**SUPPLEMENTAL DATA**

**eTable 1.** Long-range PCR conditions for amplifying the *TAF1* SVA insertion.

|  |  |
| --- | --- |
| Reagents | 1X Volume (µL) |
| HPLC H2O | 2.26 |
| 2X Xtreme Buffer | 5.00 |
| dNTPs | 1.00 |
| KOD F Primer(5’-GTTCCATTGTGTGGTTGTACCAGCGTTTGTTC-3’) | 0.30 |
| KOD R Primer(5’-CACATGAAAAGATGCCCAACATCATTAGCCATTAG-3’) | 0.30 |
| KOD Xtreme Hot Start DNA polymerase |  0.14 |
| Template DNA (75 pg) |  1.00 |
| **Total** | **10.00** |

**DNA was amplified using the following conditions:**

94° C for 2 min,

5x (98°C for 10 s, 74°C for 3 min 30 s),

5x (98°C for 10 s, 72°C for 3 min 30 s),

5x (98°C for 10 s, 70°C for 3 min 30 s),

20x (98°C for 10 s, 68°C for 3 min 30 s),

68°C for 7 min

4°C forever

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**eFigure 1. Location of guide RNAs and PCR primers.** The tracks indicate the position of the *TAF1* gene (lilac) the SVA-retrotransposon insertion (green) on the chromosome X as well as of the guide RNA used for the Cas9-targeted nanopore sequencing (gRNA1-4, red) and the PCR primers used for deep nanopore sequencing (Primer1-2, blue).



**eFigure 2. Histogram distribution of the number of (CCCTCT)n repeats in blood-, basal-ganglia- and cerebellum-derived DNA from L-7995.** Repeat number detected in DNA with (A-C) Southern blot from blood, basal ganglia or cerebellum; (D-F) Cas9-targeted enrichment and Oxford Nanopore sequencing from blood, basal ganglia or cerebellum; (G-I) PCR amplicon-based Oxford Nanopore sequencing from blood, basal ganglia or cerebellum. SB= Southern blot