G.....A.....T.....G..... AC093808
  
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-----+-----+-----+-----+-----+-----+
      2950      2960      2970      2980      2990      3000      3010
-----+-----+-----+-----+-----+
2928 ACAAATTCACAACCCTTCATGCTAAAACTCTCAATAAATTAGGTATTGATGGGACGTATTTCAAAAT L1.3spliced
2921 .....C...T.....C..... AC079018
2925 ..... AC093115
2930 .....G.....T...GC..... AF188024
2923 ..G.....G.....A...C..... AL133472
2922 .....C..C.....C AL138900
2928 ..... AL163952
2918 .....T.....T...G.....C..... AL353590
2926 .....T.....A..CC..... AL807813
2921 C.....C..... AC093808
  
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-----+-----+-----+-----+-----+-----+
      3020      3030      3040      3050      3060      3070      3080
-----+-----+-----+-----+-----+
2998 AATAAGAGCTATCTATGACAAACCCACAGCCAAATATCATACTGAATGGGCAAAAACCTGGAAGCATTCCCT L1.3spliced
2991 .....C.....A.....T..... AC079018
2993 ..... AC093115
3000 ..... AF188024
2993 .....G..T..... AL133472
2992 .....T.....T...A... AL138900
2998 .....C..... AL163952
2988 .....T..... AL353590
2996 .....C..... AL807813
2991 ..... AC093808
  
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```

-----+-----+-----+-----+-----+-----+
      3090      3100      3110      3120      3130      3140      3150
-----+-----+-----+-----+-----+
3068 TTGAAAACCGGCACAAGACAGGGATGCCCTCTCTCACCGCTCCTATTCAACATAGTGTGGGAAGTTCTGG L1.3spliced
3061 .....G..T.....A.....A.....G.....C..... AC079018
3063 .....T.....A..... AC093115
3070 .....T.....T..... AF188024
3063 .....T.....A..... AL133472
3061 .....T.....A..... AL138900
3068 .....T.....A..... AL163952
3058 .....T.....T.....A..... AL353590
3066 .....T.G.....A..... AL807813
3061 ...C...T.....A..... AC093808
  
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-----+-----+-----+-----+-----+-----+
      3160      3170      3180      3190      3200      3210      3220
-----+-----+-----+-----+-----+
3138 CCAGGGCAATCAGGCAGGAGAAGGAAATAAAGGGTATTCAATTAGGAAAAGAGGAAGTCAAATTGTCCT L1.3spliced
3131 .....T.....A.....-C...G..T..... AC079018
3133 .....A.....C.....T... AC093115
3140 .....A..... AF188024
3133 ..T.....C..... AL133472
3131 ..... AL138900
  
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3138T..... AL163952
3128C..... AL353590
3136C..... AL807813
3131A.....T..... AC093808

-----+-----+-----+-----+-----+-----+-----+
 3230 3240 3250 3260 3270 3280 3290
-----+-----+-----+-----+-----+-----+-----+
3208 GTTTGCAGACGACATGATTGTATATCTAGAAAACCCCATCGTCTCAGCCCAAATCTCCTTAAGCTGATA L1.3spliced
3200G...T.....T..... AC079018
3203T.....T..... AC093115
3210A.....CT.....A..... AF188024
3203T.....T..T.....T..... AL133472
3201T.....T..T.....C..... AL138900
3208A.....T..... AL163952
3198T.....T..... AL353590
3206T.....G.....T..T.....C..... AL807813
3201T.....C.....T.....A..... AC093808

-----+-----+-----+-----+-----+-----+-----+
 3300 3310 3320 3330 3340 3350 3360
-----+-----+-----+-----+-----+-----+-----+
3278 AGCAACTTCAGCAAAGTCTCAGGATACAAAATCAATGTACAAAATCACAAGCATCTTATACACCAACA L1.3spliced
3270G.....T..... AC079018
3273G..... AC093115
3280 AF188024
3273T..... AL133472
3271T..... AL138900
3278 AL163952
3268 GA.....G.....G.....T.....T..... AL353590
3276 G.....A.....T..... AL807813
3271T..... AC093808

-----+-----+-----+-----+-----+-----+-----+
 3370 3380 3390 3400 3410 3420 3430
-----+-----+-----+-----+-----+-----+-----+
3348 ACAGACAAACAGAGAGCCAAATCATGGGTGAACTCCCATTTCGTAATGCTTCAAAGAGAATAAAATACCT L1.3spliced
3340A.....AC.....T.. AC079018
3343A.....AC..... AC093115
3350C...AC.....AC..... AF188024
3343G.G.---A.....AC..... AL133472
3341A.....AC..... AL138900
3348G..A.....AC..... AL163952
3338A.....AC.....G..... AL353590
3346A.....AC.....A..... AL807813
3341A.....T.....AC..... AC093808

-----+-----+-----+-----+-----+-----+-----+
 3440 3450 3460 3470 3480 3490 3500
-----+-----+-----+-----+-----+-----+-----+
3418 AGGAATCCAACCTACAAGGGATGTGAAGGACCTCTCAAGGAGAACTACAAACCACTGCTCAAGGAAATA L1.3spliced
3410A...G.....A.....T..... AC079018
3409 AC093115
3420G..... AF188024
3409G.....T..C.G...T AL133472
3411 AL138900
3418C..... AL163952
3408TG.....CA.....T..... AL353590
3416CT.....T..... AL807813
3411C.....C.....T..... AC093808

-----+-----+-----+-----+-----+-----+-----+
 3510 3520 3530 3540 3550 3560 3570
-----+-----+-----+-----+-----+-----+-----+
3488 AAAGAGGACACAAACAAATGGAAGAACATTCCATGCTCATGGGTAGGAAGAATCAATATCGTGAAAATGG L1.3spliced
3480A..T..... AC079018
3479T...G..... AC093115
3490T..... AF188024
3479T.....C.....C.....T..... AL133472
3481T.....T..... AL138900
3488T.....TG..... AL163952

3478T.....T.....T..... AL353590
3486T.....T.....A.....T..... AL807813
3481T.....T.....T..... AC093808

-----+-----+-----+-----+-----+-----+
 3580 3590 3600 3610 3620 3630 3640
-----+-----+-----+-----+-----+-----+
3558 CCATACTGCCCAAGGTAATTTACAGATTCAATGCCATCCCCATCAAGCTACCAATGACTTTCTTCACAGA L1.3spliced
3550T.C.....G.....C. AC079018
3549T.....T.....T..... AC093115
3560G.....T.....T..... AF188024
3549 ..C..T.....T.....T..... AL133472
3551T.....T.....T.....T..... AL138900
3558C.....C.....C..... AL163952
3548C.....T.....T.....T..... AL353590
3555T.....T.....T.....T..... AL807813
3551T.....T.....T.....T..... AC093808

-----+-----+-----+-----+-----+-----+
 3650 3660 3670 3680 3690 3700 3710
-----+-----+-----+-----+-----+-----+
3628 ATTGGAATAAA-CTACTTTAAAGTTCATATGGAACCAAAAAGAGCCCGCATGCCAAGTCAATCCTAAG L1.3spliced
3620-.....T.....CA..... AC079018
3619-.....T.....T..... AC093115
3630-.....T.....C..... AF188024
3619-.....T.....CA..... AL133472
3621 ..A.....A.....CA..... AL138900
3628-.....G.....C..... AL163952
3618 ..G.....-...C.....C.....A.....T AL353590
3625-.....C.....A...CA..... AL807813
3621-.....T.....T..... AC093808

-----+-----+-----+-----+-----+-----+
 3720 3730 3740 3750 3760 3770 3780
-----+-----+-----+-----+-----+-----+
3697 CCAAAAAGAACAAGCTGGAGGCATCACACTACTGACTTCAAACATACTACAAGGCTACAGTAACCAAA L1.3spliced
3689C.....T.....T..... AC079018
3688T.....T.....T..... AC093115
3699G.....A.....T..... AF188024
3688T.....G.....T..... AL133472
3691T.....T.....T..... AL138900
3697T.....T.....T..... AL163952
3687C.....G.....T..... AL353590
3694T.....TG.....C..... AL807813
3690GT.....T.....C..... AC093808

-----+-----+-----+-----+-----+-----+
 3790 3800 3810 3820 3830 3840 3850
-----+-----+-----+-----+-----+-----+
3767 ACAGCATGGTACTGGTACCAAAACAGAGATATAGATCAATGGAACAGAACAGAGCCCTCAGAAATAATGC L1.3spliced
3759T.....T.....T..... AC079018
3758T.....T.....T.....C.. AC093115
3769 ..T.....T.....G.....C.. AF188024
3758T.....T.....T.....CA. AL133472
3761C.....T.....C.....G..... AL138900
3767T.....T.....T.....C.. AL163952
3757 T.....T.....C...C..... AL353590
3764A.....C...C..... AL807813
3760T.....T.....T.....C.. AC093808

-----+-----+-----+-----+-----+-----+
 3860 3870 3880 3890 3900 3910 3920
-----+-----+-----+-----+-----+-----+
3837 CGCAT----- L1.3spliced
3829T.....T.....T..... AC079018
3828 T.....T.....T.....T..... AC093115
3839 T.....T.....T.....T..... AF188024
3828CGTCTACGGCCATACCACCCCTGAACACGCCCGATCTCGTCTGATCTCGGAAGCTAAGCAGGGTCG AL133472
3831T.....T.....T..... AL138900
3837T.....T.....T..... AL163952
3827 .A.....T.....T.....T..... AL353590

3834 T.....----- AL807813
3830----- AC093808

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-----+-----+-----+-----+-----+-----+-----+
      3930      3940      3950      3960      3970      3980      3990
-----+-----+-----+-----+-----+-----+-----+
3842 -----ATCTACAACCTATCTGATCTTTGACAAACCTG L1.3spliced
3834 -----C..... AC079018
3833 -----C..... AC093115
3844 -----..... AF188024
3898 GGCCTGGTTAGTACTTGGATGGGAGAAATAACACCGCAT.....T... AL133472
3836 -----..... AL138900
3842 -----..... AL163952
3832 -----..... AL353590
3839 -----..... AL807813
3835 -----C..... AC093808
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-----+-----+-----+-----+-----+-----+-----+
      4000      4010      4020      4030      4040      4050      4060
-----+-----+-----+-----+-----+-----+-----+
3873 AGAAAAACAAGCAATGGGAAAGGATTCCCTATTTAATAAAATGGTGTCTGGGAAACTGGCTAGCCATATG L1.3spliced
3865 .C.....C.....T..... AC079018
3864 .....T..... AC093115
3875 .C..... AF188024
3968 .C..... AL133472
3867 .C.....A.....C.A AL138900
3873 ..... AL163952
3863 .....A.....G..... AL353590
3870 .C.....G.....A..... AL807813
3866 .....A.....G.....G..... AC093808
```

```
-----+-----+-----+-----+-----+-----+-----+
      4070      4080      4090      4100      4110      4120      4130
-----+-----+-----+-----+-----+-----+-----+
3943 TAGAAAGCTGAAACTGGATCCCTTCCCTTACACCTTATACAAAAATCAATTCAAGATGGATTAAAGATTTA L1.3spliced
3935 G.....T.....C... AC079018
3934 ..... AC093115
3945 .....T.....C... AF188024
4038 .....A.....T.....C.. AL133472
3937 .....C... AL138900
3943 ..... AL163952
3933 G.....C.....C.....T.....C... AL353590
3940 .....A.....G.....C... AL807813
3936 .....T.T.....T.....C... AC093808
```

```
-----+-----+-----+-----+-----+-----+-----+
      4140      4150      4160      4170      4180      4190      4200
-----+-----+-----+-----+-----+-----+-----+
4013 AACGTTAAACCTAAAACCATAAAACCCCTAGAAGAAAACCTAGGCATTACCATTTCAGGACATAGGCGTGG L1.3spliced
4005 C.T...G.....A.....A... AC079018
4004 .....G..... AC093115
4015 C...G.....A... AF188024
4107 ..A..G.....A... AL133472
4007 .....G.....C.....A... AL138900
4013 .....G.....A... AL163952
4003 ..T..G.....TG...G.....A... AL353590
4010 ..T.....A.....A... AL807813
4006 ..T..G.....A..... AC093808
```

```
-----+-----+-----+-----+-----+-----+-----+
      4210      4220      4230      4240      4250      4260      4270
-----+-----+-----+-----+-----+-----+-----+
4083 GCAAGGACTTCATGTCCAAAACACCAAAAAGCAATGGCAACAAAAGACAAAATTGACAAATGGGATCTAAT L1.3spliced
4075 .....T.....C.....A.....C...T... AC079018
4074 .....C..... AC093115
4085 .....T.....C.....C..... AF188024
4177 .....T.G.....C..... AL133472
4077 ..G.....C..T.....C..... AL138900
4083 .....C.....C.....C... AL163952
4073 .....T.....C...C..... AL353590
4074 .....T.....C.....G..... AL807813
```

```

-----+-----+-----+-----+-----+-----+
          4280      4290      4300      4310      4320      4330      4340
-----+-----+-----+-----+-----+
4153 TAAACTAAAGAGCTTCTGCACAGCAAAGAACTACCATCAGAGTGAACAGGCAACCTACAACATGGGAG L1.3spliced
4145 .....GA..... AC079018
4144 ..... AC093115
4155 .C.....G.....A..... AF188024
4247 .....A..... AL133472
4147 .....C.....A..... AL138900
4153 .....T.....A..... AL163952
4143 .....GA..... AL353590
4144 .....T.....A..... AL807813
4063 ..... AC093808

```

```

-----+-----+-----+-----+-----+-----+
          4350      4360      4370      4380      4390      4400      4410
-----+-----+-----+-----+-----+
4223 AAAATTTTCGCAACCTACTCATCTGACAAAGGGCTAATATCCAGAATCTACAATGAACTTAAACAATTT L1.3spliced
4215 .....A.....G.....C..... AC079018
4214 .....T.....C..... AC093115
4225 ..G...T.....A.....C..... AF188024
4317 ..T.C.C.....T.....T.....C..... AL133472
4217 .....G...C.....CC..... AL138900
4223 .....C..... AL163952
4213 ..C...T...T.....A.....C....C.... AL353590
4214 .....T.....C..... AL807813
4063 ..... AC093808

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-----+-----+-----+-----+-----+-----+
          4420      4430      4440      4450      4460      4470      4480
-----+-----+-----+-----+-----+
4293 ACAAGAAAAAACAACAACCCCATCAAAAAGTGGGCGAAGGACATGAACAGACACTTCTCAAAAGAAGA L1.3spliced
4285 .....A.....T.....G.....C... AC079018
4284 .....T..... AC093115
4295 .....T.....C...A..... AF188024
4387 .....G.....AA...T..... AL133472
4287 .....T.....T..... AL138900
4293 ..... AL163952
4283 .....C...A.A...T..... AL353590
4284 .....T-.....A..... AL807813
4063 ..... AC093808

```

```

-----+-----+-----+-----+-----+-----+
          4490      4500      4510      4520      4530      4540      4550
-----+-----+-----+-----+-----+
4363 CATTATGTCAGCCAAAAACACATGAAGAAATGCTCATCATCACTGGCCATCAGAGAAATGCAAATCAA L1.3spliced
4355 .....A..... AC079018
4354 .....A..... AC093115
4365 .....A.....C..... AF188024
4457 .....C.G.....A.....T.....C..... AL133472
4357 .....A.....GC..... AL138900
4363 .....G.....A.....A..... AL163952
4353 .....G.....A.....G..... AL353590
4353 .....A.....C..... AL807813
4063 ..... AC093808

```

```

-----+-----+-----+-----+-----+-----+
          4560      4570      4580      4590      4600      4610      4620
-----+-----+-----+-----+-----+
4433 ACCACTATGAGATATCATCTCACACCAGTTAGAATGGCAATCATTAATAAAGTCAGGAAACAACAGGTGCT L1.3spliced
4425 .....A.....C..... AC079018
4424 .....G..... AC093115
4435 ..G.A..... AF188024
4527 .....A.....C.....G.....T.....A... AL133472
4427 .....A.....C.....G.....A..... AL138900
4433 .....A.....C..... AL163952
4423 ..T.A.....C.....C..... AL353590
4423 .....A.....C.....TGT.....T..... AL807813
4063 ..... AC093808

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```

-----+-----+-----+-----+-----+-----+
          4630      4640      4650      4660      4670      4680      4690
-----+-----+-----+-----+-----+
4503 GGAGAGGATGCGGAGAAATAGGAACACTTTTACACTGTTGGTGGGACTGTAAACTAGTTCAACCATTGTG L1.3spliced
4495 .....T.....C..... AC079018
4494 .....T..... AC093115
4505 .....T..... AF188024
4597 .....T..... AL133472
4497 .....T.....G..... AL138900
4503 .....T.....A..... AL163952
4493 .....T..... AL353590
4493 A.....T.....T.....C.G..... AL807813
4063 ..... AL093808

```

```

-----+-----+-----+-----+-----+-----+
          4700      4710      4720      4730      4740      4750      4760
-----+-----+-----+-----+-----+
4573 GAAGTCAGTGTGGCGATTCTCAGGGATCTAGAACTAGAAATACCATTTGACCCAGCCATCCCATTACTG L1.3spliced
4565 ..... AC079018
4564 ..... AC093115
4575 .....A..... AF188024
4667 .....C.....G..... AL133472
4567 .....T.....C.....A..... AL138900
4573 ..... AL163952
4563 .....T.....GC.....C..... AL353590
4563 .....T..... AL807813
4063 ..... AC093808

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```

-----+-----+-----+-----+-----+-----+
          4770      4780      4790      4800      4810      4820      4830
-----+-----+-----+-----+-----+
4643 GGTATATACCCA-----AATGAGTATAAATCATGCTGTATAAAGACACATGCACAC L1.3spliced
4635 .....G.C..... AC079018
4634 .....G.C..... AC093115
4645 .....TTACTGGGTATATACCCA.G.C..... AF188024
4737 .....G.C.C..... AL133472
4637 .....G.C.....G AL138900
4643 .....G.C..... AL163952
4633 .....G.T.....A.....A..T AL353590
4633 .....G.T.....G..... AL807813
4063 ..... AC093808

```

```

-----+-----+-----+-----+-----+-----+
          4840      4850      4860      4870      4880      4890      4900
-----+-----+-----+-----+-----+
4695 GTATGTTTATGCGGCACTATTACACAATAGCAAAGACTTGGAAACCAACCCAAATGTCCAACAATGATAGA L1.3spliced
4687 .....G.....T..... AC079018
4686 .....G..... AC093115
4715 .....A..T..... AF188024
4789 .....T.....G..... AL133472
4689 .....A..T..... AL138900
4695 .....T..... AL163952
4685 .....A.....G.....A..... AL353590
4685 .....T..... AL807813
4063 ..... AC093808

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```

-----+-----+-----+-----+-----+-----+
          4910      4920      4930      4940      4950      4960      4970
-----+-----+-----+-----+-----+
4765 CTGGATTAAAGAAAATGTGGCACATATACACCATGGAATACTATGCAGCCATAAAAAA-TGATGAGTTCAT L1.3spliced
4757 .....-T.A..... AC079018
4756 ..... AC093115
4785 ..... AF188024
4859 .....A..... AL133472
4759 .....A..... AL138900
4765 .....G..... AL163952
4755 .....C.....C.....-A..... AL353590
4755 ..... AL807813
4063 ..... AC093808

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```

          5330      5340      5350      5360      5370      5380      5390
-----+-----+-----+-----+-----+-----+-----+
5171 AAAAAAAAAAA L1.3spliced
5162 .....TTP...-----AACAAAGAATCATTCTCTATAATTAAGTCTCATAACAGGCAACACTTCCAGAT AC079018
5157 .....G...--TG--CTGCTGGGATTTGGTA-CTGG-----AGGTGGCGGGTAGGAACATTTTGGC AC093115
5194 ..T..GT...TTTTA--AAAAAAGAAAGAGAATACACAA---TTTTTTACAGTTTATCAATACAGTGC AF188024
5267 T.....G----AAAAAAGAGAGAAGAATCAAATAGA-CACAATAAAAAATGTTAAAGGGTAGA AL133472
5167 ..G.....G.TCCAGCAAGCTGCATTCACAAAAAAAAAAAAA-AAAAAAAAAACTAGAGAAGCAAGAG AL138900
5171 ..C..C.....GTTG--AATCAAAGCTCTGTAGACTAGTCCC-TGACCTGCGTGTTC AACAGGCCCTAC AL163952
5165 C.CGCCGT..TCCCAGCACTTTGGGAGGCCGAGGTGGGCGGATCACGAGGTCAGG AL353590
5165 .....T...AATAAAAATATAAGTATAATCTGTAAGATTCACCTAAAAAAAAAACTTCACAATATAAA AL807813
4063 AC093808

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Supplemental figure 4. Alignment of the spliced L1 elements identified in the human genome. Sequences of the full-length human L1 elements that underwent splicing (SD and SA sites at positions 97 and 970 of L1.3 sequence respectively) and retrotransposed were extracted from the human genome and aligned by ClustalW method against L1.3 sequence spliced in the same manner (L1.3 spliced). Nucleotides that do not match L1.3 sequence are shown. Deletions are shown with dashes (-). Accession numbers for the contigs containing each sequence are shown on the right. AL807813 L1 belongs to the Ta family, the rest of the elements are non-Ta. The AC009487 L1 sequence has not been included in the alignment because it contains other internal rearrangements as well.

```

-----+-----+-----+-----+-----+-----+
          10         20         30         40         50         60         70
-----+-----+-----+-----+-----+
1 CGGAACTTAGGAAATTAGTCTGAACAGGAGGAGGTCCAATACAAGATATCTGCGCACCTTCCCTGTAAG
L1spaSp27to1597
1 ..... AC036146
1 ..... AC107832
1 .....TT.....C.....A..... AC122029
1 .....A..... AC122834
1 ..... AC124709
1 .....T.....C.....A.....A..... AC153559
1 ..... AL646046
1 ..... AL662923
1 ..... AL845483

```

```

-----+-----+-----+-----+-----+
          80         90        100        110        120        130        140
-----+-----+-----+-----+-----+
71 AGAGCTTGCCAGCAGAGAGTGCTCTGAGCACTGAAACTCAGAGGAGAGAATCTGTCTCCCAGGTCTGCTG
L1spaSp27to1597
69 ..... AC036146
67 ..... AC107832
70 ..... AC122029
69 ..... AC122834
69 ..... AC124709
70 ..... AC153559
69 ..... AL646046
69 ..... AL662923
69 ..... AL845483

```

```

-----+-----+-----+-----+-----+
        150        160        170        180        190        200        210
-----+-----+-----+-----+-----+
141 ATAGACGGTAACAGAATCACCAGAAGAACAATCTCTAAACAGAGTCAACTATAACTACTAACTCCAGAGA
L1spaSp27to1597
139 ..... AC036146
137 ..... AC107832
140 .G.....C... AC122029
139 ..... AC122834
139 .C..... AC124709
140 .G..... AC153559
139 ..... AL646046
139 ..... AL662923
139 ..... AL845483

```

```

-----+-----+-----+-----+-----+
        220        230        240        250        260        270        280
-----+-----+-----+-----+-----+
211 TTACCAGATGGCGAAAGGTAACGGAGGAATCTTACTAACAGGAACCAAGACCACTCACCATCACCAGAA
L1spaSp27to1597
209 ..... AC036146
207 ..... AC107832
210 .....C.....T.....C.....T..... AC122029
209 ..... AC122834
209 ..... AC124709
210 .G.....T.....C.....T..... AC153559
209 ..... AL646046
209 ..... AL662923
209 ..... AL845483

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```

-----+-----+-----+-----+-----+
        290        300        310        320        330        340        350
-----+-----+-----+-----+-----+
281 CCCAGCACACCCACTTCGCCCAGTCCAGGGAACCCCAACACACCTGAGAACCTAGACCTAGATTTAAAG
L1spaSp27to1597
279 ..... AC036146
277 ..... AC107832
280 .....T.....T.....C.....C..A..... AC122029
279 ..... AC122834
279 ..... AC124709
280 .....T.....C.....C..A..... AC153559

```

279 AL646046
279 AL662923
279 AL845483

-----+-----+-----+-----+-----+-----+
360 370 380 390 400 410 420
-----+-----+-----+-----+-----+-----+

351 CATATCTCATGATGATGGTAGAGGGCATCAAGAAGGACTTTAATAAATCACTTAAAGAAATACAGGAGAA
L1spaSp27to1597
349 A AC036146
347 A AC107832
350 A AC122029
349 A AC122834
349 A AC124709
350 A AC153559
349 A AL646046
349 A AL662923
349 A AL845483

-----+-----+-----+-----+-----+-----+
430 440 450 460 470 480 490
-----+-----+-----+-----+-----+-----+

421 CACTGCTAAAGAGTTACAAGTCCTTAAAGAAAAACAGGAAAAACACAATCAAACAGGTAGAGTCTTACA
L1spaSp27to1597
419 AC036146
417 AC107832
420 AC122029
419 AC122834
419 AC124709
420 AC153559
419 AL646046
419 AL662923
419 AL845483

-----+-----+-----+-----+-----+-----+
500 510 520 530 540 550 560
-----+-----+-----+-----+-----+-----+

491 GAAAAAGAGGAAAAACATACAAACAGGTGATGGAATGAACAAAACCATACTAGACCTAAAAAGGGAAG
L1spaSp27to1597
489 AC036146
487 AC107832
490 AC122029
489 AC122834
489 AC124709
490 AC153559
489 AL646046
489 AL662923
489 AL845483

-----+-----+-----+-----+-----+-----+
570 580 590 600 610 620 630
-----+-----+-----+-----+-----+-----+

561 TAGACACAATAAAGAAAACCTCAAAGCGAGGCAACACTAGAGATAGAAACCTAGGAAAGAAATCTGGAAC
L1spaSp27to1597
559 AC036146
557 AC107832
560 ... A T G AC122029
559 AC122834
559 AC124709
560 ... A T G AC153559
559 AL646046
559 AL662923
559 AL845483

-----+-----+-----+-----+-----+-----+
640 650 660 670 680 690 700
-----+-----+-----+-----+-----+-----+

631 CATAGATTTGAGCATCAGCAACAGAATACAAGAGATGGAAGAGAGAATCTCAGGTGCAGAACATTCCATA
L1spaSp27to1597
629 G AC036146
627 G AC107832

630G..... AC122029
629G..... AC122834
629G..... AC124709
630G..... AC153559
629G..... AL646046
629G..... AL662923
629G..... AL845483

-----+-----+-----+-----+-----+-----+-----+
710 720 730 740 750 760 770
-----+-----+-----+-----+-----+-----+-----+

701 GAGAACATCGGCACAACAATCAAAGAAAATGGAAAATGCAAAAAGATCCTAACTCAAATATCCAGGAAA
L1spaSp27to1597
699 AC036146
697 AC107832
700 AC122029
699 AC122834
699 AC124709
700 AC153559
699 AL646046
699 AL662923
699 AL845483

-----+-----+-----+-----+-----+-----+-----+
780 790 800 810 820 830 840
-----+-----+-----+-----+-----+-----+-----+

771 TCCAGGACACAATAAGAAGACCAAACGTACGGATAATAGGAGTGGATGAGAATGAAGATTTTCAACTCAA
L1spaSp27to1597
769 AC036146
767 AC107832
770G.....G.C..... AC122029
769 AC122834
769 AC124709
770G.....C..... AC153559
769 AL646046
769 AL662923
769 AL845483

-----+-----+-----+-----+-----+-----+-----+
850 860 870 880 890 900 910
-----+-----+-----+-----+-----+-----+-----+

841 AGGTCCAGCAAACATCTTCAACAATAATTTGAAGAAAACCTCCCAAATCTAAAGAATGAGATGCATATG
L1spaSp27to1597
839 AC036146
837 AC107832
840 ..A.....A.....A.....A.C..... AC122029
839 AC122834
839 AC124709
840 ..A.....A.....A.....A.C..... AC153559
839 AL646046
839 AL662923
839 AL845483

-----+-----+-----+-----+-----+-----+-----+
920 930 940 950 960 970 980
-----+-----+-----+-----+-----+-----+-----+

911 AACATACAAGAAGCCTACAGAACTCCAAATAGACTGGACCAGAAAAGAAAATTCCTCCCGACACATAATAA
L1spaSp27to1597
909 AC036146
907 AC107832
910 AC122029
909 AC122834
909 AC124709
910 AC153559
909 AL646046
909 AL662923
909 AL845483

-----+-----+-----+-----+-----+-----+-----+
990 1000 1010 1020 1030 1040 1050
-----+-----+-----+-----+-----+-----+-----+

981 TCAGAACATCAAATGCACTAAATAAGATAGAATACTAAAAGCAGTAAGGGAAAAAGGTCAAGTAACATA
 L1spaSp27to1597
 979 AC036146
 977 AC107832
 980 A G AC122029
 979 AC122834
 979 AC124709
 980 A AC153559
 979 AL646046
 979 AL662923
 979 AL845483

-----+-----+-----+-----+-----+-----+
 1060 1070 1080 1090 1100 1110 1120
 -----+-----+-----+-----+-----+-----+

1051 TAAAGGCAAGCCTATCAGAATTACACCAGATTTTTCACCAGAGACTATGAAAGCCAGAAGAGCCTGGACA
 L1spaSp27to1597
 1049 AC036146
 1047 AC107832
 1050 C AC122029
 1049 AC122834
 1049 AC124709
 1050 C AC153559
 1049 AL646046
 1049 A AL662923
 1049 AL845483

-----+-----+-----+-----+-----+-----+
 1130 1140 1150 1160 1170 1180 1190
 -----+-----+-----+-----+-----+-----+

1121 GATGTTATACAGACACTAAGAGAACACAAACTGCAGCCCAGGCTACTATACCCAGCCAAACTCTCAATTA
 L1spaSp27to1597
 1119 AC036146
 1117 AC107832
 1120 T.C AC122029
 1119 AC122834
 1119 AC124709
 1120 T.C AC153559
 1119 AL646046
 1119 AL662923
 1119 AL845483

-----+-----+-----+-----+-----+-----+
 1200 1210 1220 1230 1240 1250 1260
 -----+-----+-----+-----+-----+-----+

1191 TCATAGAGGGAGAAACCAAAGTATTCACGACAAAACCAAATTCACGCATTATCTCTCCACGAATCCAGC
 L1spaSp27to1597
 1189 A AC036146
 1187 A AC107832
 1190 C T T.A AC122029
 1189 AC122834
 1189 AC124709
 1190 C T A AC153559
 1189 AL646046
 1189 AL662923
 1189 AL845483

-----+-----+-----+-----+-----+-----+
 1270 1280 1290 1300 1310 1320 1330
 -----+-----+-----+-----+-----+-----+

1261 CCTTCAAAGGATAATAACAGAAAAAACCAATACAAGAACGGGAACACGCCTTAGAAAAAA-CAAGAAG
 L1spaSp27to1597
 1259 AC036146
 1257 AC107832
 1260 T T A AC122029
 1259 AC122834
 1259 AC124709
 1260 T T AC153559
 1259 AL646046
 1259 AL662923
 1259 AL845483

```

-----+-----+-----+-----+-----+-----+
      1340      1350      1360      1370      1380      1390      1400
-----+-----+-----+-----+-----+-----+
1330 GTAATCCCTCAACAAACCTAAAAGAAGACAGCCACAAGAACAGAATGCCACCTTTAACAACATAAAATAAC
L1spaSp27to1597
1328 ..... AC036146
1326 ..... AC107832
1329 ..... A.....A..... AC122029
1328 ..... AC122834
1328 ..... AC124709
1329 ..... A.....A..... AC153559
1328 ..... AL646046
1328 ..... AL662923
1328 ..... AL845483

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```

-----+-----+-----+-----+-----+-----+
      1410      1420      1430      1440      1450      1460      1470
-----+-----+-----+-----+-----+-----+
1400 AGGAAGCAACAATTACTTTTCCTTAATATCTCTTAACATCAATGGTCTCAACTCGCCAATAAAAAGACAT
L1spaSp27to1597
1398 ..... AC036146
1396 ..... AC107832
1399 ..... C.....C..... AC122029
1398 ..... AC122834
1398 ..... C..... AC124709
1399 ..... C..... AC153559
1398 ..... AL646046
1398 ..... AL662923
1398 ..... AL845483

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```

-----+-----+-----+-----+-----+-----+
      1480      1490      1500      1510      1520      1530      1540
-----+-----+-----+-----+-----+-----+
1470 AGACTAACAAACTGGCTACACAAACAAGACCCAACATTTTGCTGCTTACAGGAACTCATCTCAGAGAAA
L1spaSp27to1597
1468 ..... AC036146
1466 ..... AC107832
1469 ..... T.....G..A..... AC122029
1468 ..... AC122834
1468 ..... AC124709
1469 ..... T.....G..A..... AC153559
1468 ..... AL646046
1468 ..... AL662923
1468 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
      1550      1560      1570      1580      1590      1600      1610
-----+-----+-----+-----+-----+-----+
1540 AAGATAGACACTACCTCAGAATGAAAGGCTGGAAAACAATTTTCCAAGCAAATGGTATGAAGAAACAAGC
L1spaSp27to1597
1538 ..... AC036146
1536 ..... AC107832
1539 ..... A..... AC122029
1538 ..... AC122834
1538 ..... AC124709
1539 ..... A.....T.. AC153559
1538 ..... AL646046
1538 ..... AL662923
1538 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
      1620      1630      1640      1650      1660      1670      1680
-----+-----+-----+-----+-----+-----+
1610 AGGAGTAGCCATCCTAATATCTGATAAGATTGACTTCCAACCCAAAGTCATCAAAAAGACAAGGAGGGA
L1spaSp27to1597
1608 ..... AC036146
1606 ..... AC107832
1609 T.....G..... AC122029
1608 ..... AC122834
1608 ..... AC124709

```

1609 T.....G AC153559
1608 AL646046
1608 AL662923
1608 AL845483

-----+-----+-----+-----+-----+-----+-----+
 1690 1700 1710 1720 1730 1740 1750
-----+-----+-----+-----+-----+-----+-----+

1680 CACTTCATTCTCATCAAAGGTAAATCCTCCAAGAGGAACCTCAATTCTGAATATCTATGCTCCAATA
L1spaSp27to1597
1678 AC036146
1676 AC107832
1679TG.....G.....G..... AC122029
1678 AC122834
1678 AC124709
1679G..... AC153559
1678 AL646046
1678 AL662923
1678 AL845483

-----+-----+-----+-----+-----+-----+-----+
 1760 1770 1780 1790 1800 1810 1820
-----+-----+-----+-----+-----+-----+-----+

1750 CAAGAGCAGCCACATTCACTAAAGAAACTTTAGTAAAGCTCAAAGCACACATTGCGCCTCACACAATA
L1spaSp27to1597
1748 AC036146
1746 AC107832
1749G.....T.....A..... AC122029
1748 AC122834
1748 AC124709
1749G.....T.....A..... AC153559
1748 AL646046
1748 AL662923
1748 AL845483

-----+-----+-----+-----+-----+-----+-----+
 1830 1840 1850 1860 1870 1880 1890
-----+-----+-----+-----+-----+-----+-----+

1820 AGTGGGAGACTTCAACACACCACTTTCACCAATGGACAGATCATGGAAACAGAACTAAACAGGGACACA
L1spaSp27to1597
1818 AC036146
1816 AC107832
1819 AC122029
1818 AC122834
1818T..... AC124709
1819 AC153559
1818 AL646046
1818 AL662923
1818 AL845483

-----+-----+-----+-----+-----+-----+-----+
 1900 1910 1920 1930 1940 1950 1960
-----+-----+-----+-----+-----+-----+-----+

1890 CTGAAACTAACAGAAGTGATGAAACAAATGGATCTGACAGATATCTACAGAACATTTTACCCTAAACAA
L1spaSp27to1597
1888T..... AC036146
1886T..... AC107832
1889T..... AC122029
1888 AC122834
1888T..... AC124709
1889T..... AC153559
1888T..... AL646046
1888 AL662923
1888T..... AL845483

-----+-----+-----+-----+-----+-----+-----+
 1970 1980 1990 2000 2010 2020 2030
-----+-----+-----+-----+-----+-----+-----+

1960 AAGGATATACCTTCTTCTCAGCACCTCATGGTACCTTCTCCAAAATGACCACATAATAGGTCACAAATC
L1spaSp27to1597
1958 AC036146

1956 AC107832
1959 A. AC122029
1958 AC122834
1958 AC124709
1959 A. AC153559
1958 AL646046
1958 AL662923
1958 C..... AL845483

-----+-----+-----+-----+-----+-----+-----+
 2040 2050 2060 2070 2080 2090 2100
-----+-----+-----+-----+-----+-----+-----+

2030 AGGCCCTCAACAGATTAAAAAATATTGAAATTGTCCCATGTATCCTATCAGATCACCATGCACTAAGGCTG

L1spaSp27to1597

2028 C..... AC036146
2026 C..... AC107832
2029 C..... A..... AC122029
2028 C..... AC122834
2028 C..... AC124709
2029 C..... T..... AC153559
2028 C..... AL646046
2028 C..... C..... AL662923
2028 C..... AL845483

-----+-----+-----+-----+-----+-----+-----+
 2110 2120 2130 2140 2150 2160 2170
-----+-----+-----+-----+-----+-----+-----+

2100 ATCTTCAATAACAAAATAAATAACAGAAAGCCAACATTCACATGGAAACTGAACAACACTCTTCTCAATG

L1spaSp27to1597

2098 AC036146
2096 T..... C..... AC107832
2099 A..... C..... G..... AC122029
2098 AC122834
2098 AC124709
2099 A..... C..... G..... AC153559
2098 AL646046
2098 AL662923
2098 AL845483

-----+-----+-----+-----+-----+-----+-----+
 2180 2190 2200 2210 2220 2230 2240
-----+-----+-----+-----+-----+-----+-----+

2170 ATACCTTGGTCAAGGAAGGAATAAAGAAAGAAATTAAGACTTTTTAGAGTTTAATGAAAATGAAGCCAC

L1spaSp27to1597

2168 AC036146
2166 AC107832
2169 AC122029
2168 AC122834
2168 AC124709
2169 AC153559
2168 AL646046
2168 AL662923
2168 AL845483

-----+-----+-----+-----+-----+-----+-----+
 2250 2260 2270 2280 2290 2300 2310
-----+-----+-----+-----+-----+-----+-----+

2240 AACGTACCCAAACCTTTGGGACACAATGAAAGCATTCTTAAGAGGGAACTCATAGCTATGAGTGCCCTTC

L1spaSp27to1597

2238 AC036146
2236 AC107832
2239 C..... C..... AC122029
2238 AC122834
2238 AC124709
2239 C..... GC..... AC153559
2238 AL646046
2238 AL662923
2238 AL845483

-----+-----+-----+-----+-----+-----+-----+
 2320 2330 2340 2350 2360 2370 2380
-----+-----+-----+-----+-----+-----+-----+

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-----+-----+-----+-----+-----+-----+
2310 AAGAAAAAACGGGAGAGAGACATACTAGCAGCTTGACAACACATCTAAAAGCTCTAGAAAAAAGGAAG
L1spaSp27to1597
2308 ..... AC036146
2306 ..... AC107832
2309 .T...G..... AC122029
2308 ..... AC122834
2308 ..... AC124709
2309 .T...G..... AC153559
2308 ..... AL646046
2308 ..... AL662923
2308 ..... AL845483

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-----+-----+-----+-----+-----+-----+
                2390      2400      2410      2420      2430      2440      2450
-----+-----+-----+-----+-----+-----+
2380 CAAATTCACCCAAGAGGAGTAGACGGCAGGAAATAATCAAACCTCAGGGGTGAAATCAACCAAGTGGAAAC
L1spaSp27to1597
2378 ..... AC036146
2376 ..... AC107832
2379 ..... AC122029
2378 ..... AC122834
2378 ..... AC124709
2379 ..... AC153559
2378 ..... AL646046
2378 ..... AL662923
2378 ..... AL845483

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-----+-----+-----+-----+-----+-----+
                2460      2470      2480      2490      2500      2510      2520
-----+-----+-----+-----+-----+-----+
2450 AAGAAGAACTATTCAAAGAAATTAACCAAACGAGGAGTTGGTTCTTTGAGAAAATCAACAAGATAGATAAA
L1spaSp27to1597
2448 ..... AC036146
2446 ..... AC107832
2449 ..... AC122029
2448 ..... AC122834
2448 ..... AC124709
2449 ..... AC153559
2448 ..... AL646046
2448 ..... AL662923
2448 ..... AL845483

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-----+-----+-----+-----+-----+-----+
                2530      2540      2550      2560      2570      2580      2590
-----+-----+-----+-----+-----+-----+
2520 CCCTTAGCTAGACTCACTAAAGGGCACAGGGACAAAATCCTAATTAACAAAATCAGAAATGAAAAGGGAG
L1spaSp27to1597
2518 ..... AC036146
2516 ..... AC107832
2519 .....G.....A.....C..... AC122029
2518 ..... AC122834
2518 ..... AC124709
2519 .....G.....A.....C..... AC153559
2518 ..... AL646046
2518 ..... AL662923
2518 .....C..... AL845483

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-----+-----+-----+-----+-----+-----+
                2600      2610      2620      2630      2640      2650      2660
-----+-----+-----+-----+-----+-----+
2590 ACATAACAACAGATCCTGAAGAAATCAAAACACCATCAGATCCTTCTACAAAAGGCTATACTCAACAAA
L1spaSp27to1597
2588 ..... AC036146
2586 ..... AC107832
2589 ..... AC122029
2588 ..... AC122834
2588 ..... AC124709
2589 ..... AC153559
2588 ..... AL646046
2588 ..... AL662923

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2588 AL845483

-----+-----+-----+-----+-----+-----+-----+
2670 2680 2690 2700 2710 2720 2730
-----+-----+-----+-----+-----+-----+-----+

2660 ACTGGAAAACCTGGACGAAATGGACAAATTTCTGGACAGATACCAGGTACCAAAGTTGAATCAGGATCAA

L1spaSp27to1597

2658 AC036146
2656 AC107832
2659 T AC122029
2658 AC122834
2658 AC124709
2659 A AC153559
2658 AL646046
2658 AL662923
2658 AL845483

-----+-----+-----+-----+-----+-----+-----+
2740 2750 2760 2770 2780 2790 2800
-----+-----+-----+-----+-----+-----+-----+

2730 GTTGACCTTCTAAACAGTCCCATATCCCCTAAAGAAATAGAAGCAGTTATTAATAGTCTCCAGCCAAAA

L1spaSp27to1597

2728 AC036146
2726 AC107832
2729 A AC122029
2728 AC122834
2728 AC124709
2729 A AC153559
2728 AL646046
2728 AL662923
2728 AL845483

-----+-----+-----+-----+-----+-----+-----+
2810 2820 2830 2840 2850 2860 2870
-----+-----+-----+-----+-----+-----+-----+

2800 AAAGCCAGGACCAGACGGGTTTAGTGCAGAGTTCTATCAGACCTTCAAAGAAGATCTAACTCCAGTTCT

L1spaSp27to1597

2798 AC036146
2796 AC107832
2799 T AC122029
2798 AC122834
2798 AC124709
2799 G T T AC153559
2798 AL646046
2798 AL662923
2798 AL845483

-----+-----+-----+-----+-----+-----+-----+
2880 2890 2900 2910 2920 2930 2940
-----+-----+-----+-----+-----+-----+-----+

2870 GCACAACTTTTTCACAAGATAGAAGTAGAAGGTATTCTACCCAATCATTTTATGAAGCCACTATTACT

L1spaSp27to1597

2868 AC036146
2866 AC107832
2869 A C AC122029
2868 AC122834
2868 AC124709
2869 A C AC153559
2868 AL646046
2868 AL662923
2868 AL845483

-----+-----+-----+-----+-----+-----+-----+
2950 2960 2970 2980 2990 3000 3010
-----+-----+-----+-----+-----+-----+-----+

2940 CTGATACCTAAACCACAGAAAGATCCAACAAAGATAGAGAAGTTTCTTATGAACATCG

L1spaSp27to1597

2938 T AC036146
2936 T AC107832
2939 T AC122029
2938 AC122834

2938 AC124709
2939T.... AC153559
2938 AL646046
2938 AL662923
2938 AL845483

-----+-----+-----+-----+-----+-----+-----+
3020 3030 3040 3050 3060 3070 3080
-----+-----+-----+-----+-----+-----+-----+

3010 ATGCAAAAATCCTTAATAAAATTCCTCGCTAACCGAATCCAAGAACACATTAAAGCAATCATCCATCCTGA
L1spaSp27to1597
3008C..... AC036146
3006C..... AC107832
3009C..... AC122029
3008 AC122834
3008 AC124709
3009C.....T.... AC153559
3008T.... AL646046
3008 AL662923
3008T.... AL845483

-----+-----+-----+-----+-----+-----+-----+
3090 3100 3110 3120 3130 3140 3150
-----+-----+-----+-----+-----+-----+-----+

3080 CCAAGTAGGTTTTATTCCAGGGATGCAGGGATGGTTTTAATATACGAAAATCCATCAATGTAATCCATTAT
L1spaSp27to1597
3078A..... AC036146
3076A..... AC107832
3079A.....C... AC122029
3078 AC122834
3078 AC124709
3079C.....C.C. AC153559
3078 AL646046
3078 AL662923
3078 AL845483

-----+-----+-----+-----+-----+-----+-----+
3160 3170 3180 3190 3200 3210 3220
-----+-----+-----+-----+-----+-----+-----+

3150 ATAAACAAACTCAAAGACAAAACCACATGATCATCTCGTTAGATGCAGAAAAGCATTGACAAGATCC
L1spaSp27to1597
3148A..... AC036146
3146A..... AC107832
3149G..... AC122029
3148 AC122834
3148 AC124709
3149 AC153559
3148 AL646046
3148 AL662923
3148 AL845483

-----+-----+-----+-----+-----+-----+-----+
3230 3240 3250 3260 3270 3280 3290
-----+-----+-----+-----+-----+-----+-----+

3220 AACACCCATTTCATGATAAAAAGTTCCTGGAAAAGATCAGGAATTC AAGGCAATACCTAAACATGATAAAAAGC
L1spaSp27to1597
3218 AC036146
3216 AC107832
3219C..... AC122029
3218 AC122834
3218 AC124709
3219C..... AC153559
3218 AL646046
3218 AL662923
3218 AL845483

-----+-----+-----+-----+-----+-----+-----+
3300 3310 3320 3330 3340 3350 3360
-----+-----+-----+-----+-----+-----+-----+

3290 AATCTACAGCAAACCAGTAGCCAACATCAAAGTAAATGGAGAGAAGCTGGAAGCAATCCCCTAAAATCA
L1spaSp27to1597

3288 AC036146
3286 AC107832
3289 AC122029
3288 AC122834
3288 AC124709
3289 G AC153559
3288 AL646046
3288 AL662923
3288 AL845483

-----+-----+-----+-----+-----+-----+-----+
3370 3380 3390 3400 3410 3420 3430
-----+-----+-----+-----+-----+-----+-----+

3360 GGGACTAGACAAGGCTGCCCACTTTCTCCCTACCTTTTCAACATAGTACTTGAAGTATTAGCCAGAGCAA
L1spaSp27to1597
3358 AC036146
3356 T AC107832
3359 AC122029
3358 AC122834
3358 AC124709
3359 AC153559
3358 AL646046
3358 AL662923
3358 AL845483

-----+-----+-----+-----+-----+-----+-----+
3440 3450 3460 3470 3480 3490 3500
-----+-----+-----+-----+-----+-----+-----+

3430 TTCGACAACAAAAGGAGATCAAGGGGATACAAATTGGAAAAGAGGAAGTCAAATATCACTTTTTCGAGA
L1spaSp27to1597
3428 AC036146
3426 AC107832
3429 G AC122029
3428 AC122834
3428 AC124709
3429 G AC153559
3428 AL646046
3428 AL662923
3428 AL845483

-----+-----+-----+-----+-----+-----+-----+
3510 3520 3530 3540 3550 3560 3570
-----+-----+-----+-----+-----+-----+-----+

3500 TGATATGATAGTATATATAAGTGACCCTAAAAATTCCAACAGAGAAGTCTAAACCTGATAAACAGCTTC
L1spaSp27to1597
3498 AC036146
3496 AC107832
3499 C AC122029
3498 AC122834
3498 AC124709
3499 C AC153559
3498 AL646046
3498 AL662923
3498 AL845483

-----+-----+-----+-----+-----+-----+-----+
3580 3590 3600 3610 3620 3630 3640
-----+-----+-----+-----+-----+-----+-----+

3570 GGTGAAGTAGCTGGATATAAAATTAACCTCAACAAGTCAATGGCCTTTCTCTACACAAAGAATAAACAGG
L1spaSp27to1597
3568 AC036146
3566 AC107832
3569 AC122029
3568 AC122834
3568 AC124709
3569 AC153559
3568 AL646046
3568 AL662923
3568 AL845483

-----+-----+-----+-----+-----+-----+-----+

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          3650      3660      3670      3680      3690      3700      3710
-----+-----+-----+-----+-----+-----+
3640 CTGAGAAAGAAATTAGGGAAACAACACCCCTTCTCAATAGCCACAAATAATATAAAATATCTCGGCGTGAC
L1spaSp27to1597
3638 ..... AC036146
3636 ..... AC107832
3639 .....T..... AC122029
3638 .....T..... AC122834
3638 ..... AC124709
3639 .....T.....A..... AC153559
3638 ..... AL646046
3638 ..... AL662923
3638 ..... AL845483

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          3720      3730      3740      3750      3760      3770      3780
-----+-----+-----+-----+-----+
3710 TCTAACGAAGGAAGTGAAGATCTGTATGATAAAAACTTCAAGTCCCTGAAGAAAGAAATTAAGAAGAT
L1spaSp27to1597
3708 ..... AC036146
3706 ..... AC107832
3709 .....T.....T..... AC122029
3708 ..... AC122834
3708 ..... AC124709
3709 .....T.....T..... AC153559
3708 ..... AL646046
3708 ..... AL662923
3708 ..... AL845483

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          3790      3800      3810      3820      3830      3840      3850
-----+-----+-----+-----+-----+
3780 CTCAGAAGATGGAAAGATCTCCCATGCTCATGGATTGGCAGGACCAACATTGTAAAAATGGCTATCTTGC
L1spaSp27to1597
3778 ..... AC036146
3776 ..... AC107832
3779 .....T...T..... AC122029
3778 ..... AC122834
3778 ..... AC124709
3779 .....T..... AC153559
3778 ..... AL646046
3778 ..... AL662923
3778 ..... AL845483

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          3860      3870      3880      3890      3900      3910      3920
-----+-----+-----+-----+-----+
3850 CAAAAGCAATCTACAGATTCAATGCAATCCCCATTAATAATCCAACCTCAATTCTTCAACGAATTAGAAGG
L1spaSp27to1597
3848 ..... AC036146
3846 ..... AC107832
3849 .....C..... AC122029
3848 ..... AC122834
3848 ..... AC124709
3849 .....C..... AC153559
3848 ..... AL646046
3848 ..... AL662923
3848 ..... AL845483

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          3930      3940      3950      3960      3970      3980      3990
-----+-----+-----+-----+-----+
3920 AGCAATTTGCAAATTCATCTGGAATAACAAAAA-CCGAGGATAGCAAAAACCTTCTCAAGGATAAAAAG
L1spaSp27to1597
3918 ..... AC036146
3916 ..... AC107832
3919 .....T..... AC122029
3918 ..... AC122834
3918 ..... AC124709
3919 .....A..T..... AC153559
3918 ..... AL646046

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3918 AL662923
3918 AL845483

-----+-----+-----+-----+-----+-----+-----+
 4000 4010 4020 4030 4040 4050 4060
-----+-----+-----+-----+-----+-----+-----+

3989 AACCTCTGGTGAATCACCATGCCTGACCTAAAGCTTTACTACAGAGCAATTGTGATAAAAACTGCATGG
L1spaSp27to1597

3987 AC036146
3985 AC107832
3988 G..... AC122029
3987 AC122834
3987 AC124709
3989 AC153559
3987 AL646046
3987 AL662923
3987 AL845483

-----+-----+-----+-----+-----+-----+-----+
 4070 4080 4090 4100 4110 4120 4130
-----+-----+-----+-----+-----+-----+-----+

4059 TACTGGTATAGAGACAGACAAGTAGACCAATGGAATAGAAATGAAGACCCAGAAATGAACCCACACACCT
L1spaSp27to1597

4057 G..... AC036146
4055 G..... AC107832
4058 AC122029
4057 G..... AC122834
4057 G..... AC124709
4059 AC153559
4057 G..... AL646046
4057 G..... AL662923
4057 G..... AL845483

-----+-----+-----+-----+-----+-----+-----+
 4140 4150 4160 4170 4180 4190 4200
-----+-----+-----+-----+-----+-----+-----+

4129 ATGGTCACTTGATCTTCGACAAGGGAGCCAAAACCATCCAGTGAAGAAAGACAGCATTTCACAACAATTG
L1spaSp27to1597

4127 AC036146
4125 AC107832
4128 T..... A.. AC122029
4127 AC122834
4127 AC124709
4129 T..... AC153559
4127 AL646046
4127 AL662923
4127 AL845483

-----+-----+-----+-----+-----+-----+-----+
 4210 4220 4230 4240 4250 4260 4270
-----+-----+-----+-----+-----+-----+-----+

4199 GTGCTGGCACAACCTGGTTGTTATCATGTAGAAGAATGCGAATCGATCCATACTTATCTCCTTGTACTAAG
L1spaSp27to1597

4197 AC036146
4195 T..... AC107832
4198 AC122029
4197 AC122834
4197 AC124709
4199 C..... AC153559
4197 AL646046
4197 AL662923
4197 AL845483

-----+-----+-----+-----+-----+-----+-----+
 4280 4290 4300 4310 4320 4330 4340
-----+-----+-----+-----+-----+-----+-----+

4269 GTCAAATCTAAGTGGATCAAGGAACCTCACATAAAACCAGAGACACTGAAACTTATAGAGGAGAAAGTGG
L1spaSp27to1597

4267 A..... AC036146
4265 AC107832
4268 A..... A..... AC122029

4267 AC122834
4267 AC124709
4269A.....A..... AC153559
4267 AL646046
4267 AL662923
4267A.....A..... AL845483

-----+-----+-----+-----+-----+-----+-----+
4350 4360 4370 4380 4390 4400 4410
-----+-----+-----+-----+-----+-----+-----+

4339 GGAAAAGTCTTGAAGATATGGGCACAGGGGAAAAATTCCTGAACAGAACAGCAATGGCTTGTGCTGTAAG
L1spaSp27to1597
4337C..... AC036146
4335C..... AC107832
4338C..... AC122029
4337C..... AC122834
4337C..... AC124709
4339CT..... AC153559
4337C..... AL646046
4337C..... AL662923
4337C..... AL845483

-----+-----+-----+-----+-----+-----+-----+
4420 4430 4440 4450 4460 4470 4480
-----+-----+-----+-----+-----+-----+-----+

4409 ATCGAGAATTGACAAATGGGACCTAATGAACTCCAAGTTTCTGCAAGGCAAAAGACACTGTCTATAAG
L1spaSp27to1597
4407 ..T..... AC036146
4405 AC107832
4408C...A..... AC122029
4407 AC122834
4407 AC124709
4409 ..T.....C...A..... AC153559
4407 AL646046
4407 AL662923
4407 AL845483

-----+-----+-----+-----+-----+-----+-----+
4490 4500 4510 4520 4530 4540 4550
-----+-----+-----+-----+-----+-----+-----+

4479 ACAAAAAGACCACCAACAGACTGGGAAAGGATCTTTACCTATCCTAAATCAGATAGGGGACTAATATCCA
L1spaSp27to1597
4477 AC036146
4475 AC107832
4478G.....T..... AC122029
4477 AC122834
4477 AC124709
4479G.....T..... AC153559
4477 AL646046
4477 AL662923
4477 AL845483

-----+-----+-----+-----+-----+-----+-----+
4560 4570 4580 4590 4600 4610 4620
-----+-----+-----+-----+-----+-----+-----+

4549 ACATATATAAAGAACTCAAGAAGGTGGACCTCAGAAAATCAAATAACCCCTTAAAAATGGGGCTCAGA
L1spaSp27to1597
4547 AC036146
4545 AC107832
4548T.....C.....A..... AC122029
4547 AC122834
4547 AC124709
4549T.....A..... AC153559
4547 AL646046
4547 AL662923
4547 AL845483

-----+-----+-----+-----+-----+-----+-----+
4630 4640 4650 4660 4670 4680 4690
-----+-----+-----+-----+-----+-----+-----+

4619 ACTGAACAAAGAATTCTCACCTGAGGAATACCGAATGGCAGAGAAGCACCTGAAAAAATGTTCAACATCC
 L1spaSp27to1597
 4617 AC036146
 4615 AC107832
 4618 AC122029
 4617 AC122834
 4617 AC124709
 4619 AC153559
 4617 AL646046
 4617 AL662923
 4617 AL845483

-----+-----+-----+-----+-----+-----+
 4700 4710 4720 4730 4740 4750 4760
 -----+-----+-----+-----+-----+-----+

4689 TTAATCATCAGGGAAATGCAAATCAAAAACAACCCTGAGATTCCACCTCACACCAGTGAGAATGGCTAAGA
 L1spaSp27to1597
 4632 AC036146
 4685 AC107832
 4688 C.....T..... AC122029
 4687 AC122834
 4687 AC124709
 4689 C.....T..... AC153559
 4687 AL646046
 4687 A..... AL662923
 4687 AL845483

-----+-----+-----+-----+-----+-----+
 4770 4780 4790 4800 4810 4820 4830
 -----+-----+-----+-----+-----+-----+

4759 TCAAAAATTCAGGTGACAGCAGATGCTGGCGAGGATGTGGAGAAAGAGGAACACTCCTCCATTGTTGGTG
 L1spaSp27to1597
 4632 AC036146
 4755 AC107832
 4758 AC122029
 4757 AC122834
 4757 AC124709
 4759 T..... AC153559
 4757 AL646046
 4757 AL662923
 4757 AL845483

-----+-----+-----+-----+-----+-----+
 4840 4850 4860 4870 4880 4890 4900
 -----+-----+-----+-----+-----+-----+

4829 GGATTGCAGGCTTGTACAACCACTCTGGAAATCAGTCTGGCGGTTCCCTCAGAAAATGGACATAGTACTA
 L1spaSp27to1597
 4632 AC036146
 4825 AC107832
 4828 C..... AC122029
 4827 AC122834
 4827 AC124709
 4829 A.....A.....C..... AC153559
 4827 AL646046
 4827 T.....T..... AL662923
 4827 AL845483

-----+-----+-----+-----+-----+-----+
 4910 4920 4930 4940 4950 4960 4970
 -----+-----+-----+-----+-----+-----+

4899 CCGGAGGATCCAGCAATACCTCTCCTGGGCATATATCCAGAAGAAGCCCCAACTGGTAAGAAGGACACAT
 L1spaSp27to1597
 4632 AC036146
 4895 AC107832
 4898 T..... AC122029
 4897 AC122834
 4897 AC124709
 4899 A.....T..... AC153559
 4897 AL646046
 4897 AL662923
 4897 AL845483

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-----+-----+-----+-----+-----+-----+
          4980      4990      5000      5010      5020      5030      5040
-----+-----+-----+-----+-----+
4969 GCTCCACTATGTTTCATAGCAGCCTTATTTATAATAGCCAGAACTGGAAAGAACCCAGATGCCCTCAAC
L1spaSp27to1597
4632                                     AC036146
4965 ..... AC107832
4968 .....G..... AC122029
4967 ..... AC122834
4967 ..... AC124709
4969 .....G..... AC153559
4967 ..... AL646046
4967 ..... AL662923
4967 ..... AL845483

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-----+-----+-----+-----+-----+-----+
          5050      5060      5070      5080      5090      5100      5110
-----+-----+-----+-----+-----+
5039 AGAGGAATGGATACAGAAAATGTGGTACATCTACACAATGGAGTACTACTCAGCTATTA AAAAGAATGAA
L1spaSp27to1597
4632                                     AC036146
5035 ..... AC107832
5038 ..... AC122029
5037 ..... AC122834
5037 ..... AC124709
5039 ..... AC153559
5037 .....G..... AL646046
5037 ..... AL662923
5037 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          5120      5130      5140      5150      5160      5170      5180
-----+-----+-----+-----+-----+
5109 TTTATGAAATTCCTAGCCAAATGGATGGACCTGGAGAGCATCATCCTGAGTGAGGTAACACAATCACAAA
L1spaSp27to1597
4632                                     AC036146
5105 .....G..... AC107832
5108 .....G.....T..... AC122029
5107 ..... AC122834
5107 ..... AC124709
5109 .....G.....T..... AC153559
5107 ..... AL646046
5107 ..... AL662923
5107 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          5190      5200      5210      5220      5230      5240      5250
-----+-----+-----+-----+-----+
5179 GGAACTCACACAATATGTACTCACTGATAAGTGGATACTAGCCAAAACCTAGGATACCCACGATATAAG
L1spaSp27to1597
4632                                     AC036146
5175 ..... AC107832
5178 .....T.....A..... AC122029
5177 ..... AC122834
5177 ..... AC124709
5179 .....T.....A..... AC153559
5177 .....T..... AL646046
5177 ..... AL662923
5177 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          5260      5270      5280      5290      5300      5310      5320
-----+-----+-----+-----+-----+
5249 ATACAATTTCTAAACACATGAAACTCAAGAAAAATGAAGACTGAAGTGTGGACACTATGCCCTCCTTA
L1spaSp27to1597
4632                                     AC036146
5245 .....G..... AC107832
5248 ..... AC122029
5247 ..... AC122834
5247 .....G..... AC124709

```

5249 AC153559
5247 AL646046
5247 AL662923
5247 A..... AL845483

-----+-----+-----+-----+-----+-----+-----+
5330 5340 5350 5360 5370 5380 5390
-----+-----+-----+-----+-----+-----+-----+

5319 GAAGTGGGAACAAAACA---CCCATGGAAGGAGTTACAGAAACAAAGTTTGGAGCTGAGATGAAAGGAG
L1spaSp27to1597
4632 AC036146
5315----.....A.....T AC107832
5318----..T.....G.....T AC122029
5317----.....T AC122834
5317----.....T AC124709
5319AACA..T.....G.....T AC153559
5317----.....A.....T AL646046
5317----.....T.....A.....T AL662923
5317----.....A.....T AL845483

-----+-----+-----+-----+-----+-----+-----+
5400 5410 5420 5430 5440 5450 5460
-----+-----+-----+-----+-----+-----+-----+

5385 GGACCATGTAGAGACTGCCATATCCAGGGATCCACCCCATTAATCAGCATCCAAACGCTGACACCATGCA
L1spaSp27to1597
4632 AC036146
5381T.....T..... AC107832
5384 ..G.....T..... AC122029
5383 AC122834
5383 AC124709
5389T.....T..... AC153559
5383T.....T..... AL646046
5383T.....T..... AL662923
5383T.....T..... AL845483

-----+-----+-----+-----+-----+-----+-----+
5470 5480 5490 5500 5510 5520 5530
-----+-----+-----+-----+-----+-----+-----+

5455 TATACTAGCAAGATTTTATCGAAAGGACCCAGATGTAGCTGTCTCTTGTGAGACTATGCCGGGCCTAGC
L1spaSp27to1597
4632 AC036146
5451 ..C.....CT..... AC107832
5454 ..C..... AC122029
5453 AC122834
5453 AC124709
5459 ..C.....T..... AC153559
5453 ..C.....CT..... AL646046
5453 ..C.....CT..... AL662923
5453 ..C.....CT..... AL845483

-----+-----+-----+-----+-----+-----+-----+
5540 5550 5560 5570 5580 5590 5600
-----+-----+-----+-----+-----+-----+-----+

5525 AAACACAGAAGTGGATGCTCACAGTCAGCTAATGGATGGATCACAGGGCTCCCAATGGAGGAGCTAGAGA
L1spaSp27to1597
4632 AC036146
5521 AC107832
5524G.....T..... AC122029
5523 AC122834
5523 AC124709
5529C..... AC153559
5523 AL646046
5523 AL662923
5523 AL845483

-----+-----+-----+-----+-----+-----+-----+
5610 5620 5630 5640 5650 5660 5670
-----+-----+-----+-----+-----+-----+-----+

5595 AAGTACCAAGGAGCTAAAGGGATCTGCAACCCATAGGTGGAACAACATTATGAACTAACCGATACCC
L1spaSp27to1597
4632 AC036146

5591T..... AC107832
5594 AC122029
5593T..... AC122834
5593T..... AC124709
5599T..... AC153559
5593T..... AL646046
5593T..... AL662923
5593T..... AL845483

-----+-----+-----+-----+-----+-----+
5680 5690 5700 5710 5720 5730 5740
-----+-----+-----+-----+-----+-----+

5665 TGAGCTCTTGACTCTAGCTGCATATGTATCAAAAGATGGCCTAGTCGGCCATCACTGGAAAGAGAGGCC
L1spaSp27to1597
4632 AC036146
5661 AC107832
5664 A..... AC122029
5663 AC122834
5663 AC124709
5669 A..... AC153559
5663 AL646046
5663 AL662923
5663 AL845483

-----+-----+-----+-----+-----+-----+
5750 5760 5770 5780 5790 5800 5810
-----+-----+-----+-----+-----+-----+

5735 ATGGACACGCAGACTTTGTGTGCCCGGTACAGGGGAACGCCAGGGCCAAAGGGGGGGAGTGGGTGGG
L1spaSp27to1597
4632 AC036146
5731 AC107832
5734A..A....A.A....A.A.....AA.....-.....C... AC122029
5733 AC122834
5733-.....A.A.... AC124709
5739A..A....A.A....A.A.....AA.....-.....C... AC153559
5733 AL646046
5733T.....-..... AL662923
5733-.....A... AL845483

-----+-----+-----+-----+-----+-----+
5820 5830 5840 5850 5860 5870 5880
-----+-----+-----+-----+-----+-----+

5805 TAGGGGAGTGGGGGTGGGTGGGTAAGGGGGACTTTTGGTATAGCATTGAAATGTAATGAGCTAAATAC
L1spaSp27to1597
4632 AC036146
5800C.... AC107832
5803T..... AC122029
5802 AC122834
5802 AC124709
5808T.....C..... AC153559
5802 AL646046
5802A..... AC153559
5802 AL662923
5802 AL845483

-----+-----+-----+-----+-----+-----+
5890 5900 5910 5920 5930 5940 5950
-----+-----+-----+-----+-----+-----+

5875 CTAATAAAAAATGGA-AAAAAATAAAAAAA--ATAAA-ATAAAAAAAAAGACCATGAAACATAAAAAAA
L1spaSp27to1597
4632 AC036146
5870-----TGG...A.....-----..-GA.T.....A.AA.AA.GTA.CTCTTTCT AC107832
5873T.GA..G...A.....AA.A.G.C.AGG..G..GGA.A.C..CTCTC.GTGCC.G AC122029
5872A.....A.....AA.A.....-G-.T.TG-----T..CTCTCA.T-T... AC122834
5872A.....A..TTCTTAATCTC.TC.CC...G.C.TCTTTGCCTTA.A..GTC. AC124709
5878-GA..G...A.....GTGC.CGTCCTAT.CCTGCC.AGGA.AA.GTAC.GCCTTTT AC153559
5872-.....A.....TGGG...-A.....A.AA.AA..GA.....G.G AL646046
5872-----..T..AT...TT-.C...-AGC.....A.AA.AA..A.A..... AL662923
5872AAA.T.....A.....G.AAT..C.-GA...T...G.TA..GC..G..A..... AL845483

Supplemental figure 5. Alignment of the spliced L1 elements identified in the mouse genome. Sequences of the full-length mouse L1 elements that underwent splicing (SD and SA sites at positions 27 and 1597 L1spa sequence respectively) and retrotransposed were extracted from the mouse genome and aligned by ClustalW against the L1spa sequence spliced in the same manner (L1spaSp27to1597). Nucleotides that do not match L1spa sequence are shown. Accession numbers corresponding to each contig containing these sequences and chromosome numbers are shown on the right.

```
-----+-----+-----+-----+-----+-----+
          10         20         30         40         50         60         70
-----+-----+-----+-----+-----+-----+
1 CGGAACCTTAGGAAATTAGTCTGAACAGGTTGAGAGGGTGCGCCAGAGAACCTGACAGCTTCTGGAACAGGC
L1spaSp239to1597
1 ..... AC036146
1 ..... AC122834
1 .....G..... AC124709
1 ..... AL671880
1 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          80         90        100        110        120        130        140
-----+-----+-----+-----+-----+-----+
71 GGAAGCACAGAGGGCGCTGAGGCATCACCCGTGTGTGGGCCGGGACAGCCGGCCACCTTCTGGACCAGAGG
L1spaSp239to1597
69 .....G.....C....G.... AC036146
69 .....A.....G.....A.....A.....G.... AC122834
69 .....G.....T.....G....C....G.... AC124709
69 .....G.....G.....C....G.... AC671880
46 A.....G.....G.....C....G.... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          150        160        170        180        190        200        210
-----+-----+-----+-----+-----+-----+
141 ACAGGTGCCCGCCCGCTGGGGAGGCGCCTAAGCCACAGCAGCAGCGGTGCGCCATCTTGGTCCGGGACC
L1spaSp239to1597
139 .....A.... AC036146
139 ..... AC122834
139 .....T.....GG.....A.... AC124709
139 .....A.... AL671880
116 .....A..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          220        230        240        250        260        270        280
-----+-----+-----+-----+-----+-----+
211 CGCCGAACCTTAGGAAATTAGTCTGAACAGGGAGGAGGTCCAAATACAAGATATCTGCGCACCTTCCTGT
L1spaSp239to1597
209 .A.....-..... AC036146
209 .....-.....A..... AC122834
209 .....-..... AC124709
209 .A.....-..... AL671880
186 .....-..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          290        300        310        320        330        340        350
-----+-----+-----+-----+-----+-----+
281 AAGAGAGCTTGCCAGCAGAGAGTGTCTGAGCACTGAAACTCAGAGGAGAGAATCTGTCTCCAGGTCTG
L1spaSp239to1597
278 ..... AC036146
278 ..... AC122834
278 ..... AC124709
278 ..... AL671880
255 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          360        370        380        390        400        410        420
-----+-----+-----+-----+-----+-----+
351 CTGATAGACGGTAACAGAATCACCAGAAGAACAATCTCTAAACAGAGTCAACTATAACTACTAACCAG
L1spaSp239to1597
348 ..... AC036146
348 ..... AC122834
348 ...C..... AC124709
348 ..... AL671880
325 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          430        440        450        460        470        480        490
-----+-----+-----+-----+-----+-----+
421 AGATTACCAGATGGCGAAAGGTAACGGAGGAATCTTACTAACAGGAACCAAGACCACTCACCATCACCA
L1spaSp239to1597
```

```

418 ..... AC036146
418 ..... AC122834
418 ..... AC124709
418 ..... AL671880
395 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          500      510      520      530      540      550      560
-----+-----+-----+-----+-----+-----+-----+
491 GAACCCAGCACACCCACTTCGCCAGTCCAGGGAACCCCAACACACCTGAGAACCTAGACCTAGATTTAA
L1spaSp239to1597
488 ..... AC036146
488 ..... T..... AC122834
488 ..... AC124709
488 ..... AL671880
465 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          570      580      590      600      610      620      630
-----+-----+-----+-----+-----+-----+-----+
561 AAGCATATCTCATGATGATGGTAGAGGGCATCAAGAAGGACTTTAATAAATCACTTAAAGAAATACAGGA
L1spaSp239to1597
558 ..... A..... AC036146
558 ..... A..... AC122834
558 ..... A..... AC124709
558 ..... A..... AL671880
535 ..... A..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          640      650      660      670      680      690      700
-----+-----+-----+-----+-----+-----+-----+
631 GAACACTGCTAAAGAGTTACAAGTCCTTAAAGAAAAACAGGAAAAACAATCAAACAGGTAGAAGTCCTT
L1spaSp239to1597
628 ..... AC036146
628 ..... AC122834
628 ..... AC124709
628 ..... AL671880
605 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          710      720      730      740      750      760      770
-----+-----+-----+-----+-----+-----+-----+
701 ACAGAAAAAGAGGAAAAAACATACAAACAGGTGATGGAAATGAACAAAACCATACTAGACCTAAAAAGGG
L1spaSp239to1597
698 ..... AC036146
698 ..... AC122834
698 ..... AC124709
698 ..... AL671880
675 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          780      790      800      810      820      830      840
-----+-----+-----+-----+-----+-----+-----+
771 AAGTAGACACAATAAAGAAAACCTCAAAGCGAGGCAACACTAGAGATAGAAACCCTAGGAAAGAAATCTGG
L1spaSp239to1597
768 ..... AC036146
768 ..... AC122834
768 ..... AC124709
768 ..... AL671880
745 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          850      860      870      880      890      900      910
-----+-----+-----+-----+-----+-----+-----+
841 AACCATAGATTTGAGCATCAGCAACAGAATACAAGAGATGGAAGAGAGAAATCTCAGGTGCAGAACATTC
L1spaSp239to1597
838 ..... G..... AC036146
838 ..... G..... AC122834
838 ..... G..... AC124709
838 ..... G..... AL671880
815 ..... G..... AL845483

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```

-----+-----+-----+-----+-----+-----+
          920      930      940      950      960      970      980
-----+-----+-----+-----+-----+-----+
  911 ATAGAGAACATCGGCACAACAATCAAAGAAAATGGAAAATGCAAAAAGATCCTAACTCAAATATCCAGG
L1spaSp239to1597
  908 ..... AC036146
  908 ..... AC122834
  908 ..... AC124709
  908 ..... AL671880
  885 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          990      1000     1010     1020     1030     1040     1050
-----+-----+-----+-----+-----+-----+
  981 AAATCCAGGACACAATAAGAAGACCAAACGTACGGATAATAGGAGTGGATGAGAATGAAGATTTTCAACT
L1spaSp239to1597
  978 ..... AC036146
  978 ..... AC122834
  978 ..... AC124709
  978 ..... AL671880
  955 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
        1060     1070     1080     1090     1100     1110     1120
-----+-----+-----+-----+-----+-----+
 1051 CAAAGTCCAGCAAACATCTTCAACAAAATTATTGAAGAAAACCTCCCAAATCTAAAGAATGAGATGCAT
L1spaSp239to1597
 1048 ..... AC036146
 1048 ..... AC122834
 1048 ..... AC124709
 1048 ..... AL671880
 1025 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
        1130     1140     1150     1160     1170     1180     1190
-----+-----+-----+-----+-----+-----+
 1121 ATGAACATACAAGAAGCCTACAGAACTCCAATAGACTGGACCAGAAAAGAAATCCTCCCGACACATAA
L1spaSp239to1597
 1118 ..... AC036146
 1118 ..... AC122834
 1118 ..... AC124709
 1118 ..... AL671880
 1095 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
        1200     1210     1220     1230     1240     1250     1260
-----+-----+-----+-----+-----+-----+
 1191 TAATCAGAACATCAAATGCCTAAATAAAGATAGAATACTAAAAGCAGTAAGGGAAAAAGGTCAAGTAAC
L1spaSp239to1597
 1188 ..... AC036146
 1188 ..... AC122834
 1188 ..... AC124709
 1188 ..... AL671880
 1165 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
        1270     1280     1290     1300     1310     1320     1330
-----+-----+-----+-----+-----+-----+
 1261 ATATAAAGGCAAGCCTATCAGAATTACACCAGATTTTTCACCAGAGACTATGAAAGCCAGAAGAGCCTGG
L1spaSp239to1597
 1258 ..... AC036146
 1258 ..... AC122834
 1258 ..... AC124709
 1258 ..... AL671880
 1235 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
        1340     1350     1360     1370     1380     1390     1400
-----+-----+-----+-----+-----+-----+

```


1331 ACAGATGTTATACAGACACTAAGAGAACACAAACTGCAGCCCAGGCTACTATACCCAGCCAAACTCTCAA
L1spaSp239to1597
1328 AC036146
1328 AC122834
1328 AC124709
1328 AL671880
1305 AL845483

-----+-----+-----+-----+-----+-----+-----+
1410 1420 1430 1440 1450 1460 1470
-----+-----+-----+-----+-----+-----+-----+

1401 TTATCATAGAGGGAGAAACCAAAGTATTCACGACAAAACCAAATTCACGCATTATCTCTCCACGAATCC
L1spaSp239to1597
1398A..... AC036146
1398 AC122834
1398 AC124709
1398A..... AL671880
1375 AL845483

-----+-----+-----+-----+-----+-----+-----+
1480 1490 1500 1510 1520 1530 1540
-----+-----+-----+-----+-----+-----+-----+

1471 AGCCCTTCAAAGGATAATAACAGAAAAAACCAATACAAGAACGGGAACAACGCCCTAGAAAAACAAGA
L1spaSp239to1597
1468 AC036146
1468 AC122834
1468 AC124709
1468 AL671880
1445 AL845483

-----+-----+-----+-----+-----+-----+-----+
1550 1560 1570 1580 1590 1600 1610
-----+-----+-----+-----+-----+-----+-----+

1541 AGGTAATCCCTCAACAAACCTAAAAGAAGACAGCCACAAGAACAGAAATGCCACCTTTAACAACTAAAATA
L1spaSp239to1597
1538 AC036146
1538 AC122834
1538 AC124709
1538 AL671880
1515 AL845483

-----+-----+-----+-----+-----+-----+-----+
1620 1630 1640 1650 1660 1670 1680
-----+-----+-----+-----+-----+-----+-----+

1611 ACAGGAAGCAACAATTACTTTTCCTTAATATCTCTTAACATCAATGGTCTCAACTCGCCAATAAAAAAGAC
L1spaSp239to1597
1608 AC036146
1608 AC122834
1608C..... AC124709
1608 AL671880
1585 AL845483

-----+-----+-----+-----+-----+-----+-----+
1690 1700 1710 1720 1730 1740 1750
-----+-----+-----+-----+-----+-----+-----+

1681 ATAGACTAACAAACTGGCTACACAAACAAGACCCCAACATTTTGCTGCTTACAGGAACTCATCTCAGAGA
L1spaSp239to1597
1678 AC036146
1678 AC122834
1678 AC124709
1678 AL671880
1655 AL845483

-----+-----+-----+-----+-----+-----+-----+
1760 1770 1780 1790 1800 1810 1820
-----+-----+-----+-----+-----+-----+-----+

1751 AAAAGATAGACACTACCTCAGAATGAAAGGCTGGAAAACAATTTTCCAAGCAAATGGTATGAAGAAACAA
L1spaSp239to1597
1748 AC036146
1748 AC122834
1748 AC124709

```

1748 ..... AL671880
1725 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          1830      1840      1850      1860      1870      1880      1890
-----+-----+-----+-----+-----+-----+
1821 GCAGGAGTAGCCATCCTAATATCTGATAAGATTGACTTCCAACCCAAAGTCATCAAAAAAGACAAGGAGG
L1spaSp239to1597
1818 ..... AC036146
1818 ..... AC122834
1818 ..... AC124709
1818 ..... AL671880
1795 ..... AL845483

-----+-----+-----+-----+-----+-----+
          1900      1910      1920      1930      1940      1950      1960
-----+-----+-----+-----+-----+
1891 GACACTTCATTCTCATCAAAGGTAATAATCCTCCAAGAGGAACTCTCAATTCTGAATATCTATGCTCCAAA
L1spaSp239to1597
1888 ..... AC036146
1888 ..... AC122834
1888 ..... AC124709
1888 ..... AL671880
1865 ..... AL845483

-----+-----+-----+-----+-----+-----+
          1970      1980      1990      2000      2010      2020      2030
-----+-----+-----+-----+-----+
1961 TACAAGAGCAGCCACATTCCTAAAGAACTTTAGTAAAGCTCAAAGCACACATTCGCGCTCACACAATA
L1spaSp239to1597
1958 ..... AC036146
1958 ..... AC122834
1958 ..... AC124709
1958 ..... AL671880
1935 ..... AL845483

-----+-----+-----+-----+-----+-----+
          2040      2050      2060      2070      2080      2090      2100
-----+-----+-----+-----+-----+
2031 ATAGTGGGAGACTTCAACACACCCTTTCACCAATGGACAGATCATGGAACAGAACTAAACAGGGACA
L1spaSp239to1597
2028 ..... AC036146
2028 ..... AC122834
2028 ..... AC124709
2028 ..... AL671880
2005 ..... AL845483

-----+-----+-----+-----+-----+-----+
          2110      2120      2130      2140      2150      2160      2170
-----+-----+-----+-----+-----+
2101 CACTGAAACTAACAGAAGTGATGAAACAAATGGATCTGACAGATATCTACAGAACATTTTACCCTAAAAC
L1spaSp239to1597
2098 ..... T..... AC036146
2098 ..... AC122834
2098 ..... T..... AC124709
2098 ..... T..... AL671880
2075 ..... T..... AL845483

-----+-----+-----+-----+-----+-----+
          2180      2190      2200      2210      2220      2230      2240
-----+-----+-----+-----+-----+
2171 AAAAGGATATACCTTCTTCAGCACCTCATGGTACCTTCTCCAAAATTGACCACATAATAGGTCACAAA
L1spaSp239to1597
2168 ..... AC036146
2168 ..... AC122834
2168 ..... AC124709
2168 ..... AL671880
2145 ..... C..... AL845483

-----+-----+-----+-----+-----+-----+
          2250      2260      2270      2280      2290      2300      2310

```

-----+-----+-----+-----+-----+-----+
2241 TCAGGCCTCAACAGATTAAAAAATATTGAAATTGTCCCATGTATCCTATCAGATCACCATGCACTAAGGC
L1spaSp239to1597
2238C..... AC036146
2238C..... AC122834
2238C..... AC124709
2238C..... AL671880
2215C..... AL845483

-----+-----+-----+-----+-----+-----+
 2320 2330 2340 2350 2360 2370 2380
-----+-----+-----+-----+-----+-----+
2311 TGATCTTCAATAACAAAATAAATAACAGAAAGCCAACATTTCACATGGAACTGAACAACACTCTTCTCAA
L1spaSp239to1597
2308 AC036146
2308 AC122834
2308 AC124709
2308 AL671880
2285 AL845483

-----+-----+-----+-----+-----+-----+
 2390 2400 2410 2420 2430 2440 2450
-----+-----+-----+-----+-----+-----+
2381 TGATACCTTGGTCAAGGAAGGAATAAAGAAAGAAATTAAGACTTTTGTAGAGTTTAAATGAAAATGAAGCC
L1spaSp239to1597
2378 AC036146
2378 AC122834
2378 AC124709
2378 AL671880
2355 AL845483

-----+-----+-----+-----+-----+-----+
 2460 2470 2480 2490 2500 2510 2520
-----+-----+-----+-----+-----+-----+
2451 ACAACGTACCCAAACCTTTGGGACACAATGAAAGCATTCTAAGAGGGAACTCATAGCTATGAGTGCCT
L1spaSp239to1597
2448 AC036146
2448 AC122834
2448 AC124709
2448 AL671880
2425 AL845483

-----+-----+-----+-----+-----+-----+
 2530 2540 2550 2560 2570 2580 2590
-----+-----+-----+-----+-----+-----+
2521 TCAAGAAAAACGGGAGAGACACATACTAGCAGCTTGACAACACATCTAAAAGCTCTAGAAAAAAGGA
L1spaSp239to1597
2518 AC036146
2518 AC122834
2518 AC124709
2518 AL671880
2495 AL845483

-----+-----+-----+-----+-----+-----+
 2600 2610 2620 2630 2640 2650 2660
-----+-----+-----+-----+-----+-----+
2591 AGCAAATTCACCCAAGAGGAGTAGACGGCAGGAAATAATCAAACTCAGGGGTGAAATCAACCAAGTGAA
L1spaSp239to1597
2588 AC036146
2588 AC122834
2588 AC124709
2588 AL671880
2565 AL845483

-----+-----+-----+-----+-----+-----+
 2670 2680 2690 2700 2710 2720 2730
-----+-----+-----+-----+-----+-----+
2661 ACAAGAAGAACTATTCAAAGAATTAACCAAACGAGGAGTTGGTCTTTGAGAAAATCAACAAGATAGATA
L1spaSp239to1597
2658 AC036146
2658 AC122834

2658 AC124709
2658 AL671880
2635 AL845483

-----+-----+-----+-----+-----+-----+-----+
2740 2750 2760 2770 2780 2790 2800
-----+-----+-----+-----+-----+-----+-----+

2731 AACCCCTAGCTAGACTCACTAAAGGGCACAGGGACAAAATCCTAATTAAACAAAATCAGAAATGAAAAGGG
L1spaSp239to1597
2728 AC036146
2728 AC122834
2728 AC124709
2728 AL671880
2705 C AL845483

-----+-----+-----+-----+-----+-----+-----+
2810 2820 2830 2840 2850 2860 2870
-----+-----+-----+-----+-----+-----+-----+

2801 AGACATAACAACAGATCCTGAAGAAATCCAAAACACCATCAGATCCTTCTACAAAAGGCTATACTCAACA
L1spaSp239to1597
2798 AC036146
2798 AC122834
2798 AC124709
2798 AL671880
2775 AL845483

-----+-----+-----+-----+-----+-----+-----+
2880 2890 2900 2910 2920 2930 2940
-----+-----+-----+-----+-----+-----+-----+

2871 AAACCTGGAAAACCTGGACGAAATGGACAAATTTCTGGACAGATACCAGGTACCAAAGTTGAATCAGGATC
L1spaSp239to1597
2868 AC036146
2868 AC122834
2868 AC124709
2868 AL671880
2845 AL845483

-----+-----+-----+-----+-----+-----+-----+
2950 2960 2970 2980 2990 3000 3010
-----+-----+-----+-----+-----+-----+-----+

2941 AAGTTGACCTTCTAAACAGTCCCATATCCCCTAAAGAAATAGAAGCAGTTATTAATAGTCTCCCAGCCAA
L1spaSp239to1597
2938 AC036146
2938 AC122834
2938 AC124709
2938 AL671880
2915 AL845483

-----+-----+-----+-----+-----+-----+-----+
3020 3030 3040 3050 3060 3070 3080
-----+-----+-----+-----+-----+-----+-----+

3011 AAAAAGCCCAGGACCAGACGGGTTTAGTGCAGAGTTCTATCAGACCTTCAAAGAAGATCTAACTCCAGTT
L1spaSp239to1597
3008 AC036146
3008 AC122834
3008 AC124709
3008 AL671880
2985 AL845483

-----+-----+-----+-----+-----+-----+-----+
3090 3100 3110 3120 3130 3140 3150
-----+-----+-----+-----+-----+-----+-----+

3081 CTGCACAAACTTTTTACAAGATAGAAGTAGAAGGTATTCTACCCAACCTCATTTTATGAAGCCACTATTA
L1spaSp239to1597
3078 AC036146
3078 AC122834
3078 AC124709
3078 AL671880
3055 AL845483

-----+-----+-----+-----+-----+-----+-----+

```

          3160      3170      3180      3190      3200      3210      3220
-----+-----+-----+-----+-----+-----+-----+
3151 CTCTGATACCTAAACCACAGAAAGATCCAACAAAGATAGAGAACTTCAGACCAATTTCTCTTATGAACAT
L1spaSp239to1597
3148 .....T.. AC036146
3148 ..... AC122834
3148 ..... AC124709
3148 .....T.. AL671880
3125 ..... AL845483

          3230      3240      3250      3260      3270      3280      3290
-----+-----+-----+-----+-----+-----+
3221 CGATGCAAAAATCCTTAATAAAAATTCTCGCTAACCGAATCCAAGAACACATTAAGCAATCATCCATCCT
L1spaSp239to1597
3218 .....C..... AC036146
3218 ..... AC122834
3218 ..... AC124709
3218 .....C..... AL671880
3195 .....T..... AL845483

          3300      3310      3320      3330      3340      3350      3360
-----+-----+-----+-----+-----+-----+
3291 GACCAAGTAGGTTTTATTCCAGGGATGCAGGGATGGTTTAATATACGAAAATCCATCAATGTAATCCATT
L1spaSp239to1597
3288 .....A..... AC036146
3288 ..... AC122834
3288 ..... AC124709
3288 .....A..... AL671880
3265 ..... AL845483

          3370      3380      3390      3400      3410      3420      3430
-----+-----+-----+-----+-----+-----+
3361 ATATAAACAAACTCAAAGACAAAACCACATGATCATCTCTGTTAGATGCAGAAAAAGCATTTTGACAAGAT
L1spaSp239to1597
3358 .....A..... AC036146
3358 ..... AC122834
3358 ..... AC124709
3358 .....A..... AL671880
3335 ..... AL845483

          3440      3450      3460      3470      3480      3490      3500
-----+-----+-----+-----+-----+-----+
3431 CCAACACCCATTTCATGATAAAAAGTTCTGGAAAGATCAGGAATTC AAGCCAATACCTAAACATGATAAAA
L1spaSp239to1597
3428 ..... AC036146
3428 ..... AC122834
3428 ..... AC124709
3428 ..... AL671880
3405 ..... AL845483

          3510      3520      3530      3540      3550      3560      3570
-----+-----+-----+-----+-----+-----+
3501 GCAATCTACAGCAAACCAGTAGCCAACATCAAAGTAAATGGAGAGAAGCTGGAAGCAATCCCACTAAAAT
L1spaSp239to1597
3498 ..... AC036146
3498 ..... AC122834
3498 ..... AC124709
3498 ..... AL671880
3475 ..... AL845483

          3580      3590      3600      3610      3620      3630      3640
-----+-----+-----+-----+-----+-----+
3571 CAGGGACTAGACAAGGCTGCCCACTTTCTCCCTACCTTTTCAACATAGTACTTGAAGTATTAGCCAGAGC
L1spaSp239to1597
3568 ..... AC036146

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```

3568 ..... AC122834
3568 ..... AC124709
3568 ..... AL671880
3545 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          3650      3660      3670      3680      3690      3700      3710
-----+-----+-----+-----+-----+-----+-----+
3641 AATTCGACAACAAAAGGAGATCAAGGGGATACAAATTGGAAAAGAGGAAGTCAAAATATCACTTTTGGCA
L1spaSp239to1597
3638 ..... AC036146
3638 ..... AC122834
3638 ..... AC124709
3638 ..... AL671880
3615 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          3720      3730      3740      3750      3760      3770      3780
-----+-----+-----+-----+-----+-----+-----+
3711 GATGATATGATAGTATATATAAGTGACCCCTAAAAATTCCAACAGAGAACTCCTAAACCTGATAAACAGCT
L1spaSp239to1597
3708 ..... AC036146
3708 ..... AC122834
3708 ..... AC124709
3708 ..... AL671880
3685 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          3790      3800      3810      3820      3830      3840      3850
-----+-----+-----+-----+-----+-----+-----+
3781 TCGGTGAAGTAGCTGGATATAAAATTAACCTCAAACAAGTCAATGGCCTTTCTCTACACAAAGAATAAACA
L1spaSp239to1597
3778 ..... AC036146
3778 ..... AC122834
3778 ..... AC124709
3778 ..... AL671880
3755 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          3860      3870      3880      3890      3900      3910      3920
-----+-----+-----+-----+-----+-----+-----+
3851 GGCTGAGAAAGAAATTAGGGAAACAACACCCTTCTCAATAGCCACAAATAATATAAAATATCTCGGCGTG
L1spaSp239to1597
3848 ..... AC036146
3848 ..... T..... AC122834
3848 ..... AC124709
3848 ..... AL671880
3825 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          3930      3940      3950      3960      3970      3980      3990
-----+-----+-----+-----+-----+-----+-----+
3921 ACTCTAACGAAGGAAGTGAAGATCTGTATGATAAAAACCTCAAGTCCCTGAAGAAAGAAATTAAGAAG
L1spaSp239to1597
3918 ..... AC036146
3918 ..... AC122834
3918 ..... AC124709
3918 ..... AL671880
3895 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
          4000      4010      4020      4030      4040      4050      4060
-----+-----+-----+-----+-----+-----+-----+
3991 ATCTCAGAAGATGGAAAGATCTCCCATGCTCATGGATTGGCAGGACCAACATTGTAAAAATGGCTATCTT
L1spaSp239to1597
3988 ..... AC036146
3988 ..... AC122834
3988 ..... AC124709
3988 ..... AL671880
3965 ..... AL845483

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```

-----+-----+-----+-----+-----+-----+
          4070      4080      4090      4100      4110      4120      4130
-----+-----+-----+-----+-----+
4061 GCCAAAAGCAATCTACAGATTCAATGCAATCCCCATTAAAATTCCAACCAATTCTTCAACGAATTAGAA
L1spaSp239to1597
4058 ..... AC036146
4058 ..... AC122834
4058 ..... AC124709
4058 ..... AL671880
4035 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          4140      4150      4160      4170      4180      4190      4200
-----+-----+-----+-----+-----+
4131 GGAGCAATTTGCAAATTCATCTGGAATAACAAAAACCGAGGATAGCAAAAACTCTTCTCAAGGATAAAA
L1spaSp239to1597
4128 ..... AC036146
4128 ..... AC122834
4128 ..... AC124709
4128 ..... AL671880
4105 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          4210      4220      4230      4240      4250      4260      4270
-----+-----+-----+-----+-----+
4201 GAACCTCTGGTGAATCACCATGCCTGACCTAAAGCTTTACTACAGAGCAATTGTGATAAAAACTGCATG
L1spaSp239to1597
4198 ..... AC036146
4198 ..... AC122834
4198 ..... AC124709
4198 ..... AL671880
4175 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          4280      4290      4300      4310      4320      4330      4340
-----+-----+-----+-----+-----+
4271 GTACTGGTATAGAGACAGACAAGTAGACCAATGGAATAGAATTGAAGACCCAGAAATGAACCCACACACC
L1spaSp239to1597
4268 .....G..... AC036146
4268 .....G..... AC122834
4268 .....G..... AC124709
4268 .....G..... AL671880
4245 .....G..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          4350      4360      4370      4380      4390      4400      4410
-----+-----+-----+-----+-----+
4341 TATGGTCAC TTGATCTTCGACAAGGGAGCCAAAACCATCCAGTGGAGAAAGACAGCATT TCAACAATT
L1spaSp239to1597
4338 ..... AC036146
4338 ..... AC122834
4338 ..... AC124709
4338 ..... AL671880
4315 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          4420      4430      4440      4450      4460      4470      4480
-----+-----+-----+-----+-----+
4411 GGTGCTGGCACAAC TGGTTGTATCATGTAGAAGAATGCGAATCGATCCATACTTATCTCCTTGTACTAA
L1spaSp239to1597
4408 ..... AC036146
4408 ..... AC122834
4408 ..... AC124709
4408 ..... AL671880
4385 ..... AL845483

```

```

-----+-----+-----+-----+-----+-----+
          4490      4500      4510      4520      4530      4540      4550
-----+-----+-----+-----+-----+
4481 GGTCAAATCTAAGTGGATCAAGGAAC TACATAAAAACCGAGACACTGAAACTTATAGAGGAGAAAGTG
L1spaSp239to1597

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4478 .....A..... AC036146
4478 ..... AC122834
4478 ..... AC124709
4478 .....A..... AL671880
4455 .....A.....A..... AL845483

-----+-----+-----+-----+-----+-----+-----+
                4560      4570      4580      4590      4600      4610      4620
-----+-----+-----+-----+-----+-----+-----+
4551 GGGAAAAGTCTTGAAGATATGGGCACAGGGGAAAAATTCCTGAACAGAACAGCAATGGCTTGTGCTGTAA
L1spaSp239to1597
4548 .....C..... AC036146
4548 .....C..... AC122834
4548 .....C..... AC124709
4548 .....C..... AL671880
4525 .....C..... AL845483

-----+-----+-----+-----+-----+-----+-----+
                4630      4640      4650      4660      4670      4680      4690
-----+-----+-----+-----+-----+-----+-----+
4621 GATCGAGAATTGACAAATGGGACCTAATGAACTCCAAGTTTCTGCAAGGCAAAAGACACTGTCCTATAA
L1spaSp239to1597
4618 ...T..... AC036146
4618 ..... AC122834
4618 ..... AC124709
4618 ...T..... AL671880
4595 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
                4700      4710      4720      4730      4740      4750      4760
-----+-----+-----+-----+-----+-----+-----+
4691 GACAAAAAGACACCAACAGACTGGGAAAGGATCTTTACCTATCCATAAATCAGATAGGGGACTAATATCC
L1spaSp239to1597
4688 ..... AC036146
4688 ..... AC122834
4688 ..... AC124709
4688 ..... AL671880
4665 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
                4770      4780      4790      4800      4810      4820      4830
-----+-----+-----+-----+-----+-----+-----+
4761 AACATATATAAAGAAGTCAAGAAGGTGGACCTCAGAAAATCAAATAACCCCTTAAAAAATGGGGCTCAG
L1spaSp239to1597
4758 ..... AC036146
4758 ..... AC122834
4758 ..... AC124709
4758 ..... AL671880
4735 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
                4840      4850      4860      4870      4880      4890      4900
-----+-----+-----+-----+-----+-----+-----+
4831 AACTGAACAAAGAATTCTCACCTGAGGAATACCGAATGGCAGAGAAGCACCTGAAAAAATGTTCAACATC
L1spaSp239to1597
4828 ..... AC036146
4828 ..... AC122834
4828 ..... AC124709
4828 .....T..... AL671880
4805 ..... AL845483

-----+-----+-----+-----+-----+-----+-----+
                4910      4920      4930      4940      4950      4960      4970
-----+-----+-----+-----+-----+-----+-----+
4901 CTTAATCATCAGGGAAATGCAAATCAAACAACCCCTGAGATTCCACCTCACACCAGTGAGAATGGCTAAG
L1spaSp239to1597
4844 ..... AC036146
4898 ..... AC122834
4898 ..... AC124709
4898 ..... AL671880
4875 ..... AL845483

```



```
-----+-----+-----+-----+-----+-----+
          4980      4990      5000      5010      5020      5030      5040
-----+-----+-----+-----+-----+-----+
4971 ATCAAAAATTCAGGTGACAGCAGATGCTGGCGAGGATGTGGAGAAAGAGGAACACTCCTCCATTGTTGGT
L1spaSp239to1597
4844                                     AC036146
4968 ..... AC122834
4968 ..... AC124709
4968 ..... AL671880
4945 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          5050      5060      5070      5080      5090      5100      5110
-----+-----+-----+-----+-----+-----+
5041 GGGATTGCAGGCTTGTACAACCACTCTGGAAATCAGTCTGGCGGTTCCCTCAGAAAATTGGACATAGTACT
L1spaSp239to1597
4844                                     AC036146
5038 ..... AC122834
5038 ..... AC124709
5038 ..... AL671880
5015 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          5120      5130      5140      5150      5160      5170      5180
-----+-----+-----+-----+-----+-----+
5111 ACCGGAGGATCCAGCAATACCTCTCCTGGGCATATATCCAGAAGAAGCCCCAACTGGTAAGAAGGACACA
L1spaSp239to1597
4844                                     AC036146
5108 ..... AC122834
5108 ..... AC124709
5108 ..... AL671880
5085 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          5190      5200      5210      5220      5230      5240      5250
-----+-----+-----+-----+-----+-----+
5181 TGCTCCACTATGTTTCATAGCAGCCTTATTTATAATAGCCAGAAACTGGAAAGAACCAGATGCCCTCAA
L1spaSp239to1597
4844                                     AC036146
5178 ..... AC122834
5178 ..... AC124709
5178 ..... AL671880
5155 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          5260      5270      5280      5290      5300      5310      5320
-----+-----+-----+-----+-----+-----+
5251 CAGAGGAATGGATACAGAAAATGTGGTACATCTACACAATGGAGTACTACTCAGCTATTA AAAAGAATGA
L1spaSp239to1597
4844                                     AC036146
5248 ..... AC122834
5248 ..... AC124709
5248 ..... AL671880
5225 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          5330      5340      5350      5360      5370      5380      5390
-----+-----+-----+-----+-----+-----+
5321 ATTTATGAAATTCCTAGCCAAATGGATGGACCTGGAGAGCATCATCTGAGTGAGGTAACACAATCACAA
L1spaSp239to1597
4844                                     AC036146
5318 ..... AC122834
5318 ..... AC124709
5318 ..... AL671880
5295 ..... AL845483
```

```
-----+-----+-----+-----+-----+-----+
          5400      5410      5420      5430      5440      5450      5460
-----+-----+-----+-----+-----+-----+
```

5391 AGGAACTCACACAATATGTACTCACTGATAAGTGGATACTAGCCCCAAACCTAGGATACCCACGATATAA
L1spaSp239to1597
4844 AC036146
5388 AC122834
5388 AC124709
5388 AL671880
5365 AL845483

-----+-----+-----+-----+-----+-----+-----+
5470 5480 5490 5500 5510 5520 5530
-----+-----+-----+-----+-----+-----+-----+

5461 GATACAATTTCTAAACACATGAAACTCAAGAAAAATGAAGACTGAAGTGTGGACACTATGCCCTCCTT
L1spaSp239to1597
4844 AC036146
5458 AC122834
5458 AC124709
5458 AL671880
5435 AL845483

-----+-----+-----+-----+-----+-----+-----+
5540 5550 5560 5570 5580 5590 5600
-----+-----+-----+-----+-----+-----+-----+

5531 AGAAGTGGGAACAAAACACCCATGGAAGGAGTTACAGAAACAAAGTTTGGAGCTGAGATGAAAGGAGGGA
L1spaSp239to1597
4844 AC036146
5528 AC122834
5528 AC124709
5528 AL671880
5505 AL845483

-----+-----+-----+-----+-----+-----+-----+
5610 5620 5630 5640 5650 5660 5670
-----+-----+-----+-----+-----+-----+-----+

5601 CCATGTAGAGACTGCCATATCCAGGATCCACCCATAATCAGCATCCAAACGCTGACACCATTCATAT
L1spaSp239to1597
4844 AC036146
5598 AC122834
5598 AC124709
5598 AL671880
5575 AL845483

-----+-----+-----+-----+-----+-----+-----+
5680 5690 5700 5710 5720 5730 5740
-----+-----+-----+-----+-----+-----+-----+

5671 ACTAGCAAGATTTTATCGAAAGGACCCAGATGTAGCTGTCTTTGTGAGACTATGCCGGGCCTAGCAA
L1spaSp239to1597
4844 AC036146
5668 AC122834
5668 AC124709
5668 AL671880
5645 AL845483

-----+-----+-----+-----+-----+-----+-----+
5750 5760 5770 5780 5790 5800 5810
-----+-----+-----+-----+-----+-----+-----+

5741 CACAGAAGTGGATGCTCACAGTCAGCTAATGGATGGATCACAGGGCTCCCAATGGAGGAGCTAGAGAAAG
L1spaSp239to1597
4844 AC036146
5738 AC122834
5738 AC124709
5738 AL671880
5715 AL845483

-----+-----+-----+-----+-----+-----+-----+
5820 5830 5840 5850 5860 5870 5880
-----+-----+-----+-----+-----+-----+-----+

5811 TACCCAAGGAGCTAAAGGGATCTGCAACCCCTATAGGTGGAACAACATTATGAACTAACCAGTACCCCTGA
L1spaSp239to1597
4844 AC036146
5808 AC122834
5808 AC124709

```

5808 .....T..... AL671880
5875 .....T..... AL845483

-----+-----+-----+-----+-----+-----+
          5890      5900      5910      5920      5930      5940      5950
-----+-----+-----+-----+-----+
5881 GCTCTTGACTCTAGCTGCATATGTATCAAAAGATGGCCTAGTCGGCCATCACTGGAAAGAGAGGCCATT
L1spaSp239to1597
4844 ..... AC036146
5878 ..... AC122834
5878 ..... AC124709
5878 ..... AL671880
5855 ..... AL845483

-----+-----+-----+-----+-----+
          5960      5970      5980      5990      6000      6010      6020
-----+-----+-----+-----+-----+
5951 GGACACGCAGACTTTGTGTGCCCGGTACAGGGGAACGCCAGGGCCAAGGGGGGGAGTGGGTGGGTAG
L1spaSp239to1597
4844 ..... AC036146
5948 ..... AC122834
5948 ..... AC124709
5948 ..... AL671880
5925 ..... AL845483

-----+-----+-----+-----+-----+
          6030      6040      6050      6060      6070      6080      6090
-----+-----+-----+-----+-----+
6021 GGGAGTGGGGTGGGTGGGTAAAGGGGACTTTTGGTATAGCATTGGAAATGTAATGAGCTAAATACCTA
L1spaSp239to1597
4844 ..... AC036146
6017 ..... AC122834
6017 ..... AC124709
6017 ..... AL671880
5994 ..... AL845483

-----+-----+-----+-----+-----+
          6100      6110      6120      6130      6140      6150      6160
-----+-----+-----+-----+-----+
6091 ATAAAAAATGGAAAAAATAAAAAAATAAAATAAAAAAAGACC---ATGAAACATA----AAAA
L1spaSp239to1597
4844 ..... AC036146
6087 .....A.....A....A.G..T.TGTTG.TCTCA..T.....GTCTC... AC122834
6087 .....A...TT-CT...TC.C.TCTCC..AG-----AC.TCTT.G--CCTT... AC124709
6087 .....A...T.GTC...CTCC.GGTCC.G.GGATCCC.AT.CCTC.GACCTCTGC. AL671880
6064 .....AAA.T.....A.....G.A.TT.C.G...-----A---T...GG..----- AL845483

```

Supplemental figure 6. Alignment of the spliced L1 elements identified in the mouse genome. Sequences of the full-length mouse L1 elements that underwent splicing (SD and SA sites at positions 239 and 1597 L1spa sequence, respectively) and retrotransposed were extracted from the mouse genome and aligned by ClustalW against the L1spa sequence spliced in the same manner (L1spaSp239to1597). Nucleotides that do not match L1spa sequence are shown, with deleted bases as dashes. Accession numbers corresponding to each contig containing these sequences and chromosome numbers are shown on the right.

```
-----+-----+-----+-----+-----+-----+
          10         20         30         40         50         60         70
-----+-----+-----+-----+-----+-----+
1 CGGAACCTTAGGAAATTAGTCTGAACAGGTGAGAGTCTGTACCACCTGGGAACTGCCAAAGCAACACAGTG
L1spaSp27to1514
1 ..... AC078790
1 ..... AC102220
1 ..... AC125142
1 ..... AC125166
1 ..... C.. AC133495
1 ..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          80         90        100        110        120        130        140
-----+-----+-----+-----+-----+-----+
71 TCTGAGAAAGGTCCTGTTTTGGGCCTTCTTCTTCGTCCAGGAGGAGTCCAAATACAAGATATCTGCGCA
L1spaSp27to1514
69 .....G..... AC078790
69 .....G..... AC102220
69 .....G..... AC125142
69 .....G..... AC125166
69 .....G..... AC133495
69 .....G..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          150        160        170        180        190        200        210
-----+-----+-----+-----+-----+-----+
141 CCTTCCCTGTAAAGAGAGCTTGCCAGCAGAGAGTGCCTGTGAGCACTGAAACTCAGAGGAGAGAATCTGTCT
L1spaSp27to1514
139 ..... AC078790
139 ..... AC102220
139 ..... AC125142
139 ..... AC125166
139 ..... A..... AC133495
139 ..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          220        230        240        250        260        270        280
-----+-----+-----+-----+-----+-----+
211 CCCAGTCTGTGTATAGACGGTAACAGAATCACCCAGAAGAACAATCTCTAAACAGAGTCAACTATAACTA
L1spaSp27to1514
209 ..... AC078790
209 ..... AC102220
209 ..... AC125142
209 ..... AC125166
209 ..... AC133495
209 ..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          290        300        310        320        330        340        350
-----+-----+-----+-----+-----+-----+
281 CTAATCCAGAGATTACCAGATGGCGAAAGGTAAACGGAGGAATCTTACTAACAGGAACCAAGACCACTC
L1spaSp27to1514
279 .....G..... AC078790
279 ..... AC102220
279 .....G..... AC125142
279 .....G..... AC125166
279 ..... AC133495
279 .....G..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          360        370        380        390        400        410        420
-----+-----+-----+-----+-----+-----+
351 ACCATCACCAGAACCAGCACCCACTTCGCCAGTCCAGGGAACCCCAACACACCTGAGAACCTAGAC
L1spaSp27to1514
349 ..... AC078790
349 ..... AC102220
349 ..... AC125142
349 ..... AC125166
349 ..... AC133495
349 ..... AL954355
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-----+-----+-----+-----+-----+-----+
          430         440         450         460         470         480         490
-----+-----+-----+-----+-----+-----+
421 CTAGATTTAAAAGCATATCTCATGATGATGGTAGAGGGCATCAAGAAGGACTTTAATAAATCACTTAAAG
L1spaSp27to1514
419 .....A..... AC078790
419 .....A..... AC102220
419 .....A..... AC125142
419 .....A..... AC125166
419 .....A..... AC133495
419 .....A..... AL954355

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-----+-----+-----+-----+-----+-----+
          500         510         520         530         540         550         560
-----+-----+-----+-----+-----+-----+
491 AAATACAGGAGAACACTGCTAAAGAGTTACAAGTCCTTAAAGAAAAACAGGAAAAACACAATCAAACAGGT
L1spaSp27to1514
489 ..... AC078790
489 ..... AC102220
489 ..... AC125142
489 ..... AC125166
489 ..... AC133495
489 ..... AL954355

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-----+-----+-----+-----+-----+-----+
          570         580         590         600         610         620         630
-----+-----+-----+-----+-----+-----+
561 AGAAGTCCTTACAGAAAAAGAGGAAAAAACATACAACAGGTGATGGAAATGAACAAAACCATACTAGAC
L1spaSp27to1514
559 ..... AC078790
559 ..... AC102220
559 ..... AC125142
559 ..... AC125166
559 ..... AC133495
559 ..... AL954355

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-----+-----+-----+-----+-----+-----+
          640         650         660         670         680         690         700
-----+-----+-----+-----+-----+-----+
631 CTAAAAAGGGAAGTAGACACAATAAAGAAAACCTCAAAGCGAGGCAACACTAGAGATAGAAACCCTAGGAA
L1spaSp27to1514
629 ..... AC078790
629 ..... AC102220
629 ..... AC125142
629 ..... AC125166
629 ..... AC133495
629 ..... AL954355

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-----+-----+-----+-----+-----+-----+
          710         720         730         740         750         760         770
-----+-----+-----+-----+-----+-----+
701 AGAAATCTGGAACCATAGATTGAGCATCAGCAACAGAATACAAGAGATGGAAGAGAGAATCTCAGGTGC
L1spaSp27to1514
699 ..... AC078790
699 ..... AC102220
699 ..... AC125142
699 ..... AC125166
699 ..... AC133495
699 ..... AL954355

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-----+-----+-----+-----+-----+-----+
          780         790         800         810         820         830         840
-----+-----+-----+-----+-----+-----+
771 AGAACATTCCATAGAGAACATCGGCACAACAAATCAAAGAAAATGGAAAATGCAAAAAGATCCTAACTCAA
L1spaSp27to1514
769 .....G..... AC078790
769 .....G..... AC102220
769 .....G..... AC125142
769 .....G..... AC125166
769 .....G..... AC133495

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769 ....G..... AL954355
-----+-----+-----+-----+-----+-----+-----+
          850      860      870      880      890      900      910
-----+-----+-----+-----+-----+-----+-----+
841 AATATCCAGGAAATCCAGGACACAATAAGAAGACCAAACGTACGGATAATAGGAGTGGATGAGAATGAAG
L1spaSp27to1514
839 .....G.....C..... AC078790
839 .....C..... AC102220
839 .....G.....C..... AC125142
839 .....G.....C..... AC125166
839 .....C..... AC133495
839 .....G.....C..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          920      930      940      950      960      970      980
-----+-----+-----+-----+-----+-----+-----+
911 ATTTTCAACTCAAAGGTCCAGCAAACATCTTCAACAAAATTATTGAAGAAAACCTCCCAAATCTAAAGAA
L1spaSp27to1514
909 ..... AC078790
909 ..... AC102220
909 ..... AC125142
909 ..... AC125166
909 ..... AC133495
909 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          990      1000     1010     1020     1030     1040     1050
-----+-----+-----+-----+-----+-----+-----+
981 TGAGATGCATATGAACATACAAGAAGCCTACAGAACTCCAATAGACTGGACCAGAAAAGAAATTCCTCC
L1spaSp27to1514
979 ..... AC078790
979 ..... AC102220
979 ..... AC125142
979 ..... AC125166
979 ..... AC133495
979 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
        1060     1070     1080     1090     1100     1110     1120
-----+-----+-----+-----+-----+-----+-----+
1051 CGACACATAATAATCAGAACATCAAAATGCACTAAATAAAGATAGAATACTAAAAGCAGTAAGGGAAAAAG
L1spaSp27to1514
1049 ..... AC078790
1049 ..... AC102220
1049 ..... AC125142
1049 ..... AC125166
1049 ..... AC133495
1049 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
        1130     1140     1150     1160     1170     1180     1190
-----+-----+-----+-----+-----+-----+-----+
1121 GTCAAGTAACATATAAAGGCAAGCCTATCAGAATTACACCAGATTTTCACCAGAGACTATGAAAGCCAG
L1spaSp27to1514
1119 ..... AC078790
1119 ..... AC102220
1119 ..... AC125142
1119 ..... AC125166
1119 ..... AC133495
1119 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
        1200     1210     1220     1230     1240     1250     1260
-----+-----+-----+-----+-----+-----+-----+
1191 AAGAGCTGGACAGATGTTATACAGACACTAAGAGAACACAACTGCAGCCAGGCTACTATACCCAGCC
L1spaSp27to1514
1189 ..... AC078790
1189 ..... AC102220
1189 ..... AC125142
1189 ..... AC125166

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1189 ..... AC133495
1189 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1270      1280      1290      1300      1310      1320      1330
-----+-----+-----+-----+-----+-----+-----+
1261 AAACTCTCAATTATCATAGAGGGAGAAACCAAAGTATTCCACGACAAAACCAAATTCACGCATTATCTCT
L1spaSp27to1514
1259 ..... AC078790
1259 ..... AC102220
1259 ..... AC125142
1259 ..... AC125166
1259 ..... AC133495
1259 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1340      1350      1360      1370      1380      1390      1400
-----+-----+-----+-----+-----+-----+-----+
1331 CCACGAATCCAGCCCTTCAAAGGATAATAACAGAAAAAACCAATACAAGAACGGGAACAACGCCCTAGA
L1spaSp27to1514
1329 ..... AC078790
1329 ..... AC102220
1329 ..... AC125142
1329 ..... AC125166
1329 ..... AC133495
1329 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1410      1420      1430      1440      1450      1460      1470
-----+-----+-----+-----+-----+-----+-----+
1401 AAAAAACAAGAAGGTAATCCCTCAACAAACCTAAAAGAAGACAGCCACAAGAACAGAATGCCACCTTTAAC
L1spaSp27to1514
1399 ..... AC078790
1399 ..... AC102220
1399 ..... AC125142
1399 ..... AC125166
1399 ..... AC133495
1399 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1480      1490      1500      1510      1520      1530      1540
-----+-----+-----+-----+-----+-----+-----+
1471 AACTAAAATAACAGGAAGCAACAATTACTTTTCCTTAATATCTCTTAACATCAATGGTCTCAACTCGCCA
L1spaSp27to1514
1469 ..... AC078790
1469 ..... AC102220
1469 ..... AC125142
1469 ..... AC125166
1469 ..... AC133495
1469 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1550      1560      1570      1580      1590      1600      1610
-----+-----+-----+-----+-----+-----+-----+
1541 ATAAAAAGACATAGACTAACAACCTGGCTACACAAACAAGACCCAACATTTTGCTGCTTACAGGAAACTC
L1spaSp27to1514
1539 ..... AC078790
1539 ..... AC102220
1539 ..... AC125142
1539 ..... AC125166
1539 ..... AC133495
1539 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1620      1630      1640      1650      1660      1670      1680
-----+-----+-----+-----+-----+-----+-----+
1611 ATCTCAGAGAAAAAGATAGACACTACCTCAGAATGAAAGGCTGGAAAACAATTTTCCAAGCAAATGGTAT
L1spaSp27to1514
1609 ..... AC078790
1609 ..... AC102220
1609 ..... AC125142

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1609 ..... AC125166
1609 ..... AC133495
1609 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1690      1700      1710      1720      1730      1740      1750
-----+-----+-----+-----+-----+-----+-----+

1681 GAAGAAACAAGCAGGAGTAGCCATCCTAATATCTGATAAGATTGACTTCCAACCCAAAGTCATCAAAAAA
L1spaSp27to1514
1679 ..... AC078790
1679 ..... AC102220
1679 ..... AC125142
1679 ..... AC125166
1679 ..... AC133495
1679 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1760      1770      1780      1790      1800      1810      1820
-----+-----+-----+-----+-----+-----+-----+

1751 GACAAGGAGGGACACTTCATTCTCATCAAAGGTAAAATCCTCCAAGAGGAACTCTCAATTCTGAATATCT
L1spaSp27to1514
1749 ..... AC078790
1749 ..... AC102220
1749 ..... AC125142
1749 ..... AC125166
1749 ..... AC133495
1749 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1830      1840      1850      1860      1870      1880      1890
-----+-----+-----+-----+-----+-----+-----+

1821 ATGCTCCAAATACAAGAGCAGCCACATTCACATAAGAAACTTTAGTAAAGCTCAAAGCACACATTGCGCC
L1spaSp27to1514
1819 ..... AC078790
1819 ..... AC102220
1819 ..... AC125142
1819 ..... AC125166
1819 ..... AC133495
1819 ..... A..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1900      1910      1920      1930      1940      1950      1960
-----+-----+-----+-----+-----+-----+-----+

1891 TCACACAATAATAGTGGGAGACTTCAACACACCACCTTTCACCAATGGACAGATCATGGAAACAGAAACTA
L1spaSp27to1514
1889 ..... AC078790
1889 ..... AC102220
1889 ..... AC125142
1889 ..... AC125166
1889 ..... AC133495
1889 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          1970      1980      1990      2000      2010      2020      2030
-----+-----+-----+-----+-----+-----+-----+

1961 AACAGGGACACACTGAAACTAACAGAAGTGATGAAACAAATGGATCTGACAGATATCTACAGAACATTTT
L1spaSp27to1514
1959 ..... AC078790
1959 ..... AC102220
1959 ..... AC125142
1959 ..... AC125166
1959 ..... AC133495
1959 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          2040      2050      2060      2070      2080      2090      2100
-----+-----+-----+-----+-----+-----+-----+

2031 ACCCTAAAACAAAAGGATATACCTTCTTCTCAGCACCTCATGGTACCTTCTCCAAAATTGACCACATAAT
L1spaSp27to1514
2029 ..... A..... AC078790
2029 .T..... AC102220

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2029 AC125142
2029 AC125166
2029 .T..... AC133495
2029 AL954355

-----+
 2110 2120 2130 2140 2150 2160 2170
-----+
-----+
 2110 2120 2130 2140 2150 2160 2170
-----+

2101 AGGTCACAAATCAGGCCTCAACAGATTAAAAAATATTGAAATTGTCCCATGTATCCTATCAGATCACCAT
L1spaSp27to1514

2099C.....C..... AC078790
2099C..... AC102220
2099C.....C..... AC125142
2099C.....C..... AC125166
2099C..... AC133495
2099C.....C..... AL954355

-----+
 2180 2190 2200 2210 2220 2230 2240
-----+
-----+
 2180 2190 2200 2210 2220 2230 2240
-----+

2171 GCACTAAGGCTGATCTTCAATAACAAAATAAATAACAGAAAGCCAACATTCACATGGAAACTGAACAACA
L1spaSp27to1514

2169 AC078790
2169 AC102220
2169 AC125142
2169 AC125166
2169 .A..... AC133495
2169 AL954355

-----+
 2250 2260 2270 2280 2290 2300 2310
-----+
-----+
 2250 2260 2270 2280 2290 2300 2310
-----+

2241 CTCTTCTCAATGATACCTTGGTCAAGGAAGGAATAAAGAAAGAAATTAAGACTTTTTAGAGTTTAATGA
L1spaSp27to1514

2239G..... AC078790
2239 AC102220
2239G..... AC125142
2239G..... AC125166
2239 AC133495
2239G..... AL954355

-----+
 2320 2330 2340 2350 2360 2370 2380
-----+
-----+
 2320 2330 2340 2350 2360 2370 2380
-----+

2311 AAATGAAGCCACAACGTACCCAAACCTTTGGGACACAATGAAAGCATTCTAAGAGGGAAACTCATAGCT
L1spaSp27to1514

2309 AC078790
2309T.. AC102220
2309 AC125142
2309 AC125166
2309 AC133495
2309 AL954355

-----+
 2390 2400 2410 2420 2430 2440 2450
-----+
-----+
 2390 2400 2410 2420 2430 2440 2450
-----+

2381 ATGAGTGCCTTCAAGAAAAACGGGAGAGACACATACTAGCAGCTTGACAAACACATCTAAAAGCTCTAG
L1spaSp27to1514

2379 AC078790
2379AC..... AC102220
2379 AC125142
2379 AC125166
2379 AC133495
2379 AL954355

-----+
 2460 2470 2480 2490 2500 2510 2520
-----+
-----+
 2460 2470 2480 2490 2500 2510 2520
-----+

2451 AAAAAAGGAAGCAAATTCACCCAAGAGGAGTAGACGGCAGGAAATAATCAAACCTCAGGGGTGAAATCAA
L1spaSp27to1514

2449 AC078790

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2449 ..... AC102220
2449 ..... AC125142
2449 ..... AC125166
2449 ..... AC133495
2449 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          2530      2540      2550      2560      2570      2580      2590
-----+-----+-----+-----+-----+-----+-----+
2521 CCAAGTGGAAACAAGAAGAACTATTCAAAGAATTAACCAAACGAGGAGTTGGTTCTTTGAGAAAATCAAC
L1spaSp27to1514
2519 ..... AC078790
2519 ..... AC102220
2519 ..... AC125142
2519 ..... AC125166
2519 ..... AC133495
2519 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          2600      2610      2620      2630      2640      2650      2660
-----+-----+-----+-----+-----+-----+-----+
2591 AAGATAGATAAACCCCTTAGCTAGACTCACTAAAGGGCACAGGGACAAAATCCTAATTAACAAAATCAGAA
L1spaSp27to1514
2589 ..... AC078790
2589 ..... AC102220
2589 ..... AC125142
2589 ..... AC125166
2589 ..... AC133495
2589 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          2670      2680      2690      2700      2710      2720      2730
-----+-----+-----+-----+-----+-----+-----+
2661 ATGAAAAGGGAGACATAACAACAGATCCTGAAGAAATCCAAAACACCATCAGATCCTTCTACAAAAGGCT
L1spaSp27to1514
2659 ..... AC078790
2659 ..... AC102220
2659 ..... AC125142
2659 ..... AC125166
2659 ..... AC133495
2659 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          2740      2750      2760      2770      2780      2790      2800
-----+-----+-----+-----+-----+-----+-----+
2731 ATACTCAACAAAACCTGGAAAACCTGGACGAAATGGACAAATTTCTGGACAGATACCAGGTACCAAAGTTG
L1spaSp27to1514
2729 ..... AC078790
2729 ..... AC102220
2729 ..... AC125142
2729 ..... AC125166
2729 ..... AC133495
2729 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          2810      2820      2830      2840      2850      2860      2870
-----+-----+-----+-----+-----+-----+-----+
2801 AATCAGGATCAAGTTGACCTTCTAAACAGTCCCATATCCCTAAAGAAATAGAAGCAGTTATTAATAGTC
L1spaSp27to1514
2799 ..... AC078790
2799 ..... AC102220
2799 ..... AC125142
2799 ..... AC125166
2799 ..... AC133495
2799 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
          2880      2890      2900      2910      2920      2930      2940
-----+-----+-----+-----+-----+-----+-----+
2871 TCCCAGCCAAAAAAGCCCAGGACCAGACGGGTTTGTAGTCAGAGTTCTATCAGACCTTCAAAGAAGATCT
L1spaSp27to1514

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2869 ..... AC078790
2869 ..... AC102220
2869 ..... AC125142
2869 ..... AC125166
2869 ..... AC133495
2869 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
                2950      2960      2970      2980      2990      3000      3010
-----+-----+-----+-----+-----+-----+-----+
2941 AACTCCAGTTCTGCACAAACTTTTTCACAAGATAGAAGTAGAAGGTATTCTACCCAACCTCATTATGAA
L1spaSp27to1514
2939 ..... AC078790
2939 ..... AC102220
2939 ..... AC125142
2939 ..... AC125166
2939 ..... AC133495
2939 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
                3020      3030      3040      3050      3060      3070      3080
-----+-----+-----+-----+-----+-----+-----+
3011 GCCACTATTACTCTGATACCTAAACCACAGAAAGATCCAACAAAGATAGAGAACTTCAGACCAATTTCTC
L1spaSp27to1514
3009 ..... AC078790
3009 ..... AC102220
3009 ..... AC125142
3009 ..... AC125166
3009 ..... AC133495
3009 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
                3090      3100      3110      3120      3130      3140      3150
-----+-----+-----+-----+-----+-----+-----+
3081 TTATGAACATCGATGCAAAAATCCTTAATAAAAATTCTCGCTAACCGAATCCAAGAACACATTTAAAGCAAT
L1spaSp27to1514
3079 ..... AC078790
3079 ..... AC102220
3079 ..... AC125142
3079 ..... AC125166
3079 ..... AC133495
3079 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
                3160      3170      3180      3190      3200      3210      3220
-----+-----+-----+-----+-----+-----+-----+
3151 CATCCATCCTGACCAAGTAGGTTTTATTCCAGGGATGCAGGGATGGTTTAATATACGAAAATCCATCAAT
L1spaSp27to1514
3149 ..... AC078790
3149 ..... AC102220
3149 ..... AC125142
3149 ..... AC125166
3149 ..... AC133495
3149 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
                3230      3240      3250      3260      3270      3280      3290
-----+-----+-----+-----+-----+-----+-----+
3221 GTAATCCATTATATAAAACAACTCAAAGACAAAACCACATGATCATCTCGTTAGATGCAGAAAAAGCAT
L1spaSp27to1514
3219 ..... AC078790
3219 ..... AC102220
3219 ..... AC125142
3219 ..... AC125166
3219 ..... AC133495
3219 ..... AL954355

-----+-----+-----+-----+-----+-----+-----+
                3300      3310      3320      3330      3340      3350      3360
-----+-----+-----+-----+-----+-----+-----+

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3291 TTGACAAGATCCAACACCCATTCATGATAAAAAGTTCTGGAAAAGATCAGGAATTC AAGCCAATACCTAAA
L1spaSp27to1514
3289 AC078790
3289 AC102220
3289 AC125142
3289 AC125166
3289 AC133495
3289 AL954355

-----+-----+-----+-----+-----+-----+-----+
3370 3380 3390 3400 3410 3420 3430
-----+-----+-----+-----+-----+-----+-----+

3361 CATGATAAAGCAATCTACAGCAAACCAGTAGCCAACATCAAAGTAAATGGAGAGAAGCTGGAAGCAATC
L1spaSp27to1514
3359 AC078790
3359 AC102220
3359 AC125142
3359 AC125166
3359 AC133495
3359 AL954355

-----+-----+-----+-----+-----+-----+-----+
3440 3450 3460 3470 3480 3490 3500
-----+-----+-----+-----+-----+-----+-----+

3431 CCACTAAAATCAGGGACTAGACAAGGCTGCCCACTTTCTCCCTACCTTTTCAACATAGTACTTGAAGTAT
L1spaSp27to1514
3429 AC078790
3429 AC102220
3429 AC125142
3429 AC125166
3429 AC133495
3429 AL954355

-----+-----+-----+-----+-----+-----+-----+
3510 3520 3530 3540 3550 3560 3570
-----+-----+-----+-----+-----+-----+-----+

3501 TAGCCAGAGCAATTCGACAACAAAAGGAGATCAAGGGGATACAAATTGGAAAAGAGGAAGTCAAAATATC
L1spaSp27to1514
3499 AC078790
3499 AC102220
3499 AC125142
3499 AC125166
3499 AC133495
3499 AL954355

-----+-----+-----+-----+-----+-----+-----+
3580 3590 3600 3610 3620 3630 3640
-----+-----+-----+-----+-----+-----+-----+

3571 ACTTTTTCGAGATGATATGATAGTATATATAAGTGACCCTAAAAATTCCAACAGAGAACTCCTAAACCTG
L1spaSp27to1514
3569 AC078790
3569 AC102220
3569 AC125142
3569 AC125166
3569 AC133495
3569 AL954355

-----+-----+-----+-----+-----+-----+-----+
3650 3660 3670 3680 3690 3700 3710
-----+-----+-----+-----+-----+-----+-----+

3641 ATAAACAGCTTCGGTGAAGTAGCTGGATATAAAATTAAC TCAAACAAGTCAATGGCCTTTCTCTACACAA
L1spaSp27to1514
3639 AC078790
3639 AC102220
3639 AC125142
3639 AC125166
3639 AC133495
3639 AL954355

-----+-----+-----+-----+-----+-----+-----+
3720 3730 3740 3750 3760 3770 3780
-----+-----+-----+-----+-----+-----+-----+

-----+-----+-----+-----+-----+-----+-----+
3711 AGAATAAACAGGCTGAGAAAGAAATTAGGGAAACAACACCCTTCTCAATAGCCACAAATAATATAAAATA
L1spaSp27to1514
3709 AC078790
3709 T AC102220
3709 AC125142
3709 AC125166
3709 AC133495
3709 AL954355

-----+-----+-----+-----+-----+-----+-----+
3790 3800 3810 3820 3830 3840 3850
-----+-----+-----+-----+-----+-----+-----+
3781 TCTCGCGTGAAGCTCTAACGAGGAAGTGAAGATCTGTATGATAAAAACTCAAGTCCCTGAAGAAAGAA
L1spaSp27to1514
3779 AC078790
3779 AC102220
3779 AC125142
3779 AC125166
3779 T AC133495
3779 AL954355

-----+-----+-----+-----+-----+-----+-----+
3860 3870 3880 3890 3900 3910 3920
-----+-----+-----+-----+-----+-----+-----+
3851 ATTAAGAAGATCTCAGAAGATGGAAGATCTCCCATGCTCATGGATTGGCAGGACCAACATTGTAAGAA
L1spaSp27to1514
3849 AC078790
3849 AC102220
3849 AC125142
3849 AC125166
3849 AC133495
3849 AL954355

-----+-----+-----+-----+-----+-----+-----+
3930 3940 3950 3960 3970 3980 3990
-----+-----+-----+-----+-----+-----+-----+
3921 TGGCTATCTTGCCAAAAGCAATCTACAGATTCATGCAATCCCCATTAAAATCCCACTCAATCTTCAA
L1spaSp27to1514
3919 AC078790
3919 AC102220
3919 AC125142
3919 AC125166
3919 AC133495
3919 AL954355

-----+-----+-----+-----+-----+-----+-----+
4000 4010 4020 4030 4040 4050 4060
-----+-----+-----+-----+-----+-----+-----+
3991 CGAATTAGAAGGAGCAATTTGCAAATTCATCTGGAATAACAAAAACCGAGGATAGCAAAAACCTCTTCTC
L1spaSp27to1514
3989 AC078790
3989 AC102220
3989 AC125142
3989 AC125166
3989 AC133495
3989 AL954355

-----+-----+-----+-----+-----+-----+-----+
4070 4080 4090 4100 4110 4120 4130
-----+-----+-----+-----+-----+-----+-----+
4061 AAGGATAAAGAACCTCTGGTGAATCACCATGCCTGACCTAAAGCTTTACTACAGAGCAATTGTGATAA
L1spaSp27to1514
4059 AC078790
4059 AC102220
4059 AC125142
4059 AC125166
4059 AC133495
4059 AL954355

-----+-----+-----+-----+-----+-----+-----+

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          4140      4150      4160      4170      4180      4190      4200
-----+-----+-----+-----+-----+-----+-----+
4131 AAACTGCATGGTACTGGTATAGAGACAGACAAGTAGACCAATGGAATAGAATTGAAGACCCAGAAATGAA
L1spaSp27to1514
4129 .....G..... AC078790
4129 .....G..... AC102220
4129 .....G..... AC125142
4129 .....G..... AC125166
4129 .....G..... AC133495
4129 .....G..... AL954355

```

```

          4210      4220      4230      4240      4250      4260      4270
-----+-----+-----+-----+-----+-----+-----+
4201 CCCACACACCTATGGTCAC TTGATCTTCGACAAGGGAGCCAAAACCATCCAGTGGAGAAAGACAGCATT
L1spaSp27to1514
4199 ..... AC078790
4199 ..... AC102220
4199 ..... AC125142
4199 ..... AC125166
4199 ..... AC133495
4199 ..... AL954355

```

```

          4280      4290      4300      4310      4320      4330      4340
-----+-----+-----+-----+-----+-----+-----+
4271 TTCAACAATTGGTGTGCTGGCACAAC TGGTTGTTATCATGTAGAAGAATGCGAATCGATCCATACTTATCTC
L1spaSp27to1514
4269 ..... AC078790
4269 .....A..... AC102220
4269 ..... AC125142
4269 ..... AC125166
4269 ..... AC133495
4269 ..... AL954355

```

```

          4350      4360      4370      4380      4390      4400      4410
-----+-----+-----+-----+-----+-----+-----+
4341 CTTGTACTAAGGTCAAATCTAAGTGGATCAAGGAACTTCACATAAAAACGAGACACTGAAACTTATAGA
L1spaSp27to1514
4339 ..... AC078790
4339 ..... AC102220
4339 ..... AC125142
4339 ..... AC125166
4339 ..... AC133495
4339 ..... AL954355

```

```

          4420      4430      4440      4450      4460      4470      4480
-----+-----+-----+-----+-----+-----+-----+
4411 GGAGAAAGTGGGGAAAAGTCTTGAAGATATGGGCACAGGGGAAAAATTCCTGAACAGAACAGCAATGGCT
L1spaSp27to1514
4409 .....C..... AC078790
4409 .....C..... AC102220
4409 .....C..... AC125142
4409 .....C..... AC125166
4409 .....C..... AC133495
4409 .....C..... AL954355

```

```

          4490      4500      4510      4520      4530      4540      4550
-----+-----+-----+-----+-----+-----+-----+
4481 TGTGCTGTAAGATCGAGAATTGACAAATGGGACCTAATGAAACTCCAAGTTTCTGCAAGGCAAAAGACA
L1spaSp27to1514
4479 ..... AC078790
4479 ..... AC102220
4479 ..... AC125142
4479 ..... AC125166
4479 ..... AC133495
4479 ..... AL954355

```

```
-----+-----+-----+-----+-----+-----+
          4560      4570      4580      4590      4600      4610      4620
-----+-----+-----+-----+-----+
4551 CTGTCTATAAGACAAAAAGACCACCAACAGACTGGGAAAGGATCTTTACCTATCCTAAATCAGATAGGGG
L1spaSp27to1514
4549 .....T..... AC078790
4549 ..... AC102220
4549 ..... AC125142
4549 ..... AC125166
4549 ..... AC133495
4549 ..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          4630      4640      4650      4660      4670      4680      4690
-----+-----+-----+-----+-----+
4621 ACTAATATCCAACATATATAAAGAAGTCAAGAAGGTGACCTCAGAAAATCAAATAACCCCTTAAAAAA
L1spaSp27to1514
4619 ..... AC078790
4619 ..... AC102220
4619 ..... AC125142
4619 ..... AC125166
4619 ..... AC133495
4619 ..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          4700      4710      4720      4730      4740      4750      4760
-----+-----+-----+-----+-----+
4691 TGGGGCTCAGAAGTGAACAAAGAAATCTCACCTGAGGAATACCGAATGGCAGAGAAGCACCTGAAAAAAT
L1spaSp27to1514
4689 ..... AC078790
4689 .....A..... AC102220
4689 ..... AC125142
4689 ..... AC125166
4689 ..... AC133495
4689 ..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          4770      4780      4790      4800      4810      4820      4830
-----+-----+-----+-----+-----+
4761 GTTCAACATCCTTAATCATCAGGGAATGCAAATCAAACAACCCCTGAGATTCCACCTCACACCAGTGAG
L1spaSp27to1514
4759 ..... AC078790
4759 ..... AC102220
4759 ..... AC125142
4759 ..... AC125166
4759 ..... AC133495
4759 ..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          4840      4850      4860      4870      4880      4890      4900
-----+-----+-----+-----+-----+
4831 AATGGCTAAGATCAAAAATTCAGGTGACAGCAGATGCTGGCGAGGATGTGGAGAAAGAGGAACACTCCTC
L1spaSp27to1514
4829 ..... AC078790
4829 ..... AC102220
4829 ..... AC125142
4829 ..... AC125166
4829 ..... AC133495
4829 ..... AL954355
```

```
-----+-----+-----+-----+-----+-----+
          4910      4920      4930      4940      4950      4960      4970
-----+-----+-----+-----+-----+
4901 CATTGTTGGTGGGATTGCAGGCTTGTACAACCACTCTGGAATCAGTCTGGCGGTTTCCTCAGAAAATTGG
L1spaSp27to1514
4899 ..... AC078790
4899 ..... AC102220
4899 ..... AC125142
4899 .....G..... AC125166
4899 ..... AC133495
4899 ..... AL954355
```

```

-----+-----+-----+-----+-----+-----+
          4980      4990      5000      5010      5020      5030      5040
-----+-----+-----+-----+-----+
4971 ACATAGTACTACCGGAGGATCCAGCAATACCTCTCTGGGCATATATCCAGAAGAAGCCCAACTGGTAA
L1spaSp27to1514
4969 ..... AC078790
4969 ..... AC102220
4969 ..... AC125142
4969 ..... AC125166
4969 ..... AC133495
4969 ..... AL954355

```

```

-----+-----+-----+-----+-----+-----+
          5050      5060      5070      5080      5090      5100      5110
-----+-----+-----+-----+-----+
5041 GAAGGACACATGCTCCACTATGTTTCATAGCAGCCTTATTTATAATAGCCAGAAACTGGAAAGAACCCAGA
L1spaSp27to1514
5039 ..... AC078790
5039 ..... AC102220
5039 ..... AC125142
5039 ..... AC125166
5039 ..... AC133495
5039 ..... AL954355

```

```

-----+-----+-----+-----+-----+-----+
          5120      5130      5140      5150      5160      5170      5180
-----+-----+-----+-----+-----+
5111 TGCCCCTCAACAGAGGAATGGATACAGAAAATGTGGTACATCTACACAATGGAGTACTACTCAGCTATTA
L1spaSp27to1514
5109 ..... AC078790
5109 ..... AC102220
5109 ..... AC125142
5109 ..... AC125166
5109 ..... AC133495
5109 ..... AL954355

```

```

-----+-----+-----+-----+-----+-----+
          5190      5200      5210      5220      5230      5240      5250
-----+-----+-----+-----+-----+
5181 AAAAGAATGAATTTATGAAATTCCTAGCCAAATGGATGGACCTGGAGAGCATCATCCTGAGTGAGGTAAC
L1spaSp27to1514
5179 ..... AC078790
5179 ..... AC102220
5179 ..... AC125142
5179 ..... AC125166
5179 ..... AC133495
5179 ..... AL954355

```

```

-----+-----+-----+-----+-----+-----+
          5260      5270      5280      5290      5300      5310      5320
-----+-----+-----+-----+-----+
5251 ACAATCACAAGGAACCTCACACAATATGTACTCACTGATAAGTGGATAC TAGCCCAAACCTAGGATACC
L1spaSp27to1514
5249 ..... AC078790
5249 ..... AC102220
5249 ..... AC125142
5249 ..... AC125166
5249 ..... AC133495
5249 ..... AL954355

```

```

-----+-----+-----+-----+-----+-----+
          5330      5340      5350      5360      5370      5380      5390
-----+-----+-----+-----+-----+
5321 CACGATATAAGATACAATTTCTTAACACATGAAACTCAAGAAAAATGAAGACTGAAGTGTGGACTAT
L1spaSp27to1514
5319 ..... AC078790
5319 ..... AC102220
5319 ..... AC125142
5319 ..... AC125166
5319 ..... AC133495

```



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5319 ..... AL954355
-----+-----+-----+-----+-----+-----+
          5400      5410      5420      5430      5440      5450      5460
-----+-----+-----+-----+-----+-----+
5391 GCCCCTCCTTAGAAGTGGGAACAAAACACCCATGGAAGGAGTTACAGAAACAAAGTTTGGAGCTGAGATG
L1spaSp27to1514
5389 ..... AC078790
5389 ..... A..... AC102220
5389 ..... AC125142
5389 ..... AC125166
5389 ..... A..... AC133495
5389 ..... AL954355

-----+-----+-----+-----+-----+-----+
          5470      5480      5490      5500      5510      5520      5530
-----+-----+-----+-----+-----+-----+
5461 AAAGGAGGGACCATGTAGAGACTGCCATATCCAGGGATCCACCCATAATCAGCATCCAACGCTGACAC
L1spaSp27to1514
5459 .....T..... AC078790
5459 .....T.....T.....T..... AC102220
5459 .....T..... AC125142
5459 .....T..... AC125166
5459 .....T.....G.....T.....T..... AC133495
5459 .....T..... AL954355

-----+-----+-----+-----+-----+-----+
          5540      5550      5560      5570      5580      5590      5600
-----+-----+-----+-----+-----+-----+
5531 CATTGCATATACTAGCAAGATTTTATCGAAAGGACCCAGATGTAGCTGTCTCTTGTGAGACTATGCCGGG
L1spaSp27to1514
5529 ..... AC078790
5529 .....C.....CT..... AC102220
5529 ..... AC125142
5529 ..... AC125166
5529 .....C.....CT.....A..... AC133495
5529 ..... AL954355

-----+-----+-----+-----+-----+-----+
          5610      5620      5630      5640      5650      5660      5670
-----+-----+-----+-----+-----+-----+
5601 GCCTAGCAAACACAGAAGTGGATGCTCACAGTCAGCTAATGGATGGATCACAGGGCTCCCAATGGAGGAG
L1spaSp27to1514
5599 ..... AC078790
5599 ..... AC102220
5599 ..... AC125142
5599 ..... AC125166
5599 ..... AC133495
5599 ..... AL954355

-----+-----+-----+-----+-----+-----+
          5680      5690      5700      5710      5720      5730      5740
-----+-----+-----+-----+-----+-----+
5671 CTAGAGAAAGTACCCAAGGAGCTAAAGGGATCTGCAACCCTATAGGTGGAACAACATTATGAACTAACCA
L1spaSp27to1514
5669 .....T..... AC078790
5669 .....T..... AC102220
5669 .....T..... AC125142
5669 .....T..... AC125166
5669 .....T..... AC133495
5669 .....T..... AL954355

-----+-----+-----+-----+-----+-----+
          5750      5760      5770      5780      5790      5800      5810
-----+-----+-----+-----+-----+-----+
5741 GTACCCCTGAGCTCTTGACTCTAGCTGCATATGTATCAAAAGATGGCCTAGTCGGCCATCACTGGAAAGA
L1spaSp27to1514
5739 ..... AC078790
5739 ..... AC102220
5739 ..... AC125142
5739 ..... AC125166

```

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5739 ..... AC133495
5739 ..... AL954355

-----+-----+-----+-----+-----+-----+
          5820      5830      5840      5850      5860      5870      5880
-----+-----+-----+-----+-----+-----+
5811 GAGGCCCATTTGGACACGCAGACTTTGTGTGCCCGGTACAGGGGAACGCCAGGGCCAAGGGGGGGGAGT
L1spaSp27to1514
5809 ..... AC078790
5809 ..... AC102220
5809 ..... AC125142
5809 ..... AC125166
5809 ..... AC133495
5809 ..... AL954355

-----+-----+-----+-----+-----+-----+
          5890      5900      5910      5920      5930      5940      5950
-----+-----+-----+-----+-----+-----+
5881 GGGTGGGTAGGGGAGTGGGGGTGGGTGGGTAAGGGGGACTTTTGGTATAGCATTGGAATGTAATGAGC
L1spaSp27to1514
5878 ..... AC078790
5878 ..... AC102220
5878 ..... AC125142
5878 ..... AC125166
5878 ..... AC133495
5878 ..... AL954355

-----+-----+-----+-----+-----+-----+
          5960      5970      5980      5990      6000      6010      6020
-----+-----+-----+-----+-----+-----+
5951 TAAATACCTAATAAAAAATGGAAAAAATAAAAAAA-TAAATAAAAAAAAGACCATGA-AACATAA
L1spaSp27to1514
5948 .....A....T...AA.C.C...T..G.CTTGGG AC078790
5948 .....A.....AA..G.AG.T...T.T.C..TCC.AC.T.C. AC102220
5948 .....A...G...A.T.G.CTTTG...T.C.T...A.-T.G.C.. AC125142
5948 .....A.T.TCT--CTC..C.TC..TGG.CT AC125166
5948 .....AATG.....A.....AA..G.A.GCC.C.TT.GTA.GA. AC133495
5948 .....A.....AA...A.....A.GA.GAGGG.GGG.. AL954355

```

Supplemental figure 7. Alignment of the spliced L1 elements identified in the mouse genome. Sequences of the full-length mouse L1 elements that underwent splicing (SD and SA sites at positions 27 and 1514 L1spa sequence respectively) and retrotransposed were extracted from the mouse genome and aligned by ClustalW against the L1spa sequence spliced in the same manner (L1spaSp27to1514). Nucleotides that do not match L1spa sequence are shown. Accession numbers corresponding to each contig containing these sequences are shown on the right.