The amplicons in Figure 2A were fully resolved by Sanger sequencing by using the following primers, when applied: 1032R (TTTCCCCATCTTTGTGGTTTTATCT), 114R (TGAGATGAACCCAGTACCTCA), 523R (ACAGGCAGGTTTCCTTGAGCTG), 476F (AAGCTCGAACTGGGTGGAG), 1008F (AGATAAAACCACAAAGATGGGGAAA), 1615F (CAGGAAATACAGAGAACGCCA), 2056F (GGAAGAAACTGCATCAACTAATG), 2368F (ATCAAAAGAGACAAAGAAGGC), 2388R (GCCTTCTTTGTCTCTTTTGAT), 2646F (CAGAACTCTCCACCCCAAATC), 3106F (AGCAGAAGGCAAGAAATAACTAAGA), 3542R (AATTCAGCTGTGAATCCATCTGG), 3719F (ATGCAAAAATCCTCAATAAAATACTGG), 3977R (GTTCCATCAATACCGAATTTATTG), 4311F (AAAATCACAAGCATTCTTATACACCA), 4525F (GGAAGAATCAATATTGTGAAAATG), 4548R (CATTTTCACAATATTGATTCTTCC), 4891F (TCCCTATTTAATAAATGGTGCTGG), 5479F (GGAAACAACAGGTGCTGGAG), 5755F (GATTGGATTAAGAAAATGTG), 6011F (TGCATTGGGAGTTATACCTGATG), pCEP4Fw (TTTATGGTTCGTGGGGGTTA), eGFPIRv (CGACAACCACTACCTGAGCA), Chr11-5GNM-Fw (GGACAGTAGGCGGAGTTGAG), Chr11-3GNM-Rv (CCACCATGCCCAGTCTACTT), SOM5J-Fw (CTTGCGGCCGCTGATAATATAGCCCATAATAGAGAG).

The files corresponding to the L1RSsomatic amplicon in Neuron#15 are in /L1RS2SOM\_PCR (summarized in Figure 2B lower panel). Due to the close proximity of the genome\_rev\_3 (CGTTAGGTTTGGTCTCTGATTTTAGC) primer to the long 3’ poly-A tract of the insertion, we sequenced the flanking region of the amplicon by using universal M13 primers in pGEM-T easy clones (Promega). Traces from 2 different clones are included.

The files corresponding to the L1RS*PRDM4* amplicon in Liver are in /L1RS2PRMD4\_PCR (summarized in Figure 2B middle panel).

The files corresponding to the L1RS built in the eGFPI-based retrotransposition vector in Figure 2D top panel are in /L1RS2eGFPI\_RTSNvector. This same sequence was also moved into in NeoR-based retrotransposition vector in Figure 2C.

Each folder includes a MS Word document with the amplicon/vector sequence for each case, with the region covered by the Sanger sequencing files underlined.