Supplementary Online Content


eFigure. Repeat-primed PCR fragment analysis with the GeneMapper software. Electropherograms are zoomed to 800 relative fluorescence units. Numbers above the traces indicate the fragment’s lengths in base pairs. The grey vertical bars indicate the allele sizes, with the first bar indicating three GGGGCC hexanucleotide repeats. One repeat carrier from each family and one unaffected individual are represented. A typical saw-tooth pattern with a 6 bp periodicity is observed in affected individuals.

This supplementary material has been provided by the authors to give readers additional information about their work.