A search for highly variable DNA repeats in the human genome revealed a genomic fragment (TVRI-6) detecting a hypervariable distribution pattern of human DNA restriction fragments (1,2). Analysis of the primary structure of the fragment suggests that genomic instability and variability of several loci are associated with two regions of non-homologous tandem repeats. One family, termed as tau-, has the following structure: 

(C5(TC)4 TG3(TC)2 TGT)₃₆-₃₈b.p.-tandem repeats 
(1,2). A comparison of tau-repeats with GenBank nucleotide sequences permitted to unusual similarity of tau-repeats to Dr. virilis satellites (3), repeating motives of human protoenkephalin gene 1-exone and retroviral LTR ends. Other 36-38 b.p.-tandem repeats (apo-) are homologous to DNA repeats in apolipoprotein CII-gene 3-intron (4). The DNA probe containing repeats can be used for identifying individuals in human pedigrees.

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